EXPLORATIONS: AN OPEN INVITATION TO BIOLOGICAL ANTHROPOLOGY, 2ND EDITION

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13.

RACE AND HUMAN VARIATION

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This chapter is a revision from "Chapter 13: Race and Human Variation" by Michael B. C. Rivera. In Explorations: An Open Invitation to Biological Anthropology, first edition, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff, which is licensed under CC BY-NC 4.0.

Learning Objectives

- Illustrate the troubling history of "race" concepts.
- Explain human variation and evolution as the thematic roots of biological anthropology as a discipline.
- Critique earlier "race" concepts based on a contemporary understanding of the apportionment of human genetic variation.
- Explain how biological variation in humans is distributed clinally and in accordance with both isolation-by-distance and Out-of-Africa models.
- Identify phenotypic traits that reflect selective and neutral evolution.
- Extend this more-nuanced view of human variation to today's research, the implications for biomedical studies, applications in forensic anthropology, and other social/cultural/political concerns.

Humans exhibit biological variation. Humans also have a universal desire to categorize other humans in order to make sense of the world around them. Since the birth of the discipline of **biological anthropology** (or **physical anthropology**, as referred to back then), we have been interested in studying how humans vary biologically and what the sources of this variation are. Before we tackle these big problems, first consider this question: Why *should* we study human variation?

There are certainly academic reasons for studying human variation. First, it is highly interesting and important to consider the evolution of our species (see Chapters 9–12) and how our biological variation may be similar to (or different from) that of other species (e.g., other primates and apes; see Chapters 5 and 6). Second, anthropologists study modern human variation to understand how different biological traits developed over evolutionary time (see Figure 13.1). Suppose we are able to grasp the evolutionary processes that produce the differences in biology, physiology, body chemistry, behavior, and culture (**human variation**). In that case, we can make more accurate inferences about evolution and adaptation among our hominin ancestors, complementing our study of fossil evidence and the archaeological record. Third, as will be discussed in more detail later on, it is important to consider that biological variation among humans has biomedical, forensic, and sociopolitical implications. For these reasons, the study of human variation and evolution has formed the basis of anthropological inquiry for centuries and continues to be a major source of intrigue and inspiration for scientific research conducted today.

An even-more-important role of the biological anthropologist is to improve public understanding of human evolution and variation—outside of academic circles. Terms such as **race** and **ethnicity** are used in everyday conversations and in formal settings within and outside academia. The division of humankind into smaller, discrete categories is a regular occurrence in day-to-day life. This can be seen regularly when governments acquire census data with a heading like "geographic origin" or "ethnicity." Furthermore, such checkboxes and drop-down lists are commonly seen as part of the identifying information required for surveys and job applications.

According to professors of anthropology, ethnic studies, and sociology, race is often understood as rooted in biological differences, ranging from such familiar traits as skin color or eye shape to variations at the genetic level. However, race can also be studied as an "ideological construct" that goes beyond biological and genetic bases (Fuentes et al. 2019), at different times relating to our ethnicities, languages, religious beliefs, and cultural practices. Sometimes people associate racial identity with the concept of socioeconomic status or position, or they link ideas about race to what passport someone has, how long they have been in a country, or how well they have "integrated" into a population.

Figure 13.1: Humans are culturally diverse (in that cultural differences contribute to a great degree of variation between individuals), but those shown are genetically undiverse. (Top left: Hadzabe members in Tanzania; top right: Inuit family; bottom left: Andean man in Peru; bottom right: English woman.) Credit: Humans are diverse (Figure 13.1) original to Explorations: An Open Invitation to Biological Anthropology by Michael Rivera is a collective work under a CC BY-NC-SA 4.0 license. [Includes Tanzania – Hadzabe hunter (14533536392) by A_Peach, CC BY 2.0; Inuit-Kleidung 1 by Ansgar Walk, CC BY-SA 3.0; Andean Man by Cacophony, CC BY-SA 4.0; Jane Goodall GM by Floatjon, CC BY-SA 3.0.

Some of these ideas about ethnicity have huge social and political impacts, and notions of race have been part of the motivation behind various forms of racism and prejudice today, as well as many wars and genocides throughout history. **Racism** manifests in many ways—from instances of bullying between kids on school playgrounds to underpaid minorities in the workforce, and from verbal abuse hurled at people of color to violent physical behaviors against those of a certain race. **Prejudice** can be characterized as negative views toward another group based on some perceived characteristic that makes all members of that group worthy of disdain, disrespect, or exclusion (not solely along racial lines but also according to [dis]ability, gender, sexual orientation, or socioeconomic background, for example). According to Shay-Akil McLean (2014), "Racism is not something particular to the United States and race is not the same everywhere in the world. Racial categories serve particular contextual purposes depending on the society they are used in, but generally follow the base logic of the supremacy of one type of human body over all others (ordering these human bodies in a hierarchical fashion)." Choosing which biological or nonbiological features to use when discussing race is always a social process (Omi and Winant 2014). Race concepts have no validity to them unless people continue to use them in their daily lives—and, in the worst cases, to use them to justify racist behaviors and problematic ideas about racial difference or superiority/inferiority. Recent work in anthropological genetics has revealed the similarities amongst humans on a molecular level and the relatively few differences that exist between populations (Omi and Winant 2014).

The role of the biological anthropologist becomes crucial in the public sphere, because we may be able to debunk myths surrounding human variation and shed light, for the nonanthropologists around us, on how human variation is actually distributed worldwide (see Figure 13.1). Rooted in scientific observations, our work can help nonanthropologists recognize how common ideas about "race" often have no biological or genetic basis. Many anthropologists work hard to educate students on the history of where race concepts come from, why and how they last in public consciousness, and how we become more conscious of racial issues and the need to fight against racism in our societies. Throughout this chapter, I will highlight how humans cannot actually be divided into discrete "races," because most traits vary on a continuous basis and human biology is, in fact, very **homogenous** compared to the greater genetic variation we observe in closely related species. Molecular anthropology, or anthropological genetics, continues to add new layers to our understanding of human biological variation and the evolutionary processes that gave rise to the contemporary patterns of human variation. The study of human variation has not always been unbiased, and thinkers and scientists have always worked in their particular sociohistorical context. For this reason, this chapter opens with a brief overview of race concepts throughout history, many of which relied on unethical and unscientific notions about different human groups.

Special Topic: My Experiences as an Asian Academic

Figure 13.2: Michael B. C. Rivera in Hong Kong. Credit: Michael B. C. Rivera in Hong Kong original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) is under a CC BY-NC 4.0 License.

My name is Michael, and I am a biological anthropologist and archaeologist (Figure 13.2). What strikes me as most interesting to investigate is human biological variation today and the study of past human evolution. For instance, some of my research on ancient coastal populations has revealed positive effects of coastal living on dietary health and many unique adaptations in bones and teeth when living near rivers and beaches. I love talking to students and nonscientists about bioanthropologists' work, through teaching, science communication events, and writing book chapters like this one. I grew up in Hong Kong, a city in southern China. My father is from the Philippines and my mother is from Hong Kong, which makes me a mixed Filipino-Chinese academic. Growing up, I noticed that people came in all shapes, sizes, and colors. My life is very different now in that I have gained the expertise to explain those differences, and I feel a great responsibility to guide those new to anthropology toward their own understandings of diversity.

Biological anthropology is not taught extensively in Hong Kong, so I moved to the United Kingdom to earn my bachelor's, master's, and doctorate degrees. It was fascinating to me that we could answer important questions about human variation and history using scientific methods. However, I did not have many minority academic role models to look up to while I was at university. My department was made up almost exclusively of white westerner faculty, and it was hard to imagine I could one day get a job at these western institutions. While pursuing my degrees, I also remember several instances of my research contributions being overlooked or dismissed. Sometimes professors and fellow students would make racist comments toward Asian scholars (including me) and other Black, Indigenous and researchers of color, making us greatly uncomfortable in those spaces. When one of us would work up the courage to tell university leaders our experiences of being stereotyped, dismissed, or insulted, we received little support and were further excluded from research and teaching activities. This is a common experience for Black, Indigenous, and other people of color who pursue biological anthropology, and we face the difficult choice between leaving the field or bearing with such unsafe spaces.

It became important to me at that time to find other academics of color with whom to share experiences and form community. I feel inspired by all my colleagues who advocate for greater representation and diversity in universities (whether they are minority academics or not). I admire many of my fellow researchers who are underrepresented and do a great job of representing minority groups through their cutting-edge research and quality teaching at the undergraduate and graduate levels. Although I no longer work in the West, it has remained my great hope that those in the West and the "Global North" will continue to improve university culture, and I support any efforts there to welcome all scholars.

My current work is based in Hong Kong, where I am deeply dedicated to helping develop biological anthropology in East and Southeast Asia and promoting research from our home regions on the international scene. The study of anthropology really highlights how we share a common humanity and history. Being somebody who is "mixed race" and Asian likely played a key role in steering me toward the study of human variation. As this chapter hopefully shows, there is a lot to discuss about race and ethnicity regarding the discipline's history and current understandings of **human diversity**. Some scientific and technological advancements today are misused for reasons to do with money, politics, or the continuation of antiquated ideas. It is my belief, alongside many of my friends and fellow anthropologists, that science should be more about empathy toward all members of our species and contributing to the intellectual and technological nourishment of society. After speaking to many members of the public, as well as my own undergraduate students, I have received lovely messages from other individuals of color expressing thanks and appreciation for my presence and understanding as a minority scientist and mentor figure. Anthropology needs much more

diversity as well as to make room for those who have traveled different routes into the discipline. All paths taken into anthropology are valid and valuable. I would encourage everyone to study anthropology—it is a field for understanding and celebrating the intricacies of human diversity.

The History of "Race" Concepts

"Race" in the Classical Era

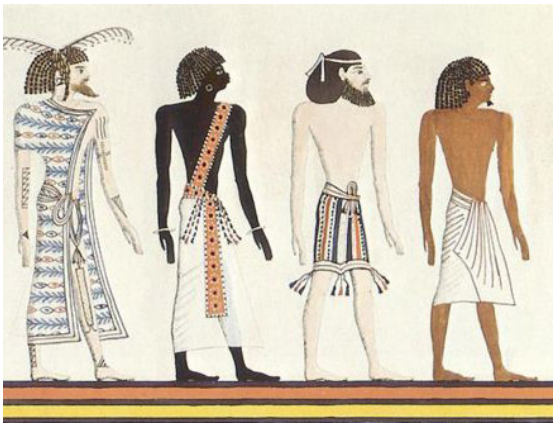


Figure 13.3: (From left to right) Depicting a Berber (Libyan), a Nubian, an Asiatic (Levantine), and an Egyptian, copied from a mural on the tomb of Seti I. Credit: Egyptian races drawing by Heinrich von Minutoli (1820) of a mural by an unknown artist from the tomb of Seti I is in the public domain.

The earliest classification systems used to understand human variation are evidenced by ancient manuscripts, scrolls, and stone tablets recovered through archaeological, historical, and literary research. The Ancient Egyptians had the *Book of Gates*, dated to the New Kingdom between 1550 B.C.E. and 1077 B.C.E (Figure 13.3). In one part of this tome dedicated to depictions of the underworld, scribes used pictures and hieroglyphics to illustrate a division of Egyptian people into the four categories known to them at the time: the Aamu (Asiatics), the Nehesu (Nubians), the Reth (Egyptians), and the Themehu (Libyans). Though not rooted in any scientific basis like our current understandings of human variation today, the Ancient Egyptians believed that each of these groups were made of a distinctive category of people, distinguishable by their skin color, place of origin, and even behavioral traits.

