Query Details

1. Your manuscript has been copy-edited in keeping with journal style. Please pay attention to any changes to the use of double and single quote marks. Double quote marks (``…") are to be used for direct quotes (when directly quoting from articles/interviews etc.), and single quote marks are for `scare' quotes. If you have any concerns, please flag them when editing your proof.

ok

2. Kindly check and confirm the edit made in the footnote 1.

Confirmed

3. Please check and confirm the edit made to the sentence 'And, of course, the microbiome is a sort of...' or amend accordingly.

Confirmed

Individual and collective identification in contemporary forensics

Simon A. Cole, [1]✉

Phone (949)824-1443
Email scole@uci.edu

Simon A. Cole is Professor of Criminology, Law and Society and Director of the Newkirk Center for Science & Society at the University of California, Irvine. He is author of *Suspect Identities* (Harvard University Press). He is Co-Editor of *Theoretical Criminology* and Associate Editor of the National Registry of Exonerations.

[1] Department of Criminology, Law & Society, University of California,

Irvine, 2340 Social Ecology II, Irvine, CA, 92697-7080 USA

Abstract

It has long been understood that individual and collective identification are inexorably intertwined. This convergence is not limited to genetics. This paper discusses the convergence of individual and collective identification in a comparative analysis of three other forensic areas: fingerprint analysis, microscopic hair comparison, and microbiome forensics. In all three case studies, we see purportedly individualizing technologies reverting, in a sense, to collective identification. Presumably, this has much to do with the perceived utility of collective identification. When knowing precisely who is the donor of a trace is not possible, or not useful, then knowing that the donor is ‘white,’ or ‘black,’ or ‘Middle Eastern’ begins to seem somehow useful. In each case, we also see that these collective identifications are ultimately founded on crude and broad, seemingly ‘commonsensical’ or ‘social,’ racial categories. These categories, meanwhile, are based on a less-than-fully-transparent combination of self-identification or official ascription. These suspect data are then transformed into seemingly persuasive scientific claims about the genetic attributes of this or that ‘race,’ ‘ethnicity,’ or ‘ancestry.’ Through this comparison the paper will explore how the individual and the collective are ‘done’ differently and similarly in different forensic disciplines.

Keywords

Race
Genetics
Forensic
Fingerprint
Microscopic hair comparison
Microbiome

Introduction

Individual and collective identification have always been inextricably intertwined. This seems paradoxical. The purpose of individual identification, after all, is to distinguish individuals from the full complement of humanity and even from groups. Yet, all efforts at individual identification seem to lead inexorably back to group identification. Presumably, this is because a mass of differentiated—or, to use a term I am campaigning against, 'unique'—individuals is not much use for doing anything. To say that each human individual is unique and different from all others is, in some sense, banal, to say nothing at all. In order to take any sort of practical action, the individuals must be reassembled into groups (Bolnick 2008, p. 71). To give just two examples, the so-called 'personalized medicine,' which genetics has promised is on the horizon, is not really personalized at all, but rather hinges on reassembling individuals into groups of individuals who share genetic propensities that are more similar within than between groups. Drugs are not actually going to be 'individualized.' Individuals are sorted into (possibly very broad) groups that may vary in their responsiveness to a particular drug (Hedgecoe 2004). The efficacy of any 'personalized' diagnoses or interventions will be achieved only statistically across the group. Their utility for any one individual in the group cannot be guaranteed, or even known. Likewise, 'individualized' penological or criminological treatments were not, in fact, individualized at all. Rather, they depended on sorting individuals into groups: first-time offenders, recidivists or various sorts, and so on (Cole 2001). Again, efficacy can only be measured statistically across the group. **AQ1**

Given the close relationship between identification technologies and various forensic technologies that likewise aim at individualized identification, it is little surprise that we observe the same phenomenon in forensic identification. The best known example is forensic DNA profiling. This technology is touted as the ultimate identifier, and it has been claimed that it can distinguish all individuals with the notable exception of homozygous twins. And, yet, rather than merely becoming an individual identification

technology, groups reappeared in forensic DNA profiling.

One notable example was the use of population groups for calculating statistical probabilities for genetic associations. In the early years of DNA profiling, the construction and use of these population groups was the subject of fierce controversy (M'charek 2000). Race mattered in forensic genetics because early statistics for DNA association were calculated under an assumption of random mating in the human population. This assumption was widely acknowledged to be false, although the extent to which correcting it would change the reported statistics was debated (Lynch et al. 2008; Aronson 2007). Today, however, the discriminating power of forensic DNA profiling has diminished the importance of these debates. And yet, the use of population groups continues (Kahn 2009). As Kahn has noted, in forensic genetics the use of race, which was seen as 'social,' is sloppy compared to the care that was taken over procedures seen as 'natural.' The racial data used in American forensic DNA profiling were in some cases based entirely on self-identification, according to U.S. census categories. The only legitimate way of interpreting these data is back onto the social category, not onto a genetic category. In other cases, the basis for racial classification was not even stated in the scientific papers. However, it seems likely that in those papers 'race' was classified through a combination of self-identification and official 'ascription' of racial identities by law enforcement authorities. Presumably they do so based on what Hammonds (1997) called "embodied race"—the assignment of people to a race based on what they look like. This may be primarily skin tone, but it presumably is also influenced by other phenotypic features and perhaps even by cultural features like attire, language, accent, attitude, and so on.

An even more charged use of race in forensic DNA profiling lay in the area of phenotypic profiling. In this practice, vendors offered a service in which they predicted the phenotypic attributes of the donor of a DNA sample whose source is unknown. These predictions were based on Ancestry Informative Markers (AIMs) (Fullwiley 2008b). This raised a number of problems including the fact that it proceeded from the gross demarcation of the human population into a small number (e.g., four) continental

population groups, searching for AIMs whose frequency differs between these groups, and then treating frequencies of AIMs as denoters of 'race,' 'the heritable component of race,' or 'biogeographical ancestry' (Sankar 2010). Exacerbating this coarse division of the population into continental groups was the way in which individual research subjects are assigned to those groups. The assignment of research subjects to racial groups was, as Cho and Sankar (2004, S9) dryly put it, "often by undescribed methods." It seems likely, however, that assignment was, again, done through self-identification or "by police officers… based on appearance rather than any knowledge of an individual's ancestry" (Cho and Sankar 2004, S10). Recording of race by police has long been routine in, for example, the United States, the United Kingdom, and France (Knepper 1996, p. 86; Skinner 2013, p. 981). Interestingly, the publication of crime statistics categorized by race by the FBI in the Uniform Crime Reports in the 1930s originated from fingerprint cards which contained racial descriptions (Knepper 1996, pp. 86–87). But these descriptions were presumably based on official ascription and perhaps self-identification. As LaFree (1995, p. 187) noted, "it seems clear that racial distinctions in most official data are probably based on… commonsense informed haphazardly and inconsistently by respondent self-identification." The recording of race by police has become controversial in some countries though. It was never practiced in Canada (Knepper 1996, p. 86), and the U.K. recently discontinued the recording of 'ethnic appearance' as part of the process of taking DNA samples (Skinner 2013, p. 987). Phenotypic assessments by police can suffer from "perception bias," and they apparently correlate poorly with ancestry measured by genetics (Ossorio 2006, p. 283; Knepper 1996, p. 95). And self-identification changes over time in response to both internal and external influences (Cho and Sankar 2004, S9). Indeed, the 'Dolezal affair' in 2015 in the U.S., in which the President of a chapter of the National Association for the Advancement of Colored People who had presented herself as black was 'exposed' as having had white ancestry and white phenotypic appearance as a child, raised the question of whether people could, or should, choose to change their 'race' in manner completely untethered to biology (Tuvel 2017; Brubaker 2016). In addition, Ossorio (2006) has noted that the phenotypic traits of minority populations are

likely to be of greater interest to the police—because they are rarer and thus denote a smaller group of suspects—and Staubach et al. (2017) argue that predictive accuracy diminishes for rarer traits "when adjusted for prevalence."

The intertwining of individualization and race in genetics is relatively well understood precisely because, in contrast to, for example, fingerprints, genes are widely believed to have both individualizing potential and group (racial) correlations (Rabinow 1992). But this convergence is not limited to genetics. This paper discusses the convergence of individual and collective identification in a comparative analysis of three forensic areas other than forensic genetics: friction ridge (or 'fingerprint') analysis, microscopic hair comparison, and microbiome forensics. Although this paper is limited to only three areas, those areas are quite disparate. The vexed relationship between individual and collective identification in these three areas may well represent a more fundamental attribute that cuts more broadly across the fields of forensics and identification. To some extent, of course, these forensic areas are 'genetic' in that the hereditary nature of the examined features is posited as the explanation for the inferences made from them. In all three of these case studies, we see purportedly individualizing technologies reverting, in a sense, to collective identification. Presumably, this has much to do with the perceived utility of collective identification. When knowing precisely who is the donor of a trace is not possible, or not useful, then knowing that the donor is 'white,' or 'black,' or 'Middle Eastern' begins to seem somehow useful (M'charek 2008).

