GENOME SAMPLING AND THE BIOPOLITICS OF RACE

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Abstract

This chapter applies Foucault's concept of biopolitics to scientific knowledge about race via a genealogy of global genome project sampling strategies. Using internal records, publications and news coverage of four major projects, I show how global genomics has moved from population-blind sampling to race/ethnicity-conscious and, finally, continent-based sampling. I argue that this tactical change was motivated by pressures from the U.S. federal government to incorporate specific sociopolitical racial redress policies. Here, the state produces a framework for accessing bodies that generates a specific definition and administration of life. Due to funding structures, this American framework has become the leading global paradigm. Understanding the brief but rich history of global genomic sampling policies can tell us much about how states and scientific fields are constructing the body, the human, and the nation.

Genomics, Biopower and Race

Genomics—the branch of genetics that studies the entire DNA sequence of organisms—is an analytical paradigm that has descended on the scientific community so thoroughly that, in less than ten years, it has not only taken center stage in genetics, but has prompted a burgeoning bioinformatics industry, spurred new models for nanotechnology, expanded research avenues for molecular and cellular biology, and created entirely new fields like pharmacogenomics and synthetic genomics. Genomics is not only the focus of the genetics arm of the U.S. National Institutes of Health (NIH), but is increasingly the focus of all government health institutes. In fact, genomics has advanced to such an influential status that *Science* named Human Genetic Variation the 2007 Breakthrough of The Year. Recent years have witnessed the entry of genomics into the consumer sector and

mass media, with the solving of high-profile criminal cases by genomic forensic services and media portrayal of celebrity genealogies and genomes.

When Michel Foucault introduced the concept of biopower in the latter quarter of the 20th century, genomics had not yet been conceived. Yet, Foucault's argument that power/knowledge would increasingly focus on the material of life itself proved prescient. Foucault articulates biopower in terms of "what brought life and its mechanisms into the realm of explicit calculations and made power/knowledge an agent of transformation of human life" (Foucault, 1978: 143). This trains our gaze on quotidian practices having to do with the body while opening state knowledge about the body politic, especially those biological sciences focused on the most intrinsic matter of life, up for analysis.

We can see this two-pronged interest in Foucault's schematics of modern disciplinary power and state racism. For Foucault, power operates on the level of the individual body and the state. He writes:

> …in thinking of the mechanisms of power, I am thinking rather of its capillary form of existence, the point where power reaches into the very grain of individuals, touches their bodies and inserts itself into their actions and attitudes, their discourses, learning processes and everyday lives. (Foucault, 1980: 39)

In his *Collège de France* seminar on race, Foucault details state racism as a modern modality. He argues that the modern state's rise to power depended upon its manipulation of society's belief in race. Emerging states claimed that there was a war of the races taking place within national bounds and that the removal of degenerate elements would ensure the greater survival of those fit for life. Sciences were enlisted to purge the national body. Family, church, and club deliberated and promoted stringent conditions of group association. Individuals internalized the idea of race, making racial identity a critical part of modern subjectivity.

Although I focus on the state's role in proliferating race policies and conditions, my interest lies in the relationship between the genomic imagination—the vision and limits of possibilities as evidenced by genome project aims and goals—and the state's own racial imagination. This follows Foucault's characterization of biopower as disciplinary power concentrated on controlling the population towards an administration of life, but also as Nikolas Rose develops it for contemporary biopolitics: "a

biopolitics that does not seek to legitimate inequality but to intervene upon its consequences…part of the economy of hope that characterizes contemporary biomedicine" (Rose, 2007: 167). This issue of hope is central to genomics, because, as I show with the case of major genome project sampling protocols, projects justify their sampling policies based on specific ethical appeals. Some of these include freeing society from racism, freeing the individual from the oppression of ascription, and addressing Eurocentrism.