Another well-known early document is the Bible, where it is written that all humankind descends from one of three sons of Noah: Shem (the ancestor to all olive-skinned Asians), Japheth (the ancestor to pale-skinned Europeans), and Ham (the ancestor to darker-skinned Africans). Similar to the Ancient Egyptians, these distinctions were based on behavioral traits and skin color. More recent work in historiography and linguistics suggest that the branches of "Hamites," "Japhethites," and "Shemites" may also relate to the formation of three independent language groups some time between 1000 and 3000 B.C.E. With the continued proliferation of Christianity, this concept of approximately three racial groupings lasted until the Middle Ages and spread as far across Eurasia as crusaders and missionaries ventured at the time.

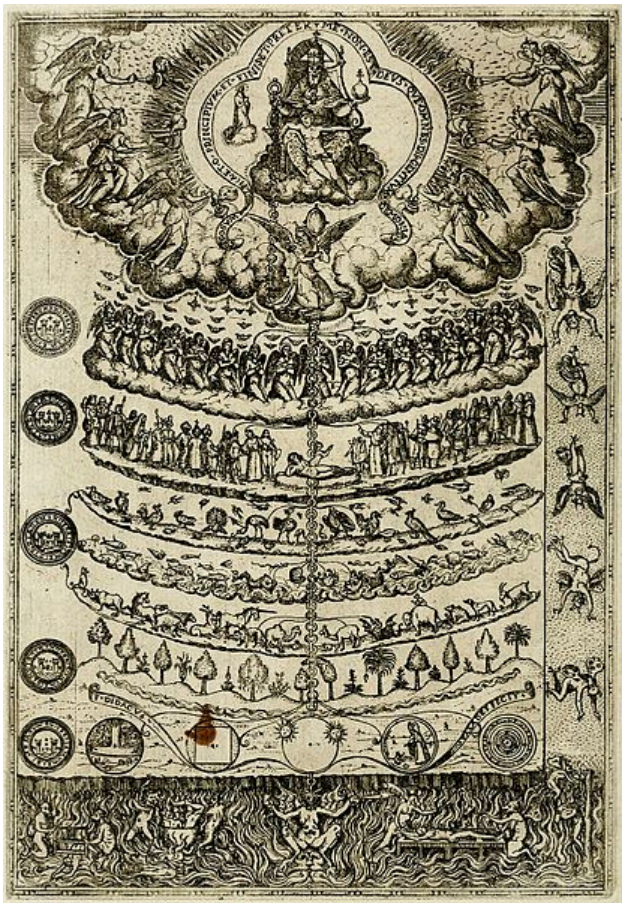


Figure 13.4: The Great Chain of Being from the Rhetorica Christiana by Fray Diego de Valades (1579). Credit: Great Chain of Being by Didacus Valades (Diego Valades 1579), print from Rhetorica Christiana (via Getty Research), is in the public domain.

There is also the "Great Chain of Being," conceived by ancient Greek philosophers like Plato (427–348 B.C.E.) and Aristotle (384–322 B.C.E.). They played a key role in laying the foundations of empirical science, whereby observations of everything from animals to humans were noted with the aim of creating taxonomic categories. Aristotle describes the Great Chain of Being as a ladder along which all objects, plants, animals, humans, and celestial bodies can be mapped in an overall hierarchy (in the order of existential importance, with humans placed near the top, just beneath divine beings; see Figure 13.4). When he writes about humans, Aristotle expressed the belief that certain people are inherently (or genetically) more instinctive rulers, while others are more natural fits for the life of a worker or enslaved person. Based on research by biological anthropologists, we currently recognize that these early systems of classification and hierarchization are unhelpful in studying human biological variation. Both behavioral traits and physical traits are coded for by multiple genes each, and how we exhibit those traits based on our genetics can vary significantly even between individuals of the same population.

"Race" during the Scientific Revolution

The 1400s to 1600s saw the beginnings of the **Scientific Revolution** in Western societies, with thinkers like Nicholas Copernicus, Galileo Galilei, and Leonardo Da Vinci publishing some of their most important findings. While by no means the first or only scholars globally to use observation and experimentation to understand the world around them, early scientists living at the end of the medieval period in Europe increasingly employed more experimentation, quantification, and rational thought in their work. This is the main difference between the work of the ancient Egyptians, Romans, and Greeks and that of later scientists such as Isaac Newton and Carl Linnaeus in the 1600s and 1700s.

Linnaeus is the author of *Systema Naturae* (1758), in which he classified all plants and animals under the formalized naming system known as **binomial nomenclature** (Figure 13.5). This system is **typological**, in that organisms are placed into groups according to how they are similar or different to others under study. What was most anthropologically notable about Linnaeus's typological system was that he was one of the first to group humans with apes and monkeys, based on the anatomical similarities between humans and nonhuman primates. However, Linnaeus viewed the world in line with **essentialism**, a problematic concept that dictates that there are a unique set of characteristics that organisms of a specific kind *must* have and that would remove organisms from taxonomic categorizations if they lacked any of the required criteria.

Figure 13.5: Carl Linnaeus. Credit: Carl von Linné by Alexander Roslin (1718-1793) is in the public domain.

Figure 13.6: A painting depicting the colonization of the Mississippi River environs by Spaniard Hernando DeSoto in 1541 (painted in 1853 by William H. Powell). Credit: Discovery of the Mississippi by William Henry Powell (photograph courtesy of Architect of the Capitol) is in the public domain.

Linnaeus subdivided the human species into four varieties, with overtly racist categories based on skin color and "inherent" behaviors. Some European scientists during this period were not aware of their own biases skewing their interpretations of biological variation, while others deliberately worked to shape public perceptions of human variation in ways that established "**otherness**" and enforced European domination and the subordination of non-European people. The conclusions and claims at which they arrived, consciously or subconsciously, often fit the times they were living through—the so-called **Age of Discovery**, when the superiority of European cultures over others was a pervasive idea throughout people's social and political lives. Although much of Eurasia was linked by spice- and silk-trading routes, the European colonial period between the 1400s and 1700s was marked by many new and unfortunately violent encounters overseas (Figure 13.6). When Europeans arrived by ship on the shores of continents that were already inhabited, it was their first meeting with the Indigenous peoples of the Americas and Australasia, who looked, spoke, and behaved differently from peoples with whom they were familiar. Building on the idea of species and "subspecies," natural historians of this time invented the term *race*, from the French *rasse* meaning "local strain."

Another scientist of the times, Johann Friedrich Blumenbach (1752–1840), classified humans into five races based on his observations of cranial form variation as well as skin color. He thus dubbed the "original" form of the human cranium the "Caucasian" form, with the idea that the ideal climate conditions for early humans would have been in the Caucasus region near the Caspian Sea. The key insight Blumenbach presented was that human variation in any particular trait should be more accurately viewed as falling along a gradation (Figure 13.7). While some of his theories were correct according to what we observe today with more knowledge in genetics, they erroneously believed that human "subspecies" were "degenerated" or "transformed" varieties of an ancestral Caucasian or European race. According to them, the Caucasian cranial dimensions were the least changed over human evolutionary time, while the other skull forms represented geographic variants of this "original." As will be discussed in greater detail later in this chapter, we have genetic and craniometric evidence for sub-Saharan Africa being the origin of the human species instead (see Chapter 12 on the fossil record that places the origins of modern *Homo sapiens* in north and east Africa). Based on work that shows how most biological characteristics are coded for by nonassociated genes, it is not reasonable to draw links between individuals' personalities and their skull shapes.

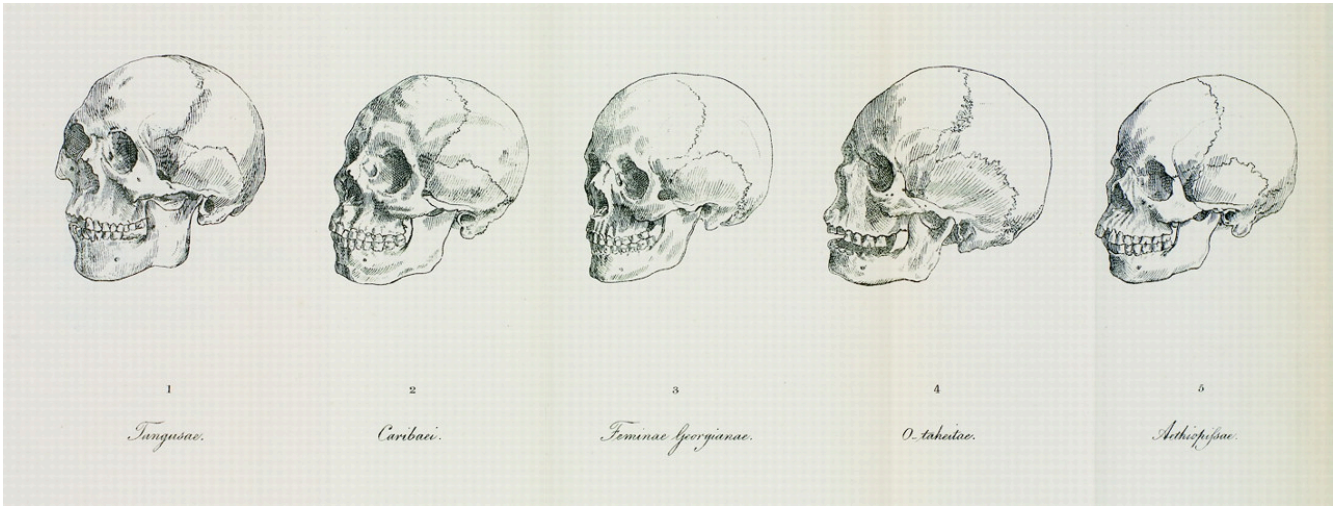


Figure 13.7: Five skull drawings representing specimens for Blumenbach's "Mongolian," "American," "Caucasian," "Malayan," and "Aethiopian" races. Credit: Blumenbach's five races by Johann Friedrich Blumenbach is in the public domain. Original in the 1795 Treatise on "De generis humani varietate nativa," unnumbered page at the end of the book titled "Tab II".

"Race" and the Dawn of Scientific Racism

Between the 1800s and mid-1900s, and contrary to what you might expect, an increased use of scientific methods to justify racial schemes developed in scholarship. Differing from earlier views, which saw all humans as environmentally deviated from one "original" humankind, classification systems after 1800 became more **polygenetic** (viewing all people as having separate origins) rather than **monogenetic** (viewing all people as having a single origin). Instead of moving closer to our modern-day understandings of human variation, there was increased support for the notion that each race was created separately and with different attributes (intelligence, temperament, and appearance).

The 1800s were an important precursor to modern biological anthropology as we know it, given that this was when the scientific measurement of human physical features (anthropometry) truly became popularized. However, empirical studies in the 1800s pushed even further the idea that Europeans were culturally and biologically superior to others. While considered one of the pioneers of American "physical" anthropology, Samuel George Morton (1799–1851) was a scholar who had a large role in perpetuating 1800s scientific racism. By measuring cranial size and shape, he calculated that "Caucasians," on average, have greater cranial volumes than other groups, such as the Indigenous peoples of the Americas and peoples Morton referred to collectively as "Negros." Today, we know that cranial size variation depends on such factors as Allen's and Bergmann's rules, which give a more likely explanation: in colder environments, it is advantageous for those living there to have larger and rounder heads because they conserve heat more effectively than more slender heads (Beals et al. 1984). The leading figures in craniometry during the 1800s instead were linked heavily with powerful individuals and wealthy sociopolitical institutions and financial bodies. Theories in support of hierarchical racial schemes using "scientific" bases certainly helped continue the exploitative and unethical trafficking and enslavement of Africans between the 1500s and 1800s.

