The tree and the net: spatio-temporal narratives of human population genomics

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Introduction

In this chapter, I examine two major spatio-temporal narratives embedded within human population genomic science: I explore what these narratives say about the evolution and history of humanity as a whole, and what their political implications are. One major narrative is embedded in a theory of evolution which tells how human populations developed in specific – often continent-sized – environmental niches, shaped by the classic evolutionary mechanisms of natural and sexual selection, endogamic mating, genetic drift, founder effects, and population bottlenecks.¹ These processes are based on concept of “population” as an entity that is located in a geographical niche and is relatively isolated for long periods of time. The key metaphor here is the tree, formed of a parental trunk and multiple branches and twigs. This metaphor underlies the DNA ancestry testing that makes genetic links between individuals and “ancestral populations”, which are often parsed as continental populations (Africans, Amerindians, Europeans, Asians), although smaller scales of resolution are given by some ancestry tests (e.g. specific regions or even ethnic groups within the continents). This kind of information is used in genomic medicine, forensic genomics and recreational genomics.² A second narrative gives a greater role to long-term inter-regional movements, mixtures and flows of people and genes, which relativize the concept of population, blur its boundaries and make it much more evidently a contingent construct. The key metaphor here is the net, with multiple interconnections and circulations over space and time.

In what follows, I explore these different narratives or metaphors for describing evolution and human pre-history, looking at their temporal and spatial dimensions. I then
discuss the implications and affordances of the narratives in terms of the claims that can be made about human unity and diversity. Finally I look at the more directly political and policy-relevant – what Kirtsoglou and Simpson (this volume) would call chonocratic – dimensions of the human futures that derive from these claims about unity and diversity, taking as an example the problem of racial disparities in health outcomes, which some people believe genetics can help to resolve.

My account raises the question of the relations between the particular theories scientists use to address specific problems, the narratives and metaphors that may underlie or overarch the theories - which may be deployed by the scientists themselves or inferred by cultural analysts - and the political implications of these narratives. Specific theories tend to hide that they deal with biocultural facts, which are “natural facts [that] have cultural information (values, ideologies, meanings) integrated into them, not layered on them” (Marks 2013: 247). In the overarching narratives and metaphors, this biocultural fusion is made more evident. If scientists themselves deploy such metaphors - as they sometimes do with the tree and the net - they may be conscious of their metaphorical character and do not take literally all their possible implications. They may well not have systematically thought through all these implications, instead using the metaphor as a convenient shorthand. This latter possibility is amplified when the metaphors are inferred by other commentators. Nevertheless, to the extent that the metaphor acts as an organizing frame for analysis, it will become reified and, as such, can have important effects. For example, socio-biological theories imply narratives of competitive individualism that underwrite the capitalist socio-economic order (Sahlins 2008); or again, some scientific ideas about human diversity - even when not explicitly racist or sexist - can legitimate hierarchies of race and gender (Fausto-Sterling 2000; Haraway 1989; Martin 1991; Wade 2002). However, talking in terms of scientific narratives as simple reflections or legitimations of dominant social orders is
theoretically too crude. Instead we need to see the narratives as being in a complex relationship of mutual constitution and co-production with social orders, such that “science” and “society” are both heterogeneous collections of elements in a shifting assemblage of relations and semiotic-material components (Jasanoff 2004; Latour 2005).

**Evolutionary narratives: tree and net**

Two key metaphors for talking about evolution are the “tree of life” and the “reticulated net” (also sometimes called the “braided stream”). These have rather different implications in terms of the role they give to spatial movement and stability, and to the relative isolation of “populations” and exchanges between them, over the long reaches of evolutionary time.

The image of the tree is very common in depicting human evolution, as well as the evolution of language and the history of families (Bouquet 1996; Doolittle 1999; Sommer 2015; Templeton 2005). Although the language of roots is closely associated with the idea of a tree, the visual depiction of the “tree of life” rarely shows the roots of the tree, only the trunk and its branches and twigs. The idea of origins is thus always singular and change is by definition upwards and outwards, implying a certain teleology. The tree image is necessarily spatio-temporal: it represents the passage of time in spatialized way – a common tendency, according to the philosopher Elizabeth Grosz, when seeking to convey an idea as elusive as time, which is “almost impossible to think or conceptualize” despite the fact that “we live time continuously” (Grosz 2004: 6, 250).

