ABSTRACT

Despite the fact that analyses of biological populations within species have become increasingly sophisticated in recent years, the language used to describe such groups has remained static, thereby reinforcing (and reifying) outdated and inadequate models of variation such as race. This problem is further amplified when the element of human culture is introduced. Drawing on Mario Bunge’s work on technoethics, in which he asserts that technology should be subject to social and moral codes, this chapter argues that the ‘race problem’ should compel anthropologists to exploit technology in order to find workable solutions. One solution to this problem may be found in modern approaches to human skeletal variation using advanced computing techniques such as geometric morphometrics, which allows for the comparison of bone morphology in three dimensions. Coupled with more complex theories of social and genetic exchange, technologically advanced methodologies will allow us to better explore the multidimensional nature of these relationships and to understand how group formation occurs, so that a dynamic approach to classification can be developed.

INTRODUCTION

Despite the fact that the race concept has been vigorously critiqued by anthropologists for over a century, it remains both a conceptual and terminological artefact in contemporary studies of human variation. This is commonly known as the ‘race problem.’ Race not only has contentious sociological connotations, but the concept itself has been shown to be inadequate on a biological level (in terms of its classificatory or taxonomic utility), whether applied specifically to humans or to other geographically variable species. Nonetheless, the race concept continues to appear in a consistently
large minority of anthropological studies (Cartmill, 1998, p. 655). Do anthropologists therefore have an ethical obligation to abandon the race concept, or at least strive to find a workable solution? In order to answer this question, this chapter will focus on four subsidiary questions: (1) what is the role of race in anthropology; (2) is race solely an anthropological problem; (3) is there an ethical dimension to the race problem; (4) how can technology be used to solve the race problem? I will argue in this chapter that Bunge’s (1976, 1977) notion of technoethics—that technology has inherent moral codes—compels us to utilize technologically sophisticated methodology for the resolution of ethical dilemmas such as the race problem. The solution I propose is a combination of old theory and new technology, using the example of 3-dimensional (3D) imaging and geometric morphometric analysis of skeletal morphology to explore the multidimensional nature of human biological relationships, moving beyond the outdated race concept.

WHAT IS THE ROLE OF RACE IN ANTHROPOLOGY?

The race concept in general, and the use of racial classification in anthropology in particular, are well researched as theoretical problems, and remain popular topics of academic inquiry. The race debate that was initiated by such esteemed anthropologists as Ashley Montagu and Claude Levi-Strauss in the 1940s and 1950s1 in response to the rising popularity of eugenics programs worldwide, seems to have reached its climax in mid-1990s, when much of the scientific world was appalled by the research coming out of the discipline of evolutionary psychology. Evolutionary psychologists such as Herrnstein and Murray (1994) and Rushton (1995) argued that inherent intellectual capabilities could be predicted by racial group membership. Much of the criticism of the race concept at that time was aimed specifically at this type of research, which drew a direct correlation between race, intelligence, and social achievement. It was presumed that these correlations were demonstrated by both differences in average brain size between racial groups and scores on intelligence tests.

Perhaps the most significant response to this line of argumentation was Gould’s *The Mismeasure of Man* (1996), in which he attacked the fundamental premise of such evolutionary psychologists: that measurable differences in average cranial capacities and/or brain size seen between so-called racial groups were indicative of differences in cognitive and cultural capabilities. Gould collected and analysed craniological data to demonstrate that the racial differences in cranial capacities that were claimed by the early craniologist, Samuel Morton (1839), were created by numerous flaws and errors in his methodology. This struck a huge blow for racial science as it clearly demonstrated that Morton had purposely manipulated his data in order to promote socially-based theories of racial inequality. Similarly, Gould argued that evolutionary psychology is based on the same pre-conceptions found in Morton’s work—misunderstood or misapplied evolutionary theory—ignoring such issues as the relationship between cranial capacity and overall body mass, sex-based differences in cranial capacities, as well as the cultural and linguistic problems inherent in applying intelligence tests to diverse groups. Unfortunately, Gould’s work represents the pinnacle of the anti-race movement in science. The majority of critical perspectives on the science of race have served to shed light on the historical development of thought about human difference and the place of humans in nature while neglecting the development of methodological solutions. Rather than demonstrating the inadequacies of racial classification and proposing solutions for moving beyond the present state of stagnation in the race debate (Billinger, 2006), many contemporary approaches focus too narrowly on particular aspects of racism (as
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a sociological problem) as opposed to racialism (as a biological problem).

As such, race remains a reality in the evolutionary sciences, including anthropology. Surveys of the current state of theoretically-based racialism in anthropological literature demonstrate that while attitudes have shifted significantly in favour of the rejection of racial categories, the use of race as an explanatory model is persistent. This is a particular problem in physical anthropology, in which analyses of skeletal morphology are used to map relationships between human groups. Cartmill (1998) reported that articles appearing in the *American Journal of Physical Anthropology (AJPA)* dealing with human variation remained consistent over 30 years in their utilisation of the race concept, with it appearing in 34% of articles in 1965 and 35% in 1996. Lieberman et al. (2003) have challenged Cartmill’s results using a slightly different methodology, explaining that the initial attacks on the racial paradigm by Montagu in 1941 and 1942, Washburn in 1953, Livingstone in 1958, Brace in 1964, and Lieberman in 1968, saw the use of the race concept decline in the *AJPA* from 78% of articles in 1931 to 36% in 1965 and down to 28% in 1996.

