

Racial Evolution in the Phylogenetic Grid of Intelligibility

David Golding✉

Division of Social Science and Humanities, Parami University

(Received: 2nd June 2025; Revised: 18th December 2025; Accepted: 8th January 2026)

Abstract

Phylogenetics produces treelike depictions of human evolutionary history that some interpret as evidence for the biological reality of discrete human races. The colonial history and purpose of phylogenetic methods are reflected in the efficacy with which they infer the evolutionary divergence of races. Contemporary phylogenetics operates through a grid of intelligibility at the confluence of several bioinformatic tools such as genetic cluster analysis, evolutionary dendrograms, island model sampling, and molecular clocks. Since the methods of using these tools are highly flexible, they can be calibrated to align with racial imaginaries and bring putative ancestral populations into focus. The human genome is thereby interpreted as a natural archive of racial evolution. In the process, the colonial history of race is obscured behind a mythical, precolonial time of relatively unadmixed racial origins. By examining the sociogenesis of racial phylogenetics, this article demonstrates the role of the phylogenetic archive in the ongoing biologization of race and the concomitant colonization of time.

Keywords: Racialization; racial science; phylogenetics; molecular clock; temporalities

✉ davidgolding@parami.edu.mm

Introduction

The exercise of colonialist authority . . . requires the production of differentiations, individuations, identity effects through which discriminatory practices can map out subject populations that are tarred with the visible and transparent mark of power. (Bhabha, 1994, p. 158)

Race is often experienced and understood to be inscribed upon or within the body. Stuart Hall (2016, p. 56) interprets Frantz Fanon's concept of epidermalization as "the writing of racial differences on the body, the inscription on the body." In some forms of epidermalization, the medium of inscription is the flesh itself, as with the branding of people subject to the transatlantic slave trade or the forcible tattooing of indigenous peoples in colonial Burma (Cole and Haebich, 2007; Browne, 2015). More commonly, epidermalization is not directed upon the skin, but rather upon other media of inscription such as certifications of identity, demographic surveys, court rulings, colonial administrative records, personal journals, family letters, genealogies, chronologies, and anthropological studies. Documentation and archivization are fundamental to the colonial project of cataloguing racial and cultural difference in order to circumscribe ethnicities as discrete, comparable, and thus governable populations (Said, 2003; Braun and Hammonds, 2008; Mbembe, 2017). A burgeoning field examines the archival practices by which racialized subjects have been governed during and after colonialism (Gikandi, 2015; Dirks, 2015). For Ann Laura Stoler (2002, p. 92), archivization is integral to the coloniality of power to the extent that "what constitutes the archive, what form it takes, and what systems of classification signal at specific times are the very substance of colonial politics." She emphasizes that critical work in the colonial archives requires "reading the colonial archives 'against their grain' of imperial history, empire builders, and the priorities and perceptions of those who wrote them" (Stoler, 2009, pp. 46–47). Much archival and counter-archival work seeks the memories of survival and resistance that have been suppressed by colonial and postcolonial regimes of truth (Morgan, 2015; Gikandi, 2015; El-Malik and Kamola, 2017). Recovering these stories of resistance also involves the "living archive" that comprises built environments, human geographies, ways of life, intentional practices, personal effects, and oral histories (Stoler, 2018; Godoy, 2021; McKemmish et al., 2019). Internalization, embodiment, and epidermalization may thus be seen as various modes of archivization. If indeed the body is the living media of the colonial archive, its politics of inscription are of visceral importance to understanding the methods by which racial categorizations are reified and sustained over time.

Although rendering the body as a living archive of racialized oppression harbors some decolonial promise, it also runs the risk of reviving colonial notions of race as biological. Consider, for example, the postulation of Himla Soodyall, Bharti Morar, and Trefor Jenkins (2002, pp. 180–191) "that the body, through its DNA, constitutes . . . a resourceful archive for testing historical data," the scrutiny of which is a practice of "reconstructing history without biases introduced from cultural data." Under this rubric, they use phylogenetic inference to support the claim to Semitic ancestry that is relayed in the oral traditions of Lemba people in South Africa. If such claims of racial origin can be verified or disproven by objective biological criteria, then the human body may very well be an archive of evidence that race is biologically real (Schramm, 2021). However convincing, it is perilous to imagine that race is written in the genome. To do so would be to mislocate the site of racial inscriptions, "mis-take their function as signifiers for their biological fact and thus read 'race' as the product of a genetic or biological schema rather than as a *discursive regime*" (Hall,

1996, p. 20). The conflation between racial inscriptions and genetic information is instrumental to the genomic and postgenomic conceptions of race that have proliferated in recent years. The work of Soodyall, Morar, and Jenkins demonstrates that genetics can be used in this manner, regardless of whether the inscription and archivization of race is truly an act of nature or a product of power. Their conceptualization of the genomic archive appears in the seminal anthology *Refiguring the Archive* (Hamilton et al., 2002). In another chapter of the anthology, Susan van Zyl (2002) addresses the idea that the human body is a “phylogenetic archive” containing the psychobiological traces of a population’s history. This present article explores the politics of inscription that order the phylogenetic archive and examines the instruments by which its contents are rendered intelligible, computable, classifiable, and temporally ordinarable.

Critical analysis of the phylogenetic archive begins with the recognition of its sociohistorical provenance. Van Zyl responds to Sigmund Freud’s (1939, 1940) theory that trauma could be phylogenetically inherited from one’s ancestors. According to van Zyl (2002, p. 45), Freud implies that “the very possibility of the archive as repository of knowledge, and thus of a history of culture, is rooted in the traces of phylogenetic memory.” She draws from Jacques Derrida’s (1996, p. 34) reading of Freud, and specifically his conjecture that the accumulation of phylogenetic memories must constitute a “biological archive.” Freud conceived of phylogenetic memory as a racial inheritance, as illustrated in his claim that the Jewish psyche is distinguished by the inherited traumas of antisemitism and the murder of Moses (Freud, 1939; see also Slavet, 2008). In opposition to Freud’s psychobiological explanation of race, Fanon (2008) argued that racial difference is sociogenic rather than phylogenetic. That line of reasoning might attend to the phylogenetic conception of race as contoured by its own sociogenesis, namely that of colonial racial science. Since the 19th century, phylogenetics has shaped a conceptual domain for thinking about the origins of racial difference. Today, phylogenetics is a burgeoning assemblage of molecular and computational instruments, methodologies, epistemologies, and databases that mostly produce treelike representations of evolutionary histories. What nanopolitics of racial inscription and archivization do they entail? What temporalities do they mobilize?

The past few decades of phylogenetic research have procured new evidence that, according to some, suggests race is biologically real. The phylogenetic race concept has been developed primarily by Robin O. Andreasen (1998, 2000, 2004, 2007) and has generated much debate. She posits that races are separate lineages that are formed through evolutionary divergence. In a sense, this way of thinking about race is nothing new. The term “phylogeny” was introduced by Ernst Haeckel (1887; see also Levit and Hossfield, 2020) in the 19th century and derives from “phylon,” a Greek word meaning race or tribe. Haeckel arranged human races hierarchically on a phylogenetic tree, with more recently diverged races appearing towards the top of the diagram (Figure 1). The field has since treated lineages as distinct units whose evolutionary histories are overwhelmingly characterized by divergence. In the 21st century, the phylogenetic conception of race is increasingly substantiated by computational methods that infer complex evolutionary histories from genetic sampling data. Though it might be imagined that molecular genetics makes visible a genomic archive that pre-exists the sampling, to do so would be to confuse a sociogenic phenomenon for a natural one. Katharina Schramm (2021, p. 64) challenges the “scientific authority” under which “the genomic archive appears as a stable, truthful, and incorruptible source of information, defined by clearly demarcated borders (the body, DNA) and neutral ordering principles (haplogroups, population affinities).” Distinct racial ancestries are produced when the genome is overlaid with what I call the *phylogenetic grid of intelligibility*.