Morton went on to write in his publication *Crania Americana* (1839) a number of views that fit with a concept called **biological determinism**. The idea behind biological determinism is that an association exists between people's physical characteristics and their behavior, intelligence, ability, values, and morals. If the idea is that some groups of people are essentially superior to others in cognitive ability and temperament, then it is easier to justify the unequal treatment of certain groups based on outward appearances. Another such problematic thinker was Paul Broca (1824–1880), after whom a region of the frontal lobe related to language use is named (Broca's area). Influenced by Morton, Broca likewise claimed that internal skull capacities could be linked with skin color and cognitive ability. He went on to justify the European colonization of other global territories by purporting it was noble for a biologically more "civilized" population to improve the "humanity" of more "barbaric" populations. Today, these theories of Morton, Broca, and others like them are known to have no scientific basis. If we could speak with them today, they would likely try to emphasize that their conclusions were based on empirical evidence and not *a priori* reasoning. However, we now can clearly see that their reasoning was biased and affected by prevailing societal views at the time.

"Race" and the Beginnings of Physical Anthropology

In the early 20th century, we saw a number of new figures coming into the science of human variation and shifting the theoretical focus within. Most notably, these included Aleš Hrdlička and Franz Boas.

Aleš Hrdlička (1869–1943) was a Czech anthropologist who moved to the United States. In 1903, he established the physical anthropology section of the National Museum of Natural History (Figure 13.8). In 1918, he founded the *American Journal of Physical Anthropology*, which remains one of the foremost scientific journals disseminating bioanthropological research. As part of his work and the scope of the journal, he differentiated "**physical anthropology**" from other kinds of anthropology: he wrote that physical anthropology is "the study of racial anatomy, physiology, and pathology" and "the study of man's variation" (Hrdlička 1918). In some ways, although the scope and technological capabilities of biological anthropologists have changed significantly, Hrdlička established an area of inquiry that has continued and prospered for over a hundred years.

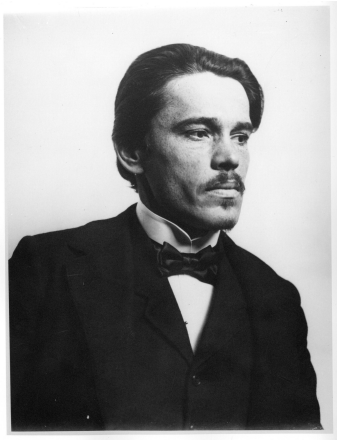


Figure 13.8: Aleš Hrdlička (1869–1943), a Czech anthropologist who founded the American Journal of Physical Anthropology. Credit: (Ales Hrdlicka) SIA2009-4246 (1903) by an unknown photographer is used for educational and non-commercial purposes as outlined by the Smithsonian.. [Smithsonian Institution Archives, Record Unit 9521, Box 1, T. Dale Stewart Oral History Interview; and Record Unit 9528, Box 1, Henry B. Collins Oral History Interview.]

Franz Boas (1858–1942) was a German American anthropologist who established the four-field anthropology system in the United States and founded the American Anthropological Association in 1902. He argued that the scientific method should be used in the study of human cultures and the comparative method for looking at human biology worldwide. One of Boas's significant contributions to biological anthropology was the study of skull dimensions with respect to race. After a long-term research project, he demonstrated how cranial form was highly dependent on cultural and environmental factors and that human behaviors were influenced primarily not by genes but by social learning. He wrote in one essay for the journal *Science*: "While individuals differ, biological differences between races are small. There is no reason to believe that one race is by nature so much more intelligent, endowed with great willpower, or emotionally more stable than another, that the difference would materially influence its culture" (Boas 1931:6). This conclusion directly contrasted with the theories of the past that relied on biological determinism. Biological anthropologists today have found evidence that corroborates Boas's explanations: societies do not exist on a hierarchy or gradation of "civilizedness" but instead are shaped by the world around them, their demographic histories, and the interactions they have with other groups.

The first half of the 1900s still involved some research that was essentialist and focused on proving racial determinism. Anthropologists like Francis Galton (1822–1911) and Earnest A. Hooton (1887–1954) created the field of **eugenics** as an attempt to formalize the social scientific study of "fitness" and "superiority" among members of 19th-century Europe. As a way of "dealing with" criminals, diseased individuals, and "uncivilized" people, eugenicists recommended prohibiting parts of the population from being married or sterilizing these members of society so they could no longer procreate (Figure 13.9). They instead encouraged "reproduction in individual families with sound physiques, good mental endowments, and demonstrable social and economic capability" (Hooton 1936). In the 1930s, Nazi Germany used this false idea of there being "pure races" to highly destructive effect. The need to be protected against admixture from "unfit" groups was their justification for their blatant racism and purging of citizens that fell under their subjective criteria.

It should be noted that eugenicist ideas were popularly discussed and debated in many non-European contexts, as in the U.S., China, and South Africa, too. The Immigration Restriction Act of 1924 was passed in the United States, with the explicit aim of reducing the country's "burden" of people considered inferior by restricting immigration of eastern European Jews, Italians, Africans, Arabs, and Asians. In the early 1900s, Chinese scientists and politicians showed great interest in eugenic ideologies, which came to dictate decisions in law-making, family life, and the medical field. Noted American anthropologist Ruth Benedict wrote extensively on Japanese culture and society during and after World War II. Her essentialist portrayals of Japanese people were heavily cited in popular discourse at the time. In 1950s South Africa, interracial marriages and sexual relations were banned by law; antimiscegenation became one of the huge focuses of apartheid resistance activists in later years. We still see the continuation of eugenics-based logic today around the world—in exclusionary immigration laws, cases of incarcerated prison inmates being forcibly sterilized, and the persistence of intelligence testing as a form of measuring people's "fitness" in a society.

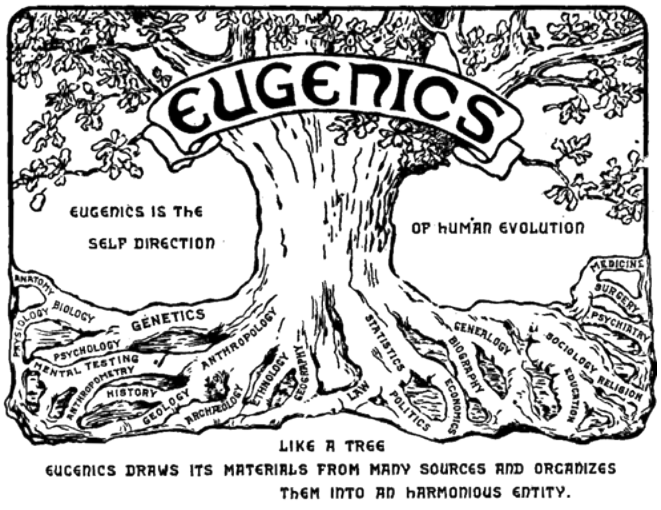


Figure 13.9: Logo of the Second International Exhibition of Eugenics, held in 1921. The text of the logo states: "Eugenics is the self-direction of human evolution. Like a tree, eugenics draws its materials from many sources and organizes them into an harmonious entity." Credit: Eugenics congress logo scanned from Harry H. Laughlin, The Second International Exhibition of Eugenics held September 22 to October 22, 1921, is in the public domain.

Shortly after World War II and the Nazi Holocaust, the full extent of essentialist, eugenicist thinking became clear. Social constructions of race, and the notion that one can predict psychological or behavioral traits based on external appearance, had become unpopular both within and outside the discipline. It was up to those in the field of physical anthropology at the time to separate physical anthropology from race concepts that supported

unscientific and socially damaging agendas. This does not mean that there are no physiological or behavioral differences between different members of the human species. However, going forward, a number of physical anthropologists saw human biological variation as more complicated than simple typologies could describe.

"The New Physical Anthropology"

After 1950, focus steered away from the concept of "race" as a unit of variation and toward understanding why variation exists in **populations** from an evolutionary perspective. This was outlined by those pioneering the "new physical anthropology," such as Sherwood Washburn, Theodosius Dobzhansky (Figure 13.10), and Julian Huxley, who borrowed this approach from contemporary population geneticists. Whether using genetic or phenotypic markers as the units of study, "groups" or "clusters" of humans differentiated by these became defined as populations that differ in the frequency of some gene or genes. Anthropologists consider what "makes" a population—a group of individuals potentially capable of or actually interbreeding due to shared geographic proximity, language, ethnicity, culture, and/or values. Put another way, a population is a local interbreeding group with reduced gene flow between themselves and other groups of humans. Members of the same population may be expected to share many genetic traits (and, as a result, many phenotypic traits that may or may not be visible outwardly).

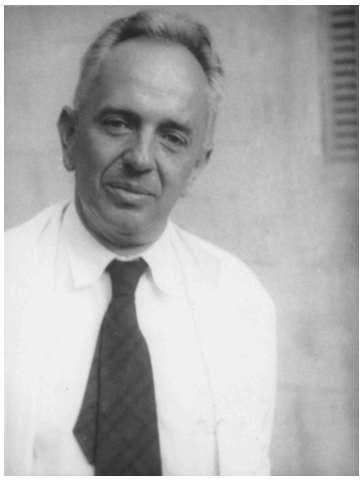


Figure 13.10: Theodosius Dobzhansky, an important scientist who formulated the 20th-century "modern synthesis" reconciling Charles Darwin's theory of evolution and Gregor Mendel's ideas on heredity. Credit: Dobzhansky no Brasil em 1943 by unknown photographer via Flickr user Cely Carmo is in the public domain.

Figure 13.11: Julian Huxley (1942). Credit: Julian Huxley 1-2 by unknown photographer is in the public domain.

Thinking of humans in terms of populations was part of Julian Huxley's (1942) "Modern Synthesis"—so named because it helped to reconcile two fundamental principles about evolution that had not been made sense of together before (Figure 13.11). As discussed in Chapter 3, Gregor Mendel (1822–1884) was able to show that inheritance was mediated by discrete particles (or genes) and not blended in the offspring. However, it was difficult for some 19th-century scientists to accept this model of genetic inheritance at the time because much of biological variation appeared to be continuous and not particulate (take skin color or height as examples). In the 1930s, it was demonstrated that traits could be polygenic and that multiple alleles could be responsible for any one phenotypic trait, thus producing the continuous variation in traits such as eye color that we see today. Thus, Huxley's "Modern Synthesis" outlines not only how human populations are capable of exchanging genes at the microevolutionary level but also how multiple alleles for one trait (polygenic exchanges) can cause gradual macroevolutionary changes.

Human Variation in Biological Anthropology Today

Many Human Traits Are Nonconcordant

In our studies of human (genetic) variation today, we understand most human traits to be nonconcordant (Figure 13.12). "**Nonconcordance**" is a term used to describe how biological traits vary independent of each other—that is, they do not get inherited in a correlative manner with other genetically controlled traits. For example, if you knew an individual had genes that coded for tall height, you would not be able to predict if they are lighter-skinned or have red hair. This is different from earlier essentialist views of human variation: the idea that skin color could predict one's brain function or even "temperament" and tendencies toward criminal behavior.

Figure 13.12: Most human biological traits are non-concordant, meaning traits vary independently and each trait has its own pattern of distribution around the world. In this image, different colors and patterns represent trait varieties. For example, the color and pattern of the head may represent hair color (dark to light), but sharing dark hair with another person does not mean you will share other traits (e.g. ability to digest lactose or ABO blood type). Credit: Nonconcordance original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

Human Variation Is Clinal/Continuous (Not Discrete)

Frank B. Livingstone (1928–2005) wrote: "There are no races, only clines" (1962: 279). A **cline** is a gradation in the frequency of an allele/trait between populations living in different geographic regions. Human variation cannot be broken into discrete "races," because most physical traits vary on a continuous or "clinal" basis. One obvious example of this is how human height does not only come in three values ("short," "medium," and "tall") but instead varies across a spectrum of vertical heights achievable by humans all over the world. On the one hand, we can describe human height as exhibiting **continuous variation**, forming a continuous pattern, but height does not vary according to where people live across the globe and does not exhibit a clinal pattern. On the other hand, skin color variation between populations does show patterning that fits quite well on to how near or far they are from each other on a world map. This makes a trait like skin color clinally distributed worldwide. When large numbers of genetic loci for large numbers of samples were sampled from human populations distributed worldwide during the 1960s and 1970s, the view that certain facets of human diversity were clinally distributed was further supported by genetic data.