Lieberman et al. (2003) also surveyed American Anthropological Association (AAA) members in 1985 and again in 1999, asking respondents to agree or disagree with the statement: “There are biological races in the species *Homo sapiens*.” In 1985, 41% of physical anthropologists surveyed disagreed with the statement, increasing to 69% in 1999. Interestingly, 53% of cultural anthropologists disagreed with the statement in 1985, with that figure rising dramatically to 80% in 1999. Striking differences were also found in physical anthropology textbooks, which predominantly presented racialist models of human variation between 1932 and 1979, but showed an almost complete abandonment of the race concept as an explanatory tool between 1980 and 1999. These results prompted Lieberman et al. (2003, p. 112) to conclude: “Data indicate that the paradigm of race has approached the point where its survival is in doubt. Even those who continue to use the concept have serious doubts about its utility.” It is also interesting to note that 42% of first authors of the included textbooks published in 1998–99 were AAA members, whereas only 4% of first authors of *AJPA* articles in 1996 were AAA members. Cartmill and Brown (2003) suggest that this difference in AAA membership indicates that the textbook authors are more representative of American anthropology, whereas the *AJPA* authorship is international; therefore, this may be more indicative of an American abandonment of the race concept, but a continued international usage.

These two studies demonstrate a significant point: a sweeping philosophical trend occurred between 1931 and 1965, in which there was a 42–43% decline in the use of racial models in the *AJPA*, followed by a period of relative stability or slight decline between 1965 and 1996. I suggest that this represents a paradigm shift in American anthropology, but a shift that has been stunted by methodological stagnancy. While the race concept itself has been questioned or abandoned, methodology has not advanced, and no workable non-racialist models for explaining human population variation yet exist. Thus, while the concept of race has changed through time, the methodologies that utilise the concept remain static. The biological aspects of this problem are further illustrated by the disjunction in results between cultural anthropologists and physical anthropologists who answered Lieberman et al.’s (2003) questionnaires. In 1985, 12% more cultural anthropologists than physical anthropologists rejected the race concept, and 11% more (even after the marked increases in rejections by both groups) in 1999.

Following Cartmill (1998), Wang et al. (2002a, 2002b) report that of 324 articles directly related to human variation printed in *Acta Anthropologica Sinica*, China’s only journal dedicated to physical anthropology, none questioned the validity of hu-
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man racial classification. Rather, several articles were mainly concerned with the biological differences among or between ‘major races.’ Wang et al. (2002b, p. 96) suggest that this focus can be considered a continuation of Weidenreich’s (1943) work in China, which emphasized regional continuity, suggesting Mongoloid roots extending back to *Homo erectus*. The irony of this focus on the so-called Mongoloid race is that studies of intra-group variation reveal that subdivision by north and south, and even further down to the ethnic or tribal level is possible (Wang et al., 2002b, p. 96). However, in China, race has proven to be a powerful political tool for uniting diverse groups within the country, since Chinese physical anthropologists have been portraying the Chinese (Mongoloid) people as a discrete biological group with a long evolutionary history.

Results of studies of Polish physical anthropologists using questionnaires based on those developed by Lieberman et al. (1989) reveal a more encouraging picture of human variation studies in central Europe. The first study, conducted in 1999, revealed that out of 55 respondents, 31% agreed with the statement “There are biological races (meaning subspecies) within the species *Homo sapiens*,” while 62% disagreed, and 7% had no opinion (Kaszycka & Štrkalj, 2002). The authors explain that there are general trends in age: Polish physical anthropologists born before, during, or shortly after World War II had a much stronger sense of race, and racial typology was taught as a major university course in some universities until the 1970s, while younger anthropologists who received more modern training were much more sceptical about the existence of biological races.

In a 2001 follow-up study, Kaszycka and Strzałko (2003) found that offering the respondents different racial concepts as options resulted in significantly different results. 75% of 100 respondents (of whom three-quarters had also responded to the 1999 survey) agreed that there are human races when allowed to choose between races defined as geographical (17%), typological (13%), populational (35%), subspecies (3%) or a combination of two of these options (7%). The rejection of race by the majority of respondents of the 1999 survey versus the much lower rate of rejection in the 2001 survey suggests that race, when construed only as a subspecies, is more problematic (at least in the Polish context) than when the term is attached to other biological concepts (Kaszycka & Štrkalj, 2002, p. 334).

The results of these studies indicate that in North America, the rejection of the race concept on an intellectual basis is more widespread amongst those who deal with it only as an organizing category (cultural anthropologists) than those who utilize race as an explanatory model (physical anthropologists) of how human groups vary biologically. In the Chinese example, race continues to be uncritically accepted by physical anthropologists, and the authors suggest that this is a result of socio-political context rather than scientific discovery. In Central Europe, the Polish studies suggest that there is general trend toward the rejection of race as a biologically meaningful concept in a strict taxonomic sense by physical anthropologists, but that it remains a persistent organizing principle in general.

In terms of anthropological methodology, critical debate over the practical usefulness of racial categorisation was most prominently played out also in the 1990s in forensic anthropological literature (Sauer, 1992; Brace, 1995; Kennedy, 1995). Although many of its practitioners contend that more advanced methods of ancestral determination are necessary (Brues, 1992; Kennedy & Chiment, 1992), and that the race debates have only served to retard such progress (Sauer, 1993), arguments that racial categories are necessary to convey socially-understandable (identifying) information are persistently made. In failing to provide progressive methods of ancestral determination, and continually relying on outdated methods of racial determination, forensic anthropologists are neglecting the scientific questions that led to
increased understanding of human variation and accuracy in their determinations.³

IS RACE SOLELY AN ANTHROPOLOGICAL PROBLEM?

The criteria used in racial classification depend upon the purpose of the classification itself (Molnar, 2002, p. 18), which may differ not only between disciplines, but also within them. We can see this in the different approaches to racial classification that are apparent between anthropological subdisciplines. Physical anthropologists are particularly influenced by both theory and method developed by colleagues in the fields of evolutionary biology and genetics, in which classification is argued to have a more objective (or pragmatic) purpose. Dunn (1951, p. 13), writing in the UNESCO publication Race and Biology, explains that “although there has been for some time a considerable measure of agreement amongst biologists about the concept of race in plants, animals and man, the word ‘race’ as used in common speech has no clear or exact meaning at all, and through frequent misuse has acquired unpleasant and distressing connotations.” While race is generally characterized as a contested term in anthropological discourse, the assumption that it has been unproblematically applied to intraspecies variation by evolutionary biologists is not at all accurate (Livingstone, 1962, p. 279; Templeton, 2002).