In each case, we also see that these collective identifications are ultimately founded on crude and broad, seemingly 'commonsensical' or 'social,' racial categories. Scientific claims about these categories, meanwhile, are based on often less-than-fully-transparent combinations of self-identification or official ascription. These suspect data are then transformed into seemingly persuasive scientific claims about the genetic attributes of this or that 'race,' 'ethnicity,' or 'ancestry.' Each of the three cases studies illustrates the seemingly inescapable persistence of race and gender as collective identities that continually recur in forensic discourse. Through this

comparison the paper will explore how the individual and the collective are 'done' differently and similarly in different forensic disciplines.

Methodologically, this study is informed by history of science's preference for what scientists write and publish over how they explain themselves in, e.g., an interview setting. Thus, a possible limitation on my findings is that they draw on textual materials, rather than interviews, and the scientists have not been permitted the opportunity to 'speak for themselves' outside the confines of their own published work.

Fingerprints

Fingerprint identification is widely believed to have nothing whatsoever to do with race. It is imagined as "pure identification." Indeed, it is often cast as the antithesis of collective identification (Rabinow 1992). As it turns out, however, this is not the case. Efforts to measure the frequency of fingerprint pattern types among the groups of interest to the scientists of the day (i.e., the nineteenth century, so the groups were 'races,' ethnic groups, the sexes, epileptics, the sane and insane, 'defectives' of various types, and so on) are almost as old, in some cases older, than the uses of fingerprints more familiar to us today. Rather than 'failing,' these efforts found small correlations between fingerprint pattern types (which are, of course, constructed categories themselves) and the ascribed groups enumerated above. These correlations were not 'wrong,' so much as they were not very useful, especially in contrast to the seemingly remarkable utility of fingerprints for criminal record-keeping and forensic investigation. Research on group correlations with fingerprint patterns was, therefore, pushed to the margins, but it never disappeared completely, and, indeed, it reappeared periodically throughout the twentieth century (e.g., Miller 2003; Löwy 2014, p. 156).

My purpose in this paper is not to rehearse this history, but rather to discuss the latest resurgence of this line of research, a paper in the *American Journal of Physical Anthropology* (Fournier and Ross 2015), "Sex, Ancestral, and Pattern Type Variation of Fingerprint Minutiae: A Forensic Perspective on Anthropological Dematoglyphics." The article's objective is

to close “the gap between researcher–practitioner by examining sex, ancestral, and pattern type variation of fingerprint minutiae.” It is worth noting that the authors’ theoretical rationale for studying fingerprints and ancestry is explicitly genetic:

> Inheritance of fingerprint traits is polygenic, which makes them less susceptible to stochastic processes such as genetic drift. Though polygenic traits are more difficult to genetically define, they remain preferable for tracing population relationships because of their stability (3, citation omitted).

In this sense, the authors are using dermatoglyphics in conjunction with genetics in much the same way that medical birth defects researchers in the 1960s did (Miller 2003).

The study sample consisted of 243 rolled impressions of right index fingers. These fingerprints were divided into four groups of approximately 60 fingerprint each, designated “African American” and “European American” with Male and Female groups for each. As with phenotypic profiling for DNA (Sankar 2010; Ossorio 2006; Fullwiley 2008a; M’charek 2008), the question arises how ancestry was assigned to research subjects in the studies underlying the predictive tools. Once again, we find a combination of self-identification and official ascription. The article first suggests that it used National Institute of Standards and Technology (NIST) software to determine ancestry:

> The Biometric Image Software (NBIS) developed by the forensic science division of the National Institute of Standards and Technology (NIST) was used to search for individuals of European and African American ancestry. Once individuals who fit the ancestry needs were identified, their prints could be searched in the local and state databases using PrintQuestVR AFIS-APIS System (4, citation omitted).

This is puzzling because it appears that NBIS cannot be "used to search for individuals of European and African American ancestry."[1] The article then states that ancestry was coded according to self-identification and official ascription:

> Once a fingerprint was determined to be of sufficient quality, sex and ancestry were ascertained based on self-identification on the individual's record. Ancestry information, therefore, was based on a priori knowledge of self-identification and demographic information of Wake County, NC. Specifically, only those individuals who self-identified as "white" or "black" were chosen for the study, racial groups that make up 62.2 and 20.3% of the 2010 population of Wake County, respectively (4–5, citation omitted).

This treatment of race as a dichotomous variable is curious given that the researchers elsewhere have made clear their awareness that a large and increasing portion of the human population can be characterized as "admixed" (Ross 2011).

AQ2

The researchers then counted the occurrence of each of five designated minutiae types (bifurcations, ridge endings, short ridges, enclosures, and dots) in each of the 243 fingerprints. The study question was whether any of the minutiae counts predicted sex or ancestry. This focus on minutiae in some sense constituted the novelty of the study. Most prior dermatoglyphic studies had focused on gross pattern type (i.e., arch, loop, whorl) rather than minutiae (e.g., Bonnevie 1924).

The answer was that one minutiae type, "bifurcations," was found to be a "significant predictor of ancestry" (6). It is perhaps worth considering the raw data behind this claim in simplified form. Table 1 reports the mean values and standard deviation of the variable "total bifurcations" for each of the four groups, rounded to one decimal place.

Table 1

Adapted from Fournier and Ross (2015)

Group	Total bifurcations	Standard deviation
European American males	21.6	1.2
European American females	19.1	1.1
African American males	23.1	1.3
African American females	24.1	1.4

Table 1 shows that most humans have around 20 bifurcations, but "African Americans" have slightly more. African American males have around 1.5 more bifurcations than European American, which is just over 1 standard deviation more. African American females have around 5 more bifurcations than European American which could be as high as 4 standard deviations more. From these data, the paper concludes that "The odds ratio of 5.61 signifies that African Americans are nearly six times more likely to have bifurcations than European Americans" (6). The wording of the claim is difficult to follow if read literally. Given an average of more than 20 bifurcations across all subjects, presumably all subject were very, very "likely to have bifurcations," and African Americans could not possibly be six times more likely. In fact, the claim means is that each additional bifurcation above the mean (of around 22) multiplies by 5.61 the odds that the subject is "African American." However, the study also shows that total bifurcations are a rather poor predictor of self-identified race. Using total bifurcations to classify "race," around 42% of the subjects classified as "African American" according to total bifurcations turned out to self-identify as "European American." And, around 43% of the subjects classified as "European American" according to total bifurcations turned out to self-identify as "African American."[2]

In short, the study began by sorting people according to a social category (self-reported "race). They then measured some biological characteristics to see if they differed according to that social category. They, then chose the

biological characteristic that seemed to differ the most and tested their ability to sort people according to that characteristic. They then tried to map this sorting back onto the social category, and found it did so poorly. And, yet the findings are still presented as having told us something about the possibility of predicting "real" race, i.e., membership in a biological, not social, category.

The paper then goes on to suggest that its findings could be used to generate a method for fingerprints analogous to phenotypic profiling for DNA (Sankar 2010):

> The logistic regression results suggest that bifurcations can be used to classify individuals into ancestry groups, a finding that could lend support to the use of statistical models based on the total number of bifurcations present to estimate biological information regarding the individual who leaves a latent fingerprint, in conjunction with point-by-point inspections in latent fingerprint comparison (7).

In other words, given an unidentified crime scene print, bifurcation-counting may allow for a binary European/African prediction of the donor's ancestry, or, more precisely, the donor's self-assigned 'race.' If this information were used in a criminal identification, it would presumably be used to tell law enforcement to look for someone of a certain 'race.' But, the phenotypic (and socio-cultural) features that such an instruction would presumably trigger in law enforcement might not be the same as those which caused the individuals in the study to self-identify as one 'race' of the other. And the overabundance of bifurcations that the study found correlates with the latter, not the former. The only legitimate way of interpreting these correlations is back onto the social category, not onto a genetic category. For instance, it might be legitimate to conclude that "this fingerprint is more likely to come from a person who self-identifies as African American, given the binary choice between African and European American." It would not, however, be legitimate to conclude that the fingerprint is more likely to come from a person from a particular genetic or

ancestral category—that is, a person whose ancestors predominantly came from the geographical entities ‘Africa’ or ‘Europe.’

But the potential applications for forensic investigation do not end there:

> It is argued here that predictive models have potential as corroborative evidence to substantiate the decisions made by latent fingerprint examiners during fingerprint comparisons, especially if some of the more rare minutia types are discovered to vary among other populations, as these would be weighted more heavily in fingerprint comparisons (7).

If I understand this claim correctly, the researchers are suggesting that, after a latent print examiner makes a decision that a particular individual is the source of a particular latent print, this decision could be corroborated by a bifurcation-count. Presumably what is meant is that if the bifurcation-count correctly predicts the ‘ancestry’ of the individual the latent print examiner decided was the donor of the latent print, this would provide corroboration for the examiner’s decision. This suggestion is rather outlandish in itself, but it raises the further question of how the ancestry of the identified individual would be determined. The paper does not say, leading one to assume that ancestry would be attributed by law enforcement based on visual assessment and other cues (e.g., voice, accent, vocabulary, attire, behavior).

Pushing this argument even further, the researchers suggest that they may be able to thus “minimize the error rate involved with making identifications” (8), a suggestion that many latent print examiners might regard as surprising if not outlandish, given that, until recently, they believed that there was no error rate for latent print identification at all (Cole, 2005). Even now that many latent print examiners have abandoned that claim, they still might recoil at the idea of corroborating a latent print decision by reference to dermatoglyphics combined with visual ancestry ascription.