In analyzing the politics by which phylogenetics can purport to chart racial evolutionary histories, I draw from Michel Foucault's (1978, p. 93) theory that mechanisms of power often operate in relation to a "grid of intelligibility of the social order." Such grids can form at the confluence of multiple, and sometimes contradictory, theories and methods that make a given phenomenon visible, measurable, and chartable. Like any apparatus of knowledge production, the phylogenetic grid can be instrumentalized towards diverse sociopolitical objectives. Phylogenetics presents a solution for what Hall (2016, pp. 55–56) identifies as "the problem for racism." The problem "is that the genetic level is not immediately visible . . . its hidden structure must therefore be *materialized*, so that it can be 'read off' in easily recognizable, visible signifiers of the body." Racial phylogenetics involves a hermeneutics by which the histories of divergent races are read off from a supposedly natural genomic archive. Yet its hermeneutics are highly subjective and contingent upon varying methods of collecting, classifying, processing, and interpreting data, as will be shown throughout this article. Computational phylogenetics often produces contradictory evolutionary histories that can be wielded to support either the conclusion that human races are biologically real or, alternatively, that they are not. This computational and interpretive adaptability of phylogenetics is not a shortcoming. Rather, these qualities animate and dynamize the field of genomic data, the empirical yet contested terrain of the debate over whether racial difference is genetic. The phylogenetic grid of intelligibility, as an apparatus that biologizes race, extrapolates from this terrain the virtual space of possible evolutionary histories that supposedly connect present-day humans with their racial origins and shed light on the temporalities of race.

The phylogenetic grid of intelligibility

Computational phylogenetics orders genetic data within its particular grid of intelligibility. One axis of the grid represents time, while the other axis represents lineage divergence. Time is expressed either in terms of years or genetic distance. The former assumes a constant mutation rate, as discussed later in this article. Evolutionary lineages are visualized in a treelike topology called a *dendrogram* (Figures 1 & 2). The dendrogram could visualize either the evolutionary histories of populations within a certain species or the evolutionary relationships between species. In either case, each node of the tree represents a common ancestor that has been inferred by a given phylogenetic method. Each branch is a divergent evolutionary lineage. The genes of plants and animals alike can be used to infer their evolutionary histories. When phylogenetic histories are inferred from human genetic data, the results are sometimes presented as evidence that distinct lineages represent divergent races, and thus that race is biologically real.

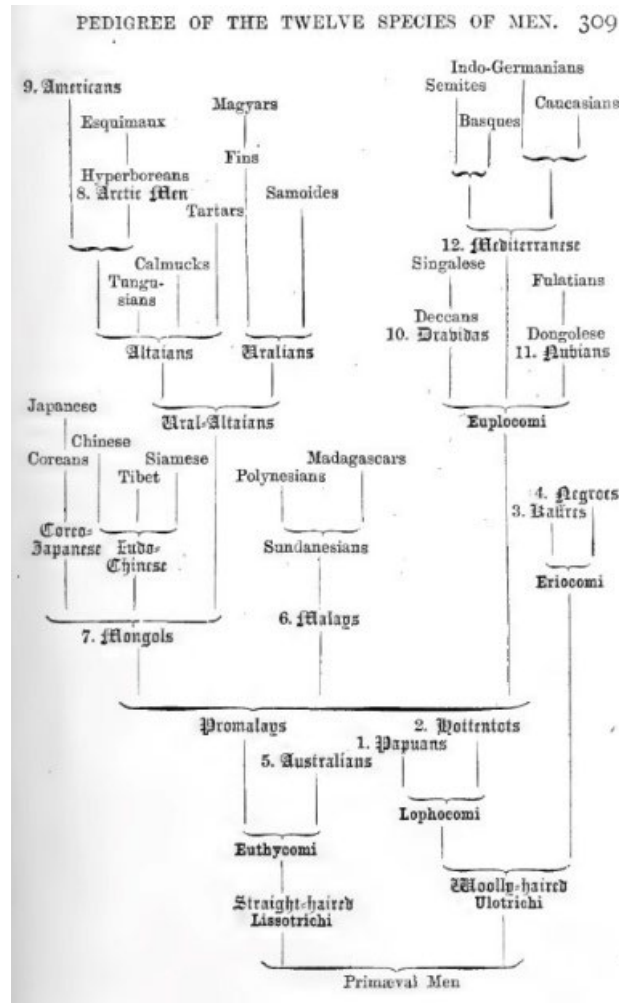


Figure 1: The first racial phylogeny (Haeckel, 1887, p. 309)

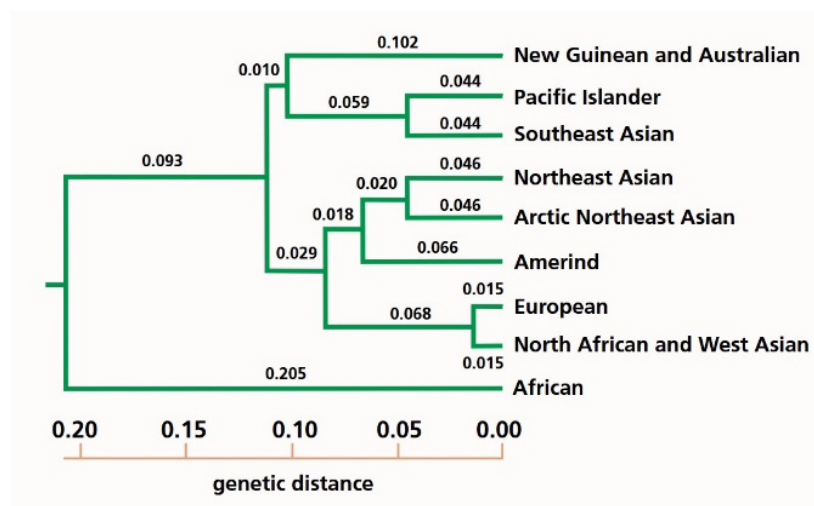


Figure 2: A contemporary human phylogenetic tree (Cavalli-Sforza & Feldman, 2003, p. 267), Reprinted with permission from Springer Nature.

That the phylogenetic grid of intelligibility so readily accommodates the racialization of human evolution is a product of its history as a late colonial technoscience. The natural

world was first overlaid with a grid of intelligibility in the 18th century. Michel Foucault limns that early taxonomy mapped “successions with the continuity of the beings and their distribution over the table” so that a “grid can be laid out over the entire vegetable or animal kingdom” (Foucault, 2002, pp. 154–164). Taxonomy has since buttressed the modern/colonial project to establish an “an absolutely certain knowledge of identities and differences” (Foucault, 2002, p. 61). Carl Linnaeus, the founder of modern taxonomy, classified humans into four continental varieties. In his taxonomy, the *Europæus* are “governed by laws,” the *Americanus* “governed by customs,” the *Asiaticus* are “governed by opinions,” and the *Afer* (i.e., *Africanus*), whom Linnaeus consistently placed last in the hierarchy, are “governed by chance” (Linnaeus, 1758, pp. 20–22, quoted in Hoquet 2014, p. 26). Taxonomy has long been employed to biologize what Edward Said calls “Orientalist knowledge” about racial and cultural difference. The production of such knowledge “was essentially the *making visible* of material, and the aim of a tableau was the construction of a sort of Benthamite Panopticon” across the colonial territories (Said, 2003, p. 127). In the 19th century, languages, texts, and organisms all became subject to treelike depictions of their historical development (Morrison, 2016). Inscriptions of natural and cultural phenomena gained currency as the calculable, ordinal, classable, and archivable material for a new grid of racial intelligibility charted by phylogenetics.

The politics of racial inscription are dynamized within the virtual space of the phylogenetic grid of intelligibility. Computational phylogenetics uses genetic data as an empirical grounding for historical inferences that were previously looser and more speculative. A decade after introducing the concept of “phylogeny” in 1866, Haeckel graphed the first phylogenetic tree of human races in 1887. The tree’s basis was ethnocultural and phenotypic rather than genetic, since scientists at the time did not know of the human genome. It subdivided humanity into 12 species and 36 races (Haeckel, 1887; see also Levit and Hossfield, 2020). “Primæval Men” form the base of Haeckel’s phylogenetic tree (Figure 1). Papuan and sub-Saharan African races are positioned towards the bottom of the tableau as direct descendants of a primitive ancestor. For the first time, colonial ethnological categories such as *ulotrichi* and *lissotrichi* were located within the topology of evolutionary history. Phylogenies of racial divergence came to influence various anthropological subfields and European fascist ideologies (Stein, 1988; Caspari, 2003; Marks, 2012; Levit and Hossfield, 2020). Phylogenetics strengthened its empirical grounding in the 20th century with the advent of molecular biology, which introduced new “practices of sampling, measuring, and classifying [that] shape and inform the archival infrastructure—the very understanding of the genome as archive” (Schramm, 2021, p. 51). These “genomic inscriptional devices and visualizations” locate racial differences within “genomic grids of intelligibility” (Wade, 2014, pp. 217–222). Genomic grids use molecular data to visualize population genetic structure. The phylogenetic grid of intelligibility can be thought of as a particular form of genomic grid that extrapolates from genetic data to infer detailed evolutionary histories.