Biologically, the race concept has equal application to plants, animals, and humans, both philosophically and methodologically. Evolutionary biologists typically refer to subspecies when discussing intraspecies variation, with the terms ‘subspecies’ and ‘geographic race’ being used interchangeably in the taxonomic literature (Mayr, 2002). In the 1940s, Ernst Mayr, perhaps the best known evolutionary biologist of the 20th century, defined a ‘subspecies’ or ‘geographic race’ as a “geographically localized subdivision of the species, which differs genetically and taxonomically from other subdivisions of the species” (1942, p. 106). However, numerous biologists found this definition to be unsuitably ambiguous when practically applied to intraspecies variation. Individuals within geographically localized populations can easily interbreed with individuals from neighbouring populations, resulting in gradients of the characters used in various classification schemes, created by continuous genetic flow. As such, subspecies designations became increasingly problematized in the 1950s, with biologists such as Wilson and Brown (1953; Brown & Wilson, 1954) arguing that the category should be abandoned altogether due to its highly arbitrary nature.

The gradations seen in physical and/or genetic characters between geographic populations within species create a major obstacle that taxonomists have not been able to overcome. This is particularly true when attempting to classify human populations. Modern molecular genetics recognizes that when major human populations are classified as (geographic) races, the amount of genetic variation at the level of morphology, karyotype, proteins and DNA within each race is substantially greater than between races (Griffiths et al., 2000, p. 782; Keita & Kittles, 1997, p. 537; Lewontin, 1972; Mettler et al., 1988, p. 269; Templeton, 1999). This has been demonstrated time and time again in human genetics studies using various loci, from blood groups to proteins, and mtDNA (Barbujani et al., 1997; Dean et al., 1994; Excoffier et al., 1992; Latter, 1980; Lewontin, 1972; Nei & Roychoudhury, 1997; Ryman et al., 1983; Sefielstad et al., 1998), showing that so-called racial variation accounts for anywhere between 2.8% and 28.0% of human variation, depending upon the method employed, with individual variation accounting for between 74.7% and 97.8%—the vast majority of overall genetic variation (Brown & Armelagos, 2001).

In a survey of the geographic distribution of genes throughout historically-situated populations, Cavalli-Sforza et al. (1994) produced nearly
five hundred maps of numerous allele frequencies from genetic samples of individuals from nearly two thousand communities. The results reinforce earlier genetic studies and demonstrate four basic rules of human variation that are important considerations for physical anthropologists in discussing human evolution on a genetic level (Cavalli-Sforza et al., 1994):

1. Individual variation is much larger than group variation.
2. In combination with the fossil record, it can be confirmed that Africa was the birthplace of humanity (i.e., Homo sapiens). Gene frequencies indicate a large genetic difference between present-day Africans and non-Africans.
3. All Europeans are thought to be hybrid populations, with approximately 65% Asian and 35% African genes (attesting to the greater antiquity of African and Asian populations).
4. Indigenous North American populations were found to be divisible into three distinct groups by blood type, representing three separate migrations from Asia.

The surprising result of these genetic analyses was that the map of world genetic variation shows Africa on one end of the spectrum and Australian aborigines at the other. What this tells us is that patterns of adaptation follow models of clinal variation, with Australian aborigines showing the greatest genetic distance from Africans, but the most similarity in terms of phenotypic constitution (i.e. skeletal morphology, and other superficial traits such as skin colour and hair texture).

Cavalli-Sforza et al. (1994) suggest that the morphological similarity seen between indigenous African and Australian populations is the simple product of adaptation to generally similar climates in regions of sub-Saharan Africa and Australia. This highlights another fundamental problem with the subspecies concept: where Mayr suggested that subspecies should differ “genetically and taxonomically” from one another, we can see that analyses of genetic and morphological data can yield different results. In this instance, the results of Cavalli-Sforza et al.’s genetic analyses do not match the population distances derived from skeletal data. Craniometric data collected by Howells (1973, 1989, 1995) have been used to test the results of the Cavalli-Sforza et al. genetic study (Cavalli-Sforza et al., 1994:72; Cavalli-Sforza & Cavalli-Sforza, 1995, pp. 116–118), but consistently grouping Australians (and Papuans) with sub-Saharan Africans as closely cognate populations.

What this demonstrates is that subspecific or racial classification fails biologically in its assumption that evolution can be studied as (evolutionary significant) branching patterns that form phylogenetic trees. This requires that geographic groups be understood as evolutionarily significant ancestor-descendant sequences of breeding populations that share a common origin. This cladistic approach inherently favours the single-origin model of modern human dispersal: that modern humans originated as a racially undifferentiated population of modern humans in Africa approximately 200,000 years ago, migrating out of Africa and forming various (approximately) reproductively isolated breeding populations, which can be represented by branches on a phylogenetic tree. When human evolution is understood as a pattern of evolutionary branching, the terminal nodes of a phylogenetic tree represent extant (monophyletic) racial groups, whose historical lineages can be traced backwards to a common ancestor (see Andreasen, 1998, 2000, 2004; Kitcher, 2003). This can be highly problematic when two or more groups being studied have morphological similarities that are the products of environment adaptations rather than biological relationships.

A hypothetical situation can further illustrate the fundamental problems with this monophyletic assumption, which causes classification at the level of subspecies to fail: group a and group b
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are both isolated groups that traditionally lived in areas A and B respectively. Neither group has encountered the other or the other’s relatives in the past. Resources become scarce in both areas A and B, and in response, one-quarter of the families in group a decide to migrate in search of better food resources, and one-quarter of the families in group b do the same, at about the same time. Both splinter groups arrive in area C, which is equidistant to areas A and B, at about the same time, and they find adequate food resources. Both groups stay and decide to settle in area C and begin to intermix, becoming group c. Who would be the common ancestor to group c? In this case, group c would be of mixed ancestry. What if food resources were to improve over time and group c was to prosper in area C and eventually spread out and recombine with group a and/or b? Cladistic theory simply cannot adequately deal with this lineage.

