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Approximating human genetic variation by means of 'self-identified race/ethnicity':
Epistemological and Ethical issues

ABSTRACT

Recent results in population genomics suggest that US race and ethnicity categories are *good* proxies for human genetic variation.¹ Using markers in the DNA of individuals selected from pre-identified populations these studies track variability in allele frequencies across human populations. Genetic data is fed to an unsupervised model-based clustering algorithm [implemented by versions of a program tellingly called *STRUCTURE*] which groups the data according to the model supplied.² The earlier of these studies call self-reported *ancestry* useful for approximating epidemiological risk.³ But recently researchers explicitly drew a link between geographic ancestry and *race*. Tang et al. (2005) report that [A]ncient geographic ancestry, which is *highly correlated with self-identified race/ethnicity*—as opposed to current residence— is the major determinant of genetic structure in the US population. (*emphasis added*)⁴

I argue that what results these studies report is biased. It is reported that the clusters accord with our common-sense race/ethnicity groups (Tang et al (2005) include Hispanic) but it is not reported that investigators have already specified an interest in say five clusters rather than two, three or seven. These clusters are also obtainable and obtained via an “unsupervised” clustering algorithm and also mark genetic variation which accords with geographic regions. But they do not mark something we have a prior interest in in the US: race.

Epistemic value is placed on the techniques of modern population genomics. But using these techniques as instruments for public policy relies on their calibration against population

¹ Rosenberg et al (2002), (2005) and Tang et al (2005).

² See Pritchard et al. (2000) for a description of the model implemented by *structure*, and Falush et al. (2003) for a description of the version implemented by *structure 2.0*

³ Rosenberg et al (2002)

⁴ Tang et al. (2005) 268

categories already defined via social, political and historical process as the ones we care to track. Genomics science measures what categories we come to care about, echoing a description Weber made of the social sciences.

Does this dependence on our values make this kind of science bad science?

I answer that it only makes it Found Science. I define found science by analogy to found art. I argue that found science 1. can be science, 2. can be useful as science. This is because FOUND science only becomes found SCIENCE, if it's founded.

<Analogy [Found Art]>

Before I draw an analogy between found art and found science, let's make sure that the familiar arm of the analogy is indeed familiar. Below are two typical examples of found art. On the left you see one of the first instances of found art, Marcel Duchamp's *Fountain*, first exhibited in 1917. On the right is a more recent found art piece, Damien Hirst's *The Void*, first exhibited in 2000 and photographed here in Berlin's Hamburger Bahnhof.



Fountain, Marcel Duchamp (1917)



The Void, Damien Hirst (2000)

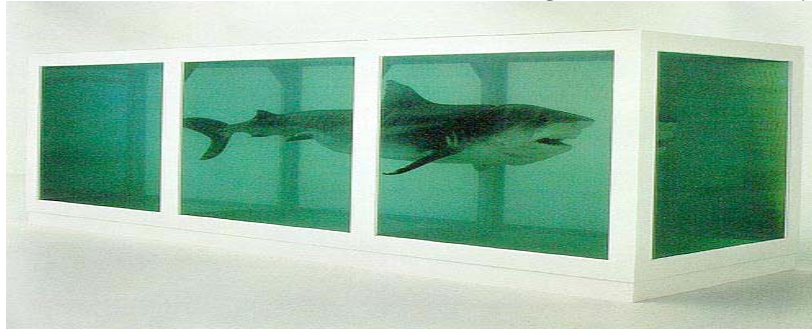
Found art has been around for approximately 100 years though, since its advent art theorists have retrospectively classified more conventional artwork as found art. Marcel Duchamp's readymades (or *objets trouvés*) were the first found art pieces. They had a pivotal role in the emergence of the avant-garde of modern art and continued to influence art through the 20th century. Found art became especially visible with the Young British Artists in the early 1990s, who counted Damien Hirst among others, in their ranks. Besides visual art, found art has influenced the performance arts and music, for example the compositions of John Cage use found sound and found rules⁵.

What I'm interested in here, is what is radical about found art. This is the claim –put to practice- that an everyday object, an object foreign to art and even *contrary* to our expectations

⁵ See Cage's use of chance to compose a piece but also as an element in the piece's performance. For example Cage used the *I Ching* to compose *Music of Changes*, solo piano (1951). His *Imaginary Landscape No. 4* (1951) is a piece for twelve radio receivers tuned to specific frequencies, volumes, etc. but with no control on what is being broadcast during the performance.

of art, like an ugly urinal, a disturbing pill, or the sound of biting an apple, can *become* art. How? It can be placed in a context which *makes it* art.

You might notice that the urinal in *Fountain* is turned upside down and written on ('R. Mutt') and the pills displayed in *The Void* are replicas of pills. Found objects are not displayed exactly as found, nor are they indeed always "found". Still, the idea is that what looks like any banal, ready-made object has a claim to being art. According to the precepts of found art: anything can be art,... -for example a shark, placed in a tank of formaldehyde, nicely titled (*The Impossibility of Death in the Mind of Someone Living*) and appropriately



authored (*by Damien Hirst* in 1991)- ...if it is placed in the artistic context⁶. But what is this "placing in an artistic context" business?

To my understanding, there are two motions involved in placing some thing somewhere: 1. a *picking up* of the thing, out of a context and 2. a *placing* of the thing *in* a context. Now, what kind of context is an artistic context?

It is a context where the thing can sit, as art!

<Analogy [Found Art (Found Shark {Found Object})]>

To work with an example, look at the piece pictured above. How is this "shark" found art? Here is my account.

First, the shark, a ready-made thing, is *found* in an artistic context. It might just be that the thing is found by an artist -as was probably the case with Hirst's imagination- but it could be that the thing is picked up by an artistic process -for example, the sound of someone mopping the stairs is picked up by Papalexandri-Alexandri's recording⁷.

Second, the shark is *founded*. It is founded in two kinds of context: a) The shark is founded in a physical context that carries the art stamp -it is put in green formaldehyde, inside a white tank, in an art studio or an art gallery and so on. b) The object is founded in a context of interests that carry the art stamp -the artist's interest in the object, the curator's interest in the object, the interest of an audience member in the object, etc.

Note that these two contexts interact. Artistic interests shape the physical context of the object and the object's physical context shapes artistic interest. Hirst wants the tank to be white and so he makes it white, the curator wants the piece installed in a specific way in an exhibition so she displays it appropriately, etc. And reversely, artistic interests are shaped by the physical

⁶ Cf. Danto (1981) p...

⁷ Cf. "Sta Skalia" ("On the Steps") Papalexandri-Alexandri (date)

context of the object: the curator likes the white tank, the buyer develops an interest after seeing the object in a famous gallery, etc. Note also that a missing interest can carry the stamp of art – for example, a lack of interest in the weight of the shark tank can distinguish it from an aquarium⁸.

Both of these artistic contexts, the physical context of the object and the context of interests in the object, found the object *as art*. And once the object is *founded* as art the whole piece *functions* as art and can be found again, *as art*⁹.