To study human traits that are clinally distributed, genetic tests must be performed to uncover the true frequencies of an allele or trait across a certain geographic space. One easily visible example of a clinal distribution seen worldwide is the patterning of human variation in skin color. Whether in southern Asia, sub-Saharan Africa, or Australia, dark brown skin is found. Paler skin tones are found in higher-latitude populations such as those who have lived in areas like Europe, Siberia, and Alaska for millennia. Skin color is easily observable as a phenotypic trait exhibiting continuous variation.

A clinal distribution still derives from genetic inheritance; however, clines often correspond to some gradually changing environmental factor. Clinal patterns arise when selective pressures in one geographic area differ from those in another as well as when people procreate and pass on genes together with their most immediate neighbors. There are several mechanisms, selective and neutral, that can lead to the clinal distribution of an allele or a biological trait. **Natural selection** is the mechanism that produced a global cline of skin color, whereby darker skin color protects equatorial populations from high amounts of UV radiation; there is a transition of lessening pigmentation in individuals that reside further and further away from the tropics (Jablonski 2004; Jablonski and Chaplin 2000; see Figure 13.13). The ability and inability to digest lactose (milk sugar) among different world communities varies according to differential practices and histories of milk and dairy-product consumption (Gerbault et al.

2011; Ingram et al. 2009). Where malaria seems to be most prevalent as a disease stressor on human populations, a clinal gradient of increasing sickle cell anemia experience toward these regions has been studied extensively by genetic anthropologists (Luzzatto 2012). Sometimes culturally defined mate selection based on some observable trait can lead to clinal variation between populations as well.

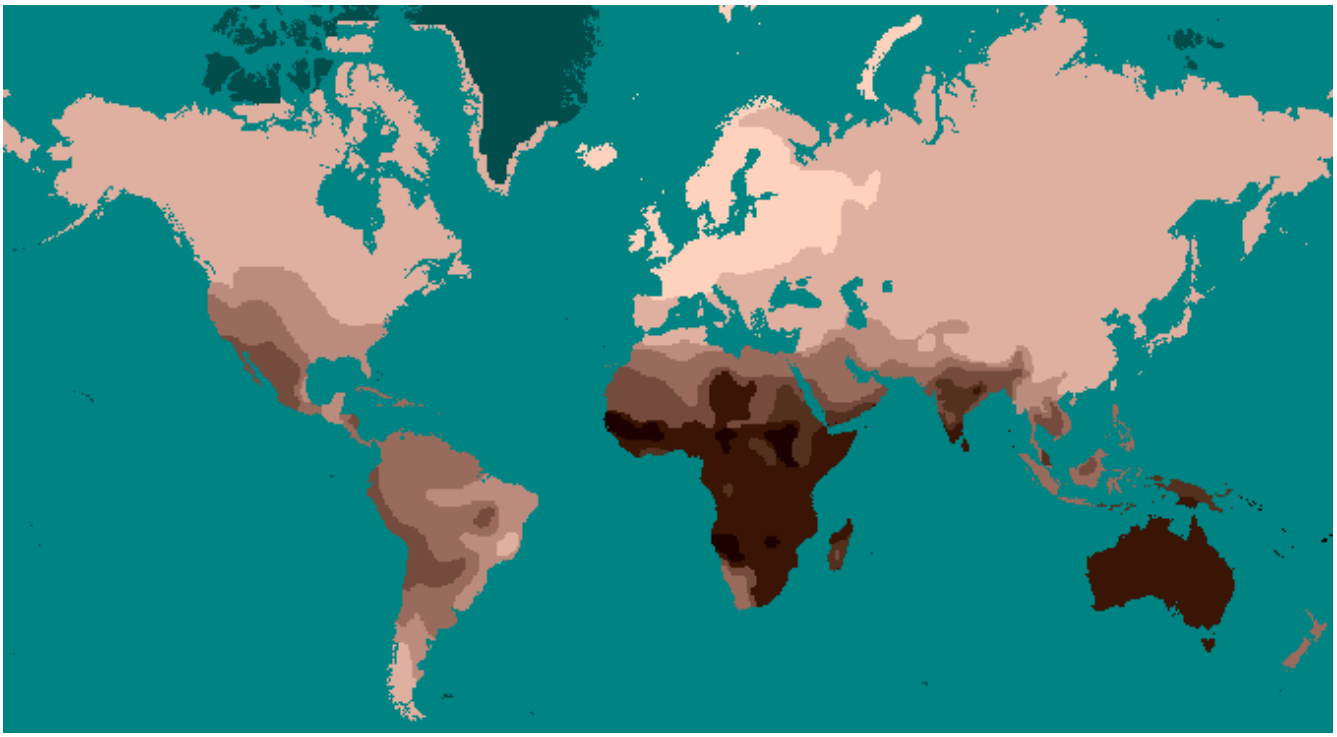
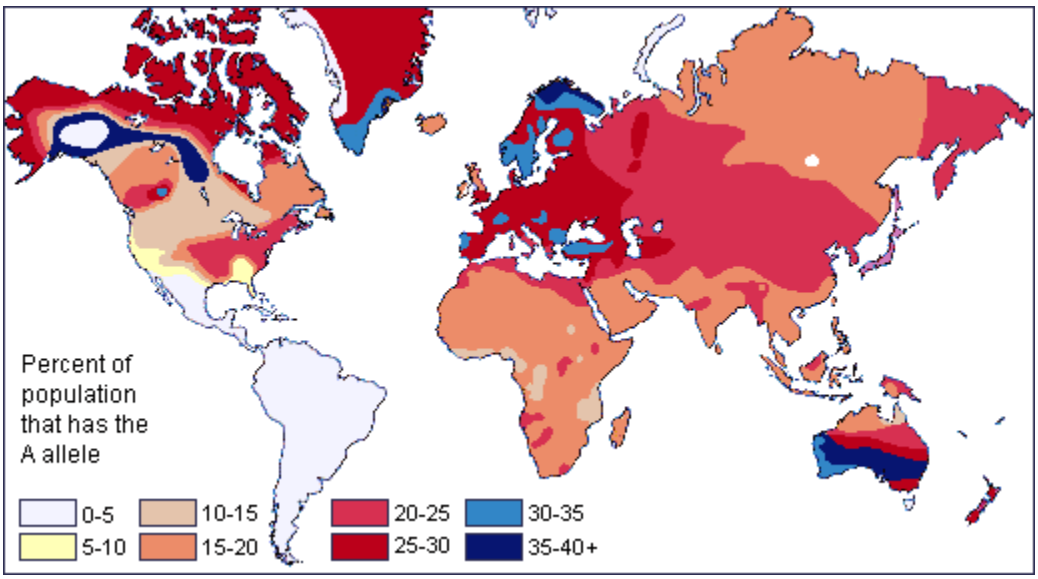
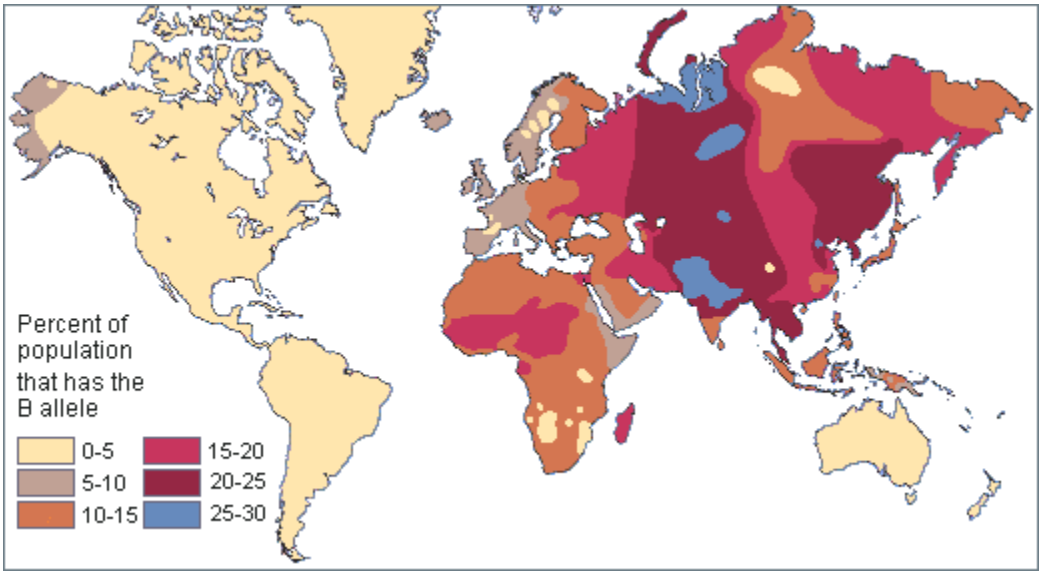


Figure 13.13: A global map of skin colors shows that dark skin pigmentation is more common in areas that receive more UV radiation (near the equator and in high altitude areas). Light skin is more common at northern and southern latitudes. It is worth bearing in mind, though, that these do not tell the full story of how human skin pigmentation varies worldwide. Each region will contain populations that exhibit a range of skin tones. In this way, this map is not perfect as an illustration of skin-color distribution. Credit: Mercator style projection map showing human skin color according to Biasutti 1940.png by Dark Tichondrias at English Wikipedia, modified (cropped) by Tuvalkin, is under a CC BY-SA 4.0 License.

Two neutral microevolutionary processes that may produce a cline in a human allele or trait are **gene flow** and **genetic drift** (see Chapter 4). The ways in which neutral processes can produce clinal distributions is seen clearly when looking at clinal maps for different blood groups in the human ABO blood group system (Figure 13.14). For instance, scientists have identified an East-to-West cline in the distribution of the blood type *B* allele across Eurasia. The frequency of *B* allele carriers decreases gradually westward when we compare the blood groups of East and Southeast Asian populations with those in Europe. This shows how populations residing nearer to one another are more likely to interbreed and share genetic material (i.e., undergo gene flow). We also see 90%–100% of native South American individuals, as well as between 70%–90% of Aboriginal Australian groups, carrying the *O* allele (Mourant, Kopeć, and Domaniewska-Sobczak 1976). These high frequencies are likely due to random genetic drift and founder effects, in which population sizes were severely reduced by the earliest *O* allele-carrying individuals migrating into those areas. Over time, the *O* blood type has remained predominant.