Phylogenetics is capable of either supporting or challenging the hypothesis that race is biological, depending on how its computational results are interpreted. The phylogenetic race concept posits that races are monophyletic groups (i.e., clades), meaning that each race comprises lineages that share a common ancestor (Andreasen, 1998, 2007). Human populations are generally admixed to some degree. To accommodate this, the phylogenetic race concept requires only a certain degree of reproductive isolation to deem a group sufficiently monophyletic to be a distinct race (Andreasen, 2004, 2007). An arbitrarily selected threshold value serves as a statistical measure against which genetic data is weighed (Brandon, 2022). Despite the empirical and objective veneer of statistically defined racial

boundaries, their composition varies greatly depending upon which and how many gene loci are sampled, the selection of sampling populations, and the chosen method of culling and pooling the genetic data (Templeton, 2002; Winther and Kaplan, 2013; Maglo et al., 2016; Osmanoglu, 2023). Disparate evolutionary histories are projected by different phylogenetic inference models (Steel and Penny, 2000; Templeton, 2004). Any racial interpretations of these histories are entirely subjective. Due to the pliability and indeterminacy of phylogenetic inference, Rasmus Grønfeldt Winther and Jonathan Michael Kaplan (2013, p. 67) caution that “we should not expect phylogenetics to provide unequivocal answers for racial ontology.” They observe that “racial realist or antirealist interpretations emerge from, and are perfectly consistent with, the genomic results” (Winther and Kaplan, 2013, p. 57). In Latin America, for example, genomic science is used alternatively to confirm and refute that race is biological (Wade et al., 2014). For these reasons, “perhaps more so in phylogenetics than in other sub-disciplines, we get out of the models what we put in” (Winther and Kaplan, 2013, p. 63). This teleological adaptability allows phylogenetic inference models to be calibrated in alignment with racial imaginaries.

With computational phylogenetics, myriad evolutionary histories can be calculated from the same genetic data. The phylogenetic grid is a retrorse projection of the genome’s virtualities or, in other words, the possible histories that can be extrapolated from genomic data. All of the phylogenies that could possibly be inferred from a particular set of genetic data are known as the *treespace*. Different phylogenetic models involve distinct methods of selecting which trees are most likely to reflect actual evolutionary histories. Given the expanding archive of genomic data that is available to an increasing array of phylogenetic inference models, the multiplicity of treespaces altogether can be envisioned as a thickening tangle of possible evolutionary trees. Peter Wade describes the virtual space of possible ancestries as:

a refiguration of race (and ethnicity, region, and nation) through the unlimited finity generated by genomics: some key foundational and reference categories are fixed and reiterated, and populations and individuals apparently located precisely in relation to them, but the very focus on invisible DNA and the approximation to it through numbers makes those precisions less stable than they appear at first sight. The endless multiplication of possible positionings in relation to the reference points—the fractionation of populations, the differentiation of individuals, the diversification of ancestries—creates a sense of movement and modulation. (Wade, 2014, p. 224)

Phylogenetic inference projects a dynamic tableau of possible evolutionary treespaces that can be explored via methodological adjustment. In this “indeterminate genomic field,” inference models can be used to “solidify a phylogenetically based racial ontology” (Winther and Kaplan, 2013, p. 65). Phylogenies in the grid of intelligibility can be calibrated and selected so that the inferred lineages comport with popular understandings of nation, culture, and race. The inscription of evolutionary histories serves to reify racial groupings while remaining pliable enough that the phylogenetic archive can be reconfigured with further accretion. Due to this flexible yet empirical grounding in genetic data, the phylogenetic grid of intelligibility is highly effective in rendering the boundaries between races as biological rather than sociogenic.

The inference of racial divergence

Until subject to phylogenetic inference, human evolutionary history does not resemble a branching tree pattern of wholly divergent lineages or races. Rather, human evolution can be more accurately visualized as a latticework in which lineages diverge and converge (i.e., reticulate) to varying extents (Cutter, 2013; Templeton, 2013; Gontier, 2015; Osmanoglu, 2023). This is because there has not been enough reproductive isolation amongst humans to form objectively distinguishable groups (Gannett, 2004). Discrete (i.e., monophyletic) population lineages are difficult to trace within the intricate latticework of the reticulating patterns of evolution. Monophyletic lineages must nevertheless be identified for race to be located within the phylogenetic grid of intelligibility. The phylogenetic race concept relies on the premise that human evolution is a branching process (Andreasen, 2004). Phylogenetic inference is fit for purpose in that “taxa with reticulate histories may not be readily identifiable using tree-based methods because they are . . . biased towards finding a taxon to be monophyletic even when it has a substantial reticulate history” (Reeves and Richards, 2007, p. 304). *Reticulation* is the convergence of previously separate lineages. Most phylogenetic inference models tend to, in essence, prune the latticework of reticulation into the shape of a branching evolutionary tree (see Andreasen, 1998; Burbrink and Gehara, 2018; Osmanoglu, 2023). The furcational methods of phylogenetic inference reifies “the old racial schema. Dendrograms are also used to illustrate the divergence of entities called human races or of populations used as their surrogates” (Keita and Kittles, 1997, p. 536). They perpetuate what S. O. Y. Keita and Rick A. Kittles term “raciotypological thinking” that persists in genetic research. In their refutation of the phylogenetic race concept, they indicate that “few human populations, even authentic breeding populations, are so well differentiated (and independent) from each other as to support the distinctness implied by tree branches.” Raciotypological thinking undergirds Andreasen’s (1998, p. 214) argument that “races are monophyletic groups; they are ancestor-descendant sequences of breeding populations, or groups of such sequences, that share a common origin.” To visualize distinct human populations and demarcate the boundaries that supposedly evince historical racial divergence, the statistical methods of genetic cluster analysis are employed.

Genetic cluster analysis divides the continuity of gradual (i.e., clinal) genetic variation into distinguishable groupings (Serre and Pääbo, 2004). Cluster analysis was first developed by early-20th-century anthropologists to categorize ethnic groups and quantify their degrees of cultural difference (Driver and Kroeber, 1932). At the end of the century, research in molecular biology and bioinformatics began applying cluster analysis to genetic datasets. The geneticization of cluster analysis did not engender objective methods by which racial clusters can be identified, but rather imbued the raciotypological maps of colonial anthropology with statistical authority. Winther (2014, p. 214) notes that “the parameter space of multilocus information is too large, and clustering possibilities too massive, to not narrow down—guide—the possible clusters using the abstract maps of culturally defined groups.” A notable example is the study *The History and Geography of Human Genes*, which Andreasen (1998, 2004, 2007) posits as empirical evidence for the phylogenetic race concept. In that study, Luigi Luca Cavalli-Sforza, Paolo Menozzi, and Alberto Piazza (1996; see also Cavalli-Sforza, 1997) reference a predefined linguistic classification system to pool, into 42 groups, genetic data from nearly two thousand sampling populations. They chose only “aboriginal populations” and “excluded all manifestly mixed populations; those stated to have 25% or more external admixture” (Cavalli-Sforza et al., 1996, p. 24). Genetic cluster analysis can be further calibrated in accordance with raciotypological groupings by adjusting the number of clusters to be inferred, which is an input variable called the *k value*. This scalar

indeterminacy presents a “grain of resolution problem” (Hochman, 2013, p. 281; see also Kitcher, 2007). In his critique of the phylogenetic race concept, Adam Hochman (2022, p. 85) explains that “there seems to be no way of determining which is the ‘racial’ grain of analysis, and thus which clusters represent ‘races,’ without appealing to convention.” When clusters are used as “thinly disguised surrogates for race,” a k value of five is usually chosen, resulting in a continental grain of resolution (Braun and Hammonds, 2008, p. 1581). These “continental clusters” are “an artifact, a construct that indicates instrumental, i.e., convenient, cutoff points for various scientific purposes,” especially those of racialization (Maglo et al., 2016, p. 6; see also Gannett, 2004). The adjustability of genetic cluster analysis yields what Philip Kitcher (2007, p. 299) calls a “nondenumerable infinity of possible accurate maps,” or in Wade’s (2014, p. 224) terminology an “unlimited finity of maps, each slightly different from the others.” Genetic cluster analysis is therefore highly effective in the “pernicious reification of our preexisting theoretical maps about groups and populations” (Winther, 2014, p. 215). Despite being instrumentally produced, population clusters are posited as traces of phylogenetic races that resulted from precolonial evolutionary divergence. As the phylogenetic grid of intelligibility is extrapolated from the genome space, racialized clusters are extruded across a temporal dimension in the form of branching (i.e., nonreticulate) lineages. Even more so than genetic clusters, these evolutionary projections are instrumentally produced and eminently configurable topologies that bear the imprints of a dendriform lens of analysis.