But note. Having the relevant contexts in place is not enough for founding an entity as art. Besides space and interest you need tools. Instruments, techniques, practices, or what I call “founding tools” are *used to* install the shark in these two types of artistic context are. So for example, the shark is bought with money; it is transported from the fishery in a vehicle; it is loaded in a tank with a crane; etc. And further, the shark is made interesting by a movie Hirst sees, or the shark is made interesting to the curator by hearing of Hirst, or the exhibit is made interesting by a public broadcast, etc.

As founding consists in an installation in multiple spatial contexts and multiple contexts of interests, different founding tools might be needed at different stages in the process of founding. Some of these founding tools will be particular artistic techniques but some will be techniques and practices not particular to art, such as scheduling, networking, popularizing, lobbying, which are undertaken with an artistic interest in mind.

So there you are. I just gave you a story about what makes the shark found art. Note that this is not a story about the artistic *merit* of this piece; it is a story about its *artistic* merit. The piece could be good or bad art by what standards we care to consider but it will be good or bad ART. Note also that this is by no means the whole story and nor an accurate story, but it is, I propose, the appropriate story for the task I have at hand which is to abstract from it!

How can this be at all relevant to science!?

For now, the relevance is an association between words.

I have been using two forms of ‘found’, an adjective and a verb form. ‘Found art’ refers to art that *is found* but also to the process needed *to found* art. In other words, the found art object is found in two ways: 1. The object is discovered –it is found. Rather than created, the object appears to be ready-made or already available. 2. The object is supported –it is founded. The object is installed in the appropriate spatial contexts of physical, discursive, social or other type of space¹⁰ and it is held there by corresponding contexts of interests –interests in values of different sorts.

⁸ Schaeffer (2000) p.289 notes the inseparability of a “processual intentionality” and “the artist’s encounter with the medium worked in”. I think of artistic intentions and artistic media more broadly here, but still as inseparable.

⁹ This does not imply that the art piece can *only* be found as art.

¹⁰ I am using “space” here to indicate answers to “where?” questions. Where is it? It could be on the table, in a magazine, on-line, at work etc. These spaces change in time, so answers to where questions are temporally indexed.

These two types of action, finding and founding, I suggest make up science practice.¹¹

<Analogy [Found Art (Found Shark {Found Object <Found Science>})]>

Following this story I just gave you for when an object is found art, when would some entity be 'found science'?

First, the already available entity (idea, object, structure...) would be *found*, maybe discovered by a scientist, maybe recorded and picked up by a scientific process and second, the entity would be *founded*, that is, supported: a) in a spatial context that carries the science stamp: in spaces where science work happens, in journals where science work is examined and shared etc. and b) in a context of interests that carry the science stamp: interests of science producers and users, *as* science producers and users.

Note again that this context of interests in the object and the spatial context of the object will interact. What interest a scientist has in the object will determine what spatial context his work takes place in (-Is he interested in the entity from a theoretical or an experimental perspective?) and where this work takes place will shape scientific interest (-Is the research published in *The Lancet* or in *JAMA*?).

Both these contexts found an entity as science. And once the entity is *founded* as science, it *functions* as science and can be found again, *as science*. And again, we could be talking about either good or bad found science¹²...

Further, to found an entity in the context of science you need to use tools. As founding consists in an installation in both a spatial context and a context of interests, founding tools will be needed for installing entities in both the spatial context of science and contexts of scientific interests. Some of these founding tools will be theories¹³, software or models, experimental apparatuses or processes¹⁴, but some will be techniques and practices not particular to science, such as scheduling, networking, popularizing, lobbying, which are undertaken with a scientific interest in mind –for example in securing a research grant, or planning a conference.

¹¹ I am using terms echoing 'discovery' and 'justification' because these terms are familiar not because they are exactly what I mean or exact, for that matter. In this account, finding is different from discovery: what is found is *not* a scientific entity until it is founded. And founding does not consist in a *mere* logical justification nor in *brute* historical process: it is an interaction of *specific* spaces and *particular* interests that sustains an entity as relevant to science. [What, if anything, we pick out as trends in these interactions again are not results of mere facts about logic or historical process –though both logic and history would help us articulate and pick out such trends.] Various types of a context distinction between discovery and justification and their confusions are reviewed in Hoyningen-Huene (1987).

¹² There has been a lot of interesting work on questions of when science is good/bad. See Hempel, Lakatos, McMullin, Longino,... This is not the question I ask. [But the –in part epistemic- process of finding/founding can have a far reaching grip which encompasses epistemic value formation.]

¹³ See Cartwright and Suarez (...) –are these founding tools?

¹⁴ Hasok? Sabina? – need to think of this part; are tools renewable? Also mathematics seems special/ analogies too; the more abstract the form of a tool, the broader its use... the more "holes" it will fit in. ---like a voucher/clincher distinction.

I started with found art, picked out [by abstraction] a rule by which the practice of found art happens and by analogy formulated a rule for how found science would operate. I now apply this rule –retrospectively– to my study of another human practice; that of the biomedical science of ‘race’ in the context of the US. The point is to show that this framework of ‘found science’ is a framework which can make visible –at least to knowers of urinals– something about science. Namely: What about the practice of science makes it *science* and what can make it *useful* as science?

<Found Science [Biomedicine (USA c.2007 {Race})]>

As a case study of found science I describe the use of ‘race’ in recent US biomedical research. I pick out uses of ‘race’ in the US biomedical discourse and install them in the frame of found science. I ask two questions: First, how is the category ‘race’ found in US biomedicine? And second, is it founded?

I look at how ready-made race classes are found in biomedical science research and practice and I describe what I see as attempts to found these ready-made categories in two different scientific contexts: 1. Human population genomics and 2. Epidemiology.

I will use this framework to talk about the conflation of different race concepts that happens when people talk across biomedical domains as a mix up of different found objects¹⁵. I also suggest a way in which the founding tools of epidemiology differ to those of genetics.

As a note of caution, I am not offering this frame as something that will sort things out. The frame is broad enough that it really is not too hard to keep coming up with ‘find/found/ings’ and to iterate. Still, it might be a useful rule for sorting things out.

<Found Science [Biomedicine (USA c.2007 {Race <Finding>})]>

‘Race and ethnicity’ categories make an officially sanctioned appearance in the US biomedical discourse after a 1977 mandate by the Office of Management and Budget (OMB) to include race/ethnicity standards in the decennial census. The standards were revised in 1997 to allow people to identify with multiple race/ethnicity categories but the original race and ethnicity categories were retained. Current race and ethnicity standards identify four races (1. Native American or American Indian, 2. Asian or Pacific Islander, 3. Black or African-American, 4. White) and one ethnicity (Hispanic).

Below is an excerpt from the OMB’s revisions to the 1977 standards. It neatly encapsulates how race and ethnicity standards are officially found in biomedical research: The categories that were developed represent a political-social construct designed to be used in the collection of data on the race and ethnicity of major broad population groups in this country, and are not anthropologically or scientifically based.

Next sentence:

¹⁵This exposition happens in the first part of the dissertation –I. Legs/Symptoms.