The limited practical significance of corroborating a fingerprint association

with an ancestry analysis suggests that dermatoglyphics may be a hammer in search of a nail. It may be an example of what Kahn (2009, p. 355) observed about race in forensic DNA profiling: “race is used because it is perceived as scientific—even if not of practical significance.”

These seemingly outlandish suggestions, however, become more understandable when we recall that the framework of the paper is to integrate two seemingly disparate disciplines that both have fingerprints as their object of study: anthropology and forensic science. As the authors note, anthropologists have tended to focus on fingerprint pattern types in an effort to correlate them with race, ethnicity, gender, disease, criminality, and other behavioral traits, whereas forensic scientists have focused on finer details, the so-called minutiae (ridge endings, bifurcations, etc.). The authors proposed to study minutiae anthropologically. “Given the applicability of ridge traits to a forensic and anthropological context,” the authors write, “it is argued here that these traits should be studied from both perspectives, ideally through collaboration (1)… [Y]et anthropologists and forensic scientists rarely collaborate in their efforts” (4).

While the paper’s claims seem rather strong, they were in fact modest compared to their characterization in the media. A North Carolina State University press release was entitled: “Study: Ancestral Background Can Be Determined by Fingerprints.” Already, we can see that the claims are being presented in the press release as stronger than even the strongest claims found in the scientific paper, as indicated by the use of the word “determined.” The press release goes on to state that “it is possible to identify an individual’s ancestral background based on his or her fingerprint characteristics.” It characterizes this as “a discovery with significant applications for law enforcement and anthropological research.” Gone is the speculative tone in the scientific paper, which said, for example, that it “could lend support to the use of statistical models” (7). Only in the second paragraph of the press release do we learn that “more work needs to be done,” that we need larger sample sizes, and to study more than two ancestral groups. In addition to the standard hyping found in many university press releases, it may be argued that this one, like many others,

heightens the popular appeal of its claims through its reference to race (ancestry), this drawing on the ever-present popular interest in claims that genetic or racial categories 'explain' human differences.

Yet even the strong claims in the press release pale in comparison to the claims in the media coverage prompted by the press release. The press release generated media coverage as far away as Italy. While one report did tone down the "determined" language in the press release by writing "latent prints can provide clues to a person's race," it also hyped the study by calling this "an astounding conclusion" (Augenstein 2015). The first author of the scientific paper is quoted stating "The results show that minutiae can tell us the probable ancestry of a person who leaves behind a latent fingerprint" and "This information is valuable evidence to corroborate the conclusion of a match based on a point-by-point comparison by a latent fingerprint examiner."

A second report summarized the study this way: "There's a new way for you to check your ancestry—look at your thumb" (Scribner 2015). It stated that the paper "suggests that one's ancestral background can be determined based on the characteristics of their thumbprint" and that the researchers "said their findings suggest that one's thumbprint can determine where their [*sic*] ancestors came from."

A third media report advised readers to "Forget all of those expensive DNA tests that claim to reveal your ancestry because a new proof-of-concept study by researchers at North Carolina State University and Washington State University demonstrates how a person's background can be identified using his/her fingerprints" (Bednar 2015).

As this last report suggests, perhaps the appeal of this news story is the way in which the seemingly humble fingerprint beats its more technically sophisticated rival at its own game: being the "code of life." If fingerprints can reveal ancestry too, they take DNA off its pedestal. Ironically, however, for criminal justice purposes, DNA *wants* off the pedestal: the acceptance of DNA as a criminal justice tool depends to some extent on reassuring the public about its *lack* of ability to predict biological futures.

Microscopic hair comparison

The second case study derives from the forensic discipline of microscopic hair comparison. Microscopic hair comparison has a long history, but it is beginning to fall into disrepute in the United States (e.g., Covey 2018). While it was already known that a large number of post-conviction DNA exonerations derived from cases in which microscopic hair comparison contributed to the wrongful conviction (Garrett 2011), the recent controversy was prompted by the exposure by the *Washington Post* of three wrongful convictions obtained in part by microscopic hair comparison (Hsu 2012). Partly in response, a joint review by the Department of Justice (DOJ), the Federal Bureau of Investigation (FBI), the Innocence Project (IP), and the National Association of Criminal Defense Lawyers (NACDL) was created to review cases in which microscopic hair comparison was used. In 2015, the group released the results of this panel's initial analysis of almost 500 cases. Most startlingly, it reported that FBI examiners gave "inaccurate" testimony in 96% of those cases. The DOJ is now working to notify all the defendants affected. The NACDL is trying to ensure that those defendants have counsel. For its part, the FBI has agreed to provide free DNA testing, and the DOJ has agreed not to invoke statutes of limitations. However, that will not necessarily apply to the majority of cases, which originated in state, not federal, courts.

That attention-getting 96% statistic is likely behind some of the rather sensational headlines that accompanied blog posts about the report, including, for example, "The FBI faked an entire field of forensic science" (Lithwick 2015) and "CSI is a Lie" (Friedersdorf 2015). One might read such reports and wonder how it is even possible to be wrong at a rate so much higher than chance. This story is perhaps a particularly stark example of what is by now a rather garden-variety finding in sociology of science: that scientific knowledge changes through the social consensus of its practitioners. By deliberately forming an organized consensus group and charging themselves with issuing a report, the four institutions (DOJ, FBI, IP, NACDL), former adversaries, whose cooperation, as Reimer (2013), Executive Director of NACDL, put it, was "once an almost inconceivable concept," were able to transform thousands of scientific results from

"accurate" to "inaccurate." When the report calls testimony "inaccurate," it does not mean that it falsely associated a hair with an individual. Rather, it means that the expert witnesses overstated the value of evidence, sometimes by claiming that the suspect was the only possible source of the hair rather than one of many possible sources, sometimes by attaching bogus statistics to a hair association.

Notably, for our purposes, many of these overstatements were claims of 'individualization'—the claim to be able to associate a crime scene hair with a single donor. What the reviewing institutions had agreed was that such claims could never be sustained for hair comparison (though they are still claimed for other forensic areas, such as fingerprints and toolmarks). Instead, hairs could only be associated with a group, and, further, in most cases the size of that group was considered unknown, and indeed unknowable. Yet, for years, FBI examiners had treated a forensic technique with relatively low discrimination as if were capable of such high discrimination that it could reduce the potential donor pool of a hair to a single individual.

The science didn't 'shift.' In fact, no scientific research was performed at all—that, after all, is the point. What happened was that relevant actors became convinced that is was not scientifically acceptable to report about a hair comparison without making a reliable estimate of the potential donor population. In essence, the relevant social actors agreed it was necessary to think about hair evidence in a probabilistic fashion. This formation of agreement could reasonably be called both a scientific act and a social one.

There is a possible explanation for this unusual turn of events: microscopic hair comparison is almost obsolete. As a National Research Council report noted:

> The availability of DNA analysis has lessened the reliance on hair examination. In a very high proportion of cases involving hair evidence, DNA can be extracted, even years after the crime has been committed. Although the DNA extraction may consist of only mitochondrial DNA (mtDNA)

> [nuclear DNA, preferable for forensic analysis, is not always retrievable from hair; mitochondrial DNA usually is], such analyses are likely to be much more specific than those conducted on the physical features of hair. For this reason, cases that might have relied heavily on hair examinations have been subjected more recently to additional analyses using DNA. Because of the inherent limitations of hair comparisons and the availability of higher-quality and higher accuracy analyses based on mtDNA, traditional hair examinations may be presented less often as evidence in the future, although microscopic comparison of physical features will continue to be useful for determining which hairs are sufficiently similar to merit comparisons with DNA analysis and for excluding suspects and assisting in criminal investigations.

The joint review was concerned with overstatements of the discriminability of hair comparison, not with ancestry attribution through hair. Nonetheless, many of the cases that were reviewed did contain statements about ancestry because hair examiners, traditionally, have made attributions of ancestry as well as individuality. In one capital case in Florida, the defense argument was that two other individuals, who happened to be Mexican, had committed the murder, but the hair analyst testified that Mexicans could be ruled out as sources of a hair (Antoun 2017).

The most dramatic case involving ancestry attribution was that of Willie Manning. At the time the joint project was underway, Willie Manning had an imminent execution date, May 7, 2013. Manning had been convicted and sentenced to death in two separate double murders in Mississippi, the 1992 murder of Tiffany Miller and Jon Steckler and the 1993 murder of Alberta Jordan and Emmoline Jimmerson (Cohen 2013). During the trial for the Miller-Steckler murder, an FBI hair analyst testified that a hair recovered from their car came from a black person. Miller and Steckler were white (Possley 2015). The analyst did not ‘individualize’ Manning as the source of that hair or provide a quantitative statement about the weight of the

evidence. But the analyst did—falsely—state that microscopic hair comparison was capable of both these things, which, arguably may have improperly increased the jury's perception of the power of the technique.