When overlaid with the phylogenetic grid of intelligibility, the reticulate patterns of human evolution result in treespaces of possible phylogenies that are themselves nonreticulate. Since most inference models are designed to produce bifurcating dendrograms without reticulation, phylogenetics is particularly suitable for the identification of monophyletic races amongst humans. Like genetic cluster analysis, the population groupings of phylogenetic inference models can be configured according to folk taxonomies of race (Templeton, 2002, 2004; Winther and Kaplan, 2013, Maglo et al., 2016). Yet phylogenetic inference adds a calibratable temporal dimension that introduces a flexibility analogous to the grain-of-resolution problem in genetic cluster analysis (Mncube, 2015). Assuming monophyly occurs in degrees rather than absolutes, “monophyletic groups occur at all levels in the genealogical hierarchy” (Osmanoglu, 2023, p. 5). Phylogenetic inference can therefore adjust its grain of resolution to accommodate various scales of racial and ethnic categorization. Given that race is sociogenic rather than phylogenetic, there is no method to objectively determine how many common ancestors are required before a clade is determined to be a race. The variable scale of phylogenetic inference enables its calibration to whichever grain of analysis is thought to reveal racial signifiers. The reticulations at multiple scales of human evolutionary history are thereby reduced to plainly divergent and monophyletic races.

The elimination of reticulation from human phylogenies serves a political purpose that originates in colonial racial science. Genealogical topologies were not predominantly treelike until the 19th century, when European evolutionary theorists sought to explain the diversity of life. Prior genealogies often depicted substantial reticulation, for example that of William the Conqueror which dates to the early 14th century (Genealogy of the Dukes of Normandy, ca. 1300). Reticulation is similarly visible in the 15th-century genealogy of Edward IV (Genealogical Chronicle of the Kings of England, ca. 1466–1467). On that scroll, his genealogy appears alongside a non-hierarchical and thoroughly reticulated diagram of the genealogical relationships between the Twelve Tribes of Israel (Figure 3). The diagram resembles a prototype of racial phylogeny, but one that visualizes admixture between groups rather than divergence. Until the 19th century, diagrams of reticulated genealogical

relationships remained common (Morrison, 2016). In 1809, Lamarck's evolutionary tree of life introduced a purely furcating topology more serviceable for the hierarchical and classificatory epistemologies of colonial technoscience and its archives (see Foucault, 2002). Its visual arrangement was adapted from previous diagrams that Linnaeus (1758) had produced to graph classificatory schema rather than evolutionary relationships. Haeckel adapted Lamarck's nonreticulate evolutionary tree to produce the first racial phylogeny (Figure 1). David A. Morrison (2016, pp. 460–461; see also Morrison 2014) discerns that dendrograms after the mid-19th century featured lineages stemming from an “explicit root, provided by the location of the common ancestor, and therefore an implicit time direction away from that ancestor. Prior networks usually lacked a time direction.” The 15th-century genealogy of the Twelve Tribes of Israel likewise lacks a linear time dimension. Instead, it depicts genealogical relationships of cyclical exchange during biblical time, marking a divine origin of intertwined lineages, long before reticulate evolution had been theorized (Figure 3). The typologizing desiderata of 19th-century raciology impelled the plotting of racial evolutionary time along a nonreticulate and linear historical dimension.

Racial evolutionary time is the temporal order that is inscribed in the raciotypological dendrograms of the phylogenetic grid. Andreasen asserts that the cladistic classification of race:

merely requires that evolution take the form of a branching process; it does not require that there be significant phenotypic or genetic differences among clades . . . Racial evolution will take this form when a species splits into two or more breeding populations that experience different evolutionary forces under a significant degree of reproductive isolation. Current work in human evolution indicates that this condition was met in the past. (Andreasen, 2004, p. 431)

Racial evolution, when projected back in time to the dawn of colonialism, concentrates upon inferred common ancestors of relatively unadmixed races. The theory has been over one hundred years in the making. As Haeckel's phylogenies were gaining influence in the early 20th century, anthropologists began theorizing about racial evolution. John T. Gulick (1905, pp. 58, 143) imagined European colonialism to be a force that diminished the “ancient segregation” of races that had resulted from “divergent racial evolution.” Racial evolutionary theory was subsequently elaborated by Griffith Taylor, who also believed that colonialism was a catalyst for admixture. For Taylor (1937, p. 86), racial evolution results in the disparities between “primitive races” and “more advanced races.” He diagrams a “racial ‘tree’ showing the relations of the five races” arranged along a vertical axis that represents time and a horizontal axis that separates a “Western Twin” and “Eastern Twin” for each level of the temporal hierarchy (Taylor, 1934, p. 241). The five racial groups are, in ascending order, “Negrito,” “Negro,” “Australoid,” “Mediterranean,” and “Alpine” (Figure 4). Towards the bottom of the hierarchy, the Eastern Twin of the “African Negro” is the “Early Melanesian.” In the Alpine group at the top, the Eastern Twin of “Europe” is “Asia.” On the racial evolutionary tree, the founder populations of each race mark more recent or anterior evolutionary divergences. The origins of racial difference are thus located within a chronology of clear divisions. In contemporary phylogenies, this temporal order is now subject to genetic sampling and the computation of treelike inference models that are used to substantiate the phylogenetic race concept. When human evolution is overlaid with the phylogenetic grid of intelligibility, races appear as fundamentally temporal units.

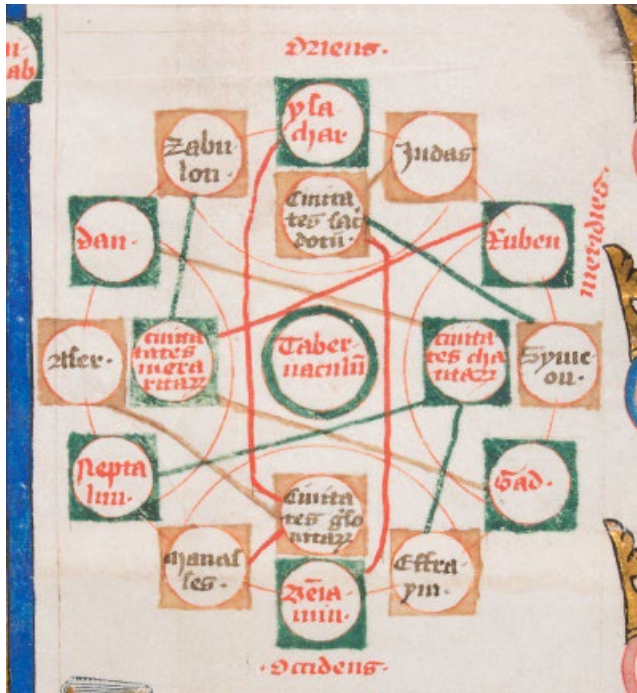


Figure 3: A prototype of racial phylogeny that shows reticulating genealogical relationships between the Twelve Tribes of Israel. (Genealogical Chronicle of the Kings of England, ca. 1466-1467)