The standards are used not only in the decennial census (which provides the "denominator" for many measures), but also in household surveys, on administrative forms (e.g., school registration and mortgage lending applications), and in medical and other research.¹⁶

Categories which are explicitly non-scientific, "not anthropologically or scientifically based", are to be used in scientific research. Race and ethnicity standards are put in the plates of, and picked up by scientists who use them to stratify their measurements. A ready-made classification, used to count populations in the context of demography, finds its way to the domains of science¹⁷.

As a result, the term 'race/ethnicity' is now found in different biomedical domains in the USA. Epidemiologists and clinical researchers measure health outcomes stratified according to 'race/ethnicity' and geneticists are pondering the existence of medically significant genetic variation between 'self-identified race/ethnicity' groups. The Department of Health and Human Services caters to the health needs of minority populations. Drug companies create markets that cater to the pharmaceutical needs of particular racial populations. Doctors prescribe treatment according to observed or self-identified race. And patients use race to identify themselves, when seeking treatment¹⁸.

Race, is found in current US biomedical science.

But is it a founded scientific entity?

<Found Science [Biomedicine (USA c.2007 {Race <Founding>})]>

'Race' is found in different biomedical contexts in the USA. I focus on the contexts of genetics and epidemiology. Though race notions are found in both contexts, some of the tools used to install race notions in each context differ. And I argue that though the tools used to found notions of race in the context of genetics work quite well in that context, found race notions founded in genetics cannot uncritically be assumed to be founded and work in the context of epidemiology: found objects will differ in important ways if installed in distinct contexts.

<Founding [Genetics]>

So on to what –I propose– is a first case of founding: installing ready-made race concepts in the context of genetics. This founding is done by developing a tool from within the context of science, and using this tool to pick out, and bring into science, these categories of race.

¹⁶See: http://www.whitehouse.gov/OMB/fedreg/directive_15.html

¹⁷ This account is obviously simplified. Race categories are not first found in U.S. biomedicine in 1977, neither were scientists strangers to the process of standardizing race and ethnicity classes [Cf. Epstein (2007)]. BUT the generalized use of these categories in U.S. biomedical research is the condition necessary for their re-discovery in terms natural to biomedical statistics: as 'appropriate' flags for aggregate rather than individual health outcomes. 'Finding' race to count aggregate health outcomes is what is relevant at this stage of my argument. (By 1997 demands for the revision of race/ethnicity standards are explicitly propelled by an interest in race not JUST as a social-political construct but also as a category which measures health disparities. For details see: http://www.whitehouse.gov/OMB/fedreg/directive_15.html Appendix 2, Report to the Office of Management and Budget on the Review of Statistical Policy Directive No. 15, Section 3.5.1.1)

¹⁸ See part I. Legs for a more detailed account.

<Founding [Genetics (Founding tool)]>

What I am referring to as a founding tool is the algorithm implemented by software STRUCTURE. This was developed by Pritchard and colleagues in 2000. It is a model-based, clustering algorithm which sorts genetic data according to similarity. STRUCTURE assumes a data-model for the genetic structure of K populations and uses this model to sort genetic data into K clusters according to genetic similarity. Each population is assumed to be characterized by a set of allele frequencies at each locus. Observations from each cluster are random draws from this parametric model and STRUCTURE infers the parameters specifying the model at the same time as it infers cluster membership. Inference is made using Bayesian methods –methods which have the benefit of incorporating in the model, in the guise of prior probabilities, some background knowledge that we have about the distribution of genetic variation across the various K populations.

I won't go into the details of the model as I don't have the expertise to evaluate this method. What I'm interested in is not the correctness of this model, but rather its aptness as a tool for genetics¹⁹. What I care to establish is that (hard) work coming from a scientific context, that of biostatistics, has gone into the development of this software. This is work done in biostatistics and aimed at studying the structure of populations in terms of structure found in their genetic samples.

Looking at the structure of the genetic data collected from some populations is one way to talk about the structure of these populations. Talking about, say their music tastes or the shape of their shoes are others. Why should we use *this* tool to infer population structure? Pritchard and colleagues answer that

The definition of populations is typically subjective, based, for example, on linguistic, cultural, or physical characters, as well as the geographic location of sampled individuals. This subjective approach is usually a sensible way of incorporating diverse types of information. However, it may be difficult to know whether a given assignment of individuals to populations based on these subjective criteria represents a natural assignment in genetic terms, and it would be useful to be able to confirm that subjective classifications are consistent with genetic information and hence appropriate for studying the questions of interest. [945]

I call this software a *founding tool*: something used for founding the ready-made into science. I put the emphasis on founding rather than finding, because 'finding' is the manifest function of the tool, but 'founding' is its target function –its use- in this context [For example, the manifest function of my cup is *to hold* coffee, but I use the cup *to pour* coffee -in my mouth].

So why call STRUCTURE a tool for founding the ready-made? This is why: what STRUCTURE operates on is the common subjective classes, and what it does to them is to bring them in a context of use and interest to genetics.

What Pritchard et al. propose is that using STRUCTURE is a way to “confirm” that already-available, subjective population classes “represent a natural assignment in genetic terms”.

¹⁹ See McAllister for a distinction of these two notions in the history of science. McAllister (1996), p...

Though the algorithm works with genetic data, its target objects –the categories of interest- are the subjective categories. It is these categories that should be checked out for their genetic appropriateness rather than the categories that STRUCTURE sorts data into at $K=n$, for some n . *Using STRUCTURE* picks out structure, and by *thus* picking out structure which corresponds to the subjective categories brings the ready-made categories into the context of genetics.²⁰

Keeping with the analogy, STRUCTURE a sorting mechanism natural to the science of genetics ‘picks up’ and out of their ordinary context the common population categories and installs them in the context of genetics. The application brings the subjective population classes in a) a spatial context of genetics –associating them with the output of a particular data-model, etc. but also b) in a context of interest to genetics. As Pritchard et al claim, if the categories are “consistent with genetic information” they are “hence appropriate for studying the questions of interest”.

So, using STRUCTURE *founds* already-found (in a “subjective” context) population classes in the new context of genetics.

I am keeping things simple here, by looking at STRUCTURE as the only founding tool in question –but this is because I limit my discussion at this level of scientific practice. The software originates in a spatial context stamped as science –the physical space of the statistics department of Oxford University, the discourse of statistics, etc- and is developed according to scientific interests particular to biostatistics –e.g. epistemic aptness, scientific authorship, model computability etc. It is a kind of founding tool particular to a scientific discourse rather than other types of tools that might found subjective population classes as of interest to genetics at different levels of science practice –textbooks possibly found subjective population classes as genetic objects by providing a narrative for ‘what geneticists do’.

Pritchard and colleagues developed software STRUCTURE to sort through genetic variation, in search of K clusters of genetically similar populations, and then see which of these, if any, match our subjective categories.

But what are the “questions of interest” that STRUCTURE is used to answer?

Besides questions generally relevant to population genomics, STRUCTURE is used to answer questions of interest to human population genomics, such as: What is the genetic structure of *human* populations?

