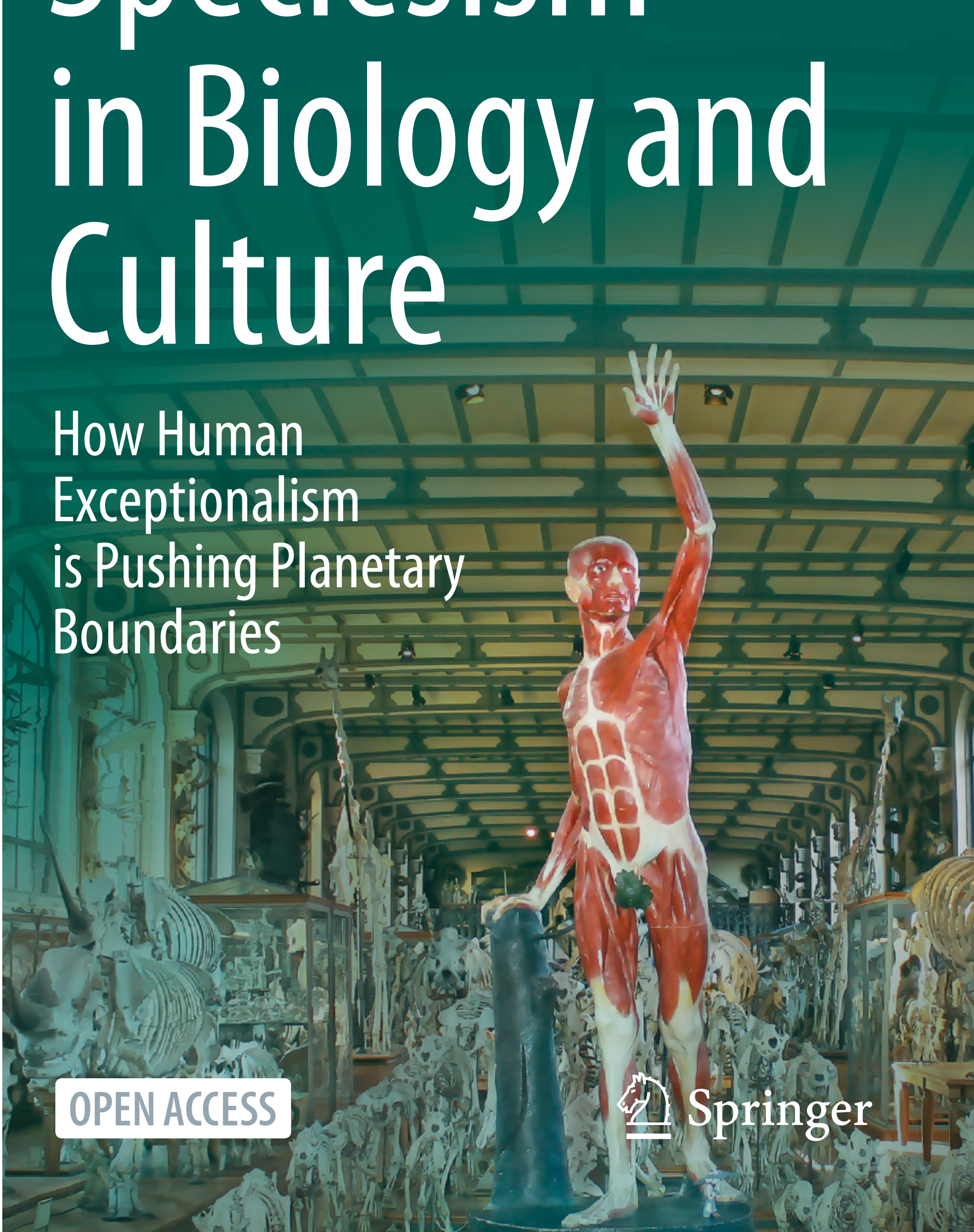
Brian Swartz · Brent D. Mishler
Editors

Speciesism in Biology and Culture

How Human Exceptionalism is Pushing Planetary Boundaries



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Cover illustration: On the cover is a photograph by Brian Swartz, taken at the Galerie de Paléontologie et d'Anatomie Comparée at the MNHN, Paris. Humans are currently in the midst of a 6th mass extinction. Our ego is front and center while skeletonized forms of close relatives lurk in our shadow. We assume we are "better" by our own self-centered standards. Our future carries so much promise. Yet even we are losing our skin, revealing how humans are animals and that humanity is inseparable from the rest of life.

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We dedicate this book to the planet's
beleaguered biodiversity and to the chance
for a bold, sustainable, and abundant future.

Foreword

Homo sapiens compulsively create and label categories—of things and even of ideas. We identify and give names, for example, to mountain peaks, rocks, languages, religions, behaviors, books, subatomic particles, elements, and living creatures. By placing a semblance of order upon what otherwise might be inchoate complexity, communication becomes easier. And, in science, categorization and insight into process have historically advanced in tandem.

In the living world, the widely used hierarchy of categories extends from the molecular and cellular subunits of individual organisms, through organs and other body parts, to the individual, the population, the species, and on up the taxonomic ladder through genus, family, order, class, phylum, kingdom, and then all of life, itself. Finer divisions arise as well, such as subfamilies, superfamilies, and subspecies, all with the same intent: to enhance communication and insight.

There, near the midpoint in the categories of life, sits what is arguably the most widely discussed category of all, at least in biology: species. In the vernacular and in the scientific literature, it is species that exhibit distinct traits, species that go extinct, species we must protect, species that provide ecosystem services, species that need to migrate under global warming if they are to survive, and species that Darwin unraveled the "origin of". Species, species, species… Why? Does a fixation on that category truly abet understanding and communication? If not, what is the alternative? Those and related questions are the focus of this book.

Linnaeus focused attention on species when he invented binomial nomenclature (a generic and a specific epithet that comprise a species name or binomen), and Darwin reified the concept in his classic work. Species are collections of twigs on the evolutionary tree of life that are considered different enough from other collections to be so designated—basically different "kinds" of organisms. It is generally agreed that sexually reproducing organisms that are sympatric (live together) without commonly interbreeding will be considered separate species. But judgments about allopatric populations (those geographically separated) are mostly matters of taste. Basically, species are arbitrary stages in a continuous evolutionary process of population differentiation. Sadly, there is a large silly literature on how to define species that does not recognize this evolutionary fact. An equivalent in silliness would be if geologists generated a long argument in print on how to define a name-able mountain, or if linguists argued about when a dialect should be called a new language, or if theologians argued endlessly about when a heresy becomes a new religion.

Despite the ambiguities, many conceptual categories that are basically chunks of continua with fuzzy borders still prove to be extremely useful—think of red, religious, sick, smart, stream, and so on. Species can be extremely useful as well. Indeed, a quick glance through the pages of The American Naturalist, Ecology, Theoretical Population Biology, Nature, Science, PNAS or any of the other journals that publish ecological research reveals that species are the most commonly used units of analysis. Models predict the forces that lead to the coexistence of some groups of species and the competitive exclusion of other species, or the flow of nutrient across species in a food web. Theories attempt to predict the distribution of abundances and body sizes of individuals across the species in an ecosystem, or the dependence of species richness on area sampled.

In some cases, however, emphasis on species can be really harmful. Perhaps the most important example is that virtually all examinations of extinction rates consider *species* extinctions, whereas *populations* within species are going extinct at rates orders of magnitude higher than those of species. Since it is those populations that deliver the ecosystem services that support civilization, the standard studies lead society to vastly underestimate the threat of the sixth mass extinction episode we are now entering.

Given the problematic nature of the species concept, its overemphasis in some contexts, and especially given the ecological and economic importance of both extant populations and, in an evolutionary context, entire lineages, it is exciting to contemplate the ways in which ecological theory can break loose from the constraints of a narrow focus on species as the organizing unit. As one example, evidence is accumulating, and theory is emerging, that predicts, that species-defined patterns in ecology, such as the distribution of abundances of trees over the species in a forest, depend strongly on the branching structure of the entire taxonomic hierarchy. In the future, those patterns will undoubtedly be shown to depend even more strongly on the structure of phylogenies. These advances provide support for the idea that entire lineages, not just extant species, need to be considered when addressing the classic question in ecology: “What patterns and processes characterize the abundance and distribution of species?”

Looking beyond this, we speculate that truly fundamental theory in ecology must break from the long tradition of rigidly using species as the dominant unit of analysis. Ecological theory that is resilient to the precise way that the units of analysis are defined, that can flexibly accommodate populations as the fundamental unit, or Linnaean units, or functional groups of individuals, or entire lineages, will provide us with the most powerful and convincing means of both understanding how nature works and predicting the probable course of the collapse of diversity and thus of the planetary life support system in the Anthropocene.

The chapters that follow in this book examine the speciesism issue from many different perspectives. We hope you enjoy the insights and find them food for thought in considering how you relate to the living world.

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Preface

This work would not have been possible without the generous support of a Sawyer Seminar grant from the Andrew W. Mellon Foundation. In the midst of a changing world where cross-disciplinary thinking is ever more critical, this project brought together a multitude of diverse minds for fresh thinking on the pressing challenges of our times. Mellon's leadership in seeing the utility of working across fields such as history, politics, law, economics, theology, paleontology, biology, anthropology, and ecology permitted participants to produce something of value that is notably different from the familiar items on our individual CVs. Funding from the Mellon Foundation allowed our thoughts to intertwine in ways that would not have been possible without their support. Mellon's funding also supported open-access publication of this book, which will allow it to reach much broader audiences.

We thank the speakers in the original Mellon-funded Sawyer Seminar Series held in 2012–2013 at the University of California, Berkeley, in order of appearance: Craig Moritz, Brent Mishler, Robert Proctor, Roberta Millstein, David Wake†, Tim White, Tony Barnosky, Jeffrey Boore, Thomas Carlson, Richard Norgaard, Paul Rabinow†, Brian Fagan, Patrick Kirch, Kent Lightfoot, Samuel Lucas, Ken Wachter, John Wilkins, Willis Jenkins, Quayshawn Spencer, Vijaya Nagarajan, Elizabeth Allison, Sam Mickey, Michael Allen, Valerie Eviner, Katherine Suding, Justin Brashares, Gary Steiner, Andrew Light, Joe Guth, Holly Doremus, David Winickoff, Eric Biber, Pamela Ronald, Jonathan Foley, Nathan Sayre, Jennifer Sowerwine, David Zilberman, Clive Hamilton, and Paul Ehrlich.

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We would like to extend a special thanks to Michael Allen, Paul Ehrlich, Scott Fitzpatrick, Saul Griffith, John Harte, Marc Lucht, Nick Matzke, Mark Moffett, Gary Steiner, John Wilkins, and Rasmus Winther for their excellent contributions to this published volume. Their insights and wit allowed more effective integration of our core pursuits. Thank you for how you see the world, for your ability to disarticulate complex subjects, and for your willingness to venture afield into the past, present, and future. On a planet now supporting over eight billion bodies and minds, we appreciate being surrounded by those who care enough to express how life can prosper on Earth and beyond.

Berkeley, USA
December 2022

Brian Swartz
Brent D. Mishler

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Brent D. Mishler is Director of the University and Jepson Herbaria and Distinguished Professor in the Department of Integrative Biology at the University of California, Berkeley, where he teaches about island biology, biodiversity, evolution, and phylogenetic analysis. He received his Ph.D. from Harvard University in 1984. His research interests are in the ecology and evolutionary biology of bryophytes (mosses and liverworts), as well as the theory of phylogenetic systematics. He has been heavily involved in developing electronic resources to present taxonomic and distributional information about plants to the public, with applications to conservation concerns. He has most recently been involved in developing new “spatial phylogenetic” tools for studying biodiversity and endemism using large-scale phylogenies and collection data in a geographic and statistical framework. He is author of over 200 scientific publications, including the recent open-access book: *What, if Anything, are Species?* (CRC Press, 2021).