Given Manning's impending execution, the FBI took the unusual step of issuing urgent letters on May 4, 2013 stating that there were errors in the hair evidence in Manning's case (Cohen 2013). The letters held that it had been error to report that a black person was the source of the hair, but still insisted that it was appropriate to report that hair "exhibits traits associated with a particular racial group":

> The scientific analysis of hair evidence permits an examiner to offer an opinion that a questioned hair possesses certain traits that are associated with a particular racial group. However, since a statistical probability cannot be determined for classification of hair into a particular racial group, it would be error for an examiner to testify that he can determine that the questioned hairs were from an individual of a particular racial group. Thus, an examiner cannot testify with any statement of probability whether the hair is from a particular racial group, but can testify that a hair exhibits traits associated with a particular racial group (Federal Bureau of Investigation 2013).

Four hours before his scheduled execution, Manning was granted a stay of execution in order to allow DNA testing on the hair. In 2015, Manning was exonerated of the Jordan-Jimmerson murder after key witnesses had recanted their original testimony and Manning's lawyers discovered that the witnesses had lied about living in the same building as the victims. Manning remains on death row for the Miller-Steckler murder (Possley 2015).

All of this is seems to suggest that microscopic hair comparison is in trouble. Nonetheless, the DOJ did recently issue a Proposed Uniform Language for Testimony and Reports (ULTR) for the Forensic Hair Examination Discipline (Department of Justice 2016a). The ULTRs are a

project that actually stemmed from the hair comparison review. The DOJ decided to do more such reviews for other forensic disciplines. As I noted above, however, carrying out such reviews requires pre-agreement on 'appropriate' and 'inappropriate' testimony. Therefore, the DOJ has committed to producing ULTRs for a range of forensic disciplines. Hair comparison was included in the first batch of draft ULTRs.

As with the FBI statement in the Manning case, the draft ULTR took the position that ancestry assignments are still appropriate, using a common crude—and arbitrary (Bolnick 2008)—three-race format:

> *Characteristics of Ancestry* The examiner may state or imply that a human hair exhibits Caucasian (European Ancestry), Negroid (African Ancestry) and/or Mongoloid (Asian or Native American Ancestry) characteristics. Ancestral group classifications are based on characteristics that are typically observed in hairs from individuals of different ancestral groups and may or may not correspond with how an individual identifies his or her race.

This raises the question whether these claims are, like others we discussed above, based on studies that rely on crude racial classification, self-identification, and official ascription. The Supporting Documentation for the ULTR stated:

> Ancestral group classifications are based on characteristics that are typically observed in hairs from individuals of different ancestral groups and may or may not correspond with how an individual identifies his or her race. Characteristics of ancestry can often be determined using features such as pigment distribution and cross-sectional shape (Department of Justice 2016b, pp. 5–6).

Ancestry groups are treated as 'scientifically real' and thus transcending both 'social race' and self-identification. The document offers two citations

in support of this statement (Franbourg et al. 2003; Khumalo et al. 2000). The first study used "African," "Caucasian," and "Asian" volunteers, but does not explain how volunteers were assigned to these groups. Notably, it found that "Chemical analysis has shown no major biochemical differences the various racial groups" (Khumalo et al. 2000, p. 814). The second study merely reports that hair samples coded "African" were taken from subjects living in France or the U.S., those coded "Asian" were taken from China or Japan, and those coded "white" were taken from Europe or Canada. Of course, this is a remarkably old fashioned conception of race that seems to selectively ignore migration. This study found that "African" hairs were different in structure, exhibited more knots, and were more often broken than hairs from other groups.

Interestingly, the ULTR did acknowledge that the crude ancestral groups it proposes "may or may not correspond with how an individual identifies his or her race." Thus, it acknowledged the 'social' nature of 'race,' but failed to address the impact that this might have on the scientific studies that supposedly support the claimed ability to make racial classifications.

Is this yet another finding founded on unwarranted assumptions about the researchers' ability to accurately sort their research subjects into ancestry? As it turns out, dermatologists have already been questioning the assignment of race in this way. In 2006, the *Journal of the American Academy of Dermatology* published a "Colloquium on Race/Ethnicity/Skin Color." In it, researchers analyzed the way in which race, ethnicity, and skin color had been reported in the journal. They found that race of patient was mentioned in 41% of case reports published in the journal. Perhaps not surprisingly, they found that the way in which race was determined was simply not reported in a full three quarters of these case reports. In the remainder, race was determined by self-identification. No studies stated that race was determined by inspection (Unaeze and Bigby 2006, p. 1068). Two editors of the journal published a "Proposed Policy on Identification of Race, Ethnicity or Skin Color in Case Reports and Studies Submitted to the *Journal of the American Academy of Dermatology*" (Unaeze and Bigby 2006). The editors concluded that "Rather than a policy, we suggest that

authors inclined to include such descriptions in their manuscripts ask themselves the following questions:

1. Is the identification of the patient's race/ethnicity/skin color important to the understanding or pedagogical value of the submitted manuscript?

2. Would the patient identify him/herself in the same way as the authors have (and how do you know)?

3. Might the descriptor be open to racist intent or interpretation?

4. What is the evidence that the race/ethnicity/color of the patient(s) plays a role in the entities described?"

Although the editors clearly have concerns beyond merely the assumption that race can be inferred from self-identification or official ascription, it is clear that is among their concerns. Elsewhere in the same issue, in a letter entitled "Describing Patients' 'Race' in Clinical Presentations Should be Abandoned," one of the editors and co-author note:

> Generally in practice, the physician decides the race of the patient on the basis of what he/she sees and his/her own biases. For most physicians, if he/she can't decide, anxiety is generated. The assessment of race is often wrong or at least at odds with what the patient considers him/herself. This conflict is absurd because there are no definitive tests or definitions of the term race (Bigby and Bernhard 2006, p. 1075, citations omitted).

In another contribution to the colloquium, one of the authors of one of the studies noted above, which was cited by the DOJ ULTR to support the proposition that hair examiners can predict ancestry, notes that "[f]or example, the definition of 'African hair' is important because this hair form is associated with a higher prevalence of specific disorders (e.g., acne keloidalis)." However, he argues:

> that race is in fact only a proxy for hair form. Within groups of ‘‘African’’ and ‘‘Asian’’ hair reside extremes of the spectrum of hair morphology, with the majority, typical of human variation, falling within these extremes. Even indigenous Africans in Africa display variations in hair form. I agree with Bigby et al. that race should be abandoned, and whilst it is a useful, albeit nonspecific, surrogate for hair form, its use suggests a lack of rigor on our part (Khumalo 2007, p. 709).

Therefore, the letter is titled “Yes, Let’s Abandon Race–It Does not Accurately Correlate with Hair Form.”

Even the famous Afro-American Studies scholar Henry Louis Gates, Jr. weighed in on the dermatological controversy. Contrary to the arguments expressed above, Gates (2006) expressed support for Taylor (2006, p. 1070), who argued, based on “the study of the Human Genome Diversity Cell Line Panel, the concept of race has seemingly been demonstrated to be more than simply a social construct, but indeed to be firmly grounded in biology.” This is generally consistent with Gates’s well known enthusiasm for exploring ancestry through the combination of genetics and history (Williams 2009), which has sometimes appeared to science studies scholars to verge on determinism (Pollock 2012, p. 108).

Given the above discussion, it would seem that the DOJ Supporting Documentation for the ULTR does not accurately reflect the current state of the field concerning the prediction of race from hairs. The citations that it offers are fairly dated, and sentiment within dermatology—including by the first author of one of the two articles cited in the Supporting Documentation—presently seems to be leaning toward describing the full continuum of hair morphology without using ‘race’ as an arbitrary way to create break points along that continuum.

As in the first case study, the slippage between biological and social categories is striking. It is entirely unclear what statements like “the hair did

(or did not) come from a ‘Mexican’ or ‘a black person’ is supposed to mean. Are these social categories, such as ‘a person who lived their childhood within the national boundaries of the country called Mexico’ or ‘a person who in the 21st-century United States is referred to as “black”’? If so, how can the scientist countenance the careless construal of these social categories as biological? Or, are these statements shorthand for more precisely defined biological categories such as ‘an ancestry group defined to capture a large portion of the current population of Mexico’ or ‘an ancestry group defined to capture individuals who ancestors several generations back lived in Africa’? If so, how can the scientist countenance the careless construal of these biological categories as social?

Even trying to found such claims on a more secure base of empirical data will be difficult because, as the dermatological literature points out, the empirical data all rest upon the assumption that self-identified ‘race’ correlates with categorical types of hair form.

We see a number of contrasts between the hair case and fingerprint case. While the fingerprint article discussed above was framed as a scientifically valid finding that was of questionable practical significance, hair comparison is “perceived as of practical significance—even if not scientific” (Kahn 2009, p. 355). Even it is recognized that hair exists along a continuum of difference, it is claimed that it is still of practical utility to say that there was a ‘black’ or ‘Mexican’ hair at a crime scene. Whereas friction ridge analysis has largely abandoned the collective identification project in order to more vigorously pursue the individual identification project, hair identification has now abandoned the individual identification project but retained the collective identification project.