<Founding [Genetics (Founding tool {Rosenberg})]>

In a now famous paper of 2002, Rosenberg and colleagues used the software STRUCTURE, to sort 377 markers in the DNA of 1056 individuals from 52 populations across the world. DNA was collected from 1056 individuals belonging to 52 “subjectively” defined populations and STRUCTURE was used to pick out genetic structure in this sample. Rosenberg and colleagues

²⁰ Hacking –representing and intervening?? [Genetic classes are like our color inventory by Wittgenstein’s terms? –you check your objects against the inventory to say their color in ‘real life’?]

report that: “program STRUCTURE picked out *six* main genetic clusters, of which five correspond to major geographic regions: America, East Asia, Pacific Islands, Africa and Eurasia.”²¹

According to Pritchard et al. STRUCTURE was developed to test whether subjective population classes are natural in genetic terms. What are the ready-made classes that STRUCTURE is used to articulate in terms “natural” to genetics by Rosenberg et al.? Rosenberg and colleagues report the fit found between *five* major geographic regions: 1. America, 2. East Asia, 3. Pacific Islands, 4. Africa and 5. Eurasia, and *five* of the clusters that occur at K=6. Rosenberg et al. claim that these five geographic regions correspond to *ancient geographical ancestry*. But what about ancient geographic ancestry dictates this fineness of grain?

Recall that STRUCTURE picks K genetic clusters, where K is a number chosen in advance. Rosenberg et al. stop at, and report K=6:

At K=5, clusters corresponded largely to major geographic regions. However, the next cluster at K=6 did not match a major region but consisted largely of individuals of the isolated Kalash group, who speak an Indo-European language and live in northwest Pakistan²².

Something goes contrary to expectation at K=6. Instead of picking out a genetic cluster corresponding to a “major region”, the cluster of genetic variation picked out by STRUCTURE corresponds to an “isolated” group of individuals from a region in Northwest Pakistan.

Two parameters seem to decide the selection of clusters at K=5 as special:

1. The clusters are produced by STRUCTURE,
2. The clusters correspond to major geographical regions.

And these two parameters matter in a specific combination. If genetic similarity and geography mattered in any combination then the genetic clusters at K=2 or K=3 or K=4 or K=6 would have been equally worth reporting as those at K=5 (the Kalash do come from an isolated geographic region). If, what mattered was matching clusters to “major” geographical regions then K=2 through 4 would satisfy this requirement. At K=2 genetic clusters were anchored by Africa and America, at K=3 genetic clusters corresponded to Africa, Eurasia-East Asia-Oceania and America and at K=4 Africa, Eurasia-East Asia, Oceania and America. If minimizing molecular variance among regions was of interest then K=7 was the right fineness of grain (the only other data provided is for K=5 which displays a higher between-regions molecular variance). If we care about genetic structure, why not study the Kalash?

Rosenberg et al. use a prior assumption about what geographical regions matter to sort through the clusters of genetic variation picked out by STRUCTURE and to decide which ones are worth reporting. They argue that this prior assumption is our evolutionary story (our theory) of what should count as ancient geographical ancestral groups²³. But this doesn’t mask the fact, and might even be historically *due to the fact*, that these geographical regions match the continental origins of what we commonly take to be five human races.²⁴

²¹ Rosenberg et al. (2002), 2381.

²² Rosenberg et al. (2002), 2381.

²³ Cf. Hardimon’s communication with Rosenberg.

²⁴ Cf. Müller-Wille and Rheinberger (in press). This is unsurprising if we accept that the notion of ‘race’ is already found in our notion of genetic heredity. Hans-Jörg Rheinberger and Staffan Müller-Wille make a convincing argument to this effect.

If our evolutionary theory had to “save” the phenomenon of five human races, who are we to extricate it from its grasp? Tools for re-articulation are there (in the guise of STRUCTURE, but also in the guise of other “subjective” criteria for deciding population structure). We still pick the fineness of grain which agrees with our prior assumptions --and which maintains continuity with our interest in race.

Is an interest in common race classifications used to a. find genetic structure -sort through what regions matter for genetic structure, and used to b. found ‘race’ -now “checked against” the terms natural to genetics- in the context of genetics?

Even if, explicitly, this is not an attempt to found races in the context of genetics; even if explicitly this is *just* an attempt to articulate ancient geographical origins in genetic terms, the conceptual affinity between races and ‘ancient geographical ancestry’ thus described, stands uncontested.

<Founding [Genetics (Founding tool {Tang})]>

In fact, forget nested meanings. We don’t need to look too far for an explicit genetic interest in race. In a paper aptly titled “Genetic structure, Self-Identified Race/Ethnicity, and confounding in case-control association studies” Hua Tang and colleagues at Stanford University examine whether self-identified race/ethnicity approximates genetic structure in the USA and they answer in the positive.

The method used to sort through genetic data was the same as the one used in Rosenberg et al. (2002) but in this study subjective population classes are explicitly defined in terms of self-identified race/ethnicity. Individuals self-identified as belonging to four major ‘racial/ethnic’ groups: white, African American, East Asian, *and Hispanic* –an officially non-racial group. Three hundred and twenty six markers in the DNA of individuals from fifteen locations in the US and in Taiwan were sorted by STRUCTURE. It is reported that of 3,636 subjects of varying race/ethnicity, only 5 people (0.14%) belonged to a genetic cluster different from their self-identified race/ethnicity (SIRE).

This result suggests a link between SIRE and genetic variation²⁵.
[A]ncient geographic ancestry, which is highly correlated with self-identified race/ethnicity —as opposed to current residence— is the major determinant of genetic structure in the U.S. population. ²⁶

Note that, once more, it is “ancient geographic ancestry” not race which is reported as the major determinant of genetic structure in the USA. But ancient geographic ancestry is now found to be “highly correlated” with self-identified race/ethnicity (SIRE).

What is the tool used to “correlate” SIRE and ancient geographic ancestry? Found STRUCTURE. As we saw, Rosenberg et al. (2002) select K=5 genetic clusters picked up by STRUCTURE as determined by ancient geographical ancestry. Tang et al. (2005) also report K=4

²⁵ Objections to the design of the study exist, as well as to how we should interpret these results. For example, it is argued that these individuals came from uncharacteristically homogeneous SIRE populations within the US.

[ref?]

²⁶ Tang et al, (2005) 268.

classes picked up by STRUCTURE as matching ancient geographical ancestry, but this claim is no longer founded in evolutionary theory but rather in the previous usage of STRUCTURE by Rosenberg et al (2002). When Tang et al (2005) report that “ancient geographic ancestry (...) is the major determinant of the genetic structure of the U.S. population” they base their report on an assumption like “program STRUCTURE clusters data according to ‘ancient geographical ancestry’” an assumption which is founded in a previous use of STRUCTURE and not proved within the context of this study. So, it is not STRUCTURE per se but rather found STRUCTURE that is used as a founding tool for installing SIRE in the context of genetics. But how is this founding SIRE in a genetic context?