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Part I
Biology and Culture

Chapter 1
Speciesism, Science, and Society

Brian Swartz and Brent D. Mishler

Abstract Speciesism is to species as racism is to race. The tenets of both are baseless on all grounds. Although our consciousness is currently raised toward the latter, the former remains persistent and infectious. Speciesism begins with how we view ourselves in relation to the natural world, and leads to behavior that challenges our future on this planet. Our naïve exceptionalism has repercussions for ecology, ethics, conservation, law, culture, and the energy and resource base that powers human society. We are merely a part of the natural world, though we have behaved for centuries through a myopia of perceived dominion. By our actions, we are now pushing against a significant number of planetary boundaries, such as threats to natural resources, climate, biodiversity, and the ecological networks that keep humanity afloat. With each passing day, the distinction blurs between the anthroposphere and the ecosphere, between humanity and the earth-system. As transformers of this planet's environment, we are one of the greatest ecosystem engineers the earth has ever seen. Yet we remain dependent upon nature, and how we behave over the next few decades will determine our prosperity on this planet and beyond.

1.1 What is Speciesism?

Academics and the general public largely remain unaware of the concept of speciesism (Jones 2020; Gunderman and White 2021). There certainly exists a familiarity with ethical issues such as factory farming, clearcutting forests, or overfishing. Yet confusion remains about speciesism itself, its underpinnings, and its extensions which transcend the history and future of life on Earth (Fjellstrom 2002; Bindig 2007; Horta 2010; Jaquet 2019). It is the purpose of this chapter, and this book as a

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whole, to expand this discussion and lay a foundation for what emerges from how we view ourselves in relation to the natural world.

If human behavior is our guide, it is clear that we view ourselves as undeniably superior to other living things. The problem is that most people do not realize they have this view, and thus can't easily see the effects that extend into other facets of the human experience (Wilson 2012). Wherever you look in human behavior, speciesism is likely found. It may start with an Instagram post with a person standing on wildflowers thus damaging the very thing they signal to care for. Yet speciesist views extend to a diverse set of topics including: the religious influences that have shaped our self-concepts and global actions; how we treat ecosystems and other organisms; how we grow food and manage the consequences of its production; and how we procure non-living natural resources such as energy that we need to thrive.

While speciesism begins with a selfish notion of perceived human specialness, it extends afield into the future of our existence in the tree of life. We are one lineage (see the definition of this and other terms in Table 1.1) that is genealogically related to millions of other lineages—all living things. Our ancestry has its roots in an extensive genealogy that has been branching and reticulating (merging) for about four billion years. We also share a global environment with all living things. *We are related to, and connected with, the rest of life, and our actions both affect and depend upon our relatives.*

1.1.1 Speciesism: Evolutionary and Ecological Thinking

It is helpful to consider "tree thinking" when visualizing humanity's relationship to other forms of life. This heuristic mindset derives from methods that biologists use to reconstruct the evolutionary relationships among organisms (Baum et al. 2005; Gregory 2008). The branching diagrams that result are called "phylogenies" or "evolutionary trees" (see Fig. 1.1). When we hear about the tree of life—or a lineage, a branch on the tree of life—it is in reference to these kinds of diagrams. "Tree thinking" is about understanding how these diagrams communicate information.

There are specific ways to read, understand, and decipher a phylogeny. For example, in Fig. 1.1, although it is intuitive to read across the tips of the branches, this would lead you to misunderstand what is being conveyed. The tips of each branch refer to living descendants of ancestor–descendant pairs. The diagram does not signal who is ancestral to whom, but rather how recently two tips shared a *common* ancestor. The depth of a shared branch indicates this. For example, you are a descendant of ancestors with a deep familial history. Your siblings and cousins are also a product of this history. Yet no one would argue that you gave rise to your aunt or that your sister came from your brother. Instead, it is a point about recency of common ancestry. You share common ancestors with your siblings (parents), just as you share common ancestors with your aunt (grandparents). These same concepts apply throughout the tree of life.

Table 1.1 A glossary of commonly-used concepts throughout this book

Concept	Meaning	Example
Lineage	Ancestor–descendant relationships through time	Example: Modern cacti are a lineage of flowering plants that share a common ancestor with oaks at one level, with conifers at a deeper level, with ferns at a still deeper level, and so forth. **See** Fig. 1.4. These lineages form the branches on the tree of life Details: Since their origin in the central Andes, cacti have spread into Central and North America across vast stretches of geographic space. Over time, their ancient ancestors gave rise to their modern-day descendants (Guerrero et al. 2019)
Clade	A cross-section of a lineage at a single time	Example: Modern cacti are a clade within flowering plants, flowering plants are a clade within seed plants, seed plants are a clade within vascular plants, and so on. These clades nest within the tree of life, as groups within groups, like Russian dolls Distinction: A lineage has a time dimension, but a clade does not. Clades are *synchronic* cross-sections of lineages, whereas lineages are *diachronic* ancestor–descendant relationships over time. Put another way: a clade is a cross-section (horizontally) through the lineages that descend from a shared common ancestor (Mishler and Wilkins 2018). A close analogy is a single movie frame (synchronic) versus the whole movie (diachronic). **See** Fig. 1.4
Phylogeny	An evolutionary tree (i.e., a phylogenetic tree)	Example: **see** Figs. 1.1–1.2, 1.4–1.5 Details: This is a branching diagram with a vertical time dimension that visually communicates how the tips of the tree relate to one another through common ancestry. The branch lengths shown may reflect changes is characteristics and/or time, depending on how the trees are constructed

(continued)

Table 1.1 (continued)

Concept	Meaning	Example
Taxon	Any formally named group of organisms, traditionally based on various criteria, but in modern phylogenetic classification is restricted to clades	Example: cacti are a taxon of flowering plants, flowering plants are a taxon of seed plants, mammals are a taxon of vertebrates, vertebrates are a taxon of animals, and so on Details: A taxon refers to a group of organisms, which in modern phylogenetic systematics is restricted to monophyletic groups (i.e., clades). A monophyletic group includes only descendants of a common ancestor. Taxon is the singular form of taxa
Taxonomic rank	A particular level in a rank-based classification system	Humans as an example: (*Domain*) eukaryotes, (*Kingdom*) animals, (*Phylum*) chordates, (*Class*) mammals, (*Order*) primates, (*Family*) hominids, (*Genus*) *Homo*, (*Species*) *sapiens* Details: These ranks are human constructs and stem from the pre-evolutionary period of history. They cut across the tree of life at varying depths and do not mean the same thing among groups (Darwin 1859, De Queiroz and Gaulthier 1994). This also applies to any category between the ranks listed above. For example, *SuperOrder* is a rank between *Class* and *Order*, *Subfamily* is a rank between *Family* and *Genus*, and so on. **See** Fig. 1.5
Adaptation	Traits that result from natural selection and increase the relative "fit" between an organism and its environment	Example: Certain groups of cacti exhibit adaptations to arid, dry environments Details: Cacti ancestrally have flat planar leaves. However, water can quickly evaporate across leaves with large surface areas. As cacti spread into drier environments, their leaves were modified into spines, losing the flat planar structure and photosynthetic function, while photosynthesis shifted to their branches. This is why the branches (stems) of desert cacti are green and why they lack planar leaves (Nobel 2002)

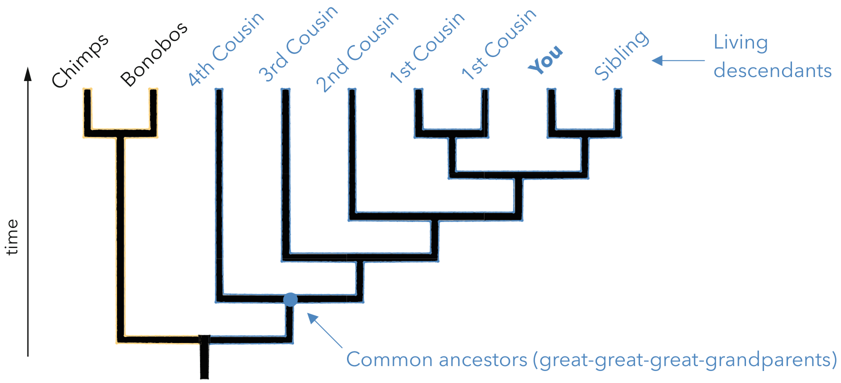

Fig. 1.1 An evolutionary tree showing the relationships among you and your nearest relatives. We do not read across the tips of branches (living descendants) to understand ancestor–descendant relationships. You did not give rise to your sibling nor did you come from your second cousin. You are all descendants of shared common ancestors. A "lineage" refers to these ancestor–descendant pairs. For simplicity, many branches have been excluded that would fall between humans and the other primates depicted

For example, reflecting on the attributes that make you unique—from personality traits to the genetic/environmental influences that shaped you—there is no other person on Earth who can fill your shoes. Comparatively, each branch on the tree of life is also unique. We all have combinations of features that make us special, and no lineage is evolutionarily "higher" or "lower" than any other.

Whereas it may seem true that humanity dominates the planet at a scale not seen by other organisms, the earth has been and likely forever will be dominated by microbes (Gould 1996) (see Fig. 1.2). The tools we use to manipulate nature circle back to remind us how much we remain a part of this microbial world. For example, despite our cleverness, we are running out of antibiotics (Stadler and Dersch 2016). This predicament partly stems from industrial farm animals spending their entire lives on rigorous antibiotic regimes (Anomaly 2015). *We are a tiny branch on the vast tree of life, and share with millions of other branches a network of dependent interactions. Humanity takes massive risks when we fail to consider our modest place in relation to the rest of nature.*

1.1.2 The Scientific Problems with Speciesism

Speciesism carries two fundamental precepts: (1) species are real; (2) one or more of these species are superior to others. The species*ist* embraces both propositions. However, the picture is nuanced and concepts are nested. For example, "species realism" is the view that species are uniquely real (Mishler 2010, 2021; Mishler

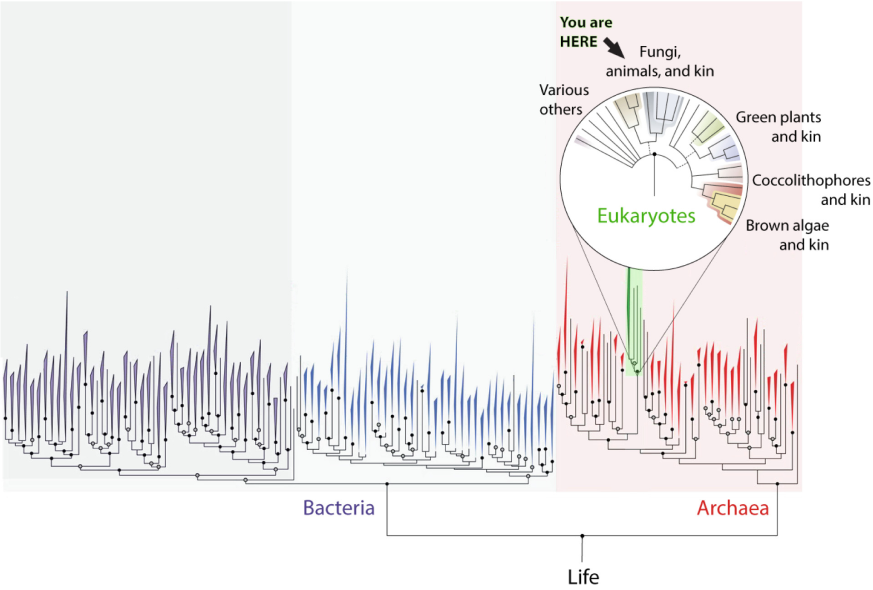

Fig. 1.2 The tree of life, modified from Hug et al. (2016) and Burki et al. (2020). There are two primary branches, Bacteria and Archaea. *Escherichia coli* are a common example of bacteria (in our GI tract). Methanogens are an example of archaeans (in the guts of cows) who produce methane from their GI tracts. Interestingly, as archaeans, humans are more closely related to methanogens than we are related to the *E. coli* in our own guts. Eukaryotes (in green) are Archaea that include organisms like ourselves with a nucleus in their cells (e.g., ALL other animals, plants, fungi, etc.)

and Wilkins 2018), while "speciesism" pairs species realism with an argument for superiority (see Fig. 1.3).