This example could apply to geographic groups within any biological species but the example becomes significantly more complex when humans are brought into the equation. This evidence should lead us to conclude that racial classifications are problematic in general, but are particularly problematic when the element of human culture is introduced. Genetic evidence has demonstrated that human mobility has resulted in a high degree of genetic mixing within so-called racial groups.

Moore (1994, p. 931) uses ethnographic evidence to support the notion that human groups have complex and intertwined historical lineages rather than being unilineal ancestor-descendant sequences:

The criticisms of synthetic theory currently being developed come largely from experienced field-workers and are based on the observation that the historical scenarios postulated by synthesists—in which ethnic groups split, evolve homogeneously within ethnic boundaries, and then split again in a cladistic manner—simply do not seem familiar

ethnographically or ethnohistorically. How many tribal societies are there in which all the members are monolingual in the same language, marry only among themselves, and are homogeneous in their traditions and material culture?

Synthetic theories such as cladism, which have been used to explain relationships and geographical distributions of language, culture, and physical types are generally weak theoretically and not particularly suitable for the study of modern human groups (Moore, 1994). Moore (1994) contrasts cladistic with rhizotic theories, explaining that where cladism emphasizes historical parent-daughter (or ancestor-descendant) relationships, rhizotic theories emphasize the extent to which each human language, culture, or biological group is derived from or rooted in several ancestral groups or lineages, which he suggests is better characterized as the process of ethnogenesis.

In Moore’s (1994, p. 927) view, ethnogenesis provides a logical alternative explanation for the global distribution of languages, cultures, physical types, and archaeological traditions, and he makes the important point that ethnogenesis stands in contrast to all hierarchical taxonomies, which, regardless of their aim or theoretical bases, are clearly meant to represent cladistic relationships. Such hierarchical models are based on the presumption, in contrast to the hypothetical example above, that once a daughter species (or subspecies, race, etc.) differentiates from its parent, it will not thereafter incorporate any genetic material from its siblings (Moore, 1994, p. 928). Cladograms and other hierarchical methods of phylogenetic reconstruction require that each terminal unit of a phylogenetic tree have only one parental unit, whereas rhizograms show the convergence of diverse roots (possibly from multiple parental stock) forming hybridized or amalgamated descendant groups (Moore, 1994, p. 930).

In a survey of tribes in California, the Great Basin, Sonora, Tierra del Fuego, and Australia, Owen (1965) found that instead of ethnically
discrete bands or tribes, that multilingualism, intermarriage across supposedly profound ethnic boundaries, and enormous cultural variation was the norm. Similarly, in a study of aboriginal band types on the Canadian plains, Sharrock (1973) found that there were three common types of interethnic social organization: alliance, intermarriage and polyethnic co-residence, and fused ethnicity (Moore, 1994, p. 936). Moore (1994, p. 938) believes that the essential difficulty between cladistic and ethnogenetic theory lies in the long term stability of ethnic groups: cladistic theory requires that ethnic groups remain stable for hundreds or thousands of years, whereas ethogenesis attempts to understand the processes in which ethnic groups are transformed through time. While this contrast might not be as problematic as Moore suggests, the general point of incommensurability is that cladistics focuses on the biological fissioning of groups, whereas ethnogenetic theory deals with transition, which in many cases involves the rearrangement or fusion of groups. Traditional methods of biological classification simply have not accounted for the complexities of population biology at the local level, looking at how social networks constrain the flow of genes within and between biological groups.

IS THERE AN ETHICAL DIMENSION TO THE RACE PROBLEM?

Although we know that racial classification has limited, if any, biological utility, we have no workable models to replace race-based models, which remain a basic starting point for discussions of intraspecies variation. A vast but underappreciated body of literature critical of biological subspecies classification has demonstrated the pragmatic problems of such classification schemes: that they are arbitrary due to the overlapping of morphological and/or genetic traits, which themselves show incongruent or inconsistent microevolutionary patterns. Nonetheless, the existing voluminous literature on race and/or racism is lacking due to the almost exclusive focus on the historical development of the race concept rather than proposing alternative methods or taxonomic schemes. As a result, even in light of new scientific evidence, perspectives on human variation continue to be structured within the racial paradigm.

Since race continues to be used as an explanatory model for human evolutionary schemes, the perpetuation of racial language gives the illusion that the race concept itself has real biological meaning. Thus, the race concept remains the basic starting point in discussions of human variation, despite ever-increasing evidence demonstrating the inability of the race concept to account for the patterns of variation seen below the level of species. In this respect, Stoler (1997, p. 198) explains that there are “fixities and fluidities” in racial discourse: despite our demonstration of the complexities of the patterns of human evolution and population biology, simple racial language has remained relatively static in our discussions of such patterns. As such, surveys of literature dealing with the changing perception of race as a biological concept provide significant proof that racial categories are fluid and not fixed, which confirms that “they can and should be undone” (Stoler, 1997, p. 198, emphasis added).

This is the ethical aspect of my argument: the more we understand about population biology, the more apparent it becomes that the race concept is fundamentally flawed. The fact that the race concept has been inaccurately perpetuated for decades, provides absolute evidence that we have an ethical obligation to find a real solution, since we are well aware of the atrocities done around the world in the name of racism. While I do not equate racialism with racism, I believe that technological advancement in the analysis of human biological variation is giving us the tools to build workable non-racial models of human variation which, when widely understood, will have obvious profoundly positive results for anti-racism movements. Such a movement will find its legitimacy in the fact that it is rooted in basic biology, and not as an explicit attack on sociological race categories.
In terms of the relationship between technology and the ethical problems inherent in using the traditional race concept, the sparse but important literature on technoethics provides an important basis for moving forward in this discussion. For Bunge (1976, p. 155), the term ‘technology’ has broad and encompassing applications, extending to material, social, conceptual, and general technologies. For the purposes of this discussion, material technology (including physical, chemical and biological science), as well as social technology (including economic, psychological, and sociological science), will be the main reference, since they are implicitly tied to the discipline of anthropology. According to Bunge (1977, p. 100), “the technologist must be held not only technically but also morally responsible for whatever he designs or executes: not only should his artifacts be optimally efficient but, far from being harmful, they should be beneficial, and not only in the short run but also in the long term.”