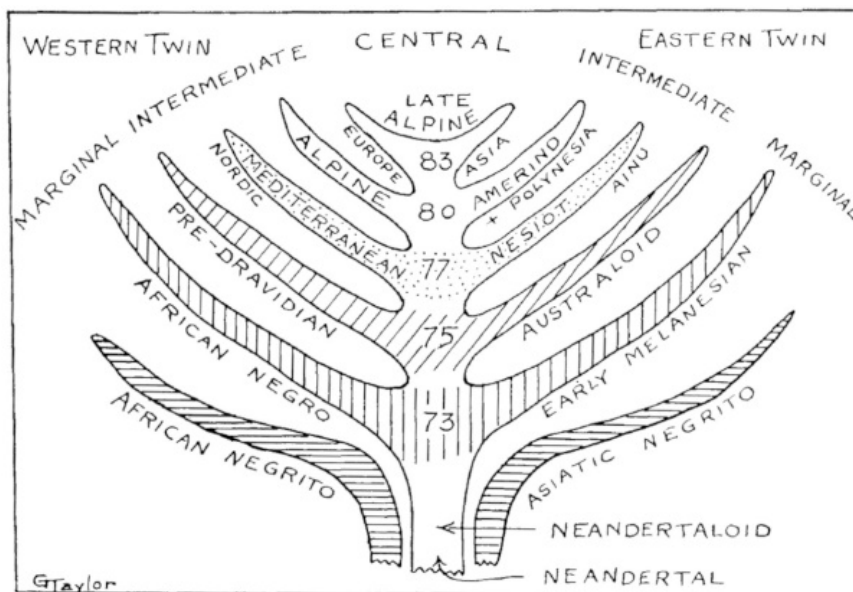


**Figure 4: Griffith Taylor's dendrogram of racial evolution (Taylor, 1934, p. 241),
Reprinted with permission from John Wiley & Sons.**

Racial evolutionary time

The phylogenetic grid of intelligibility tethers empirical evidence from the human genome to a mythical, precolonial time of racial origin. This tether stretches across *racial evolutionary time*, meaning evolutionary time as it pertains to so-called “racial evolution” (see Andreasen, 2004, p. 431). According to the theory of racial evolution, “racial divisions begin with the division of a species into founder populations, possibly due to migration or some other form of geographic separation” (Andreasen, 2007, p. 472; see also Gannett, 2004; Osmanoglu, 2023). Racial evolutionary time is hypothesized to have begun in the Late

Pleistocene, culminating in reproductively isolated “pure races” at the dawn of European colonialism (Kitcher, 2003, pp. 234–237). The planetary scale of European colonialism is surmised to have increased global admixture. Before colonialism, “*ancestral races* existed, but biological races are anastomosing” in the modern era (Andreasen, 1998, p. 216). The precolonial era is thus demarcated as a time of racial divergence, with reticulation being limited to the most recent six centuries. Since then, “the voyages of discovery, colonization and immigration have been blurring racial distinctness” (Andreasen, 1998, p. 211). Not only does this model fail to account for the precolonial prevalence of admixture and reticulation, but it is also incongruous with colonial histories of racialization, segregation, apartheid, genocide, and their effects on the human population genetic structure (Templeton, 1999; Restrepo et al., 2014; Wade et al., 2014; McLean 2019, 2020). Regardless of its validity, the inference of historical founder populations renders intelligible the evolutionary divergences between races.

The phylogenetic grid of intelligibility can be thought of as an instrument for the colonization of time. Adib and Paul Emiljanowicz understand the colonization of time to entail the imposition of a singular temporal regime in an “attempt to manipulate and project a mediated temporal imaginary,” and specifically one that is linear and measurable (2017, p. 1223). The colonial origins of race, their modes of violence, and their historical particularities are obscured behind the projection of a racial chronology onto the phylogenetic grid of intelligibility, where race appears on a precolonial and nonreticulate human evolutionary timeline. The charting of founder populations on the phylogenetic grid of intelligibility can empirically “fix a time in human prehistory, the *time of racial origination*” (Kitcher, 2003, p. 235). Shay-Akil McLean (2019, p. 172), in his critique of the phylogenetic race concept and its instrumentalization of founder populations, designates the time of racial origination as “the genetic now . . . where statements about human variation are made as if approximately 600 years ago were now.” McLean elaborates:

The entire exercise is directed toward finding a way to ignore the profoundly disruptive effects that conquest, genocidal, and settler-colonial processes have wrought on the world at many levels. More bluntly, writing race and racism out of human history is a central preoccupation of human genetics. (McLean, 2019, p. 172)

All the same, the phylogenetic grid of intelligibility serves as an inscriptive tabula for a different register of human history, that of racial evolution. The phylogenetic dehistoricization of race identified by McLean could be alternatively interpreted as a geneticization of history. When history is rendered genetically, the racializations that are recorded in sociohistorical chronologies are relocated to a racial evolutionary timeline. In the phylogenetic grid of intelligibility, the sociogenesis of racial purity appears as phylogenesis.

The genomes of indigenous people are seen as a valuable resource for the phylogenetic inference of precolonial founder populations. Andreasen (1998, p. 211; see also Andreasen, 2000) suggests that when identifying phylogenetic races, “geneticists can greatly reduce the problems posed by hybridization by studying *aboriginal populations*—breeding populations that occupied their present location before the great migratory waves that began with the voyages of discovery in the mid- to late fifteenth century.” She references the phylogenetic study by Cavalli-Sforza, Menozzi, and Piazza (1996, p. 24) that excluded populations with admixture above a certain threshold and “confined our analysis to aboriginal populations that were in their present location at the end of the fifteenth century when the great European migrations began.” The practice of selecting geographically stationary and

reproductively isolated populations has been called the “‘island model’ sampling procedure” (Maglo et al., 2016, p. 5; see also Terrell et al., 1997; Restrepo et al., 2014; Wade et al., 2014). The model “produces a misleading representation of the human genetic continuum” as if it were marked by clear discontinuities between readily distinguishable populations (Maglo et al., 2016, p. 5). This representation is amenable to essentialist ideas about purity and separateness. Kim TallBear (2013, p. 6) observes that the inference of founder populations “operates within a loop of circular reasoning. Particular, and particularly pure, biogeographic origins must be assumed in order to constitute the data that supposedly reveals those same origins.” By way of this tautological empiricism, the sociogenic myth of racial purity finds purchase as a phylogenetic phenomenon. The island model is yet another instrument by which the phylogenetic archive and its racial distinctions are biologized. Biological inscriptions of primordial groupings have long proliferated in the colonial archive, itself “an attestation to the authority of natural history, the key to the ideology of white power. Here, in the archive, the African could be reduced to the world of nature and the prehuman” (Gikandi, 2015, p. 92). Genetic data that has been sampled and archived from the bodies of indigenous peoples serve as a waypoint into the primordial time of racial evolution. The notion that indigenous peoples are spatiotemporally remote has been fundamental to racial evolutionary theory since Taylor (1937, p. 254) expounded his “First Principle of Race Evolution,” which is that “the most primitive races are found ‘pushed to the periphery.’” The principle’s reference to “the periphery” betrays a Eurocentric geography of remoteness. A principal function of island model sampling is the primordialization of indigenous genome spaces so that geneticists can access racial evolutionary time by traveling from the metropolitan core to the peripheral aborigine.

Racial evolutionary time becomes locatable on the phylogenetic grid of intelligibility with the use of a conceptual tool called the “molecular clock.” In the inference of phylogenies, “there is no absolute time scale associated with any node in the tree (or graph), and nodes in different sub-trees have no well-defined temporal order” (Loog, 2021, p. 6). A molecular clock is therefore necessary to estimate, with chronometric specificity, the divergence of lineages from each common ancestor. Molecular clocks calculate divergence times by temporally quantifying the genetic distance between populations (Figure 2). The attendant theory assumes that neutral alleles mutate at a somewhat constant rate. It has garnered substantial criticism, much of which emphasizes that human evolutionary history resembles a “changing spatial and temporal configuration of demes in a reticulating lineage” rather than a steady process of genetic mutation, drift, and diversification (Winder and Winder, 2014, p. 308; see also Schwartz and Maresca, 2006; Barnes and Dupré, 2008; Newton, 2010; Kern and Hahn, 2018). As with the dendrogram and the genetic cluster, the accuracy of the molecular clock is less important than the racial intelligibility that it affords.