To understand this, it can be helpful to draw an analogy to racism. Racism also carries two precepts: (1) races are real; (2) one or more of these races are superior

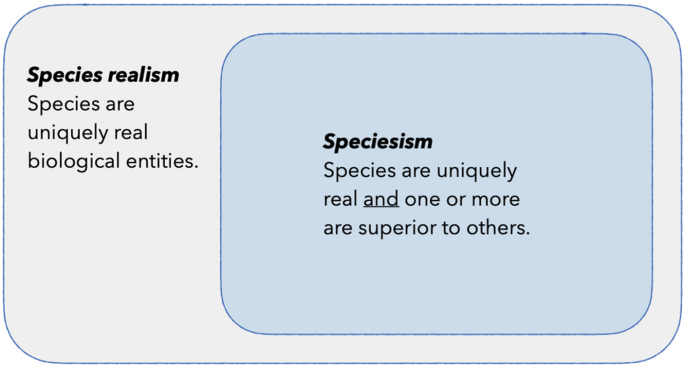

Fig. 1.3 The conceptual relationship between species realism and speciesism

to others. Like speciesism, embracing superiority encompasses the view that races are privileged categories. The parallel does not stop there. Like “species realism,” “racialism” views races as biological entities (i.e., as more than cultural constructs; Appiah 1989). One can be a racialist without being a racist as one can be a species realist without being a speciesist. However, the problem with speciesism and racism is that they are both scientifically baseless. But how so?

Consider speciesism in parts: (1) species are uniquely real; (2) at least one species is superior. See Sect. 1.4.1 below for details concerning species concepts in biology. For our purposes here, it suffices to say that whether we focus on sex, anatomy, ecological differences, or phylogeny, no species concept consistently and accurately describes life as it exists across the tree of life (Mishler 2021). It is because of this diversity that we have so many species concepts. The things called species are not uniquely real.

Curiously, we can still recognize real biological “things” across the tree of life. These “things” are lineages and clades, based on ancestor–descendant relationships that on occasion split into separate streams (Mishler and Wilkins 2018). See Table 1.1 and Fig. 1.4 for the distinction between the related but different terms “lineage” and “clade.” Ancestor–descendant relationships can be short like those shared between you and your parents or go deep into the past. Sometimes lineages split, other times they merge, and other times they go extinct, but they all together make up the tree of life.

Species realism begins to fail when humans impose taxonomic ranks onto the natural world. For example, a “species” of mammal, a “species” of plant, and a “species” of fungus are not the same thing. Comparatively, the species level is not different from any other taxonomic rank in that every level in the hierarchy is an arbitrary boundary that cuts across the tree of life at variable depths (Mishler 2021)

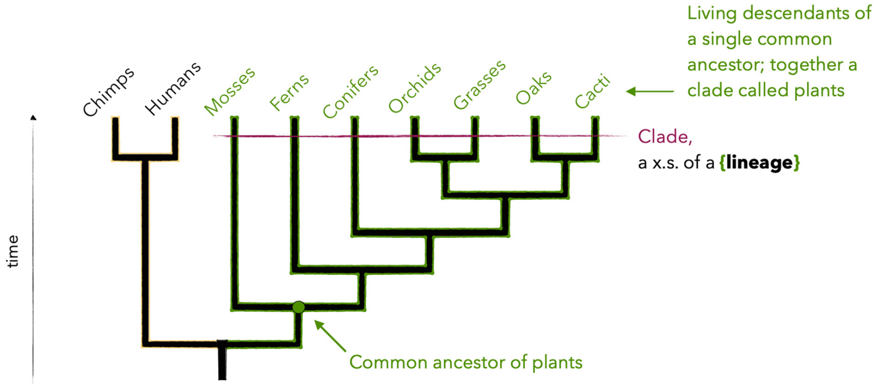

Fig. 1.4 An evolutionary tree showing the relationships among a subset of plants and animals. “Lineages” of plants are illustrated with a black core and green outline, here specifying the branches that connect the common ancestor of plants to its living descendants. A “clade” is a cross-section (x.s.) of these lineages at any level. For simplicity, many branches have been excluded that would fall between those depicted here

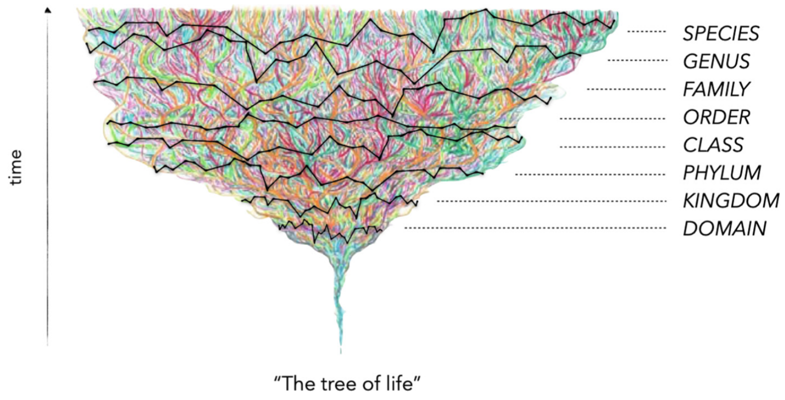

Fig. 1.5 This is the relationship between branches on the tree of life (colored lineages) and the taxonomic levels in the hierarchy (black lines) that humans have used to classify life. Lineages split and merge as they originate and go extinct. These lineages are real biological relationships that connect living things in nested groups. In comparison, taxonomic ranks (e.g., species, genus, etc.) are human constructs that are neither real nor equivalent across groups. The species level is no more special than the genus, family, phylum, or kingdom level. They are all arbitrary cut-offs along a continuum with no privileged position (colored background tree drawn by Karen Klitz)

(see Fig. 1.5). In contrast to species, lineages and clades carry the same meaning in all groups of organisms. Importantly, lineages allow us to measure the earth's biodiversity with precision without ranks, using a measure called "phylogenetic diversity" (Faith 1992; Mishler et al. 2014; Thornhill et al. 2016, 2017; Chap. 8 in this book).

Knowing that lineages make up biodiversity reveals a second issue: the tree of life is fractal. Biodiversity is about branches, from parents and offspring to deep common ancestry. An arbitrary species-level-cut exists across the tree and the depth of this cut varies among groups. This reveals that the species level is not exceptional among a continuum of lineages, bigger or smaller, and that all are important to consider for various purposes including conservation (Mishler and Baldwin 2021).

The arbitrary nature of the species level affects attitudes towards speciesism, of course. One construct cannot be superior to another construct if they are non-corresponding arbitrary entities. If the speciesist proposes the unique reality of species AND embraces superiority then both tenets fall flat. *Lineages make up the tree of life and all extant tips of this tree are equally present today, with none higher, lower, or ethically superior.*

Considering this, let us extend the parallel between species and race. Human races are not distinct branches (lineages) within humans; they are cultural constructs (Templeton 1998, 2013). Members of one so-called "race" are not always closely related. For example, one might look "Caucasian" but be more closely related to a Moroccan cousin than those cousins are related to fellow Africans in Nigeria. Races cannot be superior to others if they do not exist as biological categories. A *socially* constructed group may better at doing a particular thing, but that doesn't mean there is an underlying biological "race" that unites them. Behaviorally, this matters because how we see ourselves influences how we treat other people (racism) and how we treat other living things (speciesism).

One lineage may be empirically superior to other lineages in a specific functional trait, of course (e.g., eagles have better eyesight than humans). Yet it is essential to remember that adaptations (see Table 1.1) are about the relationship between an organism's traits and its environment (Darwin 1859). Adaptation is not universal across all traits, and there are constraints imposed by developmental relationships among traits. Humans have a mixture of traits like all other organisms, some "good" traits and some "bad" (Gould and Lewontin 1979). We may be unable to fly like bats or swim like whales, but we have a gift of foresight and planning. We are working hard to promote sustainability and venture afield on an interplanetary scale. However, aspects of our intelligence may be maladaptive in the arc of humanity's future. We are capable of some of the most astonishing accomplishments, but as emotional animals, our minds often hijack themselves (Asma and Gabriel 2019). What the future holds within our prevailing environment is an experiment in progress.

Until then, we must be keenly aware of speciesism during this time of perceived dominion. Human beings are probably the most dominant ecosystem engineers the earth has ever seen. However, we are also the worst "weed" the world has had to deal with. Over the last few hundred years, virtually no part of this planet has gone untouched. Whether we consider the energy and resources that fuel civilization or the larger earth-system that we expand into, the effects of our behavior are profound (Rockström et al. 2009; Hughes et al. 2013; O'Neill et al. 2018). Why do we behave as we do? Why do we assume that we have the right to modify the planet as we wish and subjugate other living things to our needs? We often overlook intrinsic values in organisms and natural resources ("intrinsic" as in something special about an entity in question) and instead pursue instrumental values (values that relate solely to our benefit) (Moffett 2020). *Our unquestioning attitudes about dominion over the rest of nature are strikingly similar to the unquestioning attitudes held by dominant cultures throughout history about their dominion over the rest of humanity.*

There is little doubt that we love ourselves to the exclusion of others. Perhaps this is understandable as a form of "us versus them" thinking that derives from our evolutionary past. But these tendencies cost us tremendously within the modern world (e.g., race, religion, politics) and across the tree of life (e.g., extinctions, loss of ecosystems, global climate change). As a civilization, we do not hide, or even realize the depths of our perceived superiority. We view ourselves as "better" than the rest of life.

Human actions indeed reveal deep seated speciesism. Grounding us in the natural world is probably the first best step toward dethroning our misguided exceptionalism. For millennia, we have constructed ideas and belief systems that position us at the "top" of life on Earth (Lovejoy 1963). These beliefs have placed *Homo sapiens* (wise man) as THE animal to "fill the earth and subdue it," to "have dominion over the fish of the sea and…over every living thing" (Genesis 1:28). We have done precisely this. For years, humans have debated what makes us special, be it language, tool use, culture, consciousness—all shades in a continuum with parallels and antecedents in other organisms (Lieberman 2013; Bickerton 2014; Tomasello 2014). However, there is one distinguishing point that makes the case for itself: we are likely the only organism, ever, that has spent mental effort trying to convince itself of just how exceptional it is.