Percent of population that has the A allele
0-5
5-10
10-15
15-20
20-25
25-30
30-35
35-40+


Percent of population that has the B allele
0-5
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10-15
15-20
20-25
25-30

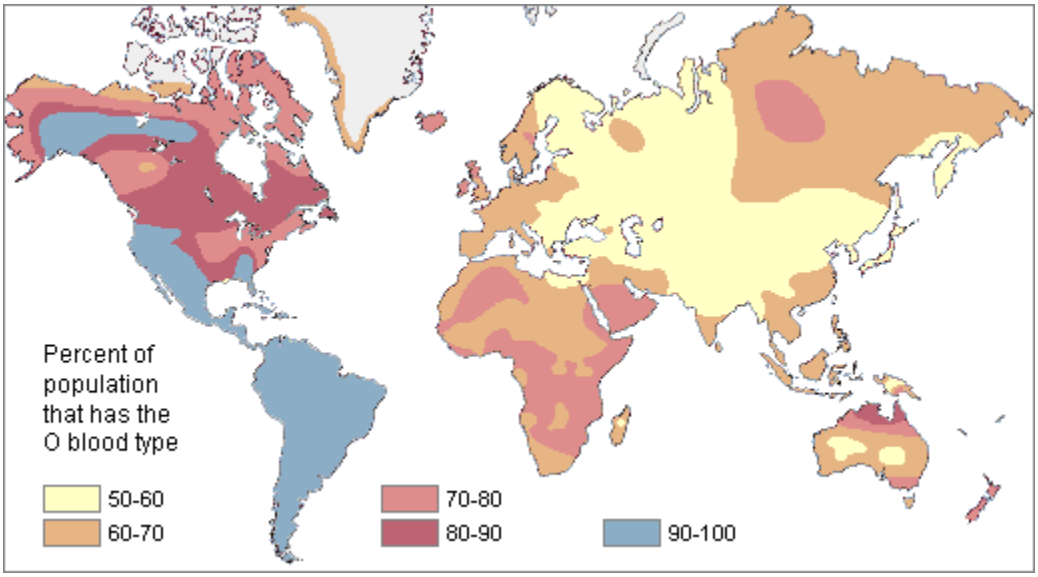

Figure 13.14a–c: a. Global distribution of blood type A. b. Global distribution of blood type B. c. Global distribution of blood type O. Credit: a. Map of blood group a by Muntuwandi at en.wikipedia is under a CC BY-SA 3.0 License. b. Map of blood group b by Muntuwandi at en.wikipedia is under a CC BY-SA 3.0 License. c. Map of blood group o is based on diagrams from http://anthro.palomar.edu/vary/vary_3.htm, reproduced from A. E. Mourant et al. (1976), and is under a CC BY-SA 3.0 License. [Image Description].

Genetic Variation Is Greater Within Group than Between Groups

One problem with race-based classifications is they relied on an erroneous idea that individuals with particular characteristics would share more similar genes with each other within a particular "race" and share less with individuals of other "races" possessing different traits and genetic makeups. However, since around 50 years ago, scientific studies have shown that the majority of human genetic differences worldwide exist *within* groups (or "races") individually rather than *between* groups. Indeed, most genetic variation we see occurs in Africa, and many variants are shared among individuals on all continents (Figure 13.15).

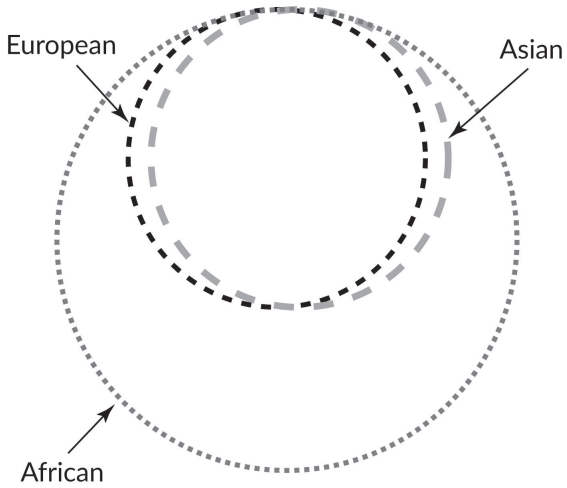

Figure 13.15: Circles represent human genetic variation. Most variants are shared among individuals on all continents. There are more variants in Africa, some of which are not found in Europe or Asia. Credit: Human Genetic Variation original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

In 2002, a landmark article by Noah Rosenberg and colleagues explored worldwide human genetic variation using an even-greater genetic data set. They used 377 highly variable markers in the human genome and sampled from 1,056 individuals representative of 52 populations. The markers chosen for study were not ones that code for any expressed genes. Because these regions of the human genome were made of unexpressed genes, we may understand these markers as neutrally derived (as opposed to selectively derived) because they do not code for functional advantages or disadvantages. These neutral genetic markers likely reflect an intricate combination of regional founder effects and population histories. Analyses of these neutral markers allowed scientists to identify that 93%–95% of global genetic differences, referred to as **variance**, can be accounted for by within-population differences, while only a small proportion of genetic variance (3%–5%) can be attributed to differences among major groups (Rosenberg et al. 2002). This research supports the theory that distinct biological races do not exist, even though misguided concepts of race may still have real social and political consequences.

Biological Data Fit Isolation-By-Distance and Out-of-Africa Models

One further note is that the world's population may be genetically divided into "groups," "subsets," "clumps," or "clusters" that reflect some degree of genetic similarity. These identifiable clusters reflect genetic or geographic distances—either with gene flow facilitated by proximity between populations or impeded by obstacles like oceans or environmentally challenging habitats (Rosenberg et al. 2005). Sometimes, inferred clusters using multiple genetic loci are interpreted by nongeneticists literally as "ancestral populations." However, it would be wrong to assume from these genetic results that highly differentiated and "pure" ancestral groups ever existed. These groupings reflect differences that have arisen over time due to clinal patterning, genetic drift, and/or restricted or unrestricted gene flow (Weiss and Long 2009). The clusters identified by scientists are arbitrary and the parameters used to split up the global population into groups is subjective and dependent on the particular questions or distinctions being brought into focus (Relethford 2009).

Additionally, research on worldwide genetic variation has shown that human variation decreases with increasing distance from sub-Saharan Africa, where there is evidence for this vast region being the geographical origin of anatomically modern humans (Liu et al. 2006; Prugnolle, Manica, and Balloux 2005; see Figures 13.16 and 13.17). Genetic differentiation decreases in human groups the further you sample data from relative to sub-Saharan Africa because of serial founder effects (Relethford 2004). Over the course of human colonization of the rest of the world outside Africa, populations broke away in expanding waves across continents into western Asia, then Europe and eastern Asia, followed by Oceania and the Americas. As a result, founder events occurred whereby genetic variation was lost, as the colonization of each new geographical region involved a smaller number of individuals moving from the original larger population to establish a new one (Relethford 2004). The most genetic variation is found across populations residing in different parts of sub-Saharan Africa, while other current populations in places like northern Europe and the southern tip of South America exhibit some of the least genetic differentiation relative to all global populations (Campbell and Tishkoff 2008).

Figure 13.16: Sub-Saharan Africa (shaded dark/green). Credit: Sub-Saharan Africa by Ezeu has been designated to the public domain (CC0).

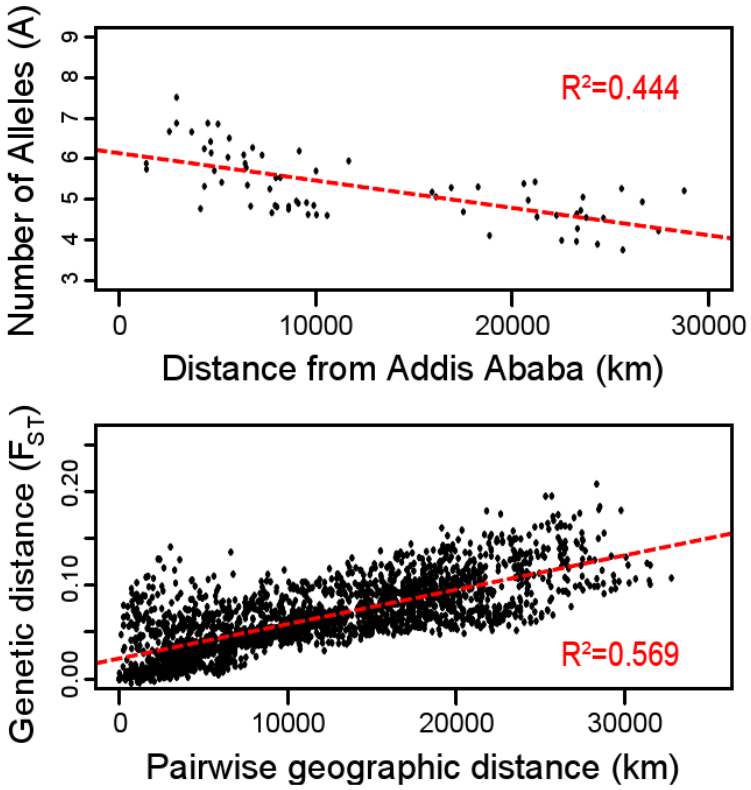

Figure 13.17: Comparison of the genetic distance and geographical distance between populations. In the top graph, the pattern reveals that genetic variation conforms to an Out-of-Africa model, as those populations further away from Addis Ababa in Ethiopia share a smaller number of alleles; in the bottom graph, we see the populations follow an isolation-by-distance model, as pairs of populations further apart geographically seem to have greater genetic distance (Kanitz et al. 2018). Credit: Complex genetic patterns (figure 1) by Kanitz et al. (2018) is under a CC BY 4.0 License.

Besides fitting nicely into the **Out-of-Africa model**, worldwide human genetic variation conforms to an **isolation-by-distance model**, which predicts that genetic similarity between groups will decrease exponentially as the geographic distance between them increases (Kanitz et al. 2018). This is because of the greater and greater restrictions to gene flow presented by geographic distance, as well as cultural and linguistic differences that occur as a result of certain degrees of isolation. Since genetic data conform to isolation-by-distance and Out-of-Africa models, these findings support the abolishment of "race" groupings. This research demonstrates that human variation is continuous and cannot be differentiated into geographically discrete categories. There are no "inherent" or "innate" differences between human groups; instead, variation derives from some degree of natural selection, as well as neutral processes like **population bottle-necking** (Figure 13.18), random **mutations** in the DNA, genetic drift, and gene flow through between-mate interbreeding.

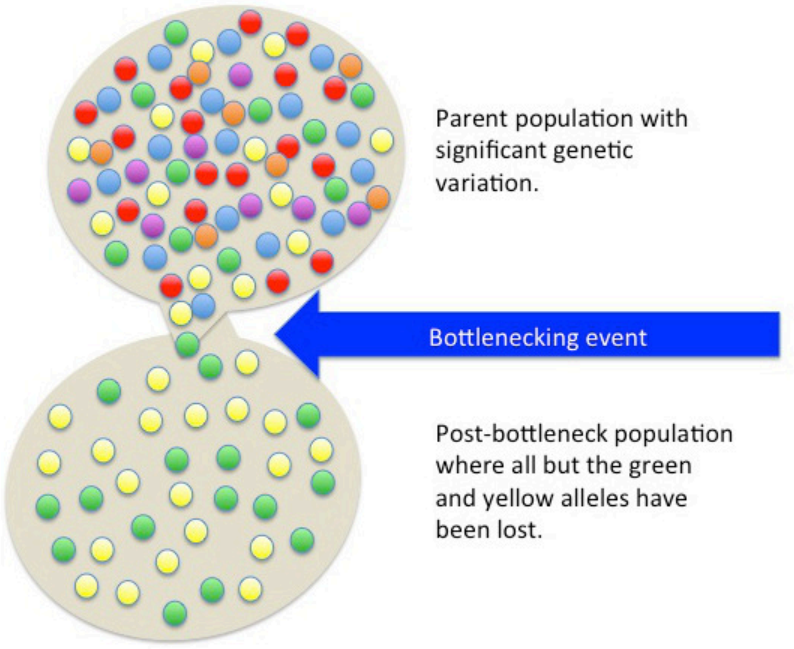

Figure 13.18: The founder effect is a change in a small population's gene pool due to a limited number of individuals breaking away from a parent population. Credit: Bottleneck effect by Tsaneda is under a CC BY 3.0 License.

Humans Have Higher Homogeneity Compared to Many Other Species

An important fact to bear in mind is that humans are 99.9% identical to one another. This means that the apportionments of human variation discussed above only concern that tiny 0.1% of difference that exists between all humans globally. Compared to other mammalian species, including the other great apes, human variation is remarkably lower. This may be surprising given that the worldwide human population has already exceeded seven billion, and, at least on the surface level, we appear to be quite phenotypically diverse. Molecular approaches to human and primate genetics tells us that external differences are merely superficial. For a proper appreciation of human variation, we have to look at our closest relatives in the primate order and mammalian class. Compared to chimpanzees, bonobos, gorillas and other primates, humans have remarkably low average genome-wide **heterogeneity** (Osada 2005).