Tang and colleagues do not install SIRE in genetics by calling *these* common categories categories natural in genetic terms. SIRE is not directly matched with the genetic clusters it is found to label because there is no causal story which is scientifically articulate and respectable for matching self-identified race/ethnicity groups with the genetic clusters that STRUCTURE associates them with²⁷. Instead, the four clusters picked out by STRUCTURE, assumed to capture ancient geographical ancestry, “are highly correlated” with SIRE. For reasons not articulated in this article, but still articulate within a broader socio-political context, it is not in the interest of biomedical science to pick up bare-handed these common race categories and install them in the context of genetics; but that doesn’t mean there is no founding going on. Tang et al perform an installation of the categories but they do it by a mechanical arm – by using the proxy ‘ancient geographical ancestry’ to recruit these ready-made classes as appropriate for answering questions of interest to genetics.

The use of STRUCTURE to select genetic structure at fineness of grain $K=5$ by Rosenberg et al. (2002) is a confirming instance of the capacity of STRUCTURE to pick out ancient geographic ancestry²⁸. Tang et al conclude that this is a capacity that STRUCTURE will exercise in similar circumstances, in their study; and this conclusion (found STRUCTURE) forms the premise of their claims. Thus when STRUCTURE picks out SIRE classes, found STRUCTURE is used to conclude that SIRE *must be associated* with ancient geographic ancestry –like a father’s hair on the skin of his newborn, it is assumed to have gotten there by accident. Well, I want to say, that newborn you are looking at is a pretty hairy one -and looks like his father too²⁹.

([**ancient geographic ancestry, which is highly correlated with self-identified race/ethnicity**] [A] —as opposed to current residence— is the major determinant of **genetic structure** in the U.S. population.) (B)

Schematically:

0. STRUCTURE clusters populations according to their genetic structure [Pritchard (2000)]
1. STRUCTURE clusters populations according to ancient geographical ancestry in at least one instance. [Rosenberg (2002)].
2. This use of STRUCTURE is similar to prior use, in all relevant ways.

HENCE by 1,2 and induction on STRUCTURE usage

²⁷ Or, there is no rule in the science language-game for matching common categories with genetic clusters.

²⁸ Tang et al, (2005) 268 --??

²⁹ [The question is, is he pretty? Can he be? –are these good questions?] The use of ‘race’ categories in Nazi medicine is an example of how these notions were used in a different historical context.

3. STRUCTURE clusters populations according to ancient geographical ancestry in this study.
4. STRUCTURE clusters are well correlated with SIRE in this case.
5. There is no causal (evolutionary) story linking SIRE to ancient geographical ancestry.

By 3, 4, 5

6. Ancient geographical ancestry is highly correlated with SIRE. [A]

Hence by 0, 6

7. Ancient geographical ancestry is highly correlated with SIRE and the major determinant of genetic structure in this population. (B)

There are problems with this reasoning.

The socially-constructed ‘race’ classifications used to count population groups are now found and founded in genomics research.

1. A founding tool, STRUCTURE, is developed from within biostatistics, to articulate subjective classes of populations in the context of genetics [Pritchard et al. (2000)].
2. This tool, STRUCTURE, founds ancient geographic ancestry in the context of genetics [Rosenberg et al. (2002)].
3. And STRUCTURE, which is founded (confirmed) as a tool for measuring ancient geographic ancestry is used to found U.S. SIRE in genetic terms [Tang et al. (2005)].

Once more, the possibility of articulating these subjective classes in genetic terms confirms their appropriateness for studying the relevant ‘questions of interest’. STRUCTURE helps install the respective subjective categories in a spatial context and a context of interests particular to population genomics. We end up with self-identified race/ethnicity classes which are found to perform relatively well what we thought ancient geographical ancestry did: measure genetic variation. Whether these categories, these found ‘races’ will turn out to be useful categories for population genomics remains to be seen. But there is every indication that this question is of interest and not just for geneticists.

Common race and ethnicity classes, sequentially founded, are offered as appropriate for answering questions of interest to genetics. But some questions interesting to geneticists also interest doctors –and their patients.

There is explicit gesturing in Rosenberg et al. (2002) towards the *medical* significance of ancient geographic ancestry. Though they do not engage in a critical argument Rosenberg et al (2002) claim that “self-reported ancestry can facilitate assessments of epidemiological risks”³⁰. Commenting on the article, John Hardy of the NIH predicts that “genetic techniques such as this will facilitate the definition of *ethnic groups* based on genomic variation and enable scientists to test the hypothesis that diseases have divergent clinical features between these groups.”³¹ The

³⁰ Rosenberg et al. (2002), 2381. Still, it is unclear that the 3-5% of genetic variability occurring between these populations will have something to do with disease. See Keita et al. (2004) on competing hypotheses regarding the medical significance of this genetic variability. This article appears in a special supplement of Nature Reviews Genetics on race and genetics, published in 2004, and used to install these questions in a discursive context of genetics.

³¹ Hardy (2003) 739

hope is that some of the alleles that cluster into different frequencies for these different groups will be causally related to disease susceptibility or to response to treatment. Though there is some research indicating that both disease susceptibilities and response to treatment are stratified according to race, there is no consensus as of yet.³²

These remarks suggest that the context of interesting questions that STRUCTURE can be used to answer can be stretched even further. We took a tool developed to articulate structure in genetic terms to articulate the structure of human populations in genetic terms and the suggestion is that the same tool can be used to explore human populations' *medically* interesting structure in genetic terms. This context of interests includes questions of interest to *both* human population genomics and *epidemiology*: Do different race and ethnicity groups approximate medically interesting genetic structure?

While race and ethnicity are installed in the context of genetics, another attempt to found common race notions happens in epidemiology. What is found in this context is different. Certain social differences and differences in health outcomes are found to be stratified according to race/ethnicity classifications. But is this an articulation of 'race' which can found it as an epidemiological object?

<Founding [Epidemiology]>

Race is a prominent category in U.S. epidemiological research. The most glaring health disparities are found to occur between blacks and whites: In 2004 the US death rate for black infants was more than double the death rate for white infants -the difference being almost fourfold for Arizona.³³ Blacks develop heart disease more rapidly and at a younger age than whites.³⁴ Diabetes mellitus is over fifty percent more common in black adults than in white adults spiking blacks' rates of end-stage renal dysfunction and lower-extremity amputation.³⁵ Blacks have three times whites' risk of dying from HIV/AIDS³⁶; almost half of new HIV/AIDS cases in 2004 were blacks though only about a tenth (12%) of the population identified as black.³⁷

These are some titles of epidemiological articles³⁸:

³² See part I. Legs.

³³ The Kaiser Family Foundation, www.statehealthfacts.org. Data Source: Arias E, Anderson RN, Hsiang-Ching K, Murphy SL, Kochanek KD. Deaths: Final Data for 2001. Division of Vital Statistics. National Vital Statistics Report, Vol 52, No. 3, Sept. 18, 2003. Hyattsville, Maryland: National Center for Health Statistics, 2003. Also see Infant Mortality Report in references.