The tree metaphor has been used for a very long time for genealogical purposes and, since the late nineteenth century, to represent human evolution. Despite some critiques in the 1930s, it became dominant during the twentieth century (Sommer 2015) and arguably remains so today, albeit in modified form. Its strongest version is found in the out-of-Africa theories of human evolution that became dominant in the 1990s.
The out-of-Africa tree

In the 1970s and 80s, the dominant idea about human evolution was the so-called multiregionalist model, which held that *Homo sapiens* or “anatomically modern” man had evolved in each Old World continental region from local archaic *Homo* ancestors. This was a tree model, because the trunk of the *Homo* genus was located in Africa, with branches into Europe and Asia, but it was displaced in the 1990s by a version known as the out-of-Africa recent replacement theory, which proposed that anatomically modern humans, had evolved in east Africa and had – relatively recently in terms of the evolutionary history of the *Homo* genus – migrated out of Africa and displaced existing archaic *Homo* species, without mixing with them or only to an insignificant extent. As in previous versions, the trunk of the tree was located in Africa, where it had already produced the *Homo sapiens* species which then migrated to all the major continental regions, where populations evolved in relative isolation from other continents, with the separate branches becoming differentiated genetically and morphologically.

A key plank in this theory was the analysis of mitochondrial DNA (mtDNA), a type of genetic material that is passed down the maternal line alone, more or less unchanged (i.e. without the recombination or “shuffling” that affects most DNA during sexual reproduction). Successive small mutations that accumulate in different lineages of mtDNA act as lineage signatures, which can be used to distinguish between maternal lineages; this makes it possible to trace population migrations across space (by mapping the geographical distribution of mutations) and time (in relative terms, by assuming that more widespread mutations are older; and in absolute terms, by calibration against a “molecular clock”, which defines how often mutations typically occur). This kind of spatio-temporal analysis typically - indeed necessarily in the case of non-recombinant DNA - results in a phylogenetic tree, showing a
common older trunk, with diverging branches and sub-branches, associated with geographically located populations (Cann, Stoneking and Wilson 1987).4

These trees are very common currency in population and evolutionary genetics and they have a common spatio-temporal narrative underlying their structure. The evolutionary story of the out-of-Africa theory says that continental-scale human diversity emerged at some notional time between the migrations out of Africa, dated about 85,000 to 100,000 years BP, which eventually led to all the world’s regions being populated by about 15,000 years BP, and a threshold at which the continental populations started to mix more intensively. This threshold varies according to the region in question, but for, say, the Americas it is not until about 1500 AD. In the intervening period, continental populations formed and became genetically differentiated by the classic evolutionary mechanisms of natural and sexual selection, endogamic mating shaped by geographic and cultural barriers, founder effects and genetic drift. Some scientists argue that major population differentiation occurred after tight population bottlenecks occurred worldwide following the volcanic winter caused by the massive Toba eruption around 71,000 years BP (Ambrose 1998). In an account directed at the general reader, which is arguably somewhat simplified, Oppenheimer (2003: 113) says that the “general rule” is that, as the Old World and Antipodes became settled, there was “little if any further inter-regional gene flow” until about 15–25,000 years ago when humans spread across the Bering Straits and into the Americas, where they formed a further continental isolate.

This view creates an image of relatively pure continental populations, which then mixed in historical times. Migration is necessarily part of this model, as humans populated the continents, but either it is seen as having lulled for tens of thousands of years, during which time continental genetic and phenotypical differentiation occurred; or it is seen in terms of “replacement”, as one human population displaced another, with little mixture taking
place. This is the assumption underlying DNA ancestry testing of “admixed” populations, which estimate the proportional contribution of ancestral populations to the genetic profile of a given sample population.5 “Admixture approaches … take as an assumption the reality of parental populations; that is, it is assumed that are, or were, such ‘pure’ human populations” (Weiss and Lambert 2014: 17). The temporal narrative invokes a tree-like structure in which the branches of the tree are continental populations, seen as more or less isolated; the narrative is underwritten by the sampling of specific reference or parental populations from particular locations, each of which represents a continental ancestry. For example, a sample of Yoruba people from Ibadan, Nigeria, is commonly used to represent “African ancestry” (Bolnick et al. 2007; International HapMap Consortium 2003). Some geneticists protest at the “selective de facto typological sampling and the assumption of statistically homogeneous source populations” involved in measurement of admixed ancestries (Weiss and Lambert 2014: 24). Another prominent scientist states: “Yes, there are differences in genetic variation at the continental level and one may refer to them as races. But why are continents the arbiter? … If humans have had this single continuous journey disobeying continental residence – and as evidence we have the continuous distribution of genetic variation across the globe, not discrete boundaries like political borders – where do we divide humanity and why?” (Chakravarti 2014: 9).