The final Approved ULTR was published by the DOJ in 2018 (Department of Justice 2018). The Supporting Documentation has apparently been discarded for all ULTRs and has not been published. Unlike the Draft ULTR, the approved document makes no mention of characteristics of ancestry.[3]

Microbiome forensics

My third case study is the emerging area of 'microbiome forensics.' The "human microbiome" refers to "both the collection of genes contained in the microbes inhabiting the human body… and the collection of different microbe species inhabiting the human body, analogous to the 'biome,' meaning the various species of flora and fauna living in a given environment, which in this case happens to be the human body" (Nothern 2016, p. 722). Non-human microbiomes—the flora and fauna living on objects and in environments—are of interest as well.

Microbiomes have emerged as an area of great scientific interest especially in health research. However, there is also interest in forensic applications. Some have suggested that the microbiome may "transform the field of law by its use in tracking and identifying criminals" (Salyards 2015, p. 58) or that it "could revolutionize future forensic investigations in much the same way DNA analysis changed investigative procedures two decades ago," and "may become the biggest advance in forensic science since the advent of DNA matching" (Steussy et al. 2015, p. 4, 11). Not surprisingly, human microbiomes have been characterized as "as unique as fingerprints" (Benezra 2016, p. 346). Enthusiasts have suggested that "Microbiomes are as unique as DNA, but since microbiomes are inadvertently left behind everywhere, they may help make tracking and catching criminals easier than DNA analysis," and "microbiomes will always be present" at crime scenes "and are impossible to conceal, which could have profound implications for the field of forensics" (Salyards 2015, pp. 59–60). Strong claims about the supposed uniqueness of each individual's microbiome are being made (Steussy et al. 2015, p. 11; Costello et al. 2009; Fierer et al. 2010). Among the potential applications envisioned for microbiome forensics are estimation of time of death, time in water, personal identification (i.e., linking a person to an object, place, or another person through a microbial trace), identification of body fluid type, soil analysis, identification of infectious strains, and "estimating the human niche of epithelial cells" (Kuiper 2016, p. 1085; Steussy et al. 2015).[4]

The human microbiome can be a very rich source of genetic information. One estimate holds that each human microbiome consists of around 100

trillion cells (Nothern 2016, p. 723). Initially, it was claimed that non-human cells in and on the human body outnumbered human cells by a factor of 10 (e.g., Costello et al. 2009, p. 1694).[5] This rather startling claim produced some philosophical musing about human identity, casting doubt on the "monogenomic" notion—so central to genetic forensics—of the human individual as defined as an agglomeration cells that are all genetically identical with one another and yet genetically different from the agglomerated cells of every other entity called a 'human body' (Dupré and O'Malley 2007, p. 842; Sapp 2007, p. 792). Perhaps instead, these seemingly special identical-yet-unique cells are in fact mere passengers—or mere parasites—on a much larger cacophony of different species and individual organisms (e.g., Gregory and Bowker 2016, p. 212; Hutter et al. 2015; Dupré and O'Malley 2007, p. 840; Landecker 2015, p. 257). Further, this perspective threatens to destabilize the longstanding orientation of forensics around the centralizing ideal of 'uniqueness' (Kirk 1963; Cole 2009) as scientists are beginning to find that microbes, far from being unique to particular places, are in fact ubiquitous: "the figure of the unique microbe is being swamped by the ubiquity of microbial presence" (Paxson and Helmreich 2014, p. 176).

Forensic microbial analysis is based on a 'metagenomic'[6] analysis of the genetic material contained in a swab taken from, say, human skin or a computer keyboard. Most forensic applications analyze the sample for an DNA sequence called 16s that encodes for RNA in the cell (for a brief history, see Sapp 2007). Thus, what is yielded by the analysis is perhaps thousands of 16s DNA sequences from "hundreds of millions of gene reads" (Benezra 2016, p. 342). To what extent these sequences represent discrete individuals or even distinct species (or taxa) is a question that must be tackled through analytic methods. In principle, this is true of forensic DNA profiling as well, especially mixtures. However, even the very complex DNA mixture samples which have famously bedeviled forensic statisticians (see, e.g., Dror and Hampikian 2011; Thompson et al. 2012; Moss 2015; Murphy 2015), consist of, say, three to five human individuals. Microbiome samples consist of thousands of different organisms from many different species or taxa. Thus, forensic microbial analysis could be conceived as

reflecting the perspective of some philosophers of biology "that the communal gene pool is evolutionarily important and that genetic material can fruitfully be thought of as the community resource for a superorganism or metaorganism, rather than the exclusive property of individual organisms" (Dupré and O'Malley 2007, p. 838).

Forensic microbial analyses begin by trying to make sense of the thousands of sampled 16s sequences. This is done by "clustering" the sequences according to their similarity with one another. 16s sequences which duplicate to some arbitrary degree (97 and 99% being the most common) are treated as belonging to a common Operational Taxonomic Unit (OTU). As the name suggests, OTUs are used a sort of convenience proxy for 'species,' while avoiding any claim that members of the same OTU are members of the same species in any strong epistemological sense.[7] Microbiology has a long history of treating the "fixed and immutable bacterial species" as an "idea" that is "required" for "orderly investigation," rather than an epistemologically determined object (Attenborough 2012, p. 58; see also Sapp 2007, p. 791). OTUs are then discussed as if they were 'species,' although it is understood that some members of the same OTU may in fact be different 'species,' and for that matter a small number of members of different OTUs may be the same species.

Different samples can be compared in terms of their overlap in OTUs. Whereas forensic DNA profiling is founded on claims about genetic material in different samples deriving from the same organism or a few of the same organisms, microbial forensics is founded on claims about the similarity of an entire microbial "community" in different samples. In this sense, microbial identification is 'collective' in a way that conventional DNA profiling is not. It essentially tries to produce individual identity through a very large group identity. Microbial identities, in this sense, are hardly individual identities at all. They are individual in the sense that they pertain to a particular keyboard or to a particular area of human skin (at a particular time). But, they are collective identities in that they are constructed out of sequences derived from multiple organisms and even species.

While it is possible to construct a microbial similarity metric based on the degree of overlap of OTUs contained in different samples alone, most microbial forensics papers do not use such metrics. 16s, the most commonly used genetic marker for forensic microbial analyses, was initially developed because of its utility for studying evolution—for measuring the distance between an organism (or species) and an ancestor (Sommerlund 2006, pp. 918–920). Perhaps for this reason, the more common practice is to use a 'phylogenetic' metric of similarity, such as UniFrac, which measures the evolutionary distance between OTUs in a sample and a common genetic ancestor. Thus, the sample, consisting of a mixture of a large number of species and even larger number of individual organisms, is characterized according its collective estimated evolutionary distance from a common microbial ancestor (e.g., Lax et al. 2015; Fierer et al. 2010). The 'identities' of microbial samples, then, are not merely 'collective'; they implicate evolutionary theory. In this way, these collective microbial identities resemble the collective human identities, such as 'race,' discussed in the previous two case studies. Both are constructed around the supposed evolutionary distance of groups of organisms from some presumed common ancestor organism.

Microbiome forensics is expected to use such phylogenetic analyses. For this reason, microbiome forensics is unlikely to produce 'matches' of the kind found in single-source human DNA analysis in which some specified number of alleles (e.g., 13) are identical between two samples. Likewise microbiome forensics is unlikely to use a statistic like the random match probability to characterize the rarity of those identical alleles. Instead the analysis will be phylogenetic and probabilistic:

> In the final analysis, phylogenetic analysis underpins virtually all microbial forensic work. There will likely never be a direct match between populations of microbes. Consequently, it will always be necessary to build an evolutionary tree through phylogenetic computations to determine how close the relatedness is between different populations. Alternatively, populations of millions of

> microbes may be compared at one time to find matching communities. In all cases, "matching" will never reveal the samples to be identical but rather so closely related that they can be used to discriminate between hypotheses put forward by court (Steussy et al. 2015, p. 26).

Even a finding of a high degree of phylogenetic similarity, however, would not address the question of how rare that phylogenetic profile is. Human DNA analysis addresses this question through reference to databases, and answering that question for microbial forensics would require "analyzing a representative number of microbiomes and building a database with relevant samples" (Kuiper 2016, p. 1086). Such databases do not currently exist (Steussy et al. 2015, p. 35, 44). Some legal scholars, however, have suggested that microbiome databases would pose a greater threat to privacy that the human DNA databases that currently exist. This is based on the argument that human DNA reveals only identity [which is not entirely correct (Joh 2006; Cole 2007)], whereas microbial DNA may reveal 'lifestyle' information, such as diet, health, location, substance use, or sexual practices (Salyards 2015, p. 73). In contrast to human DNA databases, microbiome forensics will face the challenge that microbiomes vary across both time and space: a specific individual's microbiome is constantly changing, and different parts of a single human's body contain different microbiomes (Costello et al. 2009). Steussy et al. (2015, p. 12) note that "microbes are constantly dying, reproducing, and occasionally undergoing mutations and other types of genetic change. Since bacterial cells can reproduce themselves in as little as 15 min and viruses usually within less than 24 h, their genomes may exhibit substantial differences in a very short time. A single day in the life of such a bacterial colony can produce as many generations as humans have since the time of the Peloponnesian Wars, 2500 years ago." These issues could make microbiome databases much more difficult to construct and manage than human DNA databases (Nothern 2016, p. 746; Steussy et al. 2015, p. 35, 44).