³⁴ (Root, 2003) 1174

³⁵ (Brancati et al, 67)

³⁶ (Root, 2003) 1174

³⁷ See the Kaiser Family Foundation website, www.statehealthfacts.com: http://www.statehealthfacts.org/cgi-bin/healthfacts.cgi?action=compare&category=Minority+Health&link_category=HIV%2fAIDS&link_subcategory=New+AIDS+Cases&link_topic=New+AIDS+Cases+All+Ages+by+R%2fE

Data source: Centers for Disease Control and Prevention, Division of HIV/AIDS Prevention-Surveillance and Epidemiology, Special Data Request, November 2005

³⁸ See references.

- Diabetes mellitus, *race*, and socioeconomic status; A population-based study (1996)
- Age-*race* subgroup compared with renin profile as predictors of blood pressure response to antihypertensive therapy (1998)
- *Racial* differences in the outcome of left ventricular dysfunction (1999)
- Lesser response to angiotensin-converting enzyme inhibitor therapy in *black* as compared to *white* patients with left ventricular dysfunction (2001)
- Survival variability by *race* and ethnicity in childhood acute lymphoblastic leukemia (2003)

All these studies look at complex common diseases –diabetes mellitus, blood pressure, heart disease, leukemia – and stratify subjects according to race. What is the reason for stratifying results according to race? For one, there is the interest in including race and ethnicity categories in US biomedical research so as to measure and cater to different needs that might exist across racial groups. But the question is what kinds of needs are the ones that differ across races and how do we go about catering for them?

There are two common assumptions about how race and ethnicity categories might matter for measuring and controlling health outcomes. These assumptions are made visible by the way ‘race’ is featured in the epidemiological discourse, the contexts in which it appears³⁹. First, epidemiologists commonly assume that race/ethnicity is associated with social status and social status is thought to causally determine conditions (such as education, access to care, diet, etc.) that shape health behaviours and health outcomes. Race/ethnicity, assumed to be operating as a proxy for social disparities which causally determine health disparities, can thus be found to track disparate health outcomes. Under this account, different health needs between racial groups are a trickle down effect of different social needs. Catering to the different health needs of racial groups by this account involves addressing social needs before they trickle down to medical needs. Or, in epidemiologists’ terms, it involves addressing environmental causes of disease.

A second common understanding of how race and ethnicity can track health disparities, involves notions of race and ethnicity as approximating biologically distinctive characters. Though no biologically respectable notion of race is accepted among scientists, race and ethnicity categories are commonly used in the epidemiological discourse as proxies for biologically inherited differences. Race/ethnicity is assumed to track biological differences between ancient geographical ancestral groups and ancient geographical ancestry is thought to causally determine genetic inheritance that shapes genetic disease susceptibilities and response to treatment. Under this account, different health needs between racial groups are an effect of inherited genetic differences creeping up. Catering to the different health needs of racial groups by this account involves developing race-specific drugs and pharmacogenetic techniques to prevent genetic proclivities from creeping up. Or, in epidemiologists’ terms, it involves addressing genetic causes of disease.

³⁹ See I. Legs

Both these understandings of how race matters for health outcomes are called upon to interpret epidemiological findings. And there is a live –though by no means extensive- debate about how to model the causal influence of ‘race’ on health outcomes⁴⁰. For example, some of the studies listed above do not control for social factors such as socio-economic status (SES) or education that might be causally contributing to health outcomes and be differentially distributed across racial groups. In this case differences measured in the health outcomes of racial groups could be due to environmental confounds and so attributing the differences to ‘race’ rather than say, SES, might be jumping the gun.

But some studies try to control for social differences. They select particular measures for social factors that they deem causally relevant for health outcomes and match racial populations with respect to these measures of say SES and education, before looking at whether race effects appear. What happens in many cases is that racial differences in health outcomes persist⁴¹. And in those cases, the residual effects of ‘race’ on health outcomes will be commonly put down to biologically inherited genetic differences. The thinking is: we took into consideration social differences that shape health outcomes, so what else is left but biologically determined differences and what could be causing such differences but genes?⁴²

Of course, for this reasoning to be valid, we must have adequately controlled for all the social causes of racial health disparities. Assumptions on at least three levels need to be checked: 1. The initial assumption of what candidate social factors might causally influence outcomes and be racially stratified (Is it SES and education? Is it SES, education and neighborhood? Is it financial distress, education and access to care? Etc.) 2. The selection of tools used to measure these factors (Is SES measured by annual income? Is financial distress measured by the number of times the subject has experienced distress in the last month/year? Etc.) and 3. The techniques used to apply these tools (Do subjects fill out these questionnaires? Does an examiner fill out the details? Do we use more than one measure of the factor of interest?). All of these assumptions matter!

Baffled by the complexity of ‘race’ researchers have proposed to just leave things unpacked. Controlling for environmental factors might be over-controlling for race. It’s as if ‘race’ is rushing to the clinic and it’s loaded with a messy bag of genetic and environmental causes of disease and you are worried that if you stop it and tidy things up, you will fail and make it miss its appointment. The only problem is that in that messy bag are the keys you need to open the hospital doors.

Socioeconomic status and education are consistently found to shape health outcomes and are stratified according to ‘race/ethnicity’. But disparate health outcomes persist for different racial groups, even when ‘environmental’ factors are controlled for. When ‘race’ remains an independent risk factor, racial differences in the “natural history” of the disease are

⁴⁰ See Cooper and Kaufman (),

⁴¹ See (1999) study above.

⁴² See Criqui et al (2005) –Criqui et al don’t attribute ethnic differences in outcomes of Peripheral Arterial Disease to genetic variability though they ponder its importance. Professor Criqui acknowledged the causal role of genetic differences in personal conversation (June 2006). Also see Dries, Exner et al (2001)

hypothesized.⁴³ ‘Race/ethnicity’ differences in health outcomes have been put down to differences in drug-response and genetic variation between population groups is said to explain this variation in drug-response.⁴⁴ When the OMB ‘race/ethnicity’ categories count measurable entities of biological significance like disease outcomes or drug response, questions arise, which rely on viewing the “social-political construct” of ‘race/ethnicity’ in terms of its biological causal import –and by extension its particular biological standing.

<Found Science [Application (Founding {Epidemiology <Founding tools?>})]>

A question of interest to (genetic) epidemiologists occurs in the context of genetics: Is there medically interesting genetic structure associated with race/ethnicity groups? Before answering this factual question, it is interesting to ask the normative: Can there be medically interesting genetic structure associated with race/ethnicity groups?

Michael Root, philosopher of biology, asks and answers this question in the negative. Root (2003) argues that ordinary races are not “biological races”. They *cannot* be good proxies for genetic variation. This is because human populations have not been geographically or reproductively isolated for a long enough time for any distinctive heritable characteristics to appear. He notes that 1. There is no cluster of genes possessed by all and only individuals customarily sorted as members of the same race, and that 2. The populations are differentiated “only by average frequencies of a few polymorphic genes”⁴⁵.

Root concludes that the biological differences between customary categories are “at best statistical”⁴⁶ and hence that they are *bad proxies* for medically relevant genetic variation⁴⁷. Still Root accepts that ‘race’ can be a good proxy for how social status affects health outcomes. This claim can become clear by considering an example.