1.2 A Sawyer Seminar Funded by the Andrew W. Mellon Foundation

This volume stems from a seminar series on speciesism held in 2012–2013 at the University of California, Berkeley, funded by the A.W. Mellon Foundation. This book follows the same format as the original seminar series by viewing speciesism in light of biology, culture, history, conservation, law, and sustainability. We have kept many of the same topics, though we have added new topics in the spirit of our times (e.g., the social concept of race, pandemic diseases, and the future of food and energy). Some of the seminar speakers contributed chapters to this book, and we invited additional scholars to contribute.

We first unpack speciesism by rooting humanity within the tree of life. Doing this allows us to see the evolutionary and ecological themes that connect our lineage with the rest of life. We expand this by revisiting early human civilizations to understand how smaller societies behaved on islands as humanity now acts globally. Throughout human history, islands have been microcosms of present impacts. This dissection of a "historical small" within a "current big" makes human actions tangible and clarifies how we repeat old behaviors. Will we continue these antics as we pursue interplanetary travel and treat planets as new microcosms within the universe? What insights exist in this landscape of past mistakes and future visions?

We then look into how humans are treating the current world. What does human behavior say about how we value forest resources (FAO 2020a), ocean resources (FAO 2020b), and the free services (e.g., pollination, photosynthesis, air to breathe, climate regulation, etc.) that come when these environments are intact (FAO 2020c)? How are we treating domesticated plants and animals, including soils that these organisms grow in or live upon? How do our cultural systems (e.g., religious, industrial, political, legal, medical) align with and extend from human-environment interactions? What do our cultural systems reveal about what we value? In medicine, if our microbiome (the totality of microorganisms that live in and on us) slightly outnumbers our cells by a ratio of about 1.3:1, then what does this say about what it means to be human, yet alone a "species?"

In the current landscape of pandemics and zoonotic diseases (diseases transferred between human and non-human animals), how is our perceived exceptionalism accelerating global problems? As the human population grows and we consume more resources, city centers become more dense. How will this affect our management of contagious diseases? How will we feed this world? How will energy power this future? Like any complex open system, human civilization requires energy. As we strive to wean ourselves off fossil fuels, what clean and sustainable alternatives will power a society that remains dependent upon the laws of physics? These are all questions that inevitably flow from understanding speciesism and its consequences.

1.3 Major Topics Related to Speciesism Covered in This Book

The chapters in this book follow the arc of the original seminar series, although with expanded breadth. Major themes include alignments between speciesism and racism; connections to ecology and evolution; behavioral antecedents in human prehistory; the influence of religion on human perception in relation to nature; the role of symbols as social meanings in humans and other animals; current ethical and legal manifestations as an extension of human behavior; the affects of speciesism in conservation biology; and the civilizational consequences of human actions on interplanetary scales. In this section we give short summaries of the other chapters in the book. In the following Sect. 1.4 we discuss a few additional topics that are not represented by separate chapters in the book.

1.3.1 Race and Human Genomic Variation, *Rasmus Winther*

In his chapter, Winther shows that we differ genetically far less than intuitions suggest. Compared to our differences with close relatives, there is relatively little genomic variation within *Homo sapiens*. Among the 3 billion base pairs (DNA letters) that compose our genomes (one from each parent), they are 99.9% identical among all humans. Interestingly, African genomic variation is the richest and most distinctive among all continents. Further, this pattern continually decreases as geographic distance from Africa increases; we vary less as we move away from Africa. In essence, we are all Africans, despite superficial differences in appearance or skin pigmentation.

Winther invites us to see that surface-level variants should not matter ethically or politically. If we differ by only 0.1% at most, with most differences in Africa itself, what does this say about the biological core of humanity? We are fundamentally the same. What does this imply about the basis of racism? It is empirically unfounded.

How can we pull from this insight to rally around a unified cause, a shared vision for a shared future, as members of a single lineage (*Homo sapiens*) trying to manage its existence on a finite planet? This question is more complicated, yet if we can embrace our homogeneity and act, then perhaps we can start behaving as though our future depends upon it. How we treat the world and each other affects all that we engage with, especially when our actions affect prosperity.

1.3.2 Science Without Species, Nicholas J. Matzke

In recent decades evolutionary biology has begun to move away from species as the key unit of analysis to address biological questions. In this chapter, Matzke begins by outlining how phylogenetic comparative methods have become essential tools in statistical analyses of trait relationships. Species are not statistically independent observations because they are related to different degrees on a phylogenetic tree. In fact, moving to a phylogenetic view of biodiversity can avoid a number of problems created by attempting to impose a uniform species rank across different geographic regions and clades. A major challenge in modern studies of diversification and extinction is the units of analysis and how they are defined and recognized. Taxonomic ranks including "genus" and "species" are human-defined levels imposed on a phylogenetic tree. The tree itself is the reality produced by the macroevolutionary process, and it includes every level of gradation in evolutionary divergence. Once ranks are imposed upon it, a variety of methodological problems are created as scientists compare ranks across datasets and timescales. Phylogenetic thinking can provide a solution. Matzke concludes this chapter with examples where cutting-edge science is done without need of the "species" rank.

1.3.3 Islands as Microcosms of Human Impact, Scott M. Fitzpatrick

The colonization of islands by humans in the ancient past provides study systems for human impacts on a manageable scale. In this chapter, Fitzpatrick initially focuses on the vast expanse of the Pacific, where beginning ca. 3000 years ago, Micronesian and Polynesian voyagers colonized the most remote, and final places to be reached by humans. The biota of these islands evolved independently for thousands or even millions of years, resulting in high rates of endemism and extremely fragile ecologies. The first arrival of *Homo sapiens* caused a wide variety of impacts that were greatly amplified later with Euro-American incursion. As ecologically bounded places, islands thus serve as model systems for how humans affect the earth's biosphere in the modern age.

Fitzpatrick takes this concept further, suggesting that the processes involved in the prehistoric colonization of islands are a corollary for current global impacts and extraplanetary colonization. As the possibility of extraplanetary migration becomes a reality—perhaps even a necessity to ensure our survival—Fitzpatrick invites us to ask what lessons we can learn from the archaeological study of islands. What are the consequences for us and for other forms of life on this planet and possibly others? Will we learn from our mistakes or will we bring them with us? The earth is only one of many habitable islands in the larger cosmos. How will we manage the present manifestations of human behavior, growth, sustainability, economics, ethics, disease, density, and the future of food and energy?

1.3.4 Species, God, and Dominion, John S. Wilkins

In this chapter, Wilkins argues that having a "theoretical" notion of species causes harm to science and polity. He clarifies that species as a concept is the result of theological and philosophical considerations, with deep historical roots, not any current empirical or scientific need. Yet the idea of biodiversity existing as bounded species units still holds political importance for religious ideas of *dominionism*, or supposed human supremacy over nature. It also carries tremendous impact on environmentalist and conservationist politics in the United States and elsewhere. Fundamentally, as Wilkins explains, the current concept of species is damaging since it retains much of its essentialist religious origins and emphasizes human exceptionalism to the detriment of expanding our attitudes about the rest of life.

1.3.5 Symbols and How We Came to Be Human, Mark W. Moffett

A major belief behind the idea of human exceptionalism is that *Homo sapiens* is distinct from other taxa in our use of symbols. In this chapter, Moffett considers the concept of "symbols" to describe anything with a socially shared meaning but without obvious ecological utility. Countering the argument that symbols are unique to humans, Moffett proposes that they be recognized as agents in other animals that operate in a diversity of ecologically meaningless "social markers." For example, broadly speaking, social markers might signal ingroup versus outgroup identity, and manifest in ways similar to how humans posture as they walk, express emotions, or use scents or cultural ornaments to decorate their bodies.

What does the broad tendency for "marking" traits suggest about the evolutionary origins of symbolism? Moffett critiques views of human symbolism expressed by sociologists, psychologists, anthropologists, archaeologists, and biologists. Instead, he proposes that symbolism might have arisen from behaviors in other animals which live in societies bound together by simpler "markers" of identity, such a group scents or vocalizations that do not convey ecological significance. Importantly, such markers can be essential for holding societies together.

1.3.6 Human, Non-Human, and Ecosystem Rights, Gary Steiner and Marc Lucht

Western philosophical tradition has long maintained that only humans can possess rights. In this view, attributing rights to non-human animals is dubious and attributing rights to the non-sentient natural world in nonsensical. However, in their chapter, Steiner and Lucht analyze the commitments motivating this conception of rights and reveal that it is based on self-centered prejudices of humans that their own type of sentience is required for full moral status. Steiner and Lucht show how recent research has elucidated the intellectual and emotional lives of other animals, making it necessary to rethink their moral status. More radically, they show how rejecting anthropocentrism opens the door to recognizing that certain non-living entities also deserve moral consideration and have rights to respect. The differences between the traditional and the new approach to rights draws into question the conditions for moral worth and highlights our need for a satisfactory theory of the world and understanding of the proper place for humanity within it.

1.3.7 A Phylogenetic Approach to Conservation: Michael F. Allen and Brent D. Mishler

As late as the sixteenth century, the world was a matrix of wild lands. Due to rapidly increasing technological development and population growth, we increasingly subjugated and diminished the natural world. By the eighteenth and nineteenth centuries, some pushback occurred, with calls emerging for conservation. National parks were established and laws passed that were designed to save endangered species. In this chapter, Allen and Mishler show that while the "one species at a time" approach can be credited with saving many individual taxa, it is insufficient to deal with the current biodiversity crisis given urgent pressures on remaining natural lands. They advocate moving from a "single-species approach" to an "area-based approach" that incorporates a broad phylogenetic definition of biodiversity. Biodiversity conservation should not focus on the arbitrary level at which species are named. Instead, it should be focused on the whole tree of life. Allen and Mishler discuss new spatial phylogenetic tools that leverage recently available DNA and geographic data, plus new computational tools, to incorporate all levels in the tree of life when making conservation decisions. To protect biodiversity amid increasing environmental impacts, we need to adopt cutting edge strategies for conservation to allow life to thrive and ecosystems to function.

1.3.8 Energy and Society: Toward a Sustainable Future, Saul Griffith

Energy is the single greatest lever that moves civilization. As a society, we have pulled upon fossil fuels as a historical source of energy, but have begun transitioning toward alternatives. In this chapter, Griffith explores our global move toward alternative energy, its feasibility and impacts, and the kind of world we can create with a decarbonized and electrified future. He considers how much energy we actually need, and evaluates alternative sources of energy including nuclear power. Then he examines what the effects of achieving a sustainable energy future would be, including impacts on biodiversity and land use. Throughout the chapter, Griffith explores how to achieve sustainability while avoiding destruction of the rest of biodiversity and positively uplifting humanity.

1.4 Other Topics Related to Speciesism

Speciesism connects to a variety of other subjects that we were not able to include as chapters in the book. Thus, we give an encapsulated treatment below of the nature of biodiversity, human population, health, medicine, and the integrative future of food.

1.4.1 Species, the Arbitrary Constructs of Biodiversity

It was Darwin (1859) who first realized that the species level is not unique. As he saw it, lineages diverge for various reasons, though at some point (out of convenience), a taxonomist decides to call a lineage a species even though nothing fundamental happened at that point in divergence. By the early-mid twentieth century, evolutionary biologists such as Theodosius Dobzhansky and Ernst Mayr reintroduced species as a “unique” level (Dobzhansky 1937; Mayr 1982). They used their “Biological Species Concept” (BSC), proposing that interbreeding is the key criterion that happens uniquely within species (see Mishler 2010 for detailed discussion).