This is where ethics compels us to utilise biotechnology as a tool for developing new understandings of population biology. Racial models are neither optimally efficient nor are they beneficial from a biological perspective, since they simply do not work and only serve to mischaracterize the patterns of biological variation seen within geographically diverse species. In light of this technoethical argument, any researcher who continues to use outdated models despite the availability of new technologies allowing them to explore progressive theories and methods is doing a disservice to their discipline, and the scientific community as a whole.

Technology should be subjected to moral and social controls (Bunge, 1977, p. 106). We have seen the negative personal and societal effects of the misuses of biotechnology which led to eugenic movements in Europe and North American starting in the 1930s, and which ultimately lead the Nazi Holocaust in the 1940s. In Western Canada, eugenic sterilization laws were in place from 1928 to 1972, resulting in a total of 2,832 adults and children being sterilized by government order (Wahlsten, 1997). Such atrocities were due to the lack of moral and social controls on the use of technology—even though there was a societal belief that technology was being used for the betterment of society, individual rights were widely ignored.

The technoethical approach suggests not that we suppress scientific progress because of societal pressures, but that the misuses of good technology be corrected by promoting better technology and rendering it morally and socially sensitive. As such, the technologist must be responsible not only to his or her profession, but to all those who might be affected by his or her work. Furthermore, a technologist who strives to make a contribution to alleviating social ills (including public misunderstandings of science, as in the example of the perpetuation of racial language) or to improving the quality of life is a public benefactor (Bunge, 1977, pp. 106–107).

The race problem remains unresolved because it is far too complex to be resolved by any single technologist, or group of technologists within a particular discipline, which has allowed simple answers to prevail. Racial models are remarkably simple in their explanatory powers and, as such, have general appeal in terms of relaying conceptual information to wide audiences. We are now well poised, in an age where interdisciplinary research is highly valued academically, to provide a comprehensive response to the race problem. According to Bunge (1977, p. 107), “Because no single specialist can cope with all of the many-sided and complex problems posed by large-scale technological projects, these should be entrusted to teams of experts in various fields, including applied social scientists.” Similarly, and specifically in the context of the race problem, Eze asks (2001, pp. 29–30): “If geneticists have shown that ‘race’ is not a useful concept, it may be up to the social scientists to invent new ways of making this development available to the general culture.” Anthropologists, who deal with both the social and
biological realms, are perfectly placed to make perhaps the greatest contribution to redefining human variation. As a discipline that has actively participated in perpetuating the myth of human races, this should be an obligatory goal.

If the ‘race problem’ in anthropology can be redefined rather than simply re-articulated, then new ways of exploring human variation can be developed. Histories of racial thought have filled innumerable volumes, and they have served us well, but such treatments (Billinger, 2000; Brace, 2005; Smedley, 1999) should now simply provide a background from which a new line of argumentation will take shape. The goal, then, is to bring together progressive theory and method in the analysis of human biological variation. This should not be specific to any particular anthropological subdiscipline, but a concerted effort by all anthropologists along with our colleagues in biology, medicine, history, philosophy, sociology, political science and other related disciplines.

FUTURE TRENDS: CAN TECHNOLOGY BE USED TO SOLVE THE RACE PROBLEM?

In terms of anthropologists’ approaches to the analysis of human biological relationships, there has been a rapid evolution in the technological sophistication of methodological tools. However, traditional theories of cultural and ethnic interaction typically tend to be cladistic in nature, the problems with which have already been discussed. As such, the reliance on racial classification has resulted in the relationship between ethnicity and human biology being treated in far too simplistic a manner (see Billinger, 2007a, 2007b, 2006; Crews & Bindon, 1991; Chapman, 1993; Montagu, 1997). The complex system of ethnic relations proposed by Moore, as introduced earlier, is actually derived from a relatively old and underappreciated theory of ethnic biology that can be traced back over a century.

Deniker (1900) first introduced the idea that human biology is ethnically structured, and this notion was more clearly elaborated by Huxley and Haddon (1935). Although this ethnic concept was adapted by Ashley Montagu as a genetical theory in 1942 (which was further developed by Hulse in 1969), little is understood about how it can be applied to re-building human taxonomy. Moore’s critique builds on this body of work, and provides many facets from which his cultural approach can be modified into a strong theoretical basis for new methodological strategies. If we can understand how to conceptualize the flow and/or isolation of genes and the relation to endogamous or exogamous practices, and human mobility through time, then physical anthropologists can move much closer toward understanding both the patterns and processes involved in creating the morphological variations of prehistoric, historic, and contemporary populations. This should form one part of the proposed interdisciplinary project.

I want to now use the example of how technological progress in the methodology employed by physical anthropologists can fuel this project, adapting multidimensional techniques for exploring biological patterns to fit the multidimensional theory of ethnic biology.

Perhaps the most diagnostic area for study of human morphology and phylogeny is the skull. Anatomically modern humans show considerable geographic variation in the form of the facial skeleton. Howells (1973, 1989, 1995) was a pioneer in this regard, publishing a vast global data set for use in analyses of global and regional variation in craniofacial morphology. Howells was interested in taxonomy, but saw it not as a means to an end, but rather as tool for comparative description: as an exploration of genetic populations rather than racial types. As we will see, the primary factors determining the outcome of such analyses are the types of data available and the types of analysis applied to them.