Such “typological sampling” techniques are part and parcel of a larger debate about how to sample when measuring human genetic diversity. Typically, samples are selected by named population (defined by criteria of language, ethnicity or geographical locality), whether quite specific (Yoruba from Ibadan) or more general (Cambodians, French).6 This inevitably creates a basic symmetry between social identity, locality and genetics, and presents “populations” as separate entities, despite geneticists’ simultaneous recognition that human genetic variation is mostly “clinal” in form (i.e. specific genetic traits often follow
gradient-like increases and decreases in frequency across geographical distance, with no clear borders). Also, samples taken for these kinds of studies usually include only people whose grandparents were members of the population under study or were born in the locality. The idea is to avoid the statistical “noise” created by recent migrations: the technique selects people who are genealogically rooted and thus works to “purify” the sample genetically. Overall, this creates what Palsson (2007: 179) describes as the “island model” of human biological variation: the metaphor is spatial, but it entails a temporal narrative too, as the “islands” were formed in an evolutionary process.

Underlying this island model is the very concept of population itself, which, as philosopher Naomi Zack puts it, is “not epistemologically tidy”: “There are no generally accepted answers to the following questions: How many generations of isolation are necessary to form a population? How large must a population be? What proportion of population members must reproduce in a given generation for it to qualify as a breeding unit? How much gene flow into or out of a population can take place before the population is a different population?” (Zack 2002: 69). Geneticists might respond that no “generally accepted answers” exist to these questions, because it all depends on the context and on the problem being addressed; they have also long agreed that a population can only be defined in statistical terms. On the other hand “merely to offer a genetic description of a population in terms of frequencies of various alleles [genetic variants], perhaps to make predictions about future evolutionary changes or hypothesize about past evolutionary history, assumes the existence of an entity with discernible boundaries and determinate parts” (Gannett 2003: 998). There is an underlying tension between the critical recognition (shared by many geneticists) that “population” is a conventional construct creating order from an indeterminate complex of processes and relationships, and a tendency to reify that construct as a bounded entity.
The sampling strategy based on what Pálsson calls the island model is not uncontested among geneticists. Other approaches envisage a grid or net which would sample random individuals across geographical space, without prior assignment to a socially defined group (Martínez-Cruzado et al. 2005; Pálsson 2007: 180; Reardon 2005: 77; Sommer 2015: 132). As the prominent geneticist cited above has put it:

Human evolution has always been studied with respect to such populations defined by language, geography, or cultural and physical features. Consider instead what we could decipher if we could sample a million humans (say), without regard to who they were, across a virtual grid across the world …These types of global surveys of diversity have been performed for other species and may provide the first objective description of ours, bereft of race and other labels. (Chakravarti 2014: 11)

Sommer notes that geneticist Luigi Cavalli-Sforza, who pioneered the construction of phylogenetic trees based on DNA, was aware of the problem in the 1970s: he “suggested that it [tree-building] might work only for populations that are geographically far apart, because otherwise ‘instead of a “tree” one may have to estimate a “network”; such methods do not yet exist’” (Sommer 2015: 121, citing Cavalli-Sforza). Sommer concludes: “discursively and visually foregrounding the treeness of human diversity constitutes a choice to focus on a particular kind of variation rather than another. It constitutes a choice for dichotomous visualization and narration of human evolutionary history along the lines of a root-and-branching structure” (2015: 138).
Reticulate evolution, nets and rhizomes

An alternative to the tree model is a reticulated net model, which highlights long-standing movements and particularly mixtures and gene flows between regions and populations. This metaphor was proposed as early as the 1930s by some theorists who criticized the tree model. Huxley and Haddon, in *We Europeans* (1935), a book challenging Nazi racial theories, said “the conventional ancestral tree may have some advantages for representing the descent of animal types; it is wholly unsuitable and misleading for man” because in humans “the branches constantly meet and unite and produce new types of shoots” (Huxley and Haddon 1935: 266, cited in Sommer 2015: 113). Sommer shows a map from Huxley and Haddon’s book with multiple lines of migration and evolution criss-crossing a map of Europe and the Middle East. As another alternative to the tree, Sommer also reproduces an abstract reticular diagram representing “the pedigree of *Hominidae*” by the German physical anthropologist, Franz Weidenreich, in his book *Apes, Giants, and Man* (1946), which shows multiple exchanges between lineages over time. Not surprisingly, Weidenreich also rejected contemporary ideas about races as sub-species (Sommer 2015: 114). But Sommer argues that these early critiques of the tree model did not stick and that the tree image and narrative persisted and got stronger as genetics developed; she focuses her discussion on Cavalli-Sforza and his use of trees to represent human population histories, despite his parallel recognition of the essentially random and non-teleological dynamics of evolution, which sit ill at ease with the tree metaphor.