While others have analyzed the rise of genomics in terms of informatic entanglements (Thacker, 2000, 2005), ethical frameworks (Rabinow and Bennett, 2007; Rabinow and Rose, 2003, 2006; Rose, 2007), species management (Haraway, 2003), racial ideologies (El-Haj, 2007; Reardon, 2005) and global security issues (Mukhopadyay, 2008), following Steven Epstein (2007), I investigate genomics in terms of a larger policy paradigm shift; a shift in "frameworks of ideas, standards, formal procedures, and unarticulated understandings that specify how concerns about health, medicine, and the body are made the simultaneous focus of biomedicine and state policy" (Epstein, 2007: 17). Epstein's case study of late twentieth century health policy suggests that, from the 1970s-1990s, the "one-size-fits-all" approach to biomedicine gave way to what he calls an "inclusion-and-difference" paradigm:

> The name reflects two substantive goals: the inclusion of members of various groups generally considered to have been underrepresented previously as subjects in clinical studies; and the measurement, within those studies, of differences across groups with regard to treatment effects, disease progression or biological processes. (Epstein, 2007: 6)

In other words, as scientists structure their research populations by state-sponsored categories of difference, inclusionary policy breeds a biomedical interest in studying the biological difference between those populations. Epstein elucidates the role categories play in creating cohesion, or what he terms "categorical alignment," between science, state, and society. This research picks up where Epstein leaves off, detailing inclusion-and difference from the 1990s to the present and exploring its practical nuances in the emerging field of genomics.

Genome Projects and Sampling

Due to its recent inauguration, genomics is still predominantly a research-based science. Unlike other forms of science associated with genes and the

body, genomics relies on the availability of entire sequences to make comparisons between gene structure and function and to understand the statistical presence of biological components. Thus, genomics has advanced based on large scale sequencing projects that cost billions of dollars and require the coordination of laboratories, institutions, and governments across the world. Projects target specific areas or markers of the genome in order to make research possible. Then, it is up to individual laboratories to interpret the sequence, the goal of which is to bring clinical interventions to the public.

Sampling DNA is a first and most basic step in any large-scale sequencing project. Interestingly, a review of sampling protocols finds that projects have sampled in contrary ways. Projects have gone from no interest in the ancestral origins of sampled DNA to an interest in the race and ethnicity of research subjects, and on to a disavowal of racial categories in favor of continental terms. Here, I show that each of these shifts has been precipitated by a new strategy for implementing U.S. federal policy on race. Since the early 1990s, the Department of Health and Human Services (HHS) has been reworking its current policies on population, health, and race. These policies have been incrementally incorporated into the funding guidelines for all domestic and international research. So far, four out of the five major human genome sequencing projects have been U.S. led, publicly funded projects. Because the U.S.–the world's leading spender on healthcare and the dominant member of genome industries and consortia worldwide–was the predominant funder for the public genome projects, how these projects have chosen to sample DNA and present data has evolved from a decidedly U.S. context.

- 1977 Office of Management and Budget (OMB) Directive No. 15 mandates federal agencies to use a standard set of race categories
- 1993 NIH Revitalization Act Issues a requirement for the inclusion of women and minorities in health research using OMB standards
- 1994 Healthy People 2000 specifies minority health as a priority
- 1998 Healthy People adopts OMB standards
- 1998 Food and Drug Administration's (FDA) Demographic Rule orders OMB implementation
- 1999 HHS orders OMB implementation

• 2000-1 NIH revises inclusion policy to include implementation in clinical trials
• 2003-5 FDA tightens OMB guidelines for clinical trials

Table 1. *U.S. federal race policies (1977-2007)*

The adoption of these policies by the major federal health research bodies, such as in the case of the NIH Revitalization Act and the FDA's Demographic Rule, has not only been reflected in the changing sampling protocols engendered by the major genome projects; sampling protocols have changed the terms for justifying biological research and limits of possibilities for understanding human variation. Just as Foucault argues in his detail of state racism and biopower, the state's own mandates for administrating the population prove inextricable from its preeminent technologies of knowledge. Moreover, the concept of race provides an essential pivot in the construction of such power.

The Human Genome Project

The Human Genome Project (HGP) has been a central force in contemporary biopolitics and marks the turn to genomics in molecular science. The goal of the HGP was to assemble the sequence of a single set of human chromosomes. By design, this sequence would not represent all human DNA in existence, but a sample of the DNA that *one* human passes on to or receives from his or her kin. HGP scientists needed an endlessly reproducible set of DNA to sample from, so they used immortalized cell lines already created from populations living in Utah, France, and Venezuela (called CEPH for the institute that houses them). Evolutionary biologist Ernst Mayer recalls that while other *methods* were considered, HGP planners did not address the *identity* of whom they would sample from. The race and ethnicity of the individuals who donated their DNA was not at issue in the early stages of the HGP and the idea of global population representation was not discussed (Jackson, 1998: 157). Likewise, there were no measures for minority inclusion or minority community intervention on the table.