When we look at chimpanzee genetic variation, it is fascinating that western, central, eastern, and Cameroonian chimpanzee groups have substantially more genetic variation between them than large global samples of human DNA (Bowden et al. 2012; Figure 13.19). This is surprising given that all of these chimpanzee groups live relatively near one another in Africa, while measurements of human genetic variation have been conducted using samples from entirely different continents. First, geneticists suppose that this could reflect differential experiences of the founder effect between humans and chimpanzees. Because all non-African human populations descended from a small number of anatomically modern humans who left Africa, it would be expected that all groups descended from that smaller ancestral group would be similar genetically. Second, our species is really young, given that we have only existed on the planet for around 150,000 to 300,000 years. This gave humans little time for random genetic mutations to occur as genes get passed down through genetic interbreeding and meiosis. Chimpanzees, however, have inhabited different **ecological niches**, and less interbreeding has occurred between the four chimpanzee groups over the past six to eight million years compared to the amount of gene flow that occurred between worldwide human populations (Bowden et al. 2012).

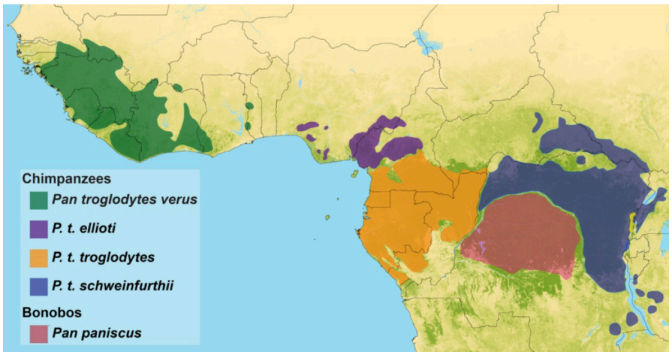

Figure 13.19: Distribution of the genus Pan, including bonobos and the four subspecies of chimpanzee, across western and central Africa (Clee et al. 2015). Credit: Chimpanzee subspecies ranges (Figure 1) by Clee et al. 2015 is under a CC BY 4.0 License. [Image Description].

Recent advances have now enabled the attainment of genetic samples from the larger family of great apes and the evaluation of genetic variation among bonobos, orangutans, and gorillas alongside that of chimpanzees and humans (Prado-Martinez et al. 2013). Collecting such data and analyzing primate genetic variation has been important not only to elucidate how different ecological, demographic, and climatic factors have shaped our evolution but also to inform upon conservation efforts and medical research. Genes that may code for genetic susceptibilities to tropical diseases that affect multiple primates can be studied through genome-wide methods. Species differences in the genomes associated with speech, behavior, and cognition could tell us more about how human individuals may be affected by genetically derived neurological or speech-related disorders and conditions (Prado-Martinez et al. 2013; Staes et al. 2017). In 2018, a great ape genomic study also reported genetic differences between chimpanzees and humans related to brain cell divisions (Kronenberg et al. 2018). From these results, it may be inferred that cognitive or behavioral variation between humans and the great apes might relate to an increased number of cortical neurons being formed during human brain development (Kronenberg et al. 2018). Comparative studies of human and nonhuman great ape genetic variation highlight the complex interactions of population histories, environmental changes, and natural selection between and within species. When viewed in the context of overall great ape variation, we may reconsider how variable the human species is relatively and how unjustified previous "race" concepts really were.

Phenotypic Traits That Reflect Neutral Evolution

Depending on the trait being observed, different patterns of phenotypic variation may be found within and among groups worldwide. In this subsection, some phenotypic traits that reflect the aforementioned patterns of genetic variation will be discussed.

Looking beyond genetic variation briefly, recent studies have revisited biological anthropology's earlier themes of externally observable traits, such as skull shape. In the last 20 or so years, anthropologists have evaluated the level to which human cranial shape variation reflects the results from genetic markers, such as those used previously to fit against Out-of-Africa models (Relethford 2004) or those used in the apportionment of human variation between and within groups (Lewontin 1972; Rosenberg et al. 2002). Using larger sample sizes of cranial data collected from thousands of skulls worldwide and a long list of cranial measurements, studies demonstrate a similar decrease in variation with distance from Africa and show that a majority of cranial variation occurs within populations rather than between populations (Betti et al. 2009; Betti et al. 2010; Manica et al. 2007; Relethford 2001; von Cramon-Taubadel and Lycett 2008; see Figure 13.20). The greatest cranial variation is found among skulls of sub-Saharan African origin, while the least variation is found among populations inhabiting places like Tierra del Fuego at the southern tip of Argentina and Chile. While ancient and historical thinkers previously thought "race" categories could reasonably be determined based on skull dimensions, modern-day analyses using more informative sets of cranial traits simply show that migrations out of Africa and the relative distances between populations can explain a majority of worldwide cranial variation (Betti et al. 2009).

Figure 13.20: Contemporary anthropologists who use many types of skeletal markers have demonstrated that a majority of cranial variation occurs within populations rather than between populations and that there is a decrease in variation with distance from Africa. Credit: Dental Anthropologist Heart Necklace by Anthro Illustrated is under a CC BY-NC 4.0 License.

Figure 13.21: Diagram of the bony labyrinth in the inner ear. Credit: Bony labyrinth by Selket has been designated to the public domain (CC0).

This same patterning in phenotypic variation has even been found in studies examining shape variation of the pelvis (Betti et al. 2013; Betti et al. 2014), the teeth (Rathmann et al. 2017), and the human **bony labyrinth** of the ear (Ponce de León et al. 2018;Figure 13.21). The skeletal morphology of these bones still varies worldwide, but a greater proportion of that variation can still be attributed to the ways in which human populations migrated across the world and exchanged genes with those closer to them rather than those further away. Human skeletal variation in these parts of the body is continuous and nondiscrete. Given the important functions of the cranium and these other skeletal parts, we may infer that the genes that underpin their development have been relatively conserved by neutral evolutionary processes such as genetic drift and gene flow. It is also important to note that while some traits such as height, weight, cranial dimensions, and body composition are determined, in part, by genes, the underlying developmental processes behind these traits are underpinned by complex polygenic mechanisms that have led to the continuous spectrum of variation in such variables among modern-day human populations.

Phenotypic Traits That Reflect Natural Selection

Even though 99.9% of our DNA is the same across all humans worldwide, and many traits reflect neutral processes, there are parts of that remaining 0.1% of the human genome that code for individual and regional differences. Similarly to craniometric analyses that have been conducted in recent decades, human variation in skin color has also been reassessed using new methods and in light of greater knowledge of biological evolution.

New technologies allow scientists to use color photometry to sample and quantify the visible wavelength of skin color, in a way 19th- and 20th-century readers could not. In one report, it was found that 87.9% of global skin color variation can be attributed to genetic differences *between* groups, 3.2% to those among local populations within regions, and 8.9% *within* local populations (Relethford 2002). This apportionment differs significantly and is the reverse situation found in the distribution of genetic differences we see when we examine genetic markers such as blood type–related alleles. However, this pattern of human skin color worldwide is not surprising, given that we now understand that past selection has occurred for darker skin near the equator and lighter skin at higher latitudes (Jablonski 2004; Jablonski and Chaplin 2000). While most genetic variation reflects neutral variation due to population migrations, geographic isolation, and restricted gene flow dynamics, some human genetic/phenotypic variation is best explained as local adaptation to environmental conditions (i.e., selection). Given that skin color variation is atypical compared to other genetic markers and biological traits, this, in fact, goes against earlier "race" typologies. This is because recent studies ironically show how so much of genetic variation relates to neutral processes, while skin color does not. It follows that skin color *cannot* be viewed as useful in making inferences about other human traits.

It is also true that some populations have not been studied extensively in skin pigmentation genetics (e.g., African, Austronesian, Melanesian, Southeast Asian, Indigenous American, and Pacific Islander populations, according to Lasisi and Shriver 2018). Earlier dispersals of these populations, and their local genetic varition, will have contributed to worldwide genetic variation, inclusive of skin pigmentation variation. Gene loci we did not previously appreciate as being linked to pigmentation are now being recognized thanks to better tools, more diverse genetic samples, and more accessible datasets (Quillen et al. 2018). Biological anthropologists look forward to further discoveries elucidating the different selective pressures and population dynamics that influence skin pigmentation evolution.

Figure 13.22: Genomicists and biological anthropologists have dedicated efforts to improving quantitative methods of measuring hair and skin variation over the last twenty years. Dr. Nina Jablonski is one such biological anthropologist specializing in the evolution and variation of human skin pigmentation. Credit: Nina Jablonski 2016 The Skin of Homo sapiens 01 (cropped) by Ptolusque is under a CC BY-SA 4.0 license.

Social Implications

To finish this chapter, we will consider the social, economic, political, and biological implications of poor understandings of race and the deliberate perpetuation of social and medical racism.

The Black Lives Matter movement (BLM) of 2013 began with the work of racial justice activists and community organizers Alicia Garza, Opal Tometi, and Patrissa Cullors. First incited by the murder of Trayvon Martin, a 17-year-old African American, and the acquittal of the man who shot him, BLM went on to protest against the deaths of numerous Black individuals, most of whom were killed by police officers (for example, Ahmaud Arbery was killed in February of 2020 by two white non-police officers). Some key characteristics of BLM from the start were its decentralized grassroots structure, the role of university students and social media in spreading awareness of the movement, and its embrace of other movements (e.g., climate justice, ending police brutality, feminist campaigns, queer activism, immigration reform, etc.). When George Floyd was murdered by a white police officer on May 25, 2020, the BLM gained new momentum, across 2,000-plus cities in the United States, and among many protesting against historic racism and police brutality in other contexts around the globe. Many in the biological anthropology community have responded to these events with a great dedication to working against systemic racism in society and institutions (American Association of Biological Anthropologists 2020).

BLM continues to be an important movement, as is evidenced in the degree of community organizing, mutual aid efforts, calls for political reform, progress toward curriculum reform and equality, inclusion and diversity (EDI) work in businesses and universities, the removal of monuments honoring historical figures associated with slavery and racism, and many other important actions. Garza (2016) writes: "The reality is that race in the United States operates on a spectrum from black to white … the closer you are to white on that spectrum, the better off you are." Tometi (2016) has stated: "We need [a human rights movement that challenges systemic racism] because the global reality is that Black people are subject to all sorts of disparities in most of our challenging issues of our day. I think about climate change, and how six of the ten worst impacted nations by climate change are actually on the continent of Africa." In the words of Cullors (2016), "Black Lives Matter is our call to action. It is a tool to reimagine a world where Black people are free to exist, free to live. It is a tool for our allies to show up differently for us." We gather from their words the importance of learning from the egregious role that anthropologists have played in the past, recognizing the legacies of "scientific" justifications for eugenics and racism in our society today, and proactively working toward environmental and social equity.

Another major industry that engages in the quantification and interpretation of human variation is medical and clinical work (National Research Council [U.S.] Committee on Human Genome Diversity 1997). Large-scale genomic studies sampling from human populations distributed worldwide have produced detailed knowledge on variation in disease resistance or susceptibility between and within populations. Let's think about drug companies who develop medicines for Black patients particularly. The predispositions to particular diseases are higher among people of African descent than some pharmaceutical businesses have taken into account. Through targeted sampling of various world groups, clinical geneticists may also identify genetic risk factors of certain common disorders such as chronic heart disease, asthma, diabetes, autoimmune diseases, and behavioral disorders. Having an understanding of population-specific biology is crucial in the development of therapies, medicines, and vaccinations, as not all treatments may be suitable for every human, depending on their genotype. During diagnosis and treatment, it is important to have an evolutionary perspective on gene-environment relationships in patients. Typological concepts of "race" are not useful, given that most racial groups (whether self-identified or not) popularly recognized lack homogeneity and are, in fact, variable. **Cystic fibrosis**, for instance, occurs in all world populations but can often be underdiagnosed in populations with African ancestry because it is thought of as a "white" disease (Yudell et al. 2016).