Later, during the 1990s, as the replacement out-of-Africa theory gained dominance, another small set of theorists placed much more emphasis on processes of movements and genetic exchange between archaic and modern populations, and between modern regional populations. Although by the 2000s no one was seriously disputing a crucial out-of-Africa migration of *Homo sapiens*, at about 100,000 years ago, which had spread across the globe,
these theorists (rather misleadingly nicknamed multiregionalists, despite their divergence from the 1970s–80s multiregionalist theories, referred to above) argued strongly that there had been a number of out-of-Africa migrations (Stringer 2014). Above all, they contended there had been significant gene flow between older and more recent types of hominids and also between regional populations. These theorists argued that it was misleading to focus on the phylogenetic trees that were constructed by looking at very specific parts of non-recombinant DNA, such as mtDNA:

If a species has extensive gene flow throughout all parts of its geographic range, the species would evolve as a single evolutionary lineage, with no intraspecific population-tree whatsoever. Instead, local populations in such a species would be genetically interrelated by a trellis or lattice-like structure, not distinct branches on a tree. Nevertheless, such a species would still have haplotype trees for all its DNA regions with no to little recombination. (Templeton 2005: 40)\(^9\)

That is, a tree-like structure could accurately characterize spatio-temporal relationships for those specific parts of the DNA that underwent little or no recombination during hereditary transmission, while being far from accurate for the species as a whole.

This reticulated net approach was strengthened by recent discoveries of Neanderthal DNA in anatomically modern human fossils and in present-day humans, indicating mixture between different lineages of “archaic” and “modern” humans. As one biological anthropologist, John Hawks, put it, “It’s mixing all the way back”: “Ancient DNA has begun to show the process of genetic exchange was not a minor player in our evolution. All human populations today evidence some mixture of ancient populations that existed well before the ‘origin of modern humans’” (Hawks 2015). Hawks and others talk of a “braided stream”,

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criss-crossed by intersecting rivulets and intersections, and of “an interwoven plexus of genetic lineages that branch out and fuse once again with the passage of time”, in which “the terms ‘archaic’ and ‘modern’ [humans] lose all meaning” (Finlayson 2013).

In this context, it is relevant that some people have been re-thinking evolution more generally in the light of biological phenomena such as polygenomic organisms, chimerism, lateral gene transfers and hybrid species, which all fit poorly with a tree model and sit better with a network model: when looked at broadly, “the history of life cannot properly be represented as a tree” (Doolittle 1999). All humans are polygenomic organisms insofar as they host multiple microbial genomes in their bodies as well as their own DNA; indeed, the human body contains at least as many microbial cells as human cells (Campbell 2016). These microbes can also affect the way human genes are expressed (Dupré 2015). Chimeras are a special case of polygenomic mosaics: they are individuals who carry two or more genetically distinct cell lines in different parts of their body, caused originally by the fusion of two zygotes (fertilized eggs) (Dupré 2015). Lateral gene transfer is a common process in which genetic variants are transferred horizontally between genealogically distinct lineages, giving rise to single organisms with genomes from multiple sources which are not phylogenetically related (Doolittle 1999). The anthropologist Stefan Helmreich, looking at microbes in deep-sea contexts and the biochemical commodities extracted from them, says they reveal that “The tree of life was always a net” and sees the advent of “a new, agenealogical, watery bare life” (Helmreich 2003: 352).

It is important to recognize that most of these examples relate to individual organisms or non-human species. The relation of these phenomena to the evolution of human populations is a little distant: processes of gene exchange across space between human social units or “populations”, even if they follow network reticulations, are not the same as chimerism, lateral gene transfer or polygenomic organisms. But the underlying conceptual
tendencies are parallel, because they highlight the role of complex trellis-like networks of biological interconnections between organisms and between populations, thus undermining a simple one-to-one correspondence between the individual physical organism and the underlying genotype, and, further, challenging the idea of a unity between the genome of the individual and that of the species (i.e. the idea that every individual of species has a characteristic species genome and only that genome); this in turn makes it harder than ever to think in terms of a simple correspondence between human social units and biological (genetic) units.

These processes relate to the concept of “reticulate evolution” as a way to adapt, rather than replace, phylogenetic tree-like models. Lateral gene transfer is one key process creating reticulation; another is hybridization between “species” to produce new fertile species, a process that goes against the conventional biological idea that most inter-specific hybrids are infertile, but which is commonly found among plants, fish, frogs, and many lineages of invertebrates (Arnold 2008). Some computational biologists add reticulation to phylogenetic trees to show genetic links between apparently separate branches, “relationships that cannot be represented by a dendrogram or a phylogenetic tree” (Legendre and Makarenkov 2002). Indeed, some people are re-imagining evolution in post-Darwinian terms as a “rhizome of life” (Mikulak 2007; Raoult 2010).