However, the recent availability of extensive genetic data within and between named species makes it abundantly clear that Darwin was right and the BSC does not apply in plants, animals, or microbes. Interbreeding and other forms of horizontal gene transfer (i.e., genetic exchange across lineages, distinct from the normal vertical transmission between ancestors and descendants) happens at multiple hierarchical levels across all life (Husnik et al. 2021). Contrariwise, there is a lack of interbreeding at many levels as well (Mishler and Donoghue 1982). There is no magical “species level” where rampant interbreeding abruptly transitions to no interbreeding. Instead, there are nested clades that are smaller and larger than the traditional species level that play essential roles in ecology and evolution.

In other words, the situation is richer and more interesting than the BSC took into account. A multi-level approach is a more accurate way to study the origin, maintenance, and conservation of biodiversity (Mishler 2021). A similar suite of processes act at various levels in the tree of life, albeit with a balance that shifts in exciting ways at various levels in different parts of the tree. A revolution in many areas of study (e.g., diversification, niche evolution, biogeography, coevolution, and conservation) will follow once a multi-level view replaces a rigid focus on the species level or other taxonomic ranks (Mishler 2022).

Granted, present methods based on taxonomic ranks do provide a rough estimate of diversity over time. In paleobiology for example, ranks provide utility since they allow discovery of patterns and processes that regulate global biodiversity (Sepkoski et al. 1981; Alroy et al. 2008, Barnosky et al. 2010). Current methods enable practitioners to reveal major historical events even if the ranks are arbitrary. For example, there have been five mass extinctions over the last 541 million years (e.g., via extraterrestrial impacts, widespread volcanic eruptions, climatic events that followed, sea-level changes, etc.). We can discover how environments and taxonomic groups were affected by these global changes. There has been fruitful research in this space, even as it aligns with the sixth mass extinction of the present day (Barnosky et al. 2010). In context, ranks represent diversity at some level and carry some utility when insufficient data make it hard to resolve phylogenetic relationships. This does not mean that ranks are natural categories, though they do allow us to roughly estimate biodiversity in the fossil record.

However, to measure diversity with the greatest precision, “systematics” (the discipline for classifying life) needs to move towards naming only clades, while eliminating ranks, including species. Much progress has been made towards that goal. The newly published *PhyloCode* (Cantino and de Queiroz 2020) is a major step in that direction, but it is still not logically complete since the species rank remains embedded within it. The community of *PhyloCode* supporters is split on this (Cellinese, Baum, & Mishler 2012), and it will be interesting to see if the *PhyloCode* can further evolve to become completely rankless as advocated by Mishler and Wilkins (2018).

Whether the species rank is formally eliminated or not, it is important to understand that the species level is arbitrary and that different entities called species have nothing necessarily in common. Instead of viewing biodiversity as “the set of species on Earth,” we should view biodiversity as “the entire tree of life,” with branches at many different levels having interest and import. *Humans are literally related to all other living things, which should affect our ethics and inform how we treat them.* The sooner we can wrap our minds around this truth, the sooner we can understand the concepts and processes at play. This realization allows us to see what speciesism means and how it weaves into the biological and cultural manifestations that emerge from it.

1.4.2 Human Population

About 300,000 years ago, *Homo sapiens* split from other branches of the *Homo* lineage (Hublin et al. 2017). Yet our origin did not proceed without extensive interbreeding (reticulation) with Neanderthals as far back as 100,000 years ago (Bergström et al. 2021). It took every year of these 300,000 for the human population to reach one billion. That happened in the year 1800. Since then, our population has grown exponentially, reaching two billion (1927), three billion (1960), four billion (1974), five billion (1987), and today (2022) has just passed eight billion. Growth rates have slowed despite the ongoing upward trajectory (Vollset et al. 2020), but many challenges have surfaced as the human population has swelled (Bradshaw et al. 2021).

The current balance between birth and death rates explains population growth rate. However, this is not the full story about environmental impacts since per capita consumption varies widely. In developing countries, birth and death rates are often higher than in developed countries, but citizens of the developed world consume many more resources on average (UNDP 2020). The balance between reproduction and consumption provides insights into our resource footprint and the number of people the earth can sustain (carrying capacity). Data suggest that we currently consume resources as if we lived on ~1.75 Earths (Global Footprint Network 2020), even though there is only… one. The earth's carrying capacity for humans is not well understood (Cohen 1995). Most published estimates suggest that it is between 8 and 16 billion (Pengra 2012). However, we have changed our carrying capacity multiple times throughout history (Goudie 2019). Since at least the industrial revolution, we consumed energy and natural resources to fuel a growing civilization (Crutzen 2002; Crutzen and Steffen 2003; Hoekstra and Wiedmann 2014). Current growth and consumption rates are unsustainable, but where are the limits and how are the resource inputs changing? *This partly depends on what standard of living is acceptable and on the accelerating rate of technological change. Is the goal to keep people alive, or some higher standard that includes space, amenities, and opportunities for humanity and the rest of biodiversity?*

One challenge is that even though developing countries have higher birth rates, the impact of each person on the environment is much greater in developed countries (UNEP and IRP 2011; Kampang and Shaoqi 2012). In part, this is why sustainable economic growth is key to many aspects of human wellbeing. If population growth outpaces economic growth, the consequence is slum-like environments where essential services are sacrificed, such as sanitation, law, medical care, clean water, etc. (Oof and Phua 2007). These environments become grounds for poverty, disease, and suffering (Marmot et al. 2008). This is a tremendous reason to support developing countries, to keep their economies sustainable, their environments intact, and to reduce birth rates while increasing prosperity. Much about human health is intimately connected to the economic, environmental, policy, and values-based decisions that accompany a growing civilization (FAO 2020d; Vollset et al. 2020).

Thus, we have many goals for the pivotal year of 2050. These include transitioning to alternative forms of energy, managing the global climate, conserving natural resources, combatting food security, leveraging exponential technologies, among countless others (Hubert et al. 2010; Griggs et al. 2013; Gates 2021). It is clear that one important way to improve prosperity is to give equal rights to women, enable their voice in decisions on family size, and provide education and healthcare to all. Around the world, data show that birth rates decrease as these resources are provided (United Nations 2017). Compassion is a precious thing, especially when the consumption of energy and natural resources has driven our economic path. We are victims of our success in many ways.

Even as birth rates decrease and societies transition demographically, greater affluence increases global consumption. Reproduction and consumption are thus interdependent, even in a sustainable world with a healthy human population and a diverse environment. By 2050, there will be about two billion more humans on Earth, for a total of about 10 billion. It will increasingly stress our infrastructure to sustain this civilization while managing the climatic, energetic, and environmental impacts that currently result from our "business as usual" path (Griggs et al. 2013; United Nations 2017).

This is one reason why it's crucial to leverage information technology and to accelerate the rate of information that we discover and return to civilization (Kurzweil 2004, 2005). Artificial intelligence, machine learning, blockchain technology, materials science, and quantum computing are examples of such tools (Kissinger et al. 2021). The compounding rate of innovation can thus permit an abundant future by changing the inputs and outputs to engineer prosperity (Diamandis and Kotler 2012, 2015, 2020; Bastani 2019). In contrast to the pace of government and policy decisions, significantly moving this dial is about catalyzing human behavior change by applying current and new technologies for the human population at scale.

1.4.3 Public Health and Medical Implications

There are health consequences that connect to every aspect of population growth at this scale. Examples include: air pollution that results from the tools that power civilization (e.g., combusted byproducts of fossil fuels, airborne industrial and agricultural wastes); climate-related extreme weather events (e.g., floods, fires, hurricanes); vector-borne diseases that spread poleward from the tropics as climate belts shift (e.g., dengue fever, West Nile virus, Rift Valley Fever); environmental toxics that accumulate and magnify in regional environments and human bodies (e.g., endocrine disruptors, carcinogens, heavy metals); challenges growing food via traditional agriculture (e.g., the depletion of soil nutrients, plants living in environments they are not adapted to, the environmental and health impacts of agricultural techniques); and the stressful mental health issues that people face amidst these challenges (WHO 2021a). In a world where the biology of stress approximates the biology of western diseases (Sapolsky 2004, 2005), what looming public health crises exist over the horizon?

Late 2019 saw an unprecedented public health crisis: SARS-CoV-2, the virus that causes COVID-19 (coronavirus disease 2019). Research into the origin of this coronavirus is ongoing (Anderson et al. 2020; Rasmussen 2021; Sallard et al. 2021; Segreto and Deigin 2021; Segreto et al. 2021; Shi 2021). Whatever the origins turn out to be, one message is simple: human population densities are as critical to public and environmental health as is the total size of our population. Both have signals that underpin sustainability and wellbeing. Harvesting resources, including wildlife, as we encroach on natural habitats increases the likelihood of encountering zoonotic diseases (i.e., the transfer of disease agents to humans from other animals; Rulli et al. 2021). We also live in a connected world where humans move and where densities can be high. Pathogens function best in these environments. This is why "social distancing” reemerged as a phenomenon in 2019, to decrease population densities (e.g., “6 feet apart”) and lower transmission likelihood.

We are no longer hunter-gatherers in a low-density world. The anthroposphere (the ecological landscape we have created) provides new situations for opportunistic microorganisms. Human culture transforms ancestral environments and microbes take advantage of shifting landscapes. It is a case when worlds collide. Humans are spectacular ecosystem engineers but there are other players on this chessboard (Darwin 1859; Van Valen 1973). Moves are met with countermoves, even if we didn’t anticipate them. While we sink our wedge deeper into this landscape (acquiring resources while displacing others), microbial players discover our vulnerabilities. 2019 revealed that these opportunists can cause global pandemics, kill millions of people, and bring economies to near standstills.

It is striking to consider how viruses reproduce in the first place (V’kovski et al. 2021). They require host cells to replicate. They inject their DNA into the genome of a host, thereby hijacking its cellular machinery and instructing it to make viruses. This process doesn’t just allow viruses to reproduce. It also leaves behind a fraction of viral DNA. It is estimated that about 8% of the human genome is viral DNA (Belshaw et al. 2004; Jern and Coffin 2008). This genetic intermixing produces an outcome that can be compared to other ways that organisms reproduce. For example, animals primarily reproduce from sperm and egg. This means that DNA in the offspring comes from the merging of paternal and maternal sources. Sexual versus viral reproduction are obviously different, but the pattern is much the same: lineages coalesce and exchange DNA at various points across the tree of life.

The frequent merging of lineages over evolutionary time illustrates how erroneous it is to think that species are uniquely real units because DNA is only shared within the same species (Mayr 1982). Evolution is about lineages, forward to the present and back to the past. They split, they merge, they go extinct; tree thinking is core to understanding this. What value does focusing on the classical species level bring to considerations of reticulation and zoonotic diseases? None: it diverts our attention from grasping the processes at play, the levels involved, the patterns that emerge, and applying this knowledge to discover tools to manage pandemic diseases.

2019 exposed us to a new lineage of coronavirus that slowed humanity to a near standstill. Its genes merged with ours and killed over five million people in two years (WHO 2021b). A pandemic at this scale was predicted during the previous decade (Gates 2015). Let COVID remind us that we are neither superior to, nor separate from, the rest of life on Earth.