Sociologists, law scholars, and professors of race studies have written extensively on how genetic/technological/medical revolutions impact people of color. In her book, *Fatal Invention: How Science, Politics, and Big Business Re-create Race in the Twenty-First Century* (2013), Professor Dorothy E. Roberts writes about how technological advances have been used in resuscitating race as a biological category for dividing humans in essentialist ways (Figure 13.23). She notes how members of law enforcement have engaged in racial profiling, sometimes with the use of machine-learning and facial-recognition technologies. Ancestry-testing services also purport to tell us "what" we are and to insist that this information is "written" in our genes. Such advertising campaigns obscure the nuances of genetic variation with the primary motive of tapping into people's desire to "know themselves" and driving up profits for their businesses. Commercial genetic testing reinforces the idea that genes map neatly onto race, all while generating massive stores of data in DNA databases. In Roberts's view, the myth of the biological concept of race being perpetuated in these ways undermines a just society and reproduces racial inequalities.

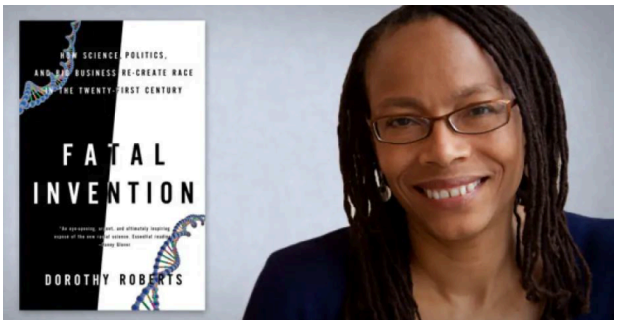

Figure 13.23: Professor Dorothy E. Roberts is a sociologist, legal scholar, and expert on the relationships among technology, medicine, bioethics, policymaking, race, and racism. Credit: Dorothy Roberts author of Fatal Invention by https://kpfa.org/ is copyrighted and used with permission.

The COVID-19 pandemic has had a significant impact on the world's population, particularly people living in the economic Global South and many Black, Indigenous and communities of color residing in the Global North. We have witnessed disproportionately high numbers of COVID-related deaths and infection cases among marginalized groups. Many immigrants and ethnic minorities in various societies have also experienced scapegoating and blame directed at them for being the source of COVID-19 spread.

To inform us on how to interpret this current worldwide pandemic, historians and anthropologists are looking back at the lessons learned from past instances of racist medicine (discriminatory practices based on broader social discrimination) and medical racism (application of discriminatory practices justified on medical grounds). Historically, who could become doctors and medical professionals was often racialized, gendered, and class specific. This made it difficult for many to overcome prejudices against women, Black people, Indigenous individuals, or other people of color from becoming doctors and clinical researchers in places such as South Africa and the United States. This, in turn, affects the sorts of information we know about health levels and health outcomes among these very groups. In the past decade, long-overdue attention is finally being paid to how race affects biological outcomes. For instance, researchers have focused on the negative legacies of racial discrimination and racism-induced stress on hormone (im)balances, mental health disorders, cardiovascular disease prevalence, and other health outcomes (Kuzawa and Sweet 2009; Shonkoff, Slopen, and WIlliams 2021; Williams 2018). The technology and standards of protocol in medical testing have been scrutinized (for more on how pulse oximeters were not designed with nonwhite patients in mind, for example, see Sjoding et al. 2020). Scholars of race and medicine have also written on how illness and disease spread have often been used to perpetuate societal prejudices. This manifests as xenophobic tendencies at a societal level, such as the blaming of "outgroups" and increased "in-group" protectiveness. Overreliance on the idea that people are "inherently" disease carriers due to genetic or biological reasons leads to improper accounting for socioeconomic or infrastructural issues that lead to differential disease prevalence amongst minority communities. (For more on race and COVID, see Tsai 2021 as well as this textbook's Chapter 16: Contemporary Topics: Human Biology and Health.)

Lastly, consider the changing field of forensic anthropology. In the past, forensic anthropologists ascribed **ancestry** or racial categories to sets of skeletons, reliant on the belief that different human groups will exhibit biologically "discrete" assortments so as to divide along culturally constructed categories (Sauer 1992). Now, a number of forensic anthropologists have argued that we should abandon these methods, both because it is unscientific and because it further validates and perpetuates this idea that race is biologically meaningful. As scientists, whether we affirm biological race as real has huge influence on the beliefs of members of the public, the judicolegal system, and law enforcement. Not all forensic experts agree with abandoning ancestry estimation. Some prefer to refocus on the neutral or selective *causes* of human biological variation, and assess how *probabilistic* it may be to assign bones of certain dimensions to one of several identified racial categories. These debates continue today as this textbook chapter is being written. More details on population affinity may be found in Chapter 15: Bioarchaeology and Forensic Anthropology.

It is important to remember that while it is possible to look for clues about one's ancestry or geographic origin based on skull morphology, again, the amount of distinctiveness in any given sample makes it impossible to distinguish whether a cranium belongs to one group (Relethford 2009). Individuals can vary in their skeletal dimensions by continental origin, country origin, regional origin, sex, age, environmental factors, and the time period in which they lived, making it difficult to assign individuals to particular categories in a completely meaningful way (Ousley, Jantz, and Freid 2009). When forensic reports and scientific journal articles give an estimation of ancestry, it is crucial to keep in mind that responsible assignments of ancestry will be done through robust statistical testing and stated as a probability estimate. Today, we also live in a more globalized world where a skeletal individual may have been born originally to parents of two separate traditional racial categories. In contexts of great heterogeneity within populations, this definitely adds difficulty to the work of forensic scientists and anthropologists preparing results for the courtroom (genetic testing may be comparatively more helpful in such situations).

Did Deeper: Measuring F_{ST}

Richard Lewontin (1929–) is a biologist and evolutionary geneticist who authored an article evaluating where the total genetic variation in humans lies. Titled "The Apportionment of Human Diversity" (Lewontin 1972), the article addressed the following question: On average, how genetically similar are two randomly chosen people from the same group when compared to two randomly chosen people from different groups?

Lewontin studied this problem by using genetic data. He obtained data for a large number of different human populations worldwide using 17 genetic markers (including alleles that code for various important enzymes and proteins, such as blood-group proteins). The statistical analysis he ran used a measure of human genetic differences in and among populations known as the fixation index (F_{ST}).

Technically, F_{ST} can be defined as the proportion of total genetic variance within a *subpopulation* relative to the total genetic variance from an *entire population*. Therefore, F_{ST} values range from 0 to 1 (or, sometimes you will see this stated as a percentage between 0% and 100%). The closer the F_{ST} value of a population (e.g., the world's population) approaches 1, the higher the degree of genetic differentiation among subpopulations relative to the overall population (see Figure 13.24 for a detailed illustration).

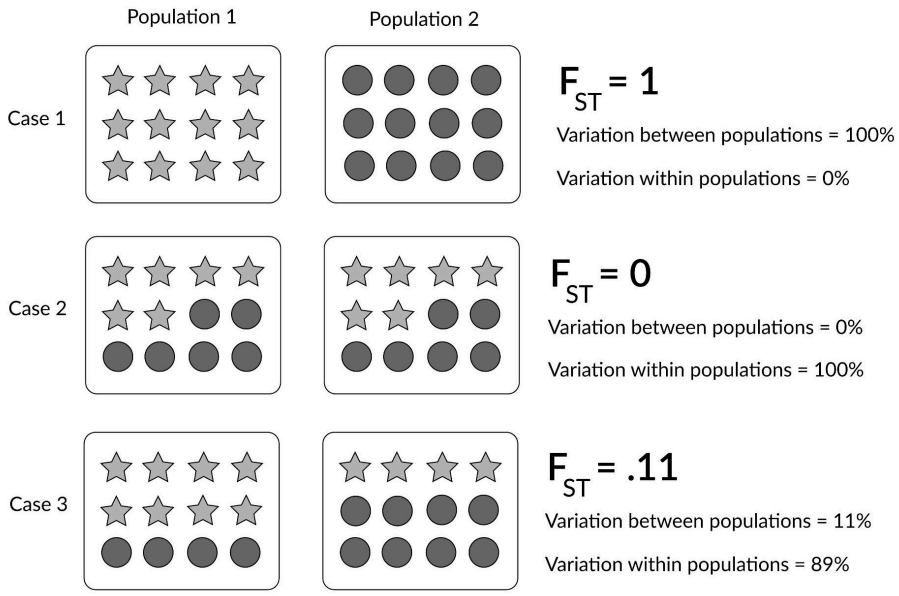

Figure 13.24: This diagram shows a range of different case studies with which we may understand how FST is calculated in different populations. In Case 1, the gene pools of Populations 1 and 2 are 100% different from each other but possess 0% variation within themselves, so FST has a value of 1. When there is no genetic variation at all between two populations and 100% variation within them, as in Case 2, we see that FST is calculated as 0. When we look at Case 3, where variation between and within are some values between 0% and 100%, we will get a decimal figure for FST dependent upon how much variation there is between and within populations. It is through such comparisons of population genetic data that we may quantify the relative similarities or differences between and within populations, and we may thus speak to the nonexistence of "racial groups" that divide up our species into broad continental or racial categories. Credit: F_{ST} original to Explorations: An Open Invitation to Biological Anthropology (2nd ed.) by Katie Nelson is under a CC BY-NC 4.0 License.

In his article, Lewontin (1972) identified that most of human genetic differences (85.4%) were found within local subpopulations (e.g., the Germans or Easter Islanders), whereas 8.3% were found between populations within continental human groups, and 6.3%

were attributable to traditional "race" groups (e.g., "Caucasian" or "Amerind"). These findings have been important for scientifically rejecting the existence of biological races (Long and Kittles 2003).

Talking About Human Biological Variation Going Forward

To conclude, utilizing the term *races* to describe human biological variation is not accurate or productive. Using a select few hundred genetic loci, or perhaps a number of phenotypic traits, it may be possible to assign individuals to a geographic ancestry, but what constitutes a bounded genetic or geographical grouping is both arbitrary and potentially harmful owing to ethical and historical reasons. The discipline of biological anthropology has moved past typological frameworks that shoehorn continuously variable human populations into discrete and socially constructed subsets. Improvements in the number of markers, the genetic technologies used to study variation, and the number of worldwide populations sampled have led to more nuanced understandings of human variation. It is of utmost importance that scientists make the following points clear to the public:

- Today, we refer to different local human groups as "populations." What constitutes a population should be carefully defined in scientific reports based on some geographical, linguistic, or cultural criteria and some degree of relativity to other closely or distantly related human groups.
- Humans have significantly less genetic variation than other primates and mammals, and all human beings on Earth share 99.9% of their overall DNA. Some of the remaining 0.1% of human variation varies on a clinal or continuous basis, such as can be seen when looking at ABO blood-type **polymorphisms** worldwide.
- Many biological characteristics in humans are actually determined nonconcordantly and/or polygenically. Therefore, superiority or inferiority in human behavior or body form cannot justifiably be linked to fixed and innate differences between groups.
- Genetic distances are correlated with geographic distances among the global human population. This is especially apparent when we consider that genetic variation is highest in sub-Saharan Africa, and average genetic heterogeneity decreases in populations further away from the African continent in accordance with the migratory history of anatomically modern *Homo sapiens*.
- The effects of gene flow, genetic drift, and population bottlenecking are reflected in some phenotypic traits, such as cranial shape.
- We recognize other traits, like skin color and lactase persistence, to be the products of many millennia of natural selective pressures influencing human biology from the external environment.