The absence of any formal dialogue over race, ethnicity, and population representation is evident in the HGP's first and second Five Year Plans. Early on, the HGP established a branch entitled "Ethical, Legal, and Social Implications" (ELSI) to address issues arising from new knowledge about human biology and the circulation of personal genetic information. ELSI's

goals in the first Five Year Plan did not address issues of population representation, nor did they ask how social groups will be affected by HGP knowledge. They focused on potential harm to the individual, such as individual privacy, confidentiality, potential discrimination by insurers or employers, and dealing with personal risk and discrimination (NIH, 1990). In the second Five Year Plan, an even more vague list of concerns was offered:

> (i) Continue to identify and define [ELSI] issues and develop policy options to address them. (ii) Develop and disseminate policy options regarding genetic testing services with potential widespread use. (iii) Foster greater acceptance of human genetic variation. (iv) Enhance and expand public and professional education that is sensitive to sociocultural and psychological issues. (Collins and Galas, 1993: 46)

The last two goals mentioning "acceptance of variation" and "social sensitivity" suggested a potential space for dialogue about the significance of race and the impact the HGP will have on popular notions, but there was still no explicit mention of race, ethnicity, or population representation.

Proceedings show that despite the inclusion of a diverse array of scientists, social scientists, ethicists, government officials, and community members, the concepts of inclusion and difference underpinning HGP sampling efforts were rarely addressed. Thus, the HGP proceeded without criticism to: 1) use samples already accessible without concern for global population representation, 2) order the removal of all population labels from the DNA to be sequenced, and 3) pool unlabeled samples for DNA amplification.

The Human Genome Diversity Project

Though the HGP advanced with a clear "no-labels, representation-neutral" policy, the U.S. government of the early 1990s was headed in a different direction. In 1990, the HHS released Healthy People 2000, a set of national health goals wherein race and ethnicity were to be of primary interest. Healthy People 2000, the second decade-spanning national health agenda following Surgeon General Julius B. Richmond's 1979 report, joined the U.S. Public Health services and the Institute of Medicine of the National Academy of the Sciences with over "300 membership organizations representing professional, voluntary, and private sectors as well as 54 State and territorial health departments" (HHS, 1994). For its

midway review, Healthy People 2000 set three broad goals for the remaining part of the decade: to "increase the span of healthy life for Americans," "reduce health disparities among Americans," and "achieve access to preventive services for all Americans" (HHS, 1994).

Contributors to the agenda stressed that an expansion of national health statistics on "non-Black" and "non-White" groups were needed (*Healthy People 2000: Citizens Chart the Course*, 1990: 51). The expansion of such databases relied on the implementation of socially-defined race and ethnicity categories as mandated by the Office of Management and Budget's Directive No. 15.[1] This focus on racial and ethnic health disparities was absent from the first Healthy People report, but soon became the focus of Healthy People campaigns. By 1998, a minimum template for population-based objectives was adopted to enforce the use of OMB categories.

Parallel to these efforts, the NIH passed the Revitalization Act, a statute setting guidelines for the inclusion and surveillance of women and minorities in clinical research and clinical trials (NIH, 1993). Investigators were directed to publish how their research would affect women and minorities and to generate "outreach programs" to ensure inclusion (NIH, 1994). Cost could not be a contributing factor to the decision over whom to include in a study. Exclusion was only permissible if the variables studied could be proven to have no differential effect on populations.

Informal communications regarding the possibility of an auxiliary human genome project began in 1989 and, by 1992, the NIH, the Department of Energy, and the National Science Foundation funded three planning workshops. In these planning stages, both the National Human Genome Research Center and the Human Genome Organization (the international coordinating body of the HGP) voiced interest in securing future funds for the project. Human Genome Organization president Sir Walter Bodmer

[1] The OMB states: "These classifications should not be interpreted as being scientific or anthropological in nature, nor should they be viewed as determinants of eligibility for participation in any Federal program. They have been developed in response to needs expressed by both the executive branch and the Congress to provide for the collection and use of compatible, nonduplicated, exchangeable racial and ethnic data by Federal agencies" (1977). The race categories in effect at this time were: White, Black, American Indian or Alaskan Native, Asian or Pacific Islander, with Hispanic as an ethnic category.

went so far as to call the Diversity Project "a cultural obligation of the [human] genome project" (Roberts, 1991: 1615).