1.4.4 Food: Nutrition, Energy, Climate, and Biotechnology

The future of food is among the most integrative subjects of our time. It includes connections that weave through nearly every facet of the global environment, and speciesism resides at its core. How we see ourselves in relation to nature determines how we treat other organisms, how we view habitats that foods come from, the methods we use to capture or cultivate these foods, and the civilizational consequences of our actions. Food entwines subjects such as energy (Pimentel and Pimental 2007), climate (Rosenzweig et al. 2020), biodiversity (Worm et al. 2006; Crist et al. 2017), soil health (McBratney et al. 2014), ocean health (Halpern et al. 2015), biotechnology (Steinwand and Ronald 2020), nutrition (Domingo et al. 2021; Meyers et al. 2017), the future of contagious diseases (Rulli et al. 2021), and the ethics that guide human behavior in these spaces (Wilson 2012).

One of humanity's grand challenges over the next 30 years will be growing food sustainably for a population of about 10 billion. The food system is a subset of human ecology, an economy of nature powered by energy. At present, fossil fuels provide most of the energy that drives food production and distribution (Shukla et al. 2019). Our food is either wild caught (e.g., fishes) or grown (e.g., agriculture or aquaculture). Amidst a more extensive energy transition, we are working to wean ourselves off fossil fuels and power all of civilization (including food) via sustainable alternatives. Yet in the meantime, about one-quarter of our carbon footprint comes from food production and how we use the land it grows upon (Ritchie and Roser 2020). Trying to feed everyone carries tremendous potential to impact the global climate and biodiversity. Presently, industrial agriculture functions ineffectively at mitigating the ethical, environmental, and public health effects of food production. This appears as deforestation, habitat loss, overfishing, monocultures, biocide and fertilizer overuse, nutrient runoff into coastal dead zones, desertification of farmed soils, depletion of soil nutrients, groundwater depletion, and the government subsidies that incentivize many of these methods (FAO 2020a, b, c, d, e). We can do better.

We are beginning to produce food using more healthy and sustainable tools. While the global energy landscape is transitioning toward alternatives, the food landscape is changing as well. Regenerative agriculture helps to mimic natural ecosystems (cycling nutrients back to their environments) while sequestering carbon from the atmosphere and giving healthy lives to farm animals that allow this to happen (Duncan 2016; Lal 2021). Hydroponics and aquaponics provide tools for growing plants indoors without abusing farmed soils with chemical fertilizers, groundwater depletion, and widespread biocide use. Healthy aquacultures are also becoming common, with algae at the base of their food systems in contrast to food pellets made from corn, soybeans, or reef fishes (Goddek et al. 2019). As a form of cellular agriculture, cultured meats are also growing (literally). We are discovering more effective ways to financially and energetically grow muscle cells to make cultured alternatives to what would otherwise emerge from a factory farm (Humbird 2020; Triech 2021). For the first time in history, cultured meats carry the potential to create food from plant and animal cells and to make many unethical practices of the modern industrial farm disappear.

Unfortunately, "ecological thinking" has challenged food production technologies since the Industrial Revolution. In modern forms, this might manifest as raising salmon or cows on a diet of corn. This diet increases the concentration of pro-inflammatory omega-6 fats because it skews the omega-3:6 ratio in their tissues (Simopoulos 2003). This happens because corn plants store omega-6 fats as energy for young seedlings, fueling their growth and the eventual synthesis of green photosynthetic leaves. Plants need a source of energy to germinate before they can begin photosynthesizing in the first place (Ai and Jane 2016). Yet when we take these foods out of context and feed them to organisms who are not adapted to them, we introduce a state of mismatch into their environments and ours. We are the next level up in this food chain, and a tighter balance of omega-3:6 is optimal for human health (DiNicolantonio and O'Keefe 2018; Taha 2020). Given the ramifications, why not first consider ecology when making food production decisions? Further, energetically, it would be better yet to skip feeding plants to animals and to eat the plants directly (Bonhommeau et al. 2013). This ecology-first approach is one great benefit from regenerative farming, which treats food systems as natural ecosystems.

Further, what can we learn from supplement markets that often extract "active ingredients" and reduce them to molecules? Do these molecules always carry the same physiological effects as their counterparts in food? For example, do omega-3 pills carry the same benefits as eating wild-caught fatty fish (ASCEND 2018, Aung et al. 2018; Bhatt et al. 2019; Hu et al. 2019; Manson et al. 2019)? Synergistic effects often emerge when eating whole foods, which can be lost when reduced to molecular building blocks (Pollan 2008). Considering the promise of cultured foods—whether as lab-grown muscle cells (from animals) or lab-grown meats (from plants)—we must think hierarchically to optimize outcomes. This framework transcends molecular, cellular, and organismic physiology. The hierarchy of food production matters since food scientists use individual molecules to enhance flavor or texture, in addition to biotechnological tools to source whole food constituents (e.g., a genetic lineage of maximally healthy muscle cells) (MacQueen et al. 2019; Furuhashi et al. 2021). If we are tailor-making plant-based steaks to create the "marbling" that people want (using omega-6 rich sunflower oils), then we must evaluate the public health consequences of our ingredients (Southey 2021; van Vliet et al. 2021). Do we want the equivalent of corn-feed beef because we did not take an appropriately integrative approach when culturing food?

We need to be careful not to create a public health crisis while trying to feed humanity. At scale, this is precisely what is happening with industrial agriculture. Most current agricultural staples are easily digestible carbohydrates that contribute to obesity, type 2 diabetes, metabolic syndrome, among various health problems (Taubes 2007; FAO 2020e; FAO et al. 2020). Therefore, the future of food is also about the ethics of human rights and giving people quality products that optimize health. If a goal over the next 30 years is to sustainably feed humanity without creating environmental or health crises, then there is much potential to flourish. Let us learn from current oversights so that we do not introduce them into innovative technologies. This applies to how food production affects the global environment and public health, and extends to zoonotic diseases and ethics as well.

Probably the greatest promise of emerging food technologies is the potential to feed humanity at scale without contributing to the environmental and ethical problems that underpin current mainstream practices. We will need a portfolio involving a combination of methods described above. With those in place, the risk of pandemic diseases, environmental impacts, and ethical mistreatment decreases. By their nature, zoonoses are diseases that humans catch from other animals. With regenerative farming practices and cultured foods from lab-controlled environments, the likelihood of zoonoses becomes exceedingly small. Comparatively, high-density farms and wild-caught animals present a vastly greater risk category. In addition, the potential for animal suffering approaches near-zero with cultured meats at the cellular level. At the organismic level, regenerative farms provide healthy environments and quality lives for domesticated animals to live and thrive in their ecosystems.

In summary, while it is important to feed the people, we also need to cease wildland conversion to agriculture and minimize all other impacts on wild biodiversity. Further, we should emphasize the sustainable use of land that we dedicate to agriculture (e.g., eating low on the food chain, intercropping to replenish soil, three-dimensional farming), move away from any use of wild caught food at scale (including fishing), and employ food production technologies as they become more energetically, monetarily, and environmentally effective than current practices.

1.5 Closing Remarks

Humanity uses nearly all suitable agricultural land, and has greatly impacted biodiversity while converting them (Martenson 2011; Ritchie and Roser 2013; Ritchie 2017, 2019). Natural lands must be protected to allow our relatives in the tree of life the space to survive. To feed humanity, this means that agricultural efficiency needs to increase tremendously while converting virtually no more land to agriculture. Even plant-based agriculture requires sustainable transformation. This includes implementing polycultures over monocultures, hydroponics and aquaponics powered by alternative energy, improved irrigation methods, the conservation of natural habitats, and the overall lessening of environmental impacts. If we can execute on this, then even plants and soil microbes will have healthier lives.

Further, suppose we can transform plant agriculture and pair it with alternative food production technologies powered by clean energy at scale. In that case, we have a shot at sustainably producing food for 10 billion people, for at least awhile. Yet exponential population growth cannot persist; we would need to grow more food every year. As discussed above, a population at 10 billion is not sustainable if we raised everyone's standard of living and consumption to levels currently present in developed countries such as the United States. Thus, unless we can continue changing human carrying capacity, the global population will need to reverse its current growth, and trend downward (Hall and Day 2009). Promisingly, data and modeling suggest precisely this kind of trend, with the global population peaking in 2064 and declining into 2100 (Vollset et al. 2020).

Our current situation arose from the self-centered actions that underlie our behavior. It would be wise to respect the proper place of other organisms in the environment that we all share. Transitioning from selfish thinking will require us to see that we are one lineage among millions in an interdependent tree of life. We are not superior to other organisms nor to the environments that we inhabit. We are a subset of nature, reliant upon its resources, and our livelihood depends upon accepting this. With a targeted strategy, we can divert and correct our path. We live amid a human behavior problem, not a human technology problem. Humanity currently possesses the tools to thrive sustainably on the earth while venturing into the cosmos. Within a reasonably short timeline, we need incentives and consistent policies to make this happen. These actions are necessary to prevent the negative feedbacks of our current behavior from catching up with us (Turner 2014; Jackson 2016; Foxon 2017; van den Bergh 2017; Hausfather and Peters 2020).

In all honesty, it is not clear if *Homo sapiens* will make the necessary transitions; we have been selfish throughout our short history. But if we can accomplish them, we will find ourselves in a place where we can live sustainably alongside nature while deploying sophisticated tools to support our unique phenotype. It does not make us less special to exist thoughtfully, with foresight for our future and consideration for our family (the rest of life on Earth). On the contrary, owning our shortcomings will allow us to overcome our predicaments. At that point, embracing humility and leaving speciesism behind will make us far more precious than our fragile exceptionalism has ever prescribed.

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Chapter 2
Race and Human Genomic Variation

Rasmus Grønfeldt Winther

Abstract How much do different groups of humans differ genetically? Starting from a thought experiment, this chapter shows that we differ less than we might think—and that, in a sense, *we are all Africans*. I draw on several key findings: that compared to many other species, *Homo sapiens* has relatively little genomic variation; that of all continental regions, African genomic variation is the richest and most encompassing; that population-level genetic variation decreases with distance from Africa; and that most genomic variation is found within local human populations (with only about 7% or so found across continental groups). This is not to deny that there are—small but somewhat systematic—group-level differences, but it is also important to recognize that these should not matter ethically or politically.

2.1 A Thought Experiment[1]

A few months after your intergalactic expedition left Earth, you arrive in a far-off world.[2] Departing your ship, you come upon some of the planet's inhabitants. They all seem to look the same. They are all more-or-less one meter tall and have the same muscular body and rounded facial features. You know that people sometimes say that other groups of people "all look the same," but in this case it seems nearly true: finding a distinguishing mark on any one of them is a challenge.

"Greetings, traveler," you hear through a universal translation device held up to the mouth of a single inhabitant who has emerged to meet you on the rock where you stand. "Please be at ease." You are told that every person on the planet looks the same; your greeter is no exception. You learn that centuries ago there was a Great

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[1] Parts of this book chapter were adapted from chapters 6 and 9 of Winther (2022a).

[2] I first presented this thought experiment in Winther (2018). This work was completed in 2015.

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Tragedy brought on by ethnic conflict including a calamitous civil war. Committed to preventing further destruction, the survivors agreed that for the rest of time they would engage in random breeding to avoid ethnic strife.

Call this Planet Unity.

Now, let's imagine a different scenario, perhaps a little more familiar: Imagine the Galápagos Islands, the natural experimental laboratory where Darwin studied evolution, with their wide variety and number of finch and tortoise species. Let's in our minds populate these islands—or any analogous archipelago—with identical small populations of early humans. Let's then add a few more dozen islands that are larger, mutually unreachable, and have distinct environments: Some are relatively cool and rainy, while others are hot and arid. What happens after tens of millions of years of evolution? Will the populations become more alike, similar to Planet Unity? Just the opposite, of course: Unlike on Planet Unity, the populations on these islands have come to be quite different from each other—not just in body and behavior, but in culture, as well.