Molecular clocks require calibration, a process by which the present-day degree of genetic variation is weighed against the timeline of evolutionary divergence suggested by the fossil record. Vincent Sarich recalls that the mid-20th-century “development of the molecular clock . . . at last provided hard numbers against which the origin of racial differences could then be computed” (Sarich and Miele, 2004, p. 76). He recounts an early effort at Berkeley to calibrate a molecular clock that used genetic samples from Papuan peoples to estimate the mutation rate of the global human population. The fossil record was interpreted to suggest that Papuan peoples had remained relatively stationary and isolated since 30,000 or 40,000 years ago. Therefore, their genes provided a much earlier calibration point than could be derived from the data of most present-day human populations. The researchers later calibrated the clock with genetic data from Native American peoples, the results of which suggested

racial evolutionary timescales three or four times shorter in duration than when the clock had been calibrated using Papuan genetic data. Preserving the validity of the molecular clock, and thus the temporal specificity of racial evolutionary time, was as simple as choosing not to publish the conflicting findings of the calibration that used Native American genes (Sarich and Miele, 2004). The temporal indeterminacy of phylogenetic inference means that a molecular clock can be calibrated in accordance with the postulates of racial evolutionary theory. The calibration's efficacy is unimpeded by the questionable validity of the clock's own theoretical basis, the island model sampling that anchors its temporality, and the underlying primordialist stereotypes about the purity of indigenous genes. All three are fraught with theoretical and empirical shortcomings (Terrell et al., 1997, 2001; Farbotko, 2010; Wilder et al., 2011; Xu et al., 2012; TallBear, 2013). These methods nonetheless transport geneticists across the colonial time of admixture and into a mythical time of racial purity.

With the molecular clock as its meter, the phylogenetic grid of intelligibility establishes the hegemony of racial evolutionary time that produces what Homi K. Bhabha calls "the time-lag of modernity":

And lest it be said that this disjunctive present of modernity is merely my theoretical abstraction, let me also remind you that a similar, signifying caesura occurs within the invention of progress in the "long imperialist nineteenth century." At the mid-point of the century questions concerning the "origin of races" provided modernity with an ontology of its present and a justification of cultural hierarchy within the West and in the East. (Bhabha, 1994, p. 246)

The racial originary myth is imperiled by the difficulty, even with the most advanced computational tools, of distinguishing races within the clinal variation of the human population genetic structure. The purity of racial origin is nonetheless preserved within the inferential virtualities of the phylogenetic grid of intelligibility. The grid visibilizes a "projective past" in which "a separation—*between* races, cultures, histories, *within* histories—a separation between *before* and *after* . . . repeats obsessively the mythical moment or disjunction" (Bhabha, 1994, pp. 82, 238). Computational phylogenetics sustains the colonization of time by charting racial origins on its grid of intelligibility. The phylogenetic grid is incapable of encapsulating what Achille Mbembe (2001, p. 16) calls "the *time of entanglement*" that is constituted by "a variety of trajectories neither convergent nor divergent but interlocked, paradoxical." Indeed, many populations are interlocked in far more complex evolutionary relationships than simple convergence or divergence. Even at the supraspecific level, the point at which lineage divergence can be said to have formed a new species is "a 'grey area' of lineage sundering where there is no scientifically objective way of deciding whether two populations are conspecific or not" (Zachos, 2018, p. 153). The colonization of evolutionary time involves the carving of distinct lineages, the severance of inoscultations, the pruning and cutting of reticulations (see Andreasen, 1998; Osmanoglu, 2023). What results is a dendrographic, nonreticulate, and unilinear temporality of racial evolution. Modern/colonial time hegemonizes the temporalities of entanglement, the "*interlocking* of presents, pasts, and futures that retain their depths of other presents, pasts, and futures, each age bearing, altering, and maintaining the previous ones" (Mbembe, 2001, p. 16, see also Hafiz, 2020). Admixture and reticulation are wholly antithetical to racial evolutionary time because they involve an entanglement that is simultaneously genealogical and temporal. The phylogenetic archive does not consist of naturally existing genetic information, but rather of the scientific records of the colonization of time.

Conclusion

Racial pride of this sort is historical. It is then appropriately directed towards something that has a temporal duration. Phylogenetic races have this sort of temporal dimension. (Brandon, 2022, p. 238)

The concept of phylogenetic race promises to strengthen racial identity by locating within the human body traces of a primordial racial purity. It explains present-day racial differences using a precolonial evolutionary timeline with empirical grounding in the plenitude of genetic data that constitutes the genomic archive. Perhaps Freud was correct that phylogenetic memory is a substance of racial identity. Yet this memory is not biologically inherited from previous generations in the way that he speculated. Rather, it is transmitted intergenerationally through the racial signifiers that circulate between the psyche and the phylogenetic archive. In the archive, phylogenetic memory is recorded as inscriptions of racial origination. Ancestral races are memorialized with particular genetic sampling methods, phylogenetic inference models, and theories of racial evolution. Phylogenetic archivization is thus a practice of historical memory or hypomnesia that racializes human experiences of time, memory, and the body. As biological records accumulate, the myth of racially pure ancestors gains an objective and scientific appearance. Unadmixed precolonial populations are affixed to precise temporal locations in the phylogenetic grid of intelligibility. Racial evolution becomes measurable by the so-called molecular clock, which is not truly a clock at all. It is not an empirical meter of the natural passage of time, but rather is a conceptual tool that transforms genetic distance into temporal distance. Together with the dendrogram and island model sampling, the molecular clock simplifies the temporal dynamics of admixture to the extent that racial evolution can be diagrammed as a purely bifurcating process of chronologically distinct divergences. Plotting racial evolution on the phylogenetic grid in effect sutures the temporal disjuncture between racially pure, precolonial ancestors and the present-day genome space. Racial identity is thereby inscribed upon the genome and ordered in the phylogenetic archive. The phylogenetic grid renders racial evolution intelligible while obscuring the nanopolitics of the genomic archive behind a veil of naturalness and objectivity.

The politics of the phylogenetic archive, as with any other colonial archive, involve the colonization of time. The intelligibility of racial history depends largely on how the archive is read. If human history is thought of as a dynamic web of relations and contestations, then it always exceeds the bounds of the archive. Racialization is a rudimentary process, fraught with contradictions and inconsistencies, as evidenced in records of colonialism and resistance. Time is too inconstant, multiplicitous, and intermeshed to fit into the rigid order of the colonial archive, at least without its disfigurement. Conversely, if human history is imagined to entail the evolutionary divergence between races, then the archive scintillates with all the possible racial histories waiting to be revealed by phylogenetic inference. Only the latter hermeneutics allow for the intelligibility of racial classifications and the authority they exert upon the body and mind. Any inscription, categorization, or epidermalization of race has the potential to leave a deep impression on the psyche. That which reifies in the phylogenetic archive may also reify as identity. Identity thus becomes subject to the genomic archive and enclosed in racial evolutionary time, which is a time that is colonized by the structuring of a primordial racial purity. To destabilize this disjunctive present, the sociogenesis of race must be foregrounded. The projective past of racial phylogenetics should be acknowledged for what it is: a virtual terrain for the ongoing biologization of race.

References

- Adib, & Emiljanowicz, P. (2019). Colonial time in tension: Decolonizing temporal imaginaries. *Time & Society*, 28(3), 1221-1271. <https://doi.org/10.1177/0961463X17718161>
- Andreasen, R. O. (1998). A new perspective on the race debate. *The British Journal for the Philosophy of Science*, 49(2), 199–225. <https://doi.org/10.1093/bjps/49.2.199>
- Andreasen, R. O. (2000). Race: Biological reality or social construct?. *Philosophy of Science*, 67(3), S653–S666. <https://doi.org/10.1086/392853>
- Andreasen, R. O. (2004). The cladistic race concept: A defense. *Biology and Philosophy*, 19, 425–442. <https://doi.org/10.1023/B:BIPH.0000036110.07449.8d>
- Andreasen, R. O. (2007). Biological conceptions of race. In M. Matthen & C. Stephens (Eds.), *The handbook of the philosophy of science* (Vol. 3) (pp. 455–481). Elsevier. <https://doi.org/10.1016/B978-044451543-8/50022-8>
- Barnes, B., & Dupré, J. (2008). *Genomes and what to make of them*. University of Chicago Press.
- Bhabha, H. K. (1994). *The Location of Culture*. Routledge.
- Burbrink, F. T., & Gehara, M. (2018). The biogeography of deep time phylogenetic reticulation. *Systematic Biology*, 67(5), 743–755. <https://doi.org/10.1093/sysbio/syy019>
- Brandon, R. N. (2022). Five advantages of the phylogenetic race concept. In L. Lorusso & R. G. Winther (Eds.), *Remapping race in a global context* (pp. 227–243). Routledge. <https://doi.org/10.4324/9781315208893-18>
- Braun, L., & Hammonds, E. (2008). Race, populations, and genomics: Africa as laboratory. *Social Science & Medicine*, 67(10), 1580–1588. <https://doi.org/10.1016/j.socscimed.2008.07.018>
- Browne, S. (2015). *Dark matters: On the surveillance of blackness*. Duke University Press. <https://doi.org/10.1215/9780822375302>
- Caspari, R. (2003). From types to populations: A century of race, physical anthropology, and the American Anthropological Association. *American Anthropologist*, 105(1), 65–76. <https://doi.org/10.1525/aa.2003.105.1.65>
- Cavalli-Sforza, L. L. (1997). Genes, peoples, and languages. *Proceedings of the National Academy of Sciences*, 94(15), 7719–7724. <https://doi.org/10.1073/pnas.94.15.7719>
- Cavalli-Sforza, L. L., & Feldman, M. W. (2003). The application of molecular genetic approaches to the study of human evolution. *Nature Genetics*, 33(S3), 266–275. <https://doi.org/10.1038/ng1113>
- Cavalli-Sforza, L. L., Menozzi, P., & Piazza, A. (1996). *The history and geography of human genes*. Princeton University Press.