The idea of a globally representative genome project came from several highly reputable molecular anthropologists and population geneticists. Yet, the two founders of the project, U.C. Berkeley biochemist Allan Wilson and Stanford geneticist Luca Cavalli-Sforza, had very different strategies for obtaining representation. Wilson was in favor of grid-sampling the globe: ignoring previous notions of relatedness and using geographical distance to mark biodiversity. Cavalli-Sforza argued that grid-sampling was too expensive and risky, and that researchers would have to pay mind to predefined populations (those marked by ethnic or linguistic ties) so as to have a rough guide to reproductive isolation. In the end, planners agreed to collect immortalized cell lines from 400 pre-defined populations, while loosely distance-sampling non-immortalized DNA (Roberts, 1992: 1205). Thus, pre-defined social categories of *ethnicity* were to be the precursor to this genomic investigation.

While the Diversity Project promised many of the same things as the HGP—a greater understanding of biology, knowledge about the role of genetics in disease, and a forum for international scientific collaboration—it also marketed itself on its ability to address *deeper social issues*. Planners openly took issue with the no-labels approach of the HGP and linked it to ethical and cultural insensitivity and Eurocentrism. Wilson and Cavalli-Sforza both remarked that the HGP's reliance on CEPH cell lines would result in a "Caucasian" or Caucasoid" sequence (Roberts, 1991: 1204; Bowcock and Cavalli-Sforza, 1991: 491). The Diversity Project, in contrast, offered a globally representative approach based on an incorporation of the self-determined identities of ethnic tribes. They planned to sample isolated populations across the world starting with those considered threatened with extinction.

As the Diversity Project met with suspicion from the public and indigenous groups around the world, their claim to alleviate racism grew into a clamor. By 1994, in a presentation to UNESCO, Cavalli-Sforza devoted one-fourth of his speech to discussing "how the Project will help combat the scourge of racism" (Human Genome Diversity Project, 1994). Although they eventually reassessed their isolate-based sampling protocol and opened the project to U.S. racial minorities and any groups who wanted to participate, their initial stance alienated government and indigenous groups alike. For the U.S. federal government, the Diversity

Project's focus on tribal ethnicity foreclosed investigation into minority biostatistics. The HHS could not accommodate an ethnic enumeration system separate from OMB. For indigenous groups, sampling was seen as a taking with little promise of return.[2] Indigenous groups all around the world signed petitions and made declarations of their unwillingness to participate in what became known as another instance of "biopiracy" and "modern-day colonialism" (Dickinson, 1996: 14). After three years of indigenous lobbying against the project, despite the production of a revised sampling protocol based on tribal consent, the Diversity Project's major funding sources withdrew support.

The Polymorphism Discovery Resource

Amidst these decisions, in 1997, the National Human Genome Research Center was elevated to the status of an institute of the NIH. As an institute, this department was invested with a new scientific leadership role and a more robust governing role. The new institute immediately moved to create a genome project that would solve the problems that plagued the Diversity Project and expand the limits of the HGP. The Polymorphism Discovery Resource was launched in 1998 as the official auxiliary to the Human Genome Project, dedicated to providing a global representation of genomic polymorphisms. In collaboration with the other HHS and NIH facilities, it aggressively sought to include DNA from people with non-European heritage. Still, once collected, DNA was de-labeled and pooled as before.