This contrasts markedly with tree metaphors that, by presenting populations as terminal points of trunk-and-branch structures, inexorably background the exchange of genes across space and “between populations”; indeed, the rhizome metaphor casts the concept of “population” in a less reified light. Trees have a scalar structure in which, at the smallest scale, all the twigs (local populations) belong only to one small branch (regional populations), and each small branch belongs only to one major branch (continental populations); thus each local population belongs to one continent only. The tree metaphor
underlies the common technique of using a single sample from a present-day Yoruba population to estimate the “African” genetic ancestry in an admixed New World population, inherited from Africans taken to the Americas centuries ago (Wade et al. 2014). Reticular networks have a very different, flatter scalar structure, which envisages individual nodes with multiple connections, or even just a heterogeneous mass of connections, without nodes.

At the more general level of how we can know the world, Deleuze and Guattari famously distinguish, in *A Thousand Plateaus*, between arborescent and rhizomic modes of knowledge. Organizing knowledge in tree-like structures invokes origins and endpoints, connected by one-way genealogical ties in a predictable scalar hierarchy. Rhizomic ways of knowing, in contrast, involve multiplicity, non-linearity, and nomadic movements in spaces without a predictable scalar relationship. Thus, “the arboreal is associated with linearity, hierarchy, origins, racism, rigidity, and carnophallogocentrism, while the rhizome embodies flexibility, openness, movement, and potentiality” (Mikulak 2007). The kind of reticulate network approaches to evolution that I have been outlining chime well with this view of rhizomatic knowledge.

**Unity and diversity in tree and net**

The tree metaphor produces a certain image of “unity in diversity”, a phrase often said to capture the subject matter of anthropology itself. In the tree image, unity is based on common roots or ancestry, at varying scales of temporal and spatial resolution, ordered in a nested hierarchy. Unity is a product of original similarity, derived from evolution in a particular space (ultimately the east African savannah); this involves a form of original immobility, as *Homo sapiens* evolved in a specific niche. Correspondingly, diversity is figured as a product of “natural” branching processes, resulting from an initial movement across space (into continents), followed by evolution over time (adaptation, genetic drift, sexual selection, etc.)
in a relatively stable and isolated location. In this picture, unity and diversity are constituted relationally, but the relation is zero-sum: more of one means less of the other. This leads to a perspectival issue: seen in one way, from the trunk upwards, it is possible to emphasize common humanity (genetically we are all “99.9% the same”); seen another way, from the twigs down, the differences can be highlighted (for example, in terms of genetic variation in humans, at least 10 million SNPs have been located; CNVs account for about 12% of the human genome; and we now know from epigenetics that environmental variation can cause the same DNA material to be expressed phenotypically in different ways in different people).  

Seen in one direction, we all share a common human nature (genetics, ontology), but have different physical manifestations (phenotypes and cultures); seen in another direction, we are different natural types (phenotypically, culturally, genetically, ontologically). This perspectival effect is clearly subject to politicized readings, with genetics supporting both an anti-racist, “we are all the same” position, and a stance that highlights genetic difference and can produce a (disavowed) racialism that, in turn, is feared by many critics to authorize an idea of racial difference that provides grist to the mill of racism (Duster 2015; Roberts 2011).

The unity/diversity pairing characteristic of the tree image has temporal dimensions too. First, the image of diversity produced draws on samples taken from present-day populations, but in genetic ancestry testing, the diversity invoked is for a period pre-1500. Genetic ancestry testing uses present-day populations as proxies for pre-diaspora continental populations; and modern diasporic “admixed” populations are usually parsed in terms of the proportions they have of the “original” components (African, Amerindian and European). This emphasizes genetic diversity and aligns it with familiar large-scale phenotypical and cultural differences (Duster 2011). Second, in the tree image, the further back one goes in time, the less diverse humans were; unity is thus calling on the deepest ancestral roots,
located not just “under the skin”, but in the far distant past. It is invisible and thus has less affective traction than the visible phenotypical and cultural differences associated with the branches of the tree (“we are all Afro-descendants” is a counter-intuitive proposition: it is technically true, but has little affective traction, because the term is generally used to designate “black” people).