- Cole, A., & Haebich, A. (2007). Corporeal colonialism and corporal punishment: A cross-cultural perspective on body modification. *Social Semiotics*, 17(3), 293–311. <https://doi.org/10.1080/10350330701448587>
- Cutter, A. D. (2013). Integrating phylogenetics, phylogeography and population genetics through genomes and evolutionary theory. *Molecular Phylogenetics and Evolution*, 69(3), 1172–1185. <https://doi.org/10.1016/j.ympev.2013.06.006>
- Derrida, J. (1996). *Archive fever: A Freudian impression*. University of Chicago Press.
- Dirks, N. B. (2015). *Autobiography of an archive: A scholar's passage to India*. Columbia University Press.
- Driver, H. E., & Kroeber, A. L. (1932). Quantitative expression of cultural relationships. *University of California Publications in American Archaeology and Ethnology*, 31(4), 211–256.
- El-Malik, S. S., & Kamola, I. A. (Eds.). (2017). *Politics of African anticolonial archive*. Rowman & Littlefield.
- Fanon, F. (2008). *Black skin, white masks*. Pluto Press.
- Farbotko, C. (2010). Wishful sinking: Disappearing islands, climate refugees and cosmopolitan experimentation. *Asia Pacific Viewpoint*, 51(1), 47–60. <https://doi.org/10.1111/j.1467-8373.2010.001413.x>
- Foucault, M. (1978). *The history of sexuality* (Vol. 1, R. Hurley, Trans.). Pantheon.
- Foucault, M. (2002). *The order of things: An archaeology of the human sciences*. Routledge.
- Freud, S. (1939). *Moses and monotheism*. Hogarth Press.
- Freud, S. (1940). An outline of psycho-analysis. *The International Journal of Psycho-Analysis*, 21, 27–84.
- Gannett, L. (2004). The biological reification of race. *British Journal for the Philosophy of Science*, 55(2), 323–345. <https://doi.org/10.1093/bjps/55.2.323>
- Genealogical Chronicle of the Kings of England. (ca. 1466–67). Metropolitan Museum of Art (The Cloisters Collection, Object 2018.631), New York, NY, United States. <https://www.metmuseum.org/art/collection/search/811798>
- Genealogy of the Dukes of Normandy. (ca. 1300). British Library (Box 6, Membrane 5, Royal Manuscripts 14), London, United Kingdom.
- Gikandi, S. (2015). Rethinking the archive of enslavement. *Early American Literature*, 50(1), 81–102. <https://doi.org/10.1353/eal.2015.0020>
- Gontier, N. (2015). Reticulate evolution everywhere. In N. Gontier (Ed.), *Reticulate evolution: Symbiogenesis, lateral gene transfer, hybridization and infectious heredity* (pp. 1–40). https://doi.org/10.1007/978-3-319-16345-1_1

- Gulick, J. T. (1905). *Evolution, racial and habitudinal*. Gibson Bros.
- Godoy, N. L. (2021). Community-driven archives: Conocimiento, healing, and justice. *Journal of Critical Library and Information Studies*, 3(2), 1–24. <https://doi.org/10.24242/jelis.v3i2.136>
- Haeckel, E. (1887). *The history of creation* (Vol. 2). D. Appleton and Company.
- Hafiz, M. (2020). Smashing the imperial frame: Race, culture, (de)coloniality. *Theory, Culture & Society*, 37(1), 113–145. <https://doi.org/10.1177/0263276419877674>
- Hall, S. (1996). The after-life of Frantz Fanon: Why Fanon? Why now? Why Black Skin, White Masks? In A. Read (Ed.), *The fact of blackness: Frantz Fanon and visual representation* (pp. 13–37). Institute of Contemporary Arts.
- Hall, S. (2016). Diasporas, or the logics of cultural translation. *MATRIZES*, 10(3), 47–58. <https://doi.org/10.11606/ISSN.1982-8160.V10I3P47-58>
- Hamilton, C., Harris, V., Taylor, J., Pickover, M., Reici, G., & Saleh, R. (Eds.). (2002). *Refiguring the archive*. Springer.
- Hochman, A. (2013). Racial discrimination: How not to do it. *Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences*, 44(3), 278–286. <https://doi.org/10.1016/j.shpsc.2013.03.003>
- Hochman, A. (2022). Racial classification without race: Edwards’ fallacy. In L. Lorusso & R. G. Winther (Eds.), *Remapping race in a global context* (pp. 74–91). Routledge. <https://doi.org/10.1016/j.shpsc.2013.03.003>
- Hoquet, T. (2014). Biologization of race and racialization of the human: Bernier, Buffon, Linnaeus. In N. Bancel, T. David, & D. Thomas (Eds.), *The invention of race: Scientific and popular representations* (pp. 17–31). Routledge. <https://doi.org/10.4324/9781315813318-2>
- Keita, S. O. Y., & Kittles, R. A. (1997). The persistence of racial thinking and the myth of divergence. *American Anthropologist*, 99(3), 534–544. <https://doi.org/10.1525/aa.1997.99.3.534>
- Kern, A. D., & Hahn, M. W. (2018). The neutral theory in light of natural selection. *Molecular Biology and Evolution*, 35(6), 1366–1371. <https://doi.org/10.1093/molbev/msy092>
- Kitcher, P. (2003). *In Mendel’s mirror: Philosophical reflections on biology*. Oxford University Press.
- Kitcher, P. (2007). Does “race” have a future?. *Philosophy & Public Affairs*, 35(4), 293–317. <https://doi.org/10.1111/j.1088-4963.2007.00115.x>
- Lamarck, J. B. P. A. (1809). *Philosophie Zoologique*. Dentu.

- Levit, G. S., & Hossfield, U. (2020). Ernst Haeckel, Nikolai Miklucho-Maclay and the racial controversy over the Papuans. *Frontiers in Zoology*, 17, e16. <https://doi.org/10.1186/s12983-020-00358-w>
- Linnaeus, C. (1758). *Systema naturæ per regna tria naturæ, secundum classes, ordines, genera, species, cum characteribus, differentiis, synonymis, locis* (10th edition). Laurentii Salvii.
- Loog, L. (2021). Sometimes hidden but always there: The assumptions underlying genetic inference of demographic histories. *Philosophical Transactions of the Royal Society B: Biological Science*, 376(1816), e20190719. <https://doi.org/10.1098/rstb.2019.0719>
- Maglo, K. N., Mersha T. B., & Martin, L. J. (2016). Population genomics and the statistical values of race: An interdisciplinary perspective on the biological classification of human populations and implications for clinical genetic epidemiological research. *Frontiers in Genetics*, 7, e22. <https://doi.org/10.3389/fgene.2016.00022>
- Marks, J. (2012). Why be against Darwin? Creationism, racism, and the roots of anthropology. *American Journal of Physical Anthropology*, 149(S55), 95–104. <https://doi.org/10.1002/ajpa.22163>
- Mbembe, A. (2001). *On the postcolony*. University of California Press.
- Mbembe, A. (2017). *Critique of black reason* (L. Dubois, Trans.). Duke University Press.
- McKemmish, S., Chandler, T., & Faulkhead, S. (2019). Imagine: A living archive of people and place “somewhere beyond custody.” *Archival Science*, 19, 281–301. <https://doi.org/10.1007/s10502-019-09320-0>
- McLean, S. (2019). Isolation by distance and the problem of the twenty-first century. *Human Biology*, 92(3), 167–179. <https://doi.org/10.13110/humanbiology.92.3.04>
- McLean, S. (2020). Social constructions, historical grounds. *Practicing Anthropology*, 42(3), 40–44.
- Mncube, Z. (2015). Are human races cladistic subspecies? *South African Journal of Philosophy*, 34(2), 163–174. <https://doi.org/10.1080/02580136.2014.998854>
- Morgan, J. L. (2015). Archives and histories of racial capitalism: An afterword. *Social Text*, 125, 153–161. <https://doi.org/10.1215/01642472-3315862>
- Morrison, D. A. (2014). Phylogenetic networks: A review of methods to display evolutionary history. *Annual Research & Review in Biology*, 4(10), 1518–1543. <https://doi.org/10.9734/arrb/2014/8230>
- Morrison, D. A. (2016). Genealogies: Pedigrees and phylogenies are reticulating networks not just divergent trees. *Evolutionary Biology*, 43(4), 456–473. <https://doi.org/10.1007/s11692-016-9376-5>
- Newton, T. (2010). Life times. *The Sociological Review*, 58(1), 196–216. <https://doi.org/10.1111/j.1467-954X.2010.01918.x>