Discovery Resource planners solved the question of how to obtain global representation by designing a sampling protocol around the racial categories of the OMB Directive No. 15. Unlike the Diversity Project, this research arm of the federal government did not have to validate its use of U.S. racial categories to comprehensively and biologically "reflect the diversity of the human population" in order to get funding (DOE, 1999). Still, planners adopted a similar antiracism, pro-inclusion argument to popularize the project. They proffered: "publicly available DNA

[2] In *Race to the Finish: Identity and Governance in an Age of Genomics*, Jenny Reardon explores the eventual failure of the project in terms of this rise of indigenous resistance. She argues that the HGDP's refusal to face the history of race relations between Anglo-American academics and indigenous subjects prevented them from seeing their project as implicated in that history. Thus, in addition to the *kind* of inclusion promoted, inclusion itself served as an important biopolitical impasse.

collections contain little African material; Native American and Asian contributions are similarly scant. As a result, say NHGRI staffers, it will be essential to collect DNA from a racially structured set of donors. Once the DNA has been sampled, however, all personal and racial data will have to be removed to protect privacy – diminishing the scientific value of the project, but bolstering its ethical foundation" (Marshall, 1997: 2047). The institute combined social inclusion and scientific representation into one method. This set a sampling precedent for future genomic research. Considering pre-defined race was incorporated as the first step in genomic sampling.

The International HapMap Project

In the late 1990s, competitive pressure from a private project and the need for the new Institute to maintain its momentum forced the National Human Genome Research Institute and the Human Genome Organization to wrap up its projects and plan the next step. In "New Goals for the U.S. Human Genome Project: 1998-2003," human variation took center stage. Under "Goal 3: Human Genome Sequence Variation," we see a first elaboration of 1) what was meant by "population," 2) the significance of measuring frequencies between individuals and populations, and 3) why population genetics would be an integral method to genomic research. Yet, the crux of the project's position on race and ethnicity came under the heading of ELSI goals. "Goal E" promised to "Explore how socioeconomic factors and concepts of race and ethnicity influence the use, understanding, and interpretation of genetic information, the utilization of genetic services, and the development of policy" (Collins et al. 1998: 688). In 1999, ELSI announced a Request for Applications entitled "Concepts of Race, Ethnicity, and Culture: Examination of the ways in which the discovery of DNA polymorphisms may interact with current concepts of race, ethnicity and culture." For the first time, scientists questioned how their research was going to effect racial and ethnic categories already in place. Behind closed doors, the National Human Genome Research Institute's National Advisory Council also began discussing the conceptual structure of race and ethnicity, while the institute began reworking its minority inclusion policy.

Likewise, the Food and Drug Administration issued a policy referred to as the Demographic Rule. It explicitly linked the issue of minority inclusion to biological processes. It warned (1) Different subgroups of the population may respond differently to a specific drug product and (2)

although the effort should be made to look for differences in effectiveness and adverse reactions among such subgroups, that effort is not being made consistently (FDA, 1998). When the NIH drafted its new policy, one that has stood since 2001, it almost point by point reflected this combined social and biological rationale (NIH, 2000).

This new orientation has been sedimented and expanded in this century's projects. While the Polymorphism Discovery Resource was the first genome project dedicated to collecting DNA to study polymorphisms, it was soon eclipsed by a *labels-on* polymorphism mapping project comprised of thirteen major pharmaceutical, genomics, and informatics companies and the HGP's British supporter, the Wellcome Trust. The SNP Consortium, founded in April 1999, aimed to generate a map of 300,000 evenly spaced single nucleotide polymorphisms (.001% of the variation in the human genome) (http://www.ornl.gov/sci/techresources/Human Genome/faq/snps.shtml#snps). In July 2000, the National Human Genome Research Institute donated 24 Discovery Resource samples hailed as "representing several racial groups," and provided database and storage infrastructure to promote the generation of 250,000 additional polymorphisms (DOE, 2000). Within months, the SNP Consortium produced a map detailing over one million polymorphisms (International SNP Map Working Group, 2001).

In August 2001, the National Human Genome Research Institute announced its plan to expand the Human Genome Project and the SNP Consortium into a genome-wide haplotype mapping project (Pennisi, 2001). The International HapMap Project was formally launched in November 2002, following a study performed on Diversity Project cell lines which suggested that there was, in fact, continental structure to the genome and an article favoring a biological concept of race.

At this time, the federal government tightened its policies on inclusion and representation around the world. The FDA circulated the draft "Guidance for Industry: Collection of Race and Ethnicity Data in Clinical Trials" (FDA, 2003) as a direct response to the foreign relocation of randomized pharmaceutical trials. The FDA sought to curb wanton incorporation of foreign-based data without consideration of its consequences for domestic "population control" measures like racial enumeration by OMB standards. Aware of the practical limitations of foreign-based research, the FDA stipulated that researchers could research sub-racial ethnic groups and tribes as long as they reported those groups in terms of OMB races (HHS,

2005). Thus, the U.S. global research orientation established by the NIH and FDA crystallized into a concerted policy wherein all globally designed research would filter through a system of categories pertinent to the U.S. sociopolitical context.