Call this Galápagos-Writ-Large.

Now the real question: are modern humans more like the inhabitants of Unity or Galápagos-Writ-Large? Where do we fall between these extremes?

When we look around us on the street or in a Zoom meeting, we can easily see differences in people's eyes, skin tone, height, and the rest. Identical twins might be a partial exception! This isn't just a point about individuals: some *groups* of people seem to share physical traits in common. And this would seem to be an argument for humans fitting the Galápagos-Writ-Large scenario.

I'm going to use this chapter to suggest the opposite: the Planet Unity scenario is a much better description of our situation. To help convince you, we'll review our best genomic evidence for the (relative) unity of the human species.

It was only in the middle of the twentieth century—long after Darwin's death—that scientists started unlocking the mysteries of genetic inheritance at the molecular level. The environment is an essential part of making you what you are, but the other side of the matter is that molecule called DNA, which encodes our genes.

A reasonable starting point for examining human diversity, then, is to ask how genes differ, if at all, between individuals and groups. How similar or dissimilar genetically is anybody from anybody else, really? Let's have a look.

The genomics of recent decades has had some surprising findings. We have learned that, compared to many other species, *Homo sapiens* has relatively little genomic variation; that of all continental regions, African genomic variation is the richest and most encompassing; that population-level genetic variation decreases with distance from Africa; and that most genomic variation is found within local human populations (with only about 7% or so found across continental groups).

What does this mean? As I will show, it means *we are all African*s. But groups also differ, and these small but somewhat systematic group-level differences explode with highly charged and controversial political and ethical debates and implications.

2.2 Relatively Little *Homo Sapiens* Intraspecies Genomic Variation

Among species for which we have good data, *Homo sapiens* has rather low average nucleotide variation. At roughly 999 base pairs out of 1000 (on average), all members of *Homo sapiens* are basically identical.[3] Given our total, haploid genome size of roughly 3 billion nucleotides, two individuals will typically and on average differ at approximately 3 million nucleotides—only a difference of about 0.1%. Our closest cousins are on either side of us in this measure, but not too far: bonobos differ by 0.076%, chimpanzees by 0.134%, and gorillas by 0.158%.[4] By contrast, the most classic model organism for genetic studies, *Drosophila* fruit flies, differ from each other by 1% on average, or about 10 times our nucleotide diversity. And maize has even more nucleotide diversity than *Drosophila*.[5]

In short, there is, according to our best genomic data, a *single overarching* human race, at least as compared to less unified species.

2.3 Out of Africa Migrations

Even so, we do differ in small ways, both at the individual level and the group level. This is what makes human evolutionary genomics so fraught and so interesting. Are there alleles associated with cancer, running speed, or intelligence, and might they be distributed unevenly across human populations? If so, what are the consequences for medicine, social policy, and our self-understanding?

It is crucial to recognize that our basic evolutionary pattern is *Out of Africa migration*. You may know the story: our species originated in Africa with a few small and highly related populations. Several times, groups left Africa, grew in size and range, and underwent evolution by natural selection, random genetic drift, and mutation. (Some migration *back* to Africa also occurred.) In this way, different human populations spanned the world, occasionally interbreeding, especially in the last tens of thousands of years.[6]

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[3] Li and Sadler (1991), Yu et al. (2002), Auton et al. (2015), Biddanda et al. (2020), Winther (2022a).

[4] Yu et al. (2004).

[5] Brown et al. (2004).

[6] For a nuanced, yet somewhat non-standard view of Out of Africa migrations, see: Templeton (1997, 1999, 2002).

2.3.1 *Of All Continental Regions, African Genomic Variation is the Richest and Most Encompassing*

African human populations are the most genetically variable in the world. African populations have roughly double the nucleotide diversity of other populations. In other words, two people whose recent ancestors are of African origin differ on average by about 1:900 nucleotides (0.11%), whereas two people whose recent ancestors are of European origin differ on average by only approximately 1:1600 (0.063%).[7] Another study found that Mandinka peoples from Mali, Guinea, and the Ivory Coast and the San peoples of South Africa harbored nucleotide diversities of 0.12% and 0.126%, respectively, while Han Chinese and Basque peoples had, respectively, 0.081% and 0.087%.[8] According to Rosenberg (2011), Africa has approximately half of the world's "private alleles"—that is, alleles at a locus unique to a geographic region.[9] Many more pieces of evidence indicate that genomic variation is generally much higher in Africa, in part due to the long periods of time of human population differentiation across the African continent. Given our Out of Africa picture, none of this is surprising.

2.3.2 *Genomic Heterozygosity of Populations Decreases with Increasing Distance from Africa, Along Human Migration Routes*

Early humans had to pass through northeastern Africa to leave it, and following this path leads to interesting insights. Genetic variation in human populations reduces in proportion to its distance from Africa, as measured along historical human migration routes. This means that the further apart two populations are along these lines, the more they differ. Here we can talk about human migration as well as *genetic* migration, or the process of gene exchange when populations mix. Genetic migration also tends to diminish along human migration routes as humans move farther from Africa.[10]

The Out of Africa migration model also aligns with the data on the decline in genomic variation as you move away from our evolutionary cradle, providing very strong evidence for a general Out-of-Africa scenario of human evolution (Fig. 2.1). This occurs because when a species migrates, relatively few individuals typically move and survive. Even fewer make it when difficult barriers such as mountains are crossed. This means two things. First, due to random genetic drift (random changes

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[7] Yu et al. (2002).

[8] Wall et al. (2008), Table 1, p. 1355; cf. Campbell and Tishkoff (2008).

[9] Rosenberg (2011), p. 667.

[10] See Fig. 1b of Ramachandran et al. (2005), 15,943; similar results are found and presented by Serre and Pääbo (2004); Lawson Handley et al. (2007).

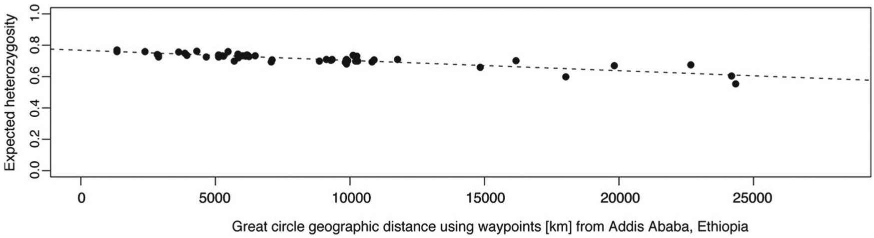

Fig. 2.1 Heterozygosity to distance from Eastern Africa global pattern. The amount of heterozygosity of each of approximately 40 worldwide populations diminishes as a function of their respective distance, along (approximate) migration routes, from Addis Ababa. (*Source* Fig. 4a, p. 15946, Support from the relationship of genetic and geographic distance in human populations for a serial founder effect originating in Africa by Ramachandran et al. (2005); https://doi.org/10.1073/pnas.0507611102 © (2005) National Academy of Sciences, U.S.A. Reprinted with permission from PNAS)

in allele frequencies across generations), small populations tend to lose genetic variation over generations (more so the smaller they are). Second, migrating natural populations experience genetic bottlenecks or a "founder effect" whenever a small group inhabits new areas.[11] Each time this happens, the founder population represents only some of the genetic variation of its parent population. These factors combine to lower the amount of genomic variation, especially outside of Africa, the home of our originary genetic variation. Interdisciplinarity and acceptance of multiple models and methods will also help paint the full picture here. For instance, archaeological and paleontological evidence can deepen and broaden our analysis.

Africa is indisputably the capital of Planet Unity—as well as the most diverse part of that planet. This is not to deny, of course, that we can see features of Galápagos-Writ-Large as a consequence of human migration and local adaptation to distinct environments.

2.3.3 Two Groundbreaking Episodes

In 1972, biologist Richard Lewontin studied the distribution of alleles across individuals from numerous groups around the globe.[12] He used genes coding for blood proteins to compare genetically different individuals within a population to individuals from other populations, both within and across continental regions. Here is his list of seven continental regions, into which he pooled populations that had been sampled and whose allele distributions (or allele frequencies) had been identified: Africans, Europeans, Asians, Southeast Asians, Indigenous Americans, Oceanians, Australian Aborigines.

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[11] Hartl and Clark (1989); Ramachandran et al. (2005); Lawson Handley et al. (2007).

[12] Lewontin (1972). For a more recent study confirming these results, see Barbujani et al. (1997). I explore Lewontin's aims and methods in Winther (2014, 2018, 2022b).

Lewontin found something astonishing: genetically, speaking, you are almost as different from someone chosen at random from your group as you are from a random person from anywhere on the globe. Our familiar racial categories are not backed up by the genetics. The human species has very little genetic variation, and it is mostly between individuals within groups—not between groups.

Nevertheless, 40 years later, a group of researchers led by Noah Rosenberg showed that even these small between-group differences provide enough information to correctly assign someone to a racial group based on knowing about 20–30 of her genes.[13]

What are we to make of this mix of results? Lewontin's work seems to suggest that races and other large human populations aren't, genetically speaking, "really real." But then how could it be possible to assign you to a race or ethnicity using just a small sample of your genes? This is not an idle question. Biologists and doctors—not to mention big pharma and insurance companies—have large stakes in understanding this puzzle.

The full answer as to why this mix of findings can co-exist would take more detail than available here. What I have elsewhere called Lewontin's "variance partitioning" and Rosenberg's "clustering analysis" are two sides of the same coin, mathematically speaking (Winther 2014). The twofold truth is this: human populations are similar in allele frequencies at many genes—but whenever we *aggregate* information about small differences across two populations, we can use this information to cluster and classify individuals into populations. Knowing an individual's multilocus genotype provides just this information. Although some refer to "Lewontin's Fallacy," I see no fallacy here: Lewontin and Rosenberg were interested in two different sets of questions and methods.

Recall our thought experiment: Planet Unity and Galápagos-Writ-Large are extremes on a spectrum. Yet, in general and on average, our species fits the Planet Unity model surprisingly well. This makes sense in light of Lewontin's results. And, in at least some places on Earth—especially big multicultural cities—our children are becoming even more Unity-like, both genetically and culturally. We see Galápagos-Writ-Large properties when we zoom in to a finer grain to explore specific genes or small populations. Admittedly, for some genes there are very large frequency differences in different parts of the world. This shows the validity of Rosenberg and colleagues' results.

2.4 Is Race Biologically Real?

Some claim that our best science indicates that human races are biologically *real* entities (e.g., Robin Andreasen, Charles Murray, Neven Sesardić, Quayshawn Spencer[14]). According to this view of *racial realism*, racial groups are clearly genetically differentiated. I believe that our best genomics obviously undercuts such a view.

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[13] Rosenberg et al. (2002). See also Rosenberg (2018).

[14] Andreasen (2000, 2007), Herrnstein and Murray (1995), Murray (2020), Sesardić (2010, 2013), Spencer (2013, 2014, 2015, 2019).

A subset of racial realists—call them "hereditarians"—argue further that the existence of biological populations explains and justifies certain social inequalities (e.g., Herrnstein and Murray 1995; Murray 2020). For them, multiple social and political inequalities, both within and between nations, are due largely to hereditary differences in the (average) innate abilities of races (as this concept is usually conceived)—intelligence, for instance. This view gives us a Galápagos-Writ-Large picture of biological race. Many hereditarians stand on the political right (e.g., conservatives, libertarians).