For instance, Billinger (2006, Chapter 5) uses Howells’ (1973, 1989) craniometric data,
supplemented with further data for North and South American indigenous populations, to test
the craniometric relationships of known world populations. Initially, a univariate method was
employed in which each of the individual cranial measurements was treated by Mayr’s (1969, pp.
187–197) coefficient of difference (CD), a simple calculation that incorporates the mean values and
standard deviations of each trait for each group. Applying this measure to the data sheds light on
whether, using the selected craniometric traits, the groups used in the analysis are differentiated
enough to form a subspecies according to Mayr’s definition. Accordingly, a CD value of 1.28 re-
veals that 90% of individuals in population a are different from 90% of individuals in population

### Table 1. Average coefficient of difference data matrix for group-by-group comparisons (from Billinger, 2006, p. 234)

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*Average calculated by taking the sum of the correlation coefficients for each group-by-group comparison for each cranio-
metric trait.
b, which is equal to 75 percent of individuals from population a differing from all individuals of population b.

Table 1 gives the results of this analysis using group-by-group comparisons, with each result being multiplied by 10. The CD value of 1.28 should also be multiplied by the same factor. Therefore, results over 12.80 show a level of differentiation over 75 percent. Based on the traits used, only the comparison of groups on the extremities of the geographic range of populations give results over 12.80, those being Siberia-Bushman, Buriat-Andaman, Siberia-Andaman, and NWT-Andaman. The remaining group-by-group comparisons show a pattern of intergradations. The relationships between each of groups based on the results of the CD were treated by cluster analysis (Figure 1) and multidimensional scaling (Figure 2) for visualisation. The results seen are not unexpected based on ‘common sense’ racial categories derived from skin colour (Andreasen, 2004, pp. 428–430).

However, it should be noted that this method calculates the mean differences between each measurement and, as such, it represents a single correlation coefficient calculated from average differences in size. For taxonomic purposes, shape is considered to be of significantly higher value than size (Corruccini, 1973, 1987). According to Howells (1973, p. 3):

*Populations have been compared (normally two populations at a time) in one measurement at a time. Such estimates of difference, or distance, do not, however, allow consideration of the shape of the skull as a whole, as this is expressed by the relations between measurements (though of course two measurements have been commonly related in a ratio or index). As a result, there had been little consideration as to whether the measurements in*
Figure 2. Multidimensional scaling of coefficient of difference results for each group in the global sample (from Billinger, 2006, p. 238)

![Multidimensional scaling](image)

Figure 3. Cluster analysis dendrogram (average linkage method) plotting Penrose’s shape distance for each group in the global sample (from Billinger, 2006, p. 249)

![Cluster analysis dendrogram](image)

use do in fact reflect the total configuration of the skull adequately for taxonomic purposes (although traditional lists naturally have attempted to cover many aspects of the skull and face).

Methods of multivariate analysis such as those developed by Penrose (1954) allow for the study of shape variation by accounting for the relations between measurements, and represent a great advancement over univariate analyses.

The second step in this study was then to apply a multivariate method for analysing shape. Figure 3 gives the resulting dendrograms created by cluster analysis of shape coefficients for each group, obtained using Penrose’s shape distance calculations for the same craniometric traits used in the univariate analysis. Figure 4 plots the shape coefficients derived from the Penrose method by multidimensional scaling. Note the discontinuities seen between the dendrograms and multidimensional scaling plots for the multivariate and univariate analyses—the difference between size and shape-based data is readily apparent.

This picture becomes increasingly complicated when attempting to place an individual into the scheme of world-wide variation for the purposes of forensic ancestral determination. In this instance, the aim was to determine the biological ancestry of the ‘Kennewick Man’ skull.11 The results show that the Kennewick skull groups with northern (Arctic) North American indigenous populations when compared to globally-distributed populations. However, when the Kennewick skull is compared only to regional American indigenous populations,12 also using Penrose’s shape distance, a very different (and more complex) picture of biological relationships appears (Figures 5 and 6).

It should be kept in mind that biological distance calculated from morphological data does not give an accurate approximation of genetic distance—it gives only the phenetic distance between the average values for each population—which is problematic because biological distance is the

Figure 4. Multidimensional scaling of Penrose’s shape distance for each group in the global sample (from Billinger, 2006, p. 250)
Figure 5. Cluster analysis dendrogram (average linkage method) plotting Penrose’s shape distance for each group in the sample of regional American indigenous populations (from Billinger, 2006, p. 256)

Figure 6. Multidimensional scaling of Penrose’s shape distance for each group in the sample of regional American indigenous populations (from Billinger, 2006, p. 257)
main factor in determining taxonomic groups and hierarchical ordering. The calculation of morphological distance is entirely dependant upon the number and type of morphological features used for the analysis, and the number of populations included. These considerations are often dependant upon the availability of published data, which may be limited. Furthermore, the ordering of the cluster analysis can only be accurately interpreted in the presence of reliable historical data on the groups used in the analysis and should not be taken as a true representation of the cladistic affinity of populations, only as an idealized model.

Standard craniometric methods do provide interesting results for studying the patterns of evolution and speciation—and the transition from univariate to multivariate analyses was a huge leap forward—but greater potential lies in moving beyond simple linear craniometric morphometrics into ‘modern morphometrics’ (Slice, 2005). Advancements in three-dimensional (3D) digital imaging provide new opportunities for progressive study of size and shape space through geometric morphometrics. Comparison of geometric morphometric coordinate data to traditional multivariate morphometrics show that although traditional caliper measurements can provide adequate results (Reig, 1996), 3D data produces more powerful statistics with higher correlation and lower probabilities of spurious results, providing a clearer picture of variation with more distinct clusters (McKeown & Jantz, 2005).