Below is a table with the ten most common causes of death for non-Hispanic blacks and non-Hispanic whites. The three leading causes of death are common across groups. (Heart Disease, Cancer, Stroke) But there are three causes of death particular to each group: Homicide, HIV, septicemia frequently kill non-Hispanic blacks and Alzheimer’s, suicide, influenza & pneumonia commonly kill non-Hispanic whites.

⁴³ See for example Brancati, Dries et al. (1999) – Greenberg and colleagues (2001) define the natural history of an illness as “the typical sequence of events” clarifying that some authors use the term ‘natural’ only for situations where there is no effective treatment for the illness and other authors use the term more broadly to describe the typical course of an illness (9). The examples I give fall under the second kind.

⁴⁴ See Bamshad (2005) for an overview of this literature.

⁴⁵ Root (2003) 1174

⁴⁶ Root (2003) 1174

⁴⁷ This is a rather weak argument. As we saw, STRUCTURE sorts through exactly such “statistical” difference –variation in the frequencies with which certain alleles appear in genome- to articulate racial categories in genetic terms. The fact that these differences are statistical does not imply that they are insignificant nor meaningless nor useless. But most importantly the notion of “self-identified geographical ancestry” could be quite *well* approximated by ‘race’ and by ‘ethnicity’ –as Tang et al. are arguing.

TABLE. Ten leading causes of death among non-Hispanic blacks and non-Hispanic whites — National Vital Statistics System, United States, 2002

Rank	Black, non-Hispanic			White, non-Hispanic		
	Cause of death	No.	(%)	Cause of death	No.	(%)
1.	Heart disease	76,604	(26.8)	Heart disease	577,761	(29.2)
2.	Cancer	61,996	(21.6)	Cancer	458,754	(23.1)
3.	Stroke	18,691	(6.5)	Stroke	133,118	(6.7)
4.	Diabetes	12,583	(4.4)	Chronic lower respiratory disease	112,128	(5.7)
5.	Unintentional injury	12,285	(4.3)	Unintentional injury	80,605	(4.1)
6.	Homicide	8,147	(2.8)	Influenza and pneumonia	55,419	(2.8)
7.	Chronic lower respiratory disease	7,730	(2.7)	Alzheimer's disease	53,486	(2.7)
8.	Human immunodeficiency virus	7,714	(2.7)	Diabetes	52,463	(2.6)
9.	Nephritis	7,410	(2.6)	Nephritis	30,669	(1.5)
10.	Septicemia	6,074	(2.1)	Suicide	26,691	(1.3)
	All others	67,249	(23.5)	All others	400,879	(20.2)
Total		286,573	(100.0)	Total	1,981,973	(100.0)

Something seems found –but is it founded? A concept of race as a proxy for social status explains why non-Hispanic Blacks tend to die more frequently of homicide. Thinking of race as a proxy for genetic variability doesn't explain it -unless there is a gene proclivity to being killed.

At the same time, it is argued that race *can* well approximate medically interesting genetic variation. Along these lines argues ethicist Peter Singer, writing with geneticist Abdallah Daar (2005). They claim that race *is* a good proxy for *medically interesting* genetic variation. They argue that there is documented genetic variation between these human populations, citing Rosenberg et al. (2002) and highlight a few “selling points” for *Nat. Rev. Genetics* readers: a. Race-specific pharmacogenomics not “*boutique ‘personalized’ medicine*” and as such seems more “ethical” to pursue, b. Race-specific pharmacogenomics is profitable: 1. There is a big market of non-whites [80% of the human population] 2. And race is a cheaper proxy for genetic variation than performing individual genetic tests⁴⁸.

We see a striking disagreement between two philosophers as to what kinds of variation ‘race’ can be assumed to approximate. Root sees races fit only as surrogates for social differences that matter to health outcomes. He does this by noticing an explanatory relevance of social difference to health outcomes. Singer proposes that races can be surrogates for genetic variation that is interesting to health outcomes. He does that by summoning the found race categories of genomics research as proxies for genetic variability. How does this disagreement occur and where is it founded? What races are these philosophers talking about and in what context?

<Found Science [Race (Found Objects Mixed up)]>

Let us reiterate:

[0. Race and ethnicity standards are introduced in biomedical research (1977)]

⁴⁸ Singer and Daar (2005), p...

1. Epidemiology associates race and ethnicity categories with significant differences in health outcomes: the categories are found to measure differences in health outcomes.
2. Population genomics associates race and ethnicity categories with identifiable genetic variability: the categories are founded as entities appropriate for answering questions of genetic interest.
3. Controlling for social risk unequally distributed between race and ethnicity groups leaves residual risk for race and ethnicity groups.
4. The genetic (statistical) differences between race and ethnicity groups acquire an explanatory role in understanding health disparities between race and ethnicity groups.
5. The marketing of race-specific medications [Cf. *BiDil* the first medication to get FDA approval for self-identified African-Americans⁴⁹] is boasted as “a step towards personalized medicine” by the FDA.

Found race notions are 1. not ‘race’ and 2. should not be assumed to match! When these ready-made categories are encountered in different biomedical contexts, they SHOULD be re-articulated and founded using context-specific founding tools.

In the context of genetics, the “subjective” self-identified race/ethnicity classes are found and founded, via STRUCTURE, as approximating a population structure that would be “natural in genetic terms” (‘ancient geographical ancestry’). When, in step 4 above, epidemiologists attribute the persistence of racial health disparities, after social differences are “controlled for” to genetic variation, what is happening is that a found object in genetics is imported in a new context, that of epidemiology, and uncritically assumed to be able to *function* as science.

But recall: “Founding” describes a picking out and a bringing in of an already-available object to a particular context that *stamps* it as science. Found science is as intrusive to the ordinary object as formaldehyde is to the shark. “The Impossibility of Death in the Mind of Someone Living” is not a shark. What makes the piece interesting and powerful *as art* is arguable related to the fact that this is a found *shark*: a symbol of masculinity, aggression, hero of movies, etc⁵⁰. But I espouse Danto’s distinction between found art and pop art as that between art “diminishing the aesthetic and testing the boundaries of art” and art “celebrating the ordinary”⁵¹.

And similarly, what makes found science good science has something to do with what entities we choose to found. What Weber says for the objects of social science, I would say for all science: the entities we choose to study are those of significance to us as humans –and of a

⁴⁹ See Kahn (2004) and Sankar and Kahn (2005) on BiDil –BiDil is a drug for heart disease approved by the FDA specifically for African-Americans in June 2005. The controversy regarding this drug is summarily this: the investigators obtained a methods patent for African Americans only and performed a prospective trial among self-identified African Americans only, though a patent was already granted to the PI for the general population in the 1990s as a “test of theory trial” –with poorly defined endpoints- suggested that the drug worked for all heart failure patients. As a result the same drug is now covered under two patents, one for a general population expiring in 2007 and another one for African-American SIRE expiring in 2020.

⁵⁰ Thanks to Hakan Sechinoglu for pointing this out.

⁵¹ Danto (1997) p132.

significance which gets re-articulated within science according to different questions of interest. But found objects will necessarily differ to unfound objects.