Third, because in the tree image unity is rooted in the past, movement forward through time (and space) equals more diversity; thus rhetorical claims that “we are all the same” actually contradict the temporal drive of the tree model towards difference. Post-1500 diaspora movements produce connections between the twigs and branches of the tree structure, but this is predicated on their prior separation. This is the model of official multiculturalism: interaction occurs but between distinct entities, only related through distant past ancestry and common human origins. In short, when allied to the tree image, the slogan “unity in diversity” becomes oxymoronic as it is not easy to see how the two concepts of “unity” and “diversity” can be anything other than inherently opposed. In this view, unity is at species level; it is what makes anyone a human; common humanity is privileged as the significant and sovereign subject in the world. In contrast, diversity is defined in terms of boundaries, divisions and the identification of difference: it is unity’s subordinated “other”.

The net metaphor offers different political affordances. Unity is derived not only from ancient evolutionary processes in Africa creating common ancestry, but also from evolutionary processes operating through long-established and, crucially, on-going exchanges and flows across space and time. The exchanges that produce unity simultaneously produce diversity, because the interactions are not homogeneous over space and time, and lead to more heterogeneity. Diversity is produced by the same set of processes that create unity, rather than emerging from a series of pendulum swings from stability (that produced sameness in Africa), to movement (manifested in the peopling of the world, which initiated
diversity), to stability again (population adaptation to continental and sub-continental niches, producing sameness in each niche and consolidating diversity world-wide).

Temporally speaking, the reticulated net means that unity is not located only in the distant past, but as an on-going process; it means that post-1500 diasporic movements are not seen as a major rupture, but rather as an intensification of processes already in place. This is the model of an alternative, more diasporic version of multiculturalism, in which interaction constitutes the relational entities that may sometimes be freeze-framed and reified as “cultures”. Thus unity and diversity are immanent in each other, rather than being related in a zero-sum balance. They co-exist in such a way that one can have more (or less) unity and more (or less) diversity at the same time. More unity can be constituted through more intensive and pervasive exchanges, which can simultaneously lead to more diversity, as exchanges do not necessarily lead to homogeneity - indeed they only do so under quite specific conditions (e.g. of monopoly capitalism); by the same token, less unity through fewer exchanges can lead to less diversity. Unity and diversity are not related as sovereign subject to dominated object, but as processes in a relation of mutual constitution.

**Genomic futures: deracialization and health for all**

What are the practical implications of the different political affordances of the tree and net images? One example comes from the area of race and racial disparities in health. On the one hand, focusing on the trunk of the tree, genomics has often been seen as helping to usher in a better future for humanity by hammering home the final scientific nail in the coffin of racism: “we are all the same”. On the other hand, genomics has been seen to usher in a brighter future in which doctors will be able to combat common disorders by understanding their genetic basis and even offer personalized medicine based on individuals’ genetic profiles. Crucially, however, it does this in part by using knowledge of how genetic variants vary according to
continental biogeographical ancestry (BGA) (Bliss 2012): i.e. it focuses now on the branches of the tree. This in itself supplies medically relevant information, but the implications of this mapping deserve attention. The tree model appears anti-racist, but it implies a temporality that reinforces continental differences, which conform to established lines of racialized difference; it also gives these differences a genetic and evolutionary basis. It is therefore deeply contradictory and ambivalent.

These contradictions emerge in approaches to racial health disparities, approaches that are by definition future-oriented, as they envisage a reduction in disparities over time. Most scientists and doctors - at least in the United States and UK - agree that racial categories should be used in health research and clinical practice as part of a social justice mission of racial inclusion: the idea is that it is necessary to recognize and measure difference in order to correct disparities that follow lines of racial difference understood as a social artifact (Bliss 2012; Epstein 2007; Smart et al. 2008). However, alongside this consensus on the ethical imperative of using racial categories in health research and clinics, there is an important gulf separating those who believe that genetic differences actually follow racial category differences in ways significant for addressing health, and those who do not.

Some geneticists say that genetic difference has some correspondence with “racial” difference; that is, the differences popularly called racial have real genetic dimensions. The terminology used here is sometimes that of “continental BGA”, in order to avoid the awkward language of race (Bliss 2012: ch. 4; Burchard et al. 2003; Mountain and Risch 2004; Risch et al. 2002). If there are medically relevant genetic differences between populations glossed in terms of race – albeit some geneticists admit that common-sense racial categories may not be the best proxy for such differences (Reich 2018: 247–73) – it is naïve, so the argument goes, to deny such differences for the sake of a misguided political correctness. Thus the focus is on the genetic differences corresponding to the branches of the
tree (Fullwiley 2008). In practical terms, this means channelling funding for health research in that direction. There may still be an anti-racist and social justice agenda operating here in the promise that genomics can produce therapies tailored to specific racial categories and thus help solve health disparities – the heart drug, Bidil, targeted at African-American men, is one example (Kahn 2013). But the reintroduction of racism is also a possibility, as shown by recent genetic research in Mexico that focuses on indigenous genetic ancestry as a predisposing factor in the very high rates of diabetes and obesity that are affecting the national population (Saldaña-Tejeda and Wade 2018).