Geometric morphometrics yield highly visual and readily interpretable results (Collard & O’Higgins, 2001; Vidarsdottir et al., 2002), offering multivariate techniques that cover all possible shape measurements of a region separately, exploring the patterns of their correlations with all possible shape measures of other regions in one single computation. Further, such analysis allows for the comparison of two distinct integrative factors—ontogeny and phylogeny—as they apply to a shared regionalization within samples of modern Homo sapiens or prehistoric hominoid crania (Bookstein et al., 2003). Geometric morphometrics provides insight into the usefulness of various traits for taxonomic purposes through the analysis of allometric (size and shape covariation) and ontogenetic trajectories for determining homology (Bastir & Rosas, 2004; Humphries, 2002; Lieberman, 2000; Mitteroecker et al., 2004). Looking at homologies between species may provide the key to isolating important microevolutionary traits within species. These trajectories also give insight into the effects of age and sex related variation in population data.

There remain, however, two fundamental questions to be asked regarding morphometric analyses and the relationship between continuously distributed morphological traits and their phylogenetic importance: can continuously distributed variables be used to make phylogenetic inferences, and can morphometric variables be used to test phylogenetic hypotheses (MacLeod & Forey, 2002)? Although the statistical complexity of shape distances lead Rohlf and Marcus (1993) to caution against assumptions that they can be safely used as measures of taxonomic distance, numerous recent studies attest to the potential for phylogenetic reconstructions using geometric morphometric data in modern humans and other hominid species. However, no studies have yet provided conclusive results. Bookstein et al. (1999) believe that refinements in methods of morphometric analysis will lead to new perspectives on phylogenetic and functional relationships among and within hominid species. The fact that 3D coordinate data collection has become much more feasible with the development of more economical portable digitizers should result in a rapid increase in the availability of data to answer these phylogenetic questions.

Neanderthals provide an especially interesting case for studying inter and intra-species variation, since it is only recently that it has been demonstrated both (geometric) morphometrically
(Harvati, 2004; Harvati et al., 2004) and through mitochondrial DNA (Currat & Excoffier, 2004; Serre et al., 2004)\(^{13}\) that the Neanderthals (*Homo neanderthalensis*) represent a distinct species and are not a subspecies of *Homo sapiens*, following years of bitter debate (Stringer, 2002).

Such phylogenetic analysis may result in immediate practical advancements as well. The results of these analyses will be important in the context of forensic anthropology, particularly in dealing with subadult forensic remains. There is, at present, no way of reliably assigning subadult remains to ancestral groups based on skeletal morphology (Vidarsdottir et al., 2002). Bringing forensic anthropological methods into the realm of human variation studies will be a benefit not only for forensic identification purposes, but also for the perceived misrepresentation of human biological patterns by forensic anthropologists.

**CONCLUSION**

Methodology must be developed on a strong theoretical basis, and as such, the methods of phylogenetic reconstruction will continue to suffer if they remain focused on unilinear patterns of evolutionary branching. Humans do not follow these simple theoretical patterns. I have argued elsewhere (Billinger, 2006) that: (a) humans follow ethnogenetic processes, and the study of these processes requires a much higher level of theoretical sophistication to decode the multiple and interlocking causation of patterns by which humans have grouped together— factors such as language, political divisions, religion, etc., not just by geography; (b) humans form ethnic groups, and such groups are fluid and historically contingent; (c) the degree to which physically or genetically distinguishable groups form is unlikely to be near a level warranting subspecies designations. This chapter has provided a summary of these arguments intended to reignite the race debate in the context of technoethical considerations. That the fluid biosocial condition outlined in this chapter exists only in human populations is enough to dismiss the notion of race at least in reference to modern humans, and likely in general biological application. The main challenge it presents is that it is simply not enough to insist on the substitution of racial terminology for neutral referents, but a wholesale re-evaluation of human taxonomy may be necessary to get at the true patterns of variation.

Eze (2001) quite correctly suggests that social scientists should assume the role of making genetic refutations of the race concept accessible to the general public. I believe that the key to destroying racist thought is by dismantling its biological basis, which has served only to reify the race concept and obscure our understanding of the nature of group biology. However, this will not eliminate racism in its social manifestation(s). In order to adequately tackle this problem, we might find a solution in the language of human rights, which is fundamentally tied to the idea of human uniqueness as our unifying feature. This perspective implicitly ties humans’ social existence to our basically biology, and provides further evidence that there is an inherent ethical argument against the perpetuation of the race problem.

Ignatieff (2000, pp. 39–40) suggests that human rights derive their force in our conscience from the sense that we all belong to a single species, and that we can recognize ourselves in every other human being we meet. In other words, “to recognize and respect a stranger is to recognize and respect ourselves,” since having an intense sense of one’s own worth is a precondition for recognizing the worth of others. Ignatieff (2000, p. 41) believes that to commit ourselves to this way of thinking about the relationship between human equality and human difference—that human equality actually manifests itself in our differences—is to understand our commonalities as human beings in the very way we differentiate ourselves (as peoples, as communities, and as individuals). As such, we humans are not simply
biologically variable, but we also display astonishingly different ways in which we decorate, adorn, perfume, and costume our bodies in order to assert our identities as individuals and members of tribes or communities. According to Ignatieff (2000, p. 53):

Marx was simply wrong when he claimed, in 1843, that rights talk reduces us all to abstract, equal individuals, held together by our biological sameness. The claim I would make is the reverse. If the supreme value that rights seek to protect is human agency, then the chief expression of human agency is difference, the ceaseless elaboration of disguises, affirmations, identities, and claims, at once individually and collectively. To believe in rights is to believe in defending difference.

It is this kind of inclusive thinking that should push anthropologists to lead the way toward progressive approaches to the study of human cultural and biological relationships. However, race and racism should not be confused with one another, and indictments against the race concept should not be based on a rejection of racist thought, but must be grounded in solid biological fact. The inconsistencies seen in various types of biological data should stimulate us to rethink the ways in which we categorize human groups. Once we have found a way to move beyond the racial paradigm in terms of the ways in which we conceive of human biological relationships, then we can start to rethink the ways in which we treat others not only as members of social or biological groups, but as individuals.

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A Technoethical Approach to the Race Problem in Anthropology


A Technoethical Approach to the Race Problem in Anthropology

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KEY TERMS

Allele Frequencies: A measure of the relative frequency of an allele (one of two or more alternative forms of a gene, which control the same inherited characteristic) on a genetic locus in a population.
Cladistic: System of biological classification that groups organisms on the basis of observed shared characteristics in order to deduce the common ancestors.