As with human DNA forensics and most other forensic identification techniques, the notion of classifying these supposedly highly

individualizing microbiomes by race has already arisen (Steussy et al. 2015, p. 43; Gunn and Pitt 2012, p. 321). If these claims are traced back to their source, we arrive at a 2011 study of vaginal microbiomes. Although this particular study was motivated by health applications, it should be noted that researchers have already targeted the vaginal microbiome as potentially important in the forensic investigation of sexual assaults (Nothern 2016, p. 736). The researchers were interested in the vaginal microbiome because, they argued, it seemed "to play a key role in preventing a number of urogenital diseases, such as bacterial vaginosis, yeast infections, sexually transmitted infections, urinary tract infections, and HIV infection," and "Common wisdom attributes this to lactic acid-producing bacteria, mainly *Lactobacillus"* (Ravel et al. 2011, p. 4680). The 396 research subjects were classified into four "ethnic" groups: "white," "black," "Hispanic," and "Asian." [As Ross (2011), an author of the fingerprint case study discussed in Section II, notes, "Hispanic" is not a biological category. It refers to "people who come from Spanish speaking countries."] The study found statistically significant differences in the microbiomes of the four ethnic groups. Most significantly, Hispanic and black women had a lower prevalence of *Lactobacillus*. Although the hosting of *Lactobacillus* is considered healthy, the study rejects the notion that black and Hispanic women are less healthy and instead proposes we rethink "the question of what kinds of bacterial communities should be considered 'normal' in Hispanic and black women." The study notes that "The reasons for these differences among ethnic groups are unknown, but it is tempting to speculate that the species composition of vaginal communities could be governed by genetically determined differences in hosts" (Ravel et al. 2011, p. 4684). Thus, the 'temptation' of genetic determinism outweighs consideration of, for example, environmental or lifestyle explanations for these individual differences.

We then turn to the question of how the racial classification of the subjects was accomplished. Again, the answer is that "ethnicity" was "self-reported" (Ravel et al. 2011, p. 4680). As with the fingerprint case study, this study began by creating human groups based on a social category, self-identified 'race.' It then sought correlations between these groups and a phenotypic

feature whose potential as an ancestry predictor has been hitherto unexplored. The only legitimate way of interpreting these correlations is back onto the social category, not onto a genetic category. For instance, it might be legitimate to conclude that "this microbiome is more likely to come from a woman who self-identifies as black or Hispanic, using U.S. Census categories." It would not, however, be legitimate to conclude that the microbiome is more likely to come from a woman from a particular genetic or ancestral category. If the data input of a scientific study consists of racial designations based on self-identification and official ascription, then the knowledge claim output of that study can only pertain to a social category of race: e.g., "this bacteria is more prevalent in the microbiomes of women who self-identify as 'black,' using U.S. Census categories."[8]

In addition to race and gender, another area of research is familial relationships. Perhaps not surprisingly, microbiomes have been found to be similar among family members (Ross et al. 2017), although the methodological definition of 'family' in such studies raises ambiguities about whether we are talking about a social or a biological construct similar to those we have already raised about 'race.' Specifically, the operational definition of family in this particular study—"10 cohabiting and sexually active couples" consisting of "healthy heterosexual adults between the ages of 20–49 years" who "had lived together for periods ranging from 4 months to 14 years… in southwestern Ontario in Canada" (Ross et al. 2017, p. 11)—might be criticized as somewhat narrow definition of a 'family.' Be that as it may, the claim of familial similarity reflects the interesting way in which microbiomes undermine the usual dichotomy between genes and environment. Microbiomes are at once thoroughly genetic and yet profoundly environmental: they are to some extent inherited, but they also reflect individuals' life histories, environments, and the other bodies with which they have regular contact. Some microbiologists have argued that inheritance reflects more than the mere passing on of human genes, but also of microbial genetic resemblances deriving, in part, from a more social meaning of 'family,' i.e., from physical proximity and sharing the same environment. Thus, "It appears that the microbiome blurs the line that separates genetic and environmental forces acting on phenotypes"

(Sandoval-Matta et al. 2017, p. 8).

Microbial family resemblances, however, revive in another form the controversy over familial searching in forensic genetics (see, e.g., Haimes 2006; Murphy 2015). Like DNA profiles, microbiomes tell us not just about an individual but about other people. In this sense, microbiome forensics proposes to identify individuals based on their families. What is racial/ethnic identification, if not that? And, of course, the microbiome is a sort of interspecies 'family' itself: a collective of individual organisms and different species that shares a common 'home.' But, as noted above, microbiomes also destabilize the very notion of the individual itself. Is the individual a human being colonized by microbes? Or is it a superorganism composed of human microbial cells?

AQ3

Conclusion

It may be useful to try to place these developments in the context of the history of forensic identification technologies. Fingerprint identification, among the earliest and most successful of these techniques, established a sort of template for the field by positing *individualized identification* as the *telos* of such technologies. The ultimate goal was a biometric identifier that would always be consistent within a human body and yet different from all other human bodies (Kirk 1963).

As noted above, interest in collective identities, such as races, emerged quickly. But group identification was relatively quickly abandoned, not because it 'didn't work,' but perhaps because it was not particularly useful for law enforcement, certainly not as useful as individualized identification. Perhaps also, group identification may have been perceived as a liability, a needless distraction from the individualized identification project.

Hair microscopy may be characterized as one of those successor technologies that molded itself in fingerprinting's image, that aimed at the *telos* posited by fingerprinting. But, hair microscopy was far from discriminating enough to even approach individualized identification, and

yet, bafflingly, went on to sometimes *claim* to have achieved it in court, at least in the U.S. These reckless claims came home to roost only decades later with the testimony review project. Its claims to individualized identification collapsing, hair microscopy took refuge in collective identification: even if claims to individualization were exaggerated and unsustainable, surely even hair microscopy could achieve the assignment of the population to three or four gross 'races.' Even these claims, now, appear to have been abandoned.

But collective identification for hair, as for everything else, runs up against the usual problems for collective identification: groups are too gross to be meaningful; arbitrary boundaries create artificial groups out of difference that exists along a continuum; assignments are made through self-identification and official ascription; and the groups purport to be biological (genotype) and yet seem to 'really' reflect "embodied race" (racialized phenotype).

Genetic identification techniques at the outset were seen as the ultimate enactment of the fingerprint paradigm: the notion that individual bodies have biometric markers that are at once consistent within that individual body and yet distinct from all other human bodies. Each cell within an individual was supposedly genetically identical with each other cell within that body and distinct from the assemblage of cells within all other bodies—or at least very rare.

This was never entirely true. It was necessary to make exceptions for homozygous twins, parasites, and chimerism (Martin 2007). The notion of the genetically homogeneous body continues to erode, most recently with findings about post-natal genetic differences in the brain cells even of a single individual (Martone 2018). But microbiome forensics threatens to explode this notion altogether. Microbiomes can distinguish identical twins, of course, and microbial analysis does not treat the human body as an undifferentiated whole—the microbiomes of different body areas will be quite different. But microbiomes may do even more. Some have read the microbiome as undermining the very distinction between the individual and

the collective, and with it the status of 'the human being' as an individual or even a unitary species. For example, Hutter et al. (2015) argue that "the individuality of human beings is better conceived as a symbiotic entity… to be human is to be multispecies." So the human being is not merely a single organism; it is not even a single species. Therefore, "we ought to consider, for biological research purposes, that the single *Homo sapiens* is not in fact the real biological individual."

The critique of collective identities constructed around notions such as 'race'—especially from the perspective of disciplines like anthropology or evolutionary biology—has long been that collective identities such as race are artificial constructs erected between two constructs that are seen as more 'real': the individual and the species. Distinctions between species, it was claimed, were indeed real, but distinctions between races were arbitrary, false boundaries created within the species. The bounded, internally homogeneous individual was likewise seen as real. What appeared to some as a 'race' was in fact merely the wondrous manifestation of the seemingly infinite potential for human variety. And yet, at the same time, this variety obscured the high degree of sameness of all those individuals within species (Marks 2002).

'Race' Marks (2015, p. 162) comments, "is a process of aggregating and classifying people, creating bounded categories of difference where none exist 'out there.'" Many social scientists are used to thinking about race in this way, but they are less accustomed to thinking about individuals or species in this way. The individual and the species are treated as privileged; indeed, fundamentally, they are conceived as the antidotes to racial thinking. The species is what unites all humans across all supposed 'races.' And, individual differences between all humans, even within supposed 'races,' are what undermine the effort collect individuals into crude groups. But what if the individual and the species are equally well "a process of aggregating and classifying people, creating bounded categories of difference where none exist 'out there'"? The microbiome threatens to undermine not just arbitrary racial categories, but all three types of identity —individual, race, species—at once (e.g., Quammen 2018). Suddenly, not

only is it absurd to consider race a biological phenomenon, but also nothing is an individual or a species anymore. What is left is a multispecies mega-collective that can be 'identified' by nothing more than 'phylogenetic similarity.' Were this to be taken seriously, identification would no longer rest on tendentious—and downright ontological—claims about the biological homogeneity of individuals and their distinctness from all other individuals. Rather, it would rest merely on measurements, in which species and individuals are just bits of data in larger 'big data' collective. Perhaps, then, we may soon do less of the familiar binary between individual and collective and start doing something else, something more complicated but that may yet afford greater opportunities for new thinking about what an identity might consist of.