Other geneticists say that social categories of race and ethnicity are irrelevant for understanding the genetics of ill-health, because there is no meaningful correspondence between these social categories and genetic variation (Bliss 2012: ch. 4; CooperKaufman and Ward 2003; Pena 2005). For these scientists, genetic factors may be important, but they cannot be adequately assessed using collective categories; instead individual genetic ancestry is important. This stance involves anti-racism as disavowal of the genetic reality of race. Health disparities between social groups are mainly due to social factors, although these may have important biological (including epigenetic) consequences, as life experiences in a given environment – e.g. living in poverty, suffering racism – can shape the body in deep-set and durable ways (Kuzawa and Sweet 2009; Kuzawa and Thayer 2013). Environmental racism, racial inequality and the experience of racism are all known to contribute strongly to racial health disparities (Gravlee 2013; Shostak and Moinester 2015: 201). From this perspective, the approach that locates a significant component of health disparities in racialized genetic difference diverts the attention of doctors and health policy-makers away from these vital social factors shaping health outcomes. The failure of medical genomics so far to produce significant or even any practical genetic therapies for common but complex disorders (diabetes, heart disease, cancer, etc.) has added grist to the mill of those who argue for greater
attention to social factors (Richardson and Stevens 2015). However, the diversion of scientific attention away from such factors is already reflected in research funding, if not yet public health policy (Bliss 2015; Montoya 2011).

Those who think race is not a useful tool for understanding the genetic basis of ill-health are cautious about continental-level genetic population difference, as represented by the branches of the tree of human life; their stance resonates with the long-term exchanges and interactions contained in the net image, which figure genetic variability as less geographically structured and more radically clinal. For them, no significant aspect of human health can be grasped by focusing on collective genetic differences of a continental population nature, which formed over long stretches of evolutionary time (differences commonly known as racial, whether or not the word “racial” is used). That is, such differences may be perceptible in the genetic data, but they explain nothing of importance, at least in relation to health. Genetic differences in general may be important, but they operate at an individual level because, in population terms, genetic exchanges over long periods have created a good deal of genetic continuity across geographic space. They emphasize social factors in creating health disparities (an aspect of diversity); implicitly they invoke the shallower time-frame of the net model, which affords an emphasis on social interventions. Health policies and research should target social factors, such as racial inequality and the neighbourhood effects produced by environmental racism and segregation. The deeper time-frame of the trunk-and-branch model is not relevant for understanding health and illness.

However, images of deep-time lineages can still have the power to colonize these shallower time-frame approaches. The increasingly influential science of epigenetics emphasizes the way the social and physical environment acts on the individual body to influence gene regulation and expression biochemically in ways that may be durable but not necessarily permanent. Durable changes to an individual’s genetic material caused by
epigenetic processes can be passed on through genetic inheritance. Richardson (2015) argues that a good deal of epigenetics focuses on the mother-foetus-child relation, as maternal experiences and behaviour especially during pregnancy can shape the foetus genetically (or rather shape the range of ways in which a foetus may develop); these changes then affect the way the female foetus develops into a reproducing adult. The end result is to produce a kind of genetic/epigenetic matriline. She shows how some geneticists talk about maternal “somatic capital”, which can be transmitted in maternal line, and how this can lead to “metabolic ghettos” of poor health. This is an indication of how lineage and genealogical thinking (related to tree thinking), with their associated temporality (in which time is a cumulative fixing agent, working on spatially located populations), can seep back into models that seem to emphasize plasticity over time (Saldaña-Tejeda and Wade 2019).

**Conclusion**

Overall, the potential of the tree model to underwrite deep-rooted diversity and geneticize (racial) difference – despite its potential to highlight unity – should be borne in mind. Attention to the various spatio-temporal models underlying different approaches to understanding genetic variation helps us to be mindful of their political and ethical – and potentially chronocratic – implications. The tree and the net are metaphors underlying different theories about (human) evolution. Scientists may be self-conscious about the implications of these metaphors, or they may not; if they are aware, they may use them anyway, perhaps as a useful shorthand.