Compare the *racial antirealism* view developed in the wake of Lewontin's (1972) paper "The Apportionment of Human Genetic Diversity" (e.g., Joshua Glasgow, Adam Hochman, Naomi Zack[15]). For the racial anti-realist, races are social fictions without a biological basis. Such a view is widespread throughout the social sciences,[16] and is widely held by those who identify with the academic left. It can be thought of as the *liberal consensus* on race. In my view, this position goes too far and is somewhat disingenuous—it simply ignores some data.

This controversy is riddled with *burden of proof arguments*: both sides like to argue that the burden lies with the other side. The left wants the right to show strong genetic evidence for specific traits, while the right wants the left to prove that no genetic explanation for between-group differences can be given.

I would suggest that our global genome leaves it open to interpretation whether we can say that racial groups exist or not. The story is complex. Interpretation differs depending on the trait—blood proteins, skin color, behaviors, etc. At any rate, our best genomic studies in the last decade have shown that racial groups aren't very strongly identifiable and don't explain very much.[17] Moreover, the Out of Africa paradigm is basically correct. Ample genomic evidence shows, beyond a doubt, that Africa is the capital of our Planet Unity (albeit the most internally diverse part). Even so, while we are all quite similar, there may be real heritable differences that could, potentially, be politically controversial, especially if they inspire public policy or medical interventions.

We should also bear in mind that the story of race, however we conceive this fraught concept and category, is not, for the most part, a genetic story. Cultural narratives, questions of identity and belonging, are central in our attempts to understand all human groups and populations, racial or otherwise. As we will see below, whether or how race is biologically real is a separate issue from whether or how it might be socially real.

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[15] Glasgow (2009), Hochman (2013, 2016), Zack (2002).

[16] For instance: Reardon (2005); Fujimura et al. (2014).

[17] For scientific and philosophical reviews of a vast literature, see, e.g., Kaplan and Winther (2014), Winther (2019).

2.5 Philosophy and Post-Racial Futures

I believe philosophical analysis of genomics of race shows that race must be characterized in both realist (social race) and antirealist (biological race) terms. (And in *conventionalist* terms for genomic race.) It all depends on which "race" you're talking about. Mills (1998) provides a useful taxonomy of views, ranging from the denial of races' existence (Glasgow 2009) to the belief in deep biological racial "essences." To me, Mills' "objective constructivism" seems the most plausible: races are socially real and are shaped by ongoing social practices. Ásta (2018) provides a similar "conferralist" framework for analyzing the social construction of race and other categories such as sex and gender. For Ásta, race is defined by a social property, namely, "social status consisting in constraints on and enablements to the individual's behavior in a context" (2018, 2). Finally, psychiatrist and philosopher Frantz Fanon illustrates the reality and consequences of social race (e.g., structural racism), in the European colonial context.[18]

Crucially, the social construction process of race is historical and contingent.[19] This means that racial categories could always be otherwise. In *When Maps Become the World,* I defended a practice of *imagining "What if…?"*:

> In posing this most capacious question, philosophy opens up a space for memories, feelings, hopes, and imagination. When we ask "What if …?," we swap one set of assumptions for another and follow the world-making consequences of each, whether in the future or in potential existence more generally. Perhaps this is a kind of future-oriented pluralistic ontologizing. … What if social relations were structured with institutions, values, and behaviors dramatically different from those in place here, today? (Winther 2020, p. 253)

Let us here briefly address one "what if…?" possibility, that of post-racial societal futures.

A post-racial future is one in which perceived membership in a racial category is no longer associated with differential access to social goods, including dignity, trust, and opportunity. For such a future to exist, we must rip up what Charles Mills calls *the racial contract*. According to Mills, the seemingly neutral social contract theory tradition—including such philosophical luminaries as Thomas Hobbes, John Locke, Jean-Jacques Rousseau, Immanuel Kant, and John Rawls—has effectively posited a social contract between just the *people who count*, which is to say white people. Plausibly, he suggests that "White supremacy is the unnamed political system that has made the modern world what it is today." A post-racial future, then, requires struggles for recognition, power, land, and a decent standard of living—for an expanded social contract that includes all.[20]

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[18] Fanon (1952/2008, 1961/2004).

[19] Hacking (1999) provides a refreshing discussion of realism and constructivism. See also the last chapter "Map Thinking Science and Philosophy" of Winther (2020).

[20] Mills (1997), pp. 3, 1. For critical analysis of whiteness, racism, and colonialism, in addition to Fanon, see, e.g., Alcoff (2015), Coulthard (2014), Galeano (1973), and Kendi (2019). TallBear (2013) and Happe (2013) show how genomics could undermine such struggles.

Post-racial societies seem possible, and perhaps desirable. They are possible if, per some of the above discussions, each of us is willing to do the hard, critical work of simultaneously feeling a sense of belonging to our respective groups and *to all of us*, and *to all of life*. In so doing, we must also work hard not to reify and naturalize social expectations and prejudice. The result of the work need not be societies in which people no longer "see" race as a social organizing principle. For instance, social race, as I have defined it, may continue to have some relevance, but not for oppressive or negatively discriminatory purposes—perhaps only to celebrate differences, as some like to say, in culture, music, or food. Whether such a society, in the absence of stereotypical racial judgments, would be more inclined to reward people based on any number of *individual* qualities, such as work ethic or charm, is a matter for further "what if…?" discussion.[21]

Allow me to put my point starkly: *genomics simply shouldn't matter to politics.*[22] Regardless of genomic results and what they could or could not tell us, we must continue to work towards equality and dignity—also for non-human life—premised on ethics and law instead of on scientific information. Normative equality simply does not depend upon factual equality. Abstracting away from genomics, I encourage us to strengthen moral and legal frameworks to guarantee equality and protection to all.

2.6 Coda: Who Are We?

Who am I? It no longer makes sense for us to ask this question. Here, on this pale simulacrum of Planet Unity, we learn more about ourselves as individuals when we ask about the collective: Who are *we*? Who *were* we? Where did *we* come from—from what places and what ancestors? Whence humanity?

These questions include another as their flipside: Who are we not? *Homo sapiens*—that collection of us oddball apes—is not *Homo erectus* or *Homo heidelbergensis*, let alone *Australopithecus anamensis*. Nor are we Neanderthals or Denisovans, although here there is much more overlap. There are morphological and (postulated) behavioral differences between all hominin species and sub-species, including differences in average brain size, presence or absence of air sacks, and the production of particular forms of tools and weapons.

Neanderthals and Denisovans both likely emerged out of Africa. Neanderthals also evolved in Europe and western Asia, and Denisovans called eastern and southern Asia—and later Oceania—their home. There are reasonably good African *Homo* fossils before 400,000 years and after 260,000 years ago. In between lies a gap. Europe, meanwhile, has a solid fossil record for Neanderthal throughout this period (Hublin 2013).

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[21] A starting point for such a discussion might be Sandel (2020).

[22] I develop this point in detail in Rasmus Grønfeldt Winther. 2022a. *Our Genes: A Philosophical Introduction to Human Evolutionary Genomics.* Cambridge University Press.

These two subspecies or sister species of *Homo sapiens* elicit much interest. After all, most humans outside of Africa today have a few percentage of Neanderthal DNA, some of which is adaptive, for example, in fighting viruses.[23] And Oceanian peoples such as Papuans and Australian aborigines often have more than 5% Denisovan DNA.[24] Recent research finds Neanderthal DNA even in contemporary African individuals, suggesting that there were "Back to Africa" migrations, perhaps even by European *Homo sapiens*, themselves carrying Neanderthal DNA, over the last 20,000 years or so.[25]

Still, we have no evidence of Neanderthal or Denisovan mitochondrial DNA or Y-chromosomal haplotypes in any modern human population. Perhaps male fetuses with Neanderthal fathers and human mothers were inviable.[26] I leave it to the interested reader to draw out various mating combinations, in order to see that both Neanderthal mitochondrial DNA and Y-chromosomes can be lost in two generations, while autosomal DNA easily introgresses into the human genealogy.[27]

While we have a few answers, many more remain: The history of *Homo* cannot but raise questions about how to untangle our DNA, "whose" DNA it is, and why Neanderthals went extinct approximately 40,000 years ago.[28] Taking a wider view, we can ask which species—and places—gave rise to our nearest contemporary cousins: bonobos, chimpanzees, and gorillas (Fig. 2.2). Such questions bring us closer to our ancestors, inviting a sense of connection and belonging across the branches of the tree of life. Our best genomics blurs all kinds of putative boundaries, showing the deep and broad connection of all life.

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[23] E.g., Enard and Petrov (2018). The divergence between Neanderthals and modern humans, *Homo sapiens* can be estimated. Mendez et al. (2016) use Y-chromosome DNA from a Neanderthal to estimate divergence time to be around 588,000 years ago; Langergraber et al. (2012) find the temporal range for the split to be 400–800,000 years ago; Gómez-Robles (2019) uses fossil teeth, not genetics, to place the split at no less than 800,000 years ago.

[24] Many central, south, and east Asian populations, as well as Indigenous Americans, have small amounts of Denisovan DNA (Jacobs et al. 2019). Typically, because of chromosomal recombination over many generations, the regions of the Neanderthal genome interspersed in our genome are less than a hundred kilobases long (Sankararaman et al. 2014). For further reviews and citations, see also Nielsen et al. (2017), Bergström et al. (2020), and Winther (2022a), especially chapter two.

[25] Chen et al. (2020).

[26] See, e.g., Mendez et al. (2016), p. 732. Or maybe any such haplotype lineages in *Homo sapiens* died out due to selection or chance (See Prüfer et al. 2014; Nielsen et al. 2017, https://humanorigins.si.edu/evidence/genetics/ancient-dna-and-neanderthals/interbreeding).

[27] Of course, it is possible that we have yet to discover a new Neanderthal Y-chromosome or mitochondrial DNA haplotype from archaic remains, perhaps present somewhere in a human population, either already sampled or not. (On the converse point of human introgression into the Neanderthal lineage, see, e.g., Raff 2017).

[28] Chen et al. (2020); Vaesen et al. (2019).

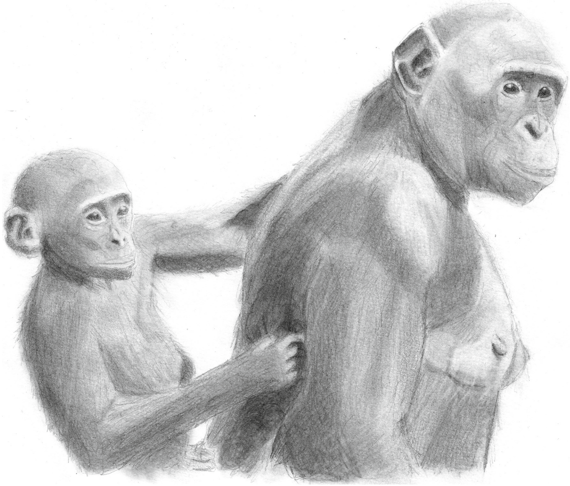

Fig. 2.2 Our cousins: Bonobos. Bonobos (*Pan paniscus*) are known for their empathy, matriarchal society, relative peacefulness, and rampant sexual activity across a range of relations (e.g., de Waal 2013, 2019). Bonobo mothers frequently permit other group members to handle their infants; 96% of these interactions were positive in one study (Klaree et al. 2018). (Illustrated by Daphné Damoiseau-Malraux. © 2020 Rasmus Grønfeldt Winther)

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