While such a future is interesting to imagine, there are good reasons to believe neither the individual nor the collective will fade away quite so easily. Indeed, the discourse around metagenomics illustrates the strong desire to perceive both individuals and collectives—organisms, species, etc.—even when the justification for these "central ontological categories" has "raised concerns" (Dupré and O'Malley 2007, p. 842). That humans tend to perceive biological things, including most notably other humans, in terms of the collective is well known. It appears that may be true of the individual as well.

Acknowledgements

This work was partially funded by the Center for Statistics and Applications in Forensic Evidence (CSAFE) through Cooperative Agreement #70NANB15H176 between the National Institute of Standards and Technology and Iowa State University, which includes activities carried out at Carnegie Mellon University, University of California Irvine, and University of Virginia. I am grateful to all the participants in both *Doing the Individual and the Collective in Forensic Genetics: Governance, Race and Restitution* workshops, at the University of Manchester in 2016 and the University of Amsterdam in 2017, for the helpful comments on draft of this paper. I am especially grateful for the editorial comments of Amade M'charek and Peter Wade. For expertise and assistance on various matters, I

am also grateful to Vanessa Antoun, Jennifer Martiny, Natasha Mesinkovska, Hal Stern, and Elham Tabassi. Responsibility for any errors is my own.

Compliance with ethical standards

Conflict of interest The author consulted on the Willie Manning case discussed in this article.

References

Antoun, V. 2017. Microscopic Hair Comparison: The NACDL Analysis Review Project. *Seventh National Seminar on Forensic Evidence and Criminal Law.* Seattle, WA.

Aronson, J.D. 2007. *Genetic Witness: Science, Law, and Controversy in the Making of DNA Profiling*. New Brunswick, NJ: Rutgers University Press.

Attenborough, F.T. 2012. 'To Rid Oneself of the Uninvited Guest': Robert Koch, Sergei Winogradsky and Competing Styles of Practice in Medical Microbiology. *Journal of Historical Sociology* 25: 50–82.

Augenstein, S. 2015. Can You Determine Race From a Fingerprint? *Forensic Magazine.*

Bednar, C. 2015. Your Fingerprint Can Reveal Your Ancestry. *redOrbit.*

Benezra, A. 2016. Datafying Microbes: Malnutrition at the Intersection of Genomics and Global Health. *BioSocieties* 11: 334–351.

Bigby, M., and J.D. Bernhard. 2006. Proposed Policy on Identification of Race, Ethnicity or Skin Color in Case Reports and Studies Submitted to the *Journal of the American Academy of Dermatology*. *Journal of the American Academy of Dermatology* 54: 1077.

Bolnick, D. 2008. Individual Ancestry Inference and the Reification of

Race as a Biological Phenomenon. In *Revisiting Race in a Genomic Age*, ed. S.S. Richardson, B.A. Koenig, and S.S.-J. Lee, 70–85. New Brunswick: Rutgers University Press.

Bonnevie, K. 1924. Studies on Papillary Patterns of Human Fingers. *Journal of Genetics* 15: 1–112.

Brubaker, R. 2016. The Dolezal Affair: Race, Gender, and the Micropolitics of Identity. *Ethnic and Racial Studies* 39: 414–448.

Cho, M.K., and P. Sankar. 2004. Forensic Genetics and Ethical, Legal and Social Implications Beyond the Clinic. *Nature Genetics* 36: S8–S12.

Cohen, A. 2013. Feds Acknowledge Scientific Errors in Testimony in Willie Manning Case. *The Atlantic.*

Cole, S.A. 2001. *Suspect Identities: A History of Fingerprinting and Criminal Identification*. Cambridge: Harvard University Press.

Cole, S.A. 2005. More Than Zero: Accounting for Error in Latent Fingerprint Identification. *Journal of Criminal Law and Criminology* 95: 985–1078.

Cole, S.A. 2007. Is the 'Junk' Designation Bunk? *Northwestern Law Review Colloquy* 102: 54–63.

Cole, S.A. 2009. Forensics without Uniqueness, Conclusions without Individualization: The New Epistemology of Forensic Identification. *Law, Probability and Risk* 8: 233–255.

Costello, E.K., C.L. Lauber, M. Hamady, et al. 2009. Bacterial Community Variation in Human Body Habitats Across Space and Time. *Science* 326: 1694–1697.

Covey, R. 2018. Suspect Evidence and Coalmine Canaries. *American Criminal Law Review* 55: forthcoming.

Department of Justice. 2016a. Proposed Uniform Language for Testimony and Report for the Forensic Hair Examination Discipline.

Department of Justice. 2016b. Supporting Documentation for Proposed Uniform Language for Testimony and Reports for the Forensic Hair Examination Discipline.

Department of Justice. 2018. Approved Uniform Language for Testimony and Reports for the Forensic Hair Discipline.

Dror, I.E., and G. Hampikian. 2011. Subjectivity and Bias in Forensic DNA Mixture Interpretation. *Science & Justice* 51: 204–208.

Dupré, J., and M.A. O'Malley. 2007. Metageonomics and Biological Ontology. *Studies in History and Philosophy of Biological and Biomedical Sciences* 38: 834–846.

Federal Bureau of Investigation. 2013. communication to Special Counsel MHCART, May 4.

Fierer, N., C.L. Lauber, N. Zhou, et al. 2010. Forensic Identification Using Skin Bacterial Communities. *Proceedings of the National Academy of Sciences* 107: 6477–6481.

Fournier, N.A., and A.H. Ross. 2015. Sex, Ancestral, and Pattern Type Variation of Fingerprint Minutiae: A Forensic Perspective on Anthropological Dematoglyphics. *American Journal of Physical Anthropology* 160: 625–632.

Franbourg, A., P. Hallegot, F. Baltenneck, et al. 2003. Current Research on Ethnic Hair. *Journal of the American Academy of Dermatology* 48: S115–S119.

Friedersdorf, C. 2015. CSI Is a Lie. *The Atlantic.*

Fullwiley, D. 2008a. The Biologistical Construction of Race. *Social*

Studies of Science 38: 695–735.

Fullwiley, D. 2008b. Can DNA 'Witness' Race? *GeneWatch.*

Garrett, B.L. 2011. *Convicting the Innocent: Where Criminal Prosecutions Go Wrong*. Cambridge: Harvard University Press.

Gates Jr., H.L. 2006. On the Right Track. *Journal of the American Academy of Dermatology* 54: 1076.

Gregory, J., and G.C. Bowker. 2016. The Data Citizen, the Quantified Self, and Personal Genomics. In *Quantified: Biosensing Technologies in Everyday Life*, ed. D. Nafus, 211–226. Cambridge: MIT Press.

Greshko, M. 2016. How Many Cells Are in the Human Body–And How Many Microbes? *National Geographic.*

Gunn, A., and S.J. Pitt. 2012. Microbes as Forensic Indicators. *Tropical Biomedicine* 29: 311–330.

Haimes, E. 2006. Social and Ethical Issues in the Use of Familial Searching in Forensic Investigations: Insights from Family and Kinship Studies. *Journal of Law, Medicine and Ethics* 34: 263–276.

Hammonds, E.M. 1997. New Technologies of Race. In *Processed Lives: Gender and Technology in Everyday Life*, ed. J. Terry and M. Calvert, 107–122. London: Routledge.

Handelsman, J. 2015. Plenary Address. *International Forensics Symposium: Forensic Science Error Management.* Arlington, Virginia: National Institute of Standards and Technology.

Hedgecoe, A. 2004. *The Politics of Personalized Medicine: Pharmacogenetics in the Clinic*. New York: Cambridge University Press.

Hsu, S.S. 2012. Convicted Defendants Left Uninformed of Forensic

Flaws Found by Justice Department. *Post.* Washington.

Hutter, T., C. Gimbert, F. Bouchard, et al. 2015. Being Human Is a Gut Feeling. *Microbiome* 3: 9.

Joh, E.E. 2006. Reclaiming 'Abandoned' DNA: The Fourth Amendment and Genetic Privacy. *Northwestern Law Review* 100: 857–884.

Kahn, J. 2009. Race, Genes, and Justice: A Call to Reform the Presentation of Forensic DNA Evidence in Criminal Trials. *Brooklyn Law Review* 74: 325–375.

Khumalo, N.P. 2007. Yes, Let's Abandon Race–It Does not Accurately Correlate with Hair Form. *Journal of the American Academy of Dermatology* 56: 709–710.

Khumalo, N.P., P.T. Doe, P.R. Dawber, et al. 2000. What is Normal Black African Hair? A Light and Scanning Electron-Microscopic Study. *Journal of the American Academy of Dermatology* 43: 814–820.

Kirk, P.L. 1963. The Ontogeny of Criminalistics. *Journal of Criminal Law, Criminology, & Police Science* 54: 235–238.

Knepper, P. 1996. Race, Racism and Crime Statistics. *Southern University Law Review* 24: 71–112.

Kuiper, I. 2016. Microbial Forensics: Next-generation Sequencing as Catalyst. *EMBO Reports* 17: 1085–1087.