- Osmanoglu, K. (2023). Against phylogenetic conceptions of race. *Global Philosophy*, 33, e6. <https://doi.org/10.1007/s10516-023-09675-1>
- Reeves, P. A., & Richards, C. M. (2007). Distinguishing terminal monophyletic groups from reticulate taxa: Performance of phenetic, tree-based, and network procedures. *Systematic Biology*, 56(2), 302–320. <https://doi.org/10.1080/10635150701324225>
- Restrepo, E., Schwartz-Marín, E., & Cárdenas, R. (2014). Nation and difference in the genetic imagination of Colombia. In P. Wade, C. L. Beltrán, & R. V. Santos (Eds.), *Mestizo genomics: Race mixture, nation, and science in Latin America* (pp. 55–84). Duke University Press. <https://doi.org/10.1215/9780822376729-003>
- Ruhlen, M. (1991). *A guide to the world's languages*. Stanford University Press.
- Said, E. W. (2003). *Orientalism*. Penguin Books.
- Sarich, V., & Miele, F. (2004). *Race: The reality of human differences*. Routledge.
- Schramm, K. (2021). Race, genealogy, and the genomic archive in post-apartheid South Africa. *Social Analysis: The International Journal of Anthropology*, 65(4), 49–69. <https://doi.org/10.3167/sa.2021.650403>
- Schwartz, J. H., & Maresca, B. (2006). Do molecular clocks run at all? A critique of molecular systematics. *Biological Theory*, 1, 357–371. <https://doi.org/10.1162/biot.2006.1.4.357>
- Slavet, E. (2008). Freud's "Lamarckism" and the politics of racial science. *Journal of the History of Biology*, 41, 37–80. <https://doi.org/10.1007/s10739-007-9138-4>
- Soodyall, H., Morar, B., & Jenkins, T. (2002). The human genome as archive: Some illustrations from the South. In C. Hamilton, V. Harris, J. Taylor, M. Pickover, G. Reici, & R. Saleh (Eds.), *Refiguring the archive* (pp. 179–192). Springer.
- Steel, M., & Penny, D. (2000). Parsimony, likelihood, and the role of models in molecular phylogenetics. *Molecular Biology and Evolution*, 17(6), 839–850. <https://doi.org/10.1093/oxfordjournals.molbev.a026364>
- Stein, G. J. (1988). Biological science and the roots of Nazism. *American Scientist*, 76(1), 50–58.
- Stoler, A. L. (2002). Colonial archives and the arts of governance. *Archival Science*, 2, 87–109. <https://doi.org/10.1007/BF02435632>
- Stoler, A. L. (2009). *Along the archival grain: Epistemic anxieties and colonial common sense*. Princeton University Press.
- Stoler, A. L. (2018). "On archiving as dissensus." *Comparative Studies of South Asia, Africa and the Middle East*, 38(1), 43–56. <https://doi.org/10.1215/1089201x-4389967>
- TallBear, K. (2013). *Native American DNA: Tribal belonging and the false promise of genetic science*. University of Minnesota Press.

- Taylor, G. (1934). The ecological basis of anthropology. *Ecology*, 15, 223–242.
<https://doi.org/10.2307/1932465>
- Taylor, G. (1937). *Environment, race, and migration*. University of Chicago Press.
- Templeton, A. R. (1999). Human races: A genetic and evolutionary perspective. *American Anthropologist*, 100, 632–650. <https://doi.org/10.1525/aa.1998.100.3.632>
- Templeton, A. R. (2002). Out of Africa again and again. *Nature*, 416(6786), 45–51.
<https://doi.org/10.1038/416045a>
- Templeton, A. R. (2004). Human races in the context of recent human evolution: A molecular genetic perspective. In A. Goodman, D. Heath, & M. S. Lindee (Eds.), *Genetic nature/culture* (pp. 234–257). Lawrence Earlbaum Associates.
<https://doi.org/10.1525/9780520929975-016>
- Templeton, A. R. (2013). Biological races in humans. *Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences*, 44(3), 262–271. <https://doi.org/10.1016/j.shpsc.2013.04.010>
- Terrell, J. E., Hunt, T. L., & Gosden, C. (1997). The dimensions of social life in the Pacific: Human diversity and the myth of the primitive isolate. *Current Anthropology*, 38(2), 155–195. <https://doi.org/10.1086/204604>
- Terrell, J. E., Kelly, K. M., & Rainbird, P. (2001). Foregone conclusions? In search of ‘Papuan’ and “Austronesians.” *Current Anthropology*, 42(1), 97–124.
<https://doi.org/10.1086/318436>
- Van Zyl, S. (2002). Psychoanalysis and the archive: Derrida’s *Archive Fever*. In C. Hamilton, V. Harris, J. Taylor, M. Pickover, G. Reici, & R. Saleh (Eds.), *Refiguring the archive* (pp. 39–59). Springer.
- Wade, P. (2014). Race, multiculturalism, and genomics in Latin America. In P. Wade, C. L. Beltrán, & R. V. Santos (Eds.), *Mestizo genomics: Race mixture, nation, and science in Latin America* (pp. 211–239). Duke University Press.
<https://doi.org/10.1215/9780822376729-009>
- Wade, P., Deister, V. G., Kent, M., & Olarte-Sierra, M. F. (2014). Social categories and laboratory practices in Brazil, Colombia, and Mexico: A comparative overview. In P. Wade, C. L. Beltrán, & R. V. Santos (Eds.), *Mestizo genomics: Race mixture, nation, and science in Latin America* (pp. 183–209). Duke University Press.
<https://doi.org/10.1215/9780822376729-008>
- Wilder, J. A., Cox, M. P., Paquette, A. M., Alford, R., Satyagraha, A. W., Harahap, A., & Sudoyo, H. (2011). Genetic continuity across a deeply divergent linguistic contact zone in North Maluku, Indonesia. *BMC Genetics*, 12, e100.
<https://doi.org/10.1186/1471-2156-12-100>
- Winder, I. C., & Winder, N. P. (2014). Reticulate evolution and the human past: An anthropological perspective. *Annals of Human Biology*, 41(4), 300–311.
<https://doi.org/10.3109/03014460.2014.922613>

- Winther, R. G. (2014). The genetic reification of “race?” The story of two mathematical methods. *Critical Philosophy of Race*, 2(2), 204–223. <https://doi.org/10.1353/por.2014.0008>
- Winther, R. G., & Kaplan, J. M. (2013). Ontologies and politics of biogenomic “race.” *Theoria*, 60(3), 54–80. <https://doi.org/10.3167/th.2013.6013605>
- Xu, S., Pugach, I., Stoneking, M., Kayser, M., Jin, L., & HUGO Pan-Asian SNP Consortium. (2012). Genetic dating indicates that the Asian-Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. *Proceedings of the National Academy of Sciences*, 109(12), 4574–4579. <https://doi.org/10.1073/pnas.1118892109>
- Zachos, F. E. (2018). Mammals and meaningful taxonomic units: The debate about species concepts and conservation. *Mammal Review*, 48(3), 153–159. <https://doi.org/10.1111/mam.12121>