In the end, HapMap planners designed an OMB-friendly *continent-based* approach wherein they would sample one well-defined ethnic group from each region of the globe and refer to samples in geographic terms.[3] This original proposition was altered when Native American groups opted out of the project. The tribal representatives that were contacted requested that HapMap not knowingly include any Native American samples. It was altered a second time as representatives from China and Japan both expressed their intent on participating. Both China and Japan were included, yet their sample contributions were each halved. Thus, the HapMap's Phase I DNA pool represents a sample of equal European, African, and Asian proportions. While these limited groupings overlap with OMB standards, they are not completely coincident. They provide a first glimpse of a move away from strict adherence to Directive No. 15.

It is important to note that many HapMap scientists questioned the implementation of OMB categories from the outset. Planners wanted the project to be a beacon guiding the world toward a more just existence based on the evident truths of our biology, not a hegemonic reflex of one nation's population standards. Therefore, once the planning group took on the status of an official consortium, the HapMap Project decided to avoid suggesting comprehensive global representation would be achieved. Instead, they generated a set of "Guidelines for Referring to the HapMap Populations in Publications and Presentations" that instruct all users of HapMap data to adhere to the immediate geographic, location-specific descriptors they provide (this consists of a town, city or ethnic label accompanied by the state or nation where that sample was collected). The guidelines reason that rules must be followed in order to assure scientific consistency, but also to show respect for the communities sampled. "Guidelines" makes clear that labels are generated to reflect exactly where samples were obtained; therefore using a continental shorthand is impermissible (http://www.hapmap.org/citinghapmap.html).

[3] Troy Duster has written extensively on the reification of racial categories since the Human Genome Project. Regarding the HapMap project's continental scheme, he asks: "Why was the question [of variation] raised in this manner?" (Duster, 2005: 1050). See Duster 2005 and 2006.

However, slippages have proved impossible to avoid. In the HapMap Project's official introductory article in *Nature*, the consortium justified their sampling in terms of its ability to engender global representation based on continental ancestry. The consortium called the Yoruba in Ibadan, Nigeria; Japanese in Tokyo, Japan; Han Chinese in Beijing, China; and CEPH "four large populations [that] will include a substantial amount of the genetic variation found in all populations throughout the world" (The International HapMap Consortium, 2003: 791).

Thus, despite HapMap's attempts to disentangle its practices of social inclusion, scientific representation, and taxonomy, its continental focus has precipitated the current sampling paradigm that divides the globe into genomic regions coincident with OMB standards. Again, this paradigm not only guides the scientific elaboration of research populations but provides the social, political, and ethical justification for the genomic research itself.

Conclusion

This portrayal of the major genome projects of the genome era shows that while each of them faced innumerable challenges, in the end, none could survive without engaging with the U.S. federal interest in race. The HapMap is clearly moving things in a new direction with the disavowal of overt OMB categories, but its continental ancestry protocol keeps the population framework squarely located in the government's "population control" scheme. To return to Foucault's notion of biopower, genome projects are successful insofar as they are relevant to larger sociopolitical projects useful in the administration of life. Race provides an invaluable tool for organizing populations as well as scientific knowledge about those populations.

This portrayal also shows how critical ethical appeals are in garnering support for biopolitical projects. From the outset, projects made communication with the public first on their agenda. They articulated their strategies in the language of promises for a better social future and the personal relevance of scientific policies to all citizens of the world. Projects that previously ignored race were forced to align ethical visions with the dominant social concerns of the U.S. context, making racial strategy and dialogue a priority.

Rose gives this shift toward "attempts to shape the conduct of human beings by acting upon their sentiments, beliefs, values" the name "ethopolitics."

> If "discipline" individualizes and normalizes, and "biopolitics" collectivizes and socializes, "ethopolitics" concerns itself with the self-techniques by which human beings should judge and act upon themselves to make themselves better than they are. (Rose, 2007: 27)

While Rose urges us to see contemporary race in terms of the latter forms of politics, my analysis indicates that, indeed, all of these forms of power co-exist