There is also a very important sense in which scientists continuously try to improve their theories and this changes the metaphors they use and their political implications. For example, while I have focused on the tree and the net as substantially different metaphors, recent approaches see the expansion of *Homo sapiens* as having been shaped by serial
founder effects, which occurred as small groups of humans migrated into new niches and expanded there. According to this theory, the series of founder effects have left a tree-like structure of nested genetic differentiation, detected as underlying signatures of ancient processes of genetic drift, which remain despite inter-regional gene flow. This model posits a tree metaphor but does not require an assumption of persistent relative isolation between regions or “branches” (Deshpande et al. 2009; HennCavalli-Sforza and Feldman 2012). Nevertheless, the tree and net metaphors I have focused on still operate in science – the tree image in particular has a good deal of traction outside the specialized realm of biological theory. So it is necessary to be attentive to the political and ethical implications of these metaphors, and in particular the way the tree metaphor can underwrite racialized thinking, while seeming to dissolve it, and thus produce chronocratic effects.

This analysis of metaphors may seem distant from medical genomic research and further still from clinical practice and health policy. But it is important to trace the connections between different areas of the assemblage in which various domains of scientific research practice (evolutionary theory, medical genomics) are linked directly or indirectly with each other and with other realms of practice (clinical medicine, health policy-making, recreational genomics). It is important to see that debates about race, genetics and health, or the meaning of DNA ancestry testing, are related to debates about human evolution and the peopling of the world, through underlying metaphors, such as the tree of life or the rhizome of life, that tell particular narratives about humans in time and space.

Notes

1 Sexual selection is a form of natural selection that occurs when individuals of one sex preferentially choose members of the opposite sex, based on certain characteristics, which then become more frequent in the “breeding population” and more accentuated. Mating is
endogamic when it happens more frequently within a breeding population, whether by cultural preference or geographic barriers. Genetic drift refers to the process by which certain individuals, by accident, leave fewer copies of their genes in the next generation than others; over time, this can lead to some genetic variants in a breeding population disappearing or becoming very scarce. Founder effects occur when a small number of individuals found a new colony or breeding population: their genetic variants will be common in successive generations. Population bottlenecks occur when a population is severely reduced, by accidental demographic forces (famine, disease), for at least one generation. This will reduce genetic variability and accentuate genetic drift and founder effects. All these effects depend on the notion of (breeding) population, which is not easy to delimit - see below for a discussion.

2 Data on ancestry are used in genomic medicine to help localize disease-related genetic variants; in forensic genomics, they are used to help predict the physical appearance of a suspect and to support claims to identity-related resources, such as compensation for damages (e.g. death of a relative), return of bodily remains, or lucrative membership in a Native American tribe; and in recreational genomics, they are deployed in narratives of identity and belonging which can satisfy or pique the curiosity of roots seekers.

3 See, for example, the image from Louis Leakey’s 1934 book *Adam’s Ancestors* reproduced at http://www.talkorigins.org/faqs/homs/leakeydiag.html; and the image of Old World language evolution by Minna Sundberg at http://www.sssscomic.com/comic.php?page=196.

4 For examples, see the paper by Cann, Stoneking and Wilson (1987) and also https://courses.lumenlearning.com/wm-nmbiology1/chapter/reading-phylogenetic-trees-2/.

5 Strictly speaking all humans are “admixed”, but in genetics the term usually refers to populations such as African-Americans and Latin Americans who have been formed by the
recent mixture of populations previously assumed to have been more or less genetically isolated from each other.


7 For an example, see Templeton (2012), available online:
http://dx.doi.org/10.1002/9780470015902.a0020795.pub2.

8 The same tension between accounts that emphasize replacement and ones that highlight mixture can be seen in debates about the pre-history of Vanuatu, in the Pacific. One theory proposed that original migrants who came from East Asia about 5,000 years ago had been replaced by more recent ones from Melanesia, with little mixture having taken place; a counter-theory held that these two populations had mixed together over a period of some 500 years (Bedford et al. 2018; Lewis-Kraus 2019). Both theories allowed for sweeping processes of migration, but saw the human interactions deriving from those processes in quite different ways.

9 A haplotype is a set of genetic variants that tend to be inherited together across generations; thus a haplotype tree is a phylogenetic tree of the type I have already referred to.

10 For an image of a braided stream, see the photo of the Stikine River delta by Sam Beebe (Ecotrust), available online:

11 Previous estimates gave the ratio of microbial to human cells as 10:1, a figure that is still widely repeated (American Society for Microbiology 2008; Dupré 2015).

12 Geneticists may be aware of the short-hand approximations underlying this technique, but they use it nevertheless, as do commercial DNA ancestry testing companies (Bolnick et al. 2007).
SNPs (single nucleotide polymorphisms) are single “letter” locations on the DNA sequence where a difference occurs between individuals in a species, with some regularity (usually more than 1% of the total population). CNVs (copy number variants) occur when the number of copies of a particular letter sequence varies from one individual to the next (Clancy 2008; Redon et al. 2006).

References cited


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