Ethnogenesis: The creation of a new ethnic group identity through the separation or combination of existing groups.

Homology: Similar evolutionary characteristics that are a product of descent from a common ancestor rather than a product of a similar environment.

Morphometrics: Measurement of skeletal morphological features, captured using calipers or 3D imaging.

Ontogeny: The development of an individual organism from a fertilized ovum to maturity, as contrasted with the development of a group or species (phylogeny).

Phenetic: System of biological classification based on the quantification of overall physical similarities between organisms rather than on their genetic or developmental relationships.

Phylogenetic: The development over time of a species, genus, or group, as contrasted with the development of an individual (ontogeny).

Rhizotic: System of classification that emphasizes the extent to which each element (e.g., human language, culture, or population) is considered to be derived from or rooted in several different antecedent groups.

Skeletal Morphology: The form and structure of the skeletal system and its individual elements.

Taxonomic: Relating to the practice or principles of systematic classification.

ENDNOTES

1. According to Montagu (1941, p. 243), “The idea of race is one of the most fundamental if not the most fundamental of the concepts with which the anthropologist has habitually worked.” Furthermore, Levi-Strauss (1958, p. 8) asserted, “The original sin of anthropology … consists in its confusion of the idea of race, in the purely biological sense (assuming that there is any factual basis for the idea, even in this limited field—which is disputed by modern genetics), with the sociological and psychological production of human civilizations.”

2. See also Teschler-Nicola (2004) for a critical analysis of National Socialist race theory in Austria and central Europe, which also demonstrates the changing perceptions of human classification in the post-war period.

3. To add to this problem, popular fictional novels and crime drama television programs have provided a wildly inaccurate image of the techniques uses by anthropologists in the analysis of biological variation and forensic identification.

4. Clinal variation is the graded intensity of adaptive traits according to geographic distance. Thus, genetic distance and geographic distance are highly correlated (Templeton, 1999, p. 639).

5. Patterns of clinal variation follow the so-called Bergmann-Allen rules. Bergmann’s rule explains that in warm-blooded species, as groups move geographically towards more polar regions, overall body mass is expected to increase. Similarly, Allen’s rule explains that as groups move towards warmer (equatorial) geographic areas, the length of the extremities increases. In recent human groups, this clinal variation shows a very strong negative correlation (-.60) between body mass and mean annual temperature (Marks, 1995; Molnar, 2002, pp. 199–201).
Conflicting human evolutionary models remain unresolved in this respect (see Billinger, 2006, Chapter 2; Collard & Wood, 2000; Hawks & Wolpoff, 2003). The cladistic approach inherently favours the branching pattern of the Out-of-Africa hypothesis of human origins (Stringer, 1996; Templeton, 2002) over the Multiregional Continuity Model (Brace, 1996, p. 221; see also Wolpoff et al., 1984; Wolpoff & Caspari, 1997, 2000). For a discussion of the competing models of human evolution and phylogeny and how they relate to race or subspecies, see particularly Cartmill (1997) and Billinger (2000, Chapter 3).

Montagu (1942, p. 375) was the only one of these authors to offer a definition of an ethnic group: “[O]ne of a number of populations comprising the single species Homo sapiens, which individually maintain their differences, physical and cultural, by means of isolating mechanisms such as geographic and social barriers. These differences will vary as the power of the geographic and social barriers, acting upon the original genetic differences, vary. Where these barriers are of low power neighboring groups will intergrade, or hybridize, with one another. Where these barriers are of high power such ethnic groups will tend to remain distinct or replace each other geographically or ecologically.”

The populations chosen by Howells (1973, 1989) represent 6 major groups: Europe (Norse, Zalavar, Berg), Africa (Egypt, Teita, Dogon, Zulu, Bushman), Australo-Melanesia (Australia, Tasmania, Tolai), Far East (North Japan, South Japan, Hainan Island), America (Arikara, Peru), and Other (Andaman, Ainu, Buriat, Eskimo). Howells’ American data is supplemented by data for Navajo, Mexico, as well as Arctic (Siberia, Northwest Territories [NWT]), and the “Kennewick Man” skull (see Billinger, 2006, p. 149). Only male data has been included here. Female data show similar patterns. Please refer to Billinger (2006) for the complete analysis.

10 craniofacial traits were used at this stage of the analysis: GOL (maximum cranial length), XCB (maximum cranial breadth), ZYB (bizygomatic diameter), BBH (basion-bregma height), MAB (maxillo-alveolar breadth), NPH (upper facial height), NLH (nasal height), NLB (nasal breadth), OBB (orbital breadth), and OBH (orbital height).

Mayr developed the CD as a method to quantify difference in response to critiques of his definition of subspecies as arbitrary. The “Kennewick Man” skull, found on the shores of the Columbia River in Washington State, is one of the oldest known cranial specimens in North America, at 9500–9000 years old (Chatters, 2000; McManamon, 2000). This specimen is particularly interesting for this study because the assignment of ancestral affinity to this skull has been a highly contentious endeavour (Thomas, 2000; Morell, 1998).

American/Arctic data (Arikara, Peru Navajo, Mexico, Siberia, Northwest Territories [NWT], Ainu, Buriat, Eskimo, Kennewick) has further been supplemented with the addition of Northwest Coast [NWC], Haida, Tsimshian, Greenville, Prince Rupert Harbour [PRH], Namu, Blue Jackets Creek [BJC], and a Paleoindian sample. Only 4 craniofacial traits were used at this stage of analysis, based on the availability of published data: GOL, XCB, ZYB, and NPH (see Billinger, 2006, p. 253).

Templeton (2005, p. 52) finds the designation of Neanderthals as a separate species based on mtDNA evidence to be questionable, arguing that genetic, fossil, and archaeological data should be integrated in order to draw significant conclusions about evolutionary models.