LaFree, G. 1995. Race and Crime Trends in the United States, 1946-1990. In *Ethnicity, Race and Crime: Perspectives across Time and Place*, ed. D.F. Hawkins, 169–193. Albany: State University of New York Press.

Landecker, H. 2015. Being and Eating: Losing Grip on the Equation. *BioSocieties* 10: 253–258.

Lax, S., J.T. Hampton-Marcell, S.M. Gibbons, et al. 2015. Forensic Analysis of the Microbiome of Phones and Shoes. *Microbiome* 3: 21.

Lithwick, D. 2015. Pseudoscience in the Witness Box. *Slate.*

Löwy, I. 2014. How Genetics Came to the Unborn: 1960–2000. *Studies in History and Philosophy of Biological and Biomedical Sciences* 47: 154–162.

Lynch, M., S.A. Cole, R. McNally, et al. 2008. *Truth Machine: The Contentious History of DNA Fingerprinting*. Chicago: University of Chicago Press.

M'charek, A. 2000. Technologies of Population: Forensic DNA Testing Practices and the Making of Differences and Similarities. *Configurations* 8: 121–158.

M'charek, A. 2008. Silent Witness, Articulate Collective: DNA Evidence and the Inference of Visible Traits. *Bioethics* 22: 519–528.

Marks, J. 2002. *What It Means to Be 98% Chimpanzee*. Berkeley: University of California Press.

Marks, J. 2015. *Tales of the Ex-Apes: How We Think about Human Evolution*. Berkeley: University of California Press.

Martin, A. 2007. The Chimera of Liberal Individualism: How Cells Became Selves in Human Clinical Genetics. *Osiris* 22: 205–222.

Martone, R. 2018. Life Experience: It's in Your DNA. *Scientific American.*

Miller, F.A. 2003. Dermatoglyphics and the Persistence of 'Mongolism': Networks of Technology, Disease and Discipline. *Social Studies of Science* 33: 75–94.

Moss, K.L. 2015. The Admissibility of TrueAllele: A Computerized DNA Interpretation System. *Washington and Lee Law Review* 72: 1033–1076.

Murphy, E.E. 2015. *Inside the Cell: The Dark Side of Forensic DNA*. New York: Nation Books.

Nothern, K. 2016. How Research into the Human Microbiome Can Be Used to Solve Crimes. *Southern California Interdisciplinary Law Journal* 25: 721–751.

Ossorio, P.N. 2006. About Face: Forensic Genetic Testing for Race and Visible Traits. *Journal of Law, Medicine and Ethics* 34: 277–292.

Paxson, H., and S. Helmreich. 2014. The Perils and Promises of Microbial Abundance: Novel Natures and Model Ecosystems, from Artisanal Cheese to Alien Seas. *Social Studies of Science* 44: 165–193.

Pollock, A. 2012. *Medicating Race: Heart Disease and Durable Preoccupations with Difference*. Durham: Duke University Press.

Possley, M. 2015. *Willie Manning*. https://www.law.umich.edu/special/exoneration/Pages/casedetail.aspx?caseid=4679.

Quammen, D. 2018. *The Tangled Tree: A Radical New History of Life*. New York: Simon & Schuster.

Rabinow, P. 1992. Galton's Regret: Of Types and Individuals. In *DNA on Trial: Genetic Identification and Criminal Justice*, ed. P.R. Billings, 5–18. Plainview, NY: Cold Spring Harbor Laboratory Press.

Ravel, J., P. Gajer, Z. Abdo, et al. 2011. Vaginal Microbiome of Reproductive-Age Women. *Proceedings of the National Academy of Sciences* 108: 4680–4687.

Reimer, N.L. 2013. The Hair Microscopy Review Project: An Historic

Breakthrough for Law Enforcement and A Daunting Challenge for the Defense Bar. *The Champion.* 16.

Rekdal, O.B. 2014. Academic Urban Legends. *Social Studies of Science* 44: 638–654.

Ross, A.A., A.C. Doxey, and J.D. Neufeld. 2017. The Skin Microbiome of Cohabiting Couples. *mSystems* 2: e00043-17.

Ross, A.H. 2011. The Concept of 'Race': A Forensic Anthropological Perspective on Human Variation. *Advances in Forensic Anthropology.* National Forensic Science Technology Center.

Salyards, J. 2015. Microbiomes Germ Clouds and the Future of DNA Jurisprudence. *Journal of Technology Law & Policy* 16: 58–75.

Sandoval-Matta, S., M. Aldana, E. Martinez-Romero, et al. 2017. The Human Microbiome and the Missing Heritability Problem. *Frontiers in Genetics* 8: 80.

Sankar, P. 2010. Forensic DNA Phenotyping: Reinforcing Race in Law Enforcement. In *What's the Use of Race? Modern Governance and the Biology of Difference*, ed. I. Whitmarsh and D.S. Jones, 49–62. Cambridge: MIT Press.

Sapp, J. 2007. The Structure of Microbial Evolutionary Theory. *Studies in History and Philosophy of Biological and Biomedical Sciences* 38: 780–795.

Scribner, H. 2015. What Your Thumb Can Tell You about Your Family History. *News.* Deseret.

Skinner, D. 2013. 'The NDNAD Has No Ability in Itself to be Discriminatory': Ethnicity and the Governance of the UK National DNA Database. *Sociology* 47: 976–992.

Sommerlund, J. 2006. Classifying Microorganisms. *Social Studies of Science* 36: 909–928.

Staubach, F., N. Buchanan, A. Köttgen, et al. 2017. Note Limitations of DNA Legislation. *Nature* 545: 30.

Steussy, E.E., J.A. Eisen, E.J. Imwinkelried, et al. 2015. Microbial Forensics: The Biggest Thing Since DNA? *UC Davis Legal Studies Research Paper Series.*

Tabassi, E. 2016. Email communication to XXXX, June 29.

Taylor, S.C. 2006. As Simple as Black and White? *Journal of the American Academy of Dermatology* 54: 1070–1071.

Thompson, W.C., L. D. Mueller, and D.E. Krane. 2012. Forensic DNA Statistics: Still Controversial in Some Cases. *The Champion.* 12–23.

Tuvel, R. 2017. Defense of Transracialism. *Hypatia* 32: 263–278.

Unaeze, J., and M. Bigby. 2006. The Frequency of Reporting of Race/Ethnicity in Case Reports. *Journal of the American Academy of Dermatology* 54: 1067–1070.

Williams, P. 2009. The Elusive Variability of Race. *GeneWatch.*

Yatsunenko, T., F.E. Rey, M.J. Manary, et al. 2012. Human Gut Microbiome Viewed Across Age and Geography. *Nature* 486: 222–227.

---

[1] The website for the NBIS states that it contains eight “utilities”: (1) A data interchange standard. (2) A fingerprint image quality algorithm. (3) A neural-network-based fingerprint pattern classification system. (4) A minutiae detector. (5) A collection of general-purpose image utilities. (6) A fingerprint matching algorithm. (7) A fingerprint segmentation algorithm for separating multiple images on a fingerprint card into separate images. (8) A spectral validation/verification metric for fingerprint images (http://www.nist.gov/itl/iad

/ig/nbis.cfm).

It does not allow a "search for individuals of European or African American ancestry," nor can it estimate the ancestry (or ethnicity) of the source of a print (Tabassi 2016).

[2] 49/117 = 41.9%. 54/126 = 42.9%. These figures represent a preferable way of reporting the data in the study than the characterization in the article:

> The article uses the total number of subjects in the study (243) as the denominator, rather than the total number of subjects classified as a particular 'race' according to total bifurcations, thus considerably understating the "error rate."

[3] On September 1, 2016, I submitted a public comment on the draft ULTR—after the deadline for public comment had closed, unfortunately—summarizing the argument made in this article. I suggested that "The DOJ should consider discontinuing the practice of attributing ancestry to hair. Alternatively, it should consult with the dermatological community on the current thinking on this issue." I make no causal claim about this action.

[4] What this last item means is not clear, and the references listed by Kuiper are no help.

[5] The 10:1 claim, however, turned out to be premature, and it has recently been revised downward significantly and has been characterized as what Rekdal (2014) would call an "academic urban legend" (Greshko 2016).

[6] In a curious coincidence, the coiner of the term "metagenonics," Jo Handelsman, went on to serve as Associate Director for Science at the White House Office of Science and Technology Policy from 2014 to 2017. In that capacity, she made some important statements about the importance of forensic reform (Handelsman 2015).

[7] Even the use of the term 'species' in this context is imprecise. Some use the term 'species or taxa' because it is incorrect or contested to refer to some forms of microbes, such as fungi or viruses, as 'species.'

[8] In another comparative microbiome study of differences between geographic groups (Yatsunenko et al. 2012), the researchers unselfconsciously mixed two geographic groups and one 'racial' group. Two groups were defined by their country of residence: "residents of rural Malawian communities, and inhabitants of USA metropolitan areas." These groups were compared to a group defined racially: "healthy Amerindians from the Amazonas of Venezuela." In the rest of the paper, the groups are describes as Malawian, Amerindian, and USA, not, for example, Malawian, Venezuelan, and American.