Taken together, genetic analyses of human variation do not support 20th-century (or even-earlier) concepts of race. In discussions about human variation, these genomic results help clarify how biological variation is distributed across the human population today. Taking care to think about and debate the nature of human variation is important, because although the effects and events that produced genetic differences among groups occurred in the ancient past, sociocultural concepts about race and ethnicity continue to have real social, economic, and political consequences.

Beyond talking about variation in the university setting, it is important that teachers, researchers, and students of anthropology recognize and assume the responsibility of influencing public perspectives of human variation. Race-based classification systems were developed during the colonial era, the transatlantic trafficking of kidnapped Africans and the so-called "Scientific Revolution" by the first "anthropologists" and scholars of humankind's variation. Unfortunately, some of their early ideas have persisted and evolved into present-day lived realities. Some of today's politicians and socioeconomic bodies have racially charged agendas that promote racism or certain kinds of economic or racial inequalities. As anthropologists, we must acknowledge that while human "races" are not a biological reality, their status as a (misguided) social construction does have real consequences for many people (Antrosio 2011).

In other words, while "race" is a sociocultural invention, the treatment different individuals receive due to their perceived "race" can have significant financial, emotional, sociopolitical, and physiological costs. However—and importantly assuming a "color-blind" position when it comes to the topics of "race" and ethnicity (especially in political discussions) is actually counterproductive, because the negative social consequences of modern "race" ideas could be ignored, making it harder to examine and address instances of discrimination properly (Wise 2010). Rather than shy away from these topics, we can use our scientific findings to establish socially relevant and biologically accurate ideas concerning human diversity.

Today, research into genetic and phenotypic differentiation among and within various human populations continues to expand in its scope, its technological capabilities, its sample sizes, and its ethical concerns. It is thanks to such scientific work done in the past few decades that we now have a deeper understanding not only of how humans vary but also of how we are biologically a rather homogenous, intermixing world population.

Review Questions

- How is the genetic variation of the human species distributed worldwide?
- What evolutionary processes are responsible for producing genotypic/phenotypic variation within and between human populations?
- Should we continue to attribute any value to "race" concepts older than 1950, based on our current understandings of human biological variation?
- How should we communicate scientific findings about human biological variation more accurately and responsibly to those outside the anthropological discipline?

Key Terms

Age of Discovery: A period between the late 1400s and late 1700s when European explorers and ships sailed extensively across the globe in pursuit of new trading routes and territorial conquest.

Ancestry: Biogeographical information about an individual, traced either through the study of an individual's genome, skeletal characteristics, or some other form of forensic/archaeological evidence. Anthropologists carry out probabilistic estimates of ancestry. They attribute sets of human remains to distinctive "ancestral" groups using careful statistical testing and should report ancestry estimations with statistical probability values.

Binomial nomenclature: A system of naming living things developed by Linnaeus in the 1700s. It employs a scientific name made up of two italicized Latin or Greek words, with the first word capitalized and representative of an organism's genus and the second word indicating an organism's species (e.g., *Homo sapiens*, *Australopithecus afarensis*, *Pongo tapanuliensis*, etc.).

Biological anthropology: A branch of study under anthropology (the study of humankind) that focuses on when and where humans and our human ancestors first originated, how we have evolved and adapted globally over time, and the reasons why we see biological variation among humans worldwide today.

Biological determinism: The erroneous concept that an individual's behavioral characteristics are innate and determined by genes, brain size, or other physiological attributes—and, notably, without the influence of social learning or the environment around the individual during development.

Bony labyrinth: A system of interconnected canals within the auditory (ear- or hearing-related) apparatus, located in the inner ear and responsible for balance and the reception of sound waves.

Cline: A gradient of physiological or morphological change in a single character or allele frequency among a group of species across environmental or geographical lines (e.g., skin color varies clinally, as, over many generations, human groups living nearer the equator have adapted to have more skin pigmentation).

Continuous variation: This term refers to variation that exists between individuals and cannot be measured using distinct categories. Instead, differences between individuals within a population in relation to one particular trait are measurable along a smooth, continuous gradient.

Cystic fibrosis: A genetic disorder in which one defective gene causes overproduction and buildup of mucus in the lungs and other bodily organs. It is most common in northern Europeans (but also occurs in other world populations).

Ecological niche: The position or status of an organism within its community and/or ecosystem, resulting from the organism's structural and functional adaptations (e.g., bipedalism, omnivorous diets, lactose digestion, etc.).

Essentialism: A belief or view that an entity, organism, or human grouping has a specific set of characteristics that are fundamentally necessary to its being and classification into definitive categories.

Ethnicity: A term used commonly in an interchangeable way with the term *race*, complicated because how different people define this term depends on the qualities and characteristics they use to assign a label or identity to themselves and/or others (which may include aspects of family background, skin color, language(s) spoken, religion, physical proportions, behavior and temperament, etc.).

Eugenics: A set of beliefs and practices that involves the controlled selective breeding of human populations with the hope of improving their heritable qualities, especially through surgical procedures like sterilization and legal rulings that affect marriage rights for interracial couples.

Gene flow: A neutral (or nonselective) evolutionary process that occurs when genes get shared between populations.

Genetic drift: A neutral evolutionary process in which allele frequencies change from generation to generation due to random chance.

Heterogeneity: The quality of being diverse genetically.

Homogenous: The quality of being uniform genetically.

Human diversity: Human diversity is a measure of variation that may describe how many different forms of human there are, separated or clustered into groups according to some genetic, phenotypic, or cultural trait(s). The term can be applied to culture (in which case humans can be described as significantly diverse) or genetics (in which case humans are not diverse because all humans on Earth share a majority of their genes).

Human variation: Differences in biology, physiology, body chemistry, behavior, and culture. By measuring these differences, we understand the degrees of variation between individuals, groups, populations, or species.

Isolation-by-distance model: A model that predicts a positive relationship between genetic distances and geographical distances between pairs of populations.

Monogenetic: Pertaining to the idea that the origin of a species is situated in one geographic region or time (as opposed to *polygenetic*).

Mutation: A gene alteration in the DNA sequence of an organism. As a random, neutral evolutionary process that occurs over the course of meiosis and early cell development, gene mutations are possible sources of variation in any given human gene pool. Genetic mutations that occur in more than 1% of a population are termed *polymorphisms*.

Natural selection: An evolutionary process whereby certain traits are perpetuated through successive generations, likely owing to the advantages they give organisms in terms of chances of survival and/or reproduction.

Nonconcordance: The fact of genes or traits not varying with one another and instead being inherited independently.

Otherness: In postcolonial anthropology, we now understand "othering" to mean any action by someone or some group that establishes a division between "us" and "them" in relation to other individuals or populations. This could be based on linguistic or cultural differences, and it has largely been based on external characteristics throughout history.

Out-of-Africa model: A model that suggests that all humans originate from one single group of *Homo sapiens* in (sub-Saharan) Africa who lived between 100,000 and 315,000 years ago and who subsequently diverged and migrated to other regions across the globe.

Physical anthropology: This used to be the more common name given to the subdiscipline of anthropology centered upon the study of human origins, evolution and variation (also see *biological anthropology* above). This name for the field has gradually become less popular due to two reasons: first, it may not reflect our interests in other aspects of humankind that are not physical (such as those behavioral, cultural and spiritual), and second, using this term popular in the early decades of our field may be viewed by some as harkening back to a time when biological anthropologists conducted their work in unethical ways.

Polygenetic: Having many different ancestries, as in older theories about human origins that involved multiple traditional groupings of humans evolving concurrently in different parts of the world before they merged into one species through interbreeding and/or intergroup warfare. These earlier suggestions have now been overwhelmed by insurmountable evidence for a single origin of the human species in Africa (see the "Out-of-Africa model").

Polymorphism: A genetic variant within a population (caused either by a single gene or multiple genes) that occurs at a rate of over 1% among the population. Polymorphisms are responsible for variation in phenotypic traits such as blood type and skin color.

Population: A group of humans living in a particular geographical area, with more local interbreeding within-group than interbreeding with other groups. A limited or restricted amount of gene flow between populations can occur due to geographical, cultural, linguistic, or environmental factors.

Population bottlenecking: An event in which genetic variation is significantly reduced owing to a sharp reduction in population size. This can occur when environmental disaster strikes or as a result of human activities (e.g., genocides or group migrations). An important example of this loss in genetic variation occurred over the first human migrations out of Africa and into other continental regions.

Prejudice: An unjustified attitude toward an individual or group that is not based on reason, whether positive (and showing preference for one group of people over another) or negative (and resulting in harm or injury to others).

Race: The identification of a group based on a perceived distinctiveness that makes that group more similar to each other than they are to others outside the group. This may be based on cultural differences, genetic parentage, physical characteristics, behavioral attributes, or something arbitrarily and socially constructed. As a social or demographic category, perceptions of "race" can have real and serious consequences for different groups of people. This is despite the fact that biological anthropologists and geneticists have demonstrated that all humans are genetically homogenous and that more differences can be found within populations than between them in the overall apportionment of human biological variation. This term is sometimes used interchangeably with *ethnicity*.

Racism: Any action or belief that discriminates against someone based on perceived differences in race or ethnicity.

Scientific Revolution: A period between the 1400s and 1600s when substantial shifts occurred in the social, technological, and philosophical sense, when a scientific method based on the collection of empirical evidence through experimentation was emphasized and inductive reasoning was used to test hypotheses and interpret their results.

Typological: Of or describing an assortment system that relies on the interpretation of qualitative similarities or differences in the study of variation among objects or people. The categorization of cultures or human groups according to "race" was performed with a typological approach in the earliest practice of anthropology, but this practice has since been discredited and abandoned.

Variance: In statistics, variance measures the dispersal of a set of data around the mean or average value.

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Michael B. C. Rivera is a biological anthropologist and human bioarchaeologist who studies human evolution and history and works to develop these disciplines in Hong Kong, East/Southeast Asia, and the "Global South." His doctoral thesis focused on the transition into agriculture in coastal environments and adaptations of ancient people along the beach. He is the only biological anthropologist working at the University of Hong Kong and the lead archaeologist managing the excavation of a WWII military aircraft that crashed in Hong Kong in 1945.

Michael is also an advocate for greater inclusion, diversity, equality, and access to learning in academia. Much of his work also includes science communication and public engagement activities online, in schools, and in collaboration with museums.

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Image Descriptions

Figure 13.14a: This world map is colored in to reflect the percent of populations that have the A allele (for ABO bloodtypes). The lightest color reflects populations with 0-5% allele A, and these increase at 5% intervals to the darkest color for 35-40% allele A. The lightest colors are in the Americas, particularly in South America. The darkest colors are in Europe, Australia, and very northern North America.

Figure 13.14b: This world map is colored in to reflect the percent of populations that have the B allele (for ABO bloodtypes). The lightest color reflects populations with 0-5% allele B, and these increase at 5% intervals to the darkest color for 25-30% allele B. The lightest color covers most of North and South America and Australia. The darkest colors are found in central Asia.

Figure 13.14c: This world map is colored in to reflect the percent of populations that have the O allele (the most common allele for ABO bloodtypes). The lightest color reflects populations with 50-60% allele O, and these increase at 10% intervals to the darkest color for 90-100% allele O. The lightest color is in central Asia, and the darkes colors are in North and South America.

Figure 13.19: This map shows the distribution of the four subspecies of chimpanzees and bonobos across west and central Africa.

Chimpanzees:

- Pan troglodytes verus: found across many nations in West Africa including Guinea, Sierra Leone, Liberia, and the Ivory Coast
- Pan troglodytes ellioti: found only in Nigeria and Cameroon
- Pan troglodytes troglodytes: found in Cameroon and Congo Basin
- Pan troglodytes schweinfurthii: found in Burundi, Central African Republic, Congo, Democratic Republic of Congo, Rwanda, South Sudan, Tanzania, and Uganda.

Bonobos:

- Pan paniscus: Found in the Democratic Republic of Congo