So it is with race. Found race notions will differ from ordinary race concepts once founded in well-defined scientific contexts, and race notions founded in different scientific contexts will be intrinsically different to each other. If these scientific contexts have no bridge principles to link them up, they will be inherently disjointed. If there is an interest to joining scientific contexts then the work needed is extra work and should be visible as such⁵². Distinguishing between these found ‘races’ matters for understanding what medical science is and *can be* doing.

<Found Science [Application (Found Freedom)]>

Though Root points out a way in which race and ethnicity categories might be significant for biomedical research –as categories which approximate social disparities that influence health outcomes, there is no articulation of precisely which social features that matter to health outcomes, in what combinations and with what relative weights shape health profiles along racial lines. Geneticists enjoy the luxury of dealing with data on the genetic level but epidemiologists do not. Which variables should be featured in the corresponding parametric model of a founding tool for epidemiology? How do we cluster individuals in terms “natural” to epidemiology and cross-reference our results with the common (subjective) race categories occurring outside the epidemiological context?⁵³

These are pressing questions for founding ‘race’ in epidemiology. What usually happens in social science domains is that the common categories are taken up wholesale. And there is a normative requirement that the social sciences do this, in order to study the phenomena at hand⁵⁴. But why are characteristics exhibited on a macroscopic level demanded to be inviolable by this theory?

Here is one answer⁵⁵: faith to social macroscopic phenomena is demanded just because these are articulated in terms that overlap with what Paul Churchland calls “folk” theory. There is no appropriate distance between our social science language and common vernacular to allow the unperturbed founding of these phenomena in science. And though with scientific domains such as physics or genetics folk claims can co-exist with our scientific theories⁵⁶, the discourse of social science is not allowed the creative freedoms of genetics. Social science cannot shield its work in a formally closed domain and nurture it to the point of developing its own founding tools.

As I propose here, this is a mistaken approach founded on an unfounded worry. Developing *scientific* theories for life cannot eliminate other *theorems* of life; ways in which we

⁵² The notion of invisible work I have in mind is one used by Mirmalek (ref?) to describe the work done by NASA scientists on the Rover mission when adjusting their lives to follow both Earth and Mars times.

⁵³ Many thanks to Damien Fennel who asked these questions.

⁵⁴ Ref...? Nancy? Weber?

⁵⁵ I came up with this answer in conversation with Richard Tutton, so thanks for that. ---Who gives this answer??

⁵⁶ --my paper on Cartwright in reply to the dispute between Nagel and Churchland on qualia touches on this question...

come to theorize life that lie outside a scientific context⁵⁷. The unmediated correspondence of social science terms and common phenomena expected of social science is unfounded. It is not immediately expected of other scientific domains so why should social science face these extra constraints?

This account suggests that some intrusion to the founded entities “original” place is unavoidable and in fact required to properly found them in a scientific context. The extra work of matching the founded objects to *functions* [?] of the common objects must be made visible and taken up as extra work, happening in specific spaces and contexts of interest. Geneticists and epidemiologists are not to be expected to study races in a scientific context. They cannot. At the same time, they also cannot assume that these common objects can be reduced to one of these multiple foundings of them.

This fact is demonstrated by the case study of race. Found race notions are, to begin with, different kinds of notions: they make use of ‘race’ to get at either a social kind or a biological kind. They are either what Hardimon (forthcoming) calls socialrace or what I term biorace notions of race. Contrary to our common categories which are commonly discussed as composite entities, carrying forth what Rabinow terms and Hacking discusses as “biosocial” identities⁵⁸, the categories used in science practice are either proxies for social groups or proxies for biological differences. Public health policy targets (social) minority groups to eliminate racial health disparities, epidemiology looks at races as capturing both social differences that matter to health and biologically inherited differences that shape health outcomes and genetics treats races as proxies for biologically inherited variations. Further, what socialrace or biorace notions are articulated, within each context cannot be *assumed* to match, but rather, have to *be* matched: i.e. re-articulated and founded across contexts.

<Found Science [Application (Found Objects: Socialrace and Biorace)]>

Revisiting the philosophical debate with the distinction in mind helps articulate the source of the dispute between Root (2003) and Daar and Singer (2005). Daar and Singer (2005):

- Do not demonstrate that what genetic variation occurs between human populations is medically interesting.
- They don’t worry about the trans-global applicability of these ‘race’ categories.
- And, surprisingly for professional ethicists, they don’t worry about the socio-political risks for the populations sampled.

Under my account this is because 1. Daar and Singer work with some biorace notion of race to the exception of socialrace and 2. They assume that biorace notions in genetics will match those found to be relevant in epidemiology.

Root (2003) on the other hand:

⁵⁷ This elimination has not yet occurred, and I disagree with Churchland that this kind of un-mediated knowledge is at all possible in a world that is evolving and changing through human mediation. The emergence of new phenomena, to-be-reduced, would prevent the complete elimination of folk epistemology.

⁵⁸ Hacking (2006)

- Accepts that race correlates well with disease.
- Rejects the *medical usefulness* of associations between race and genetics because our evolutionary (causal) story does not feature ‘race’.
- Proposes self-identified geographical ancestry as a *better proxy* for genetic variation, *but* lacks any data to that end. Tang et al. (2005) actually find ‘self-identified race/ethnicity’ [surely not a part of our evolutionary story], to be well correlated with ancient geographical ancestry.

This is because Root’s working notion of ‘race’ as socialrace, prevents him from examining the significance of biorace notions of ‘race’, found and founded in the context of genetics.

<Found Science [Application (Prescription)]>

In a time when political interest in addressing the disparate health needs of US race/ethnicity groups is driving research, the risk of essentializing socialraces and the risk of taking them for bioraces is great. Jumping across scientific contexts without any bridge principles in place, and taking ready-made concepts to be founded when there are merely found is reckless science. To ask and hope to answer the right questions about how ‘race’ relates to ‘health’ we must distinguish between ways race can become found race in science and then to try and translate across found race notions. We must develop theoretical and pragmatic tools to found entities within scientific contexts and to get the found entities to be found again and founded, across scientific domains.

<Found Science [Telos]>

Arthur Danto writes that one of the concerns of *Fluxus* was “overcoming the gap between art and life”⁵⁹. Taking commonplace objects, sounds, gestures, and installing them in the spaces and contexts that make them function as art displaces, along with the objects, our attitude towards them. Found art comes with the realization that as we change our attitude towards given, mundane objects the objects come to function in different ways.

Similarly, a point of “finding” science is overcoming the gap between science and life. And this should be a two-way process. As life gets founded in science, science must be founded in life. The capacity to take what is given, and to place it in the context of science, call this physics, psychology or genetics, comes with the responsibility of letting the found entity function *as science*, in life.

Found science can only be good science if it uses its freedom and is responsible for its functions. And for this to happen it is necessary that found science is founded with care for each other and for the spaces that sustain us.

⁵⁹ Danto (2000)

Damien Hirst – All Works (excluding prints)
Chart 4: Adjusted Average Sale Price and Mean Estimate



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Placing the things we find interesting in this life in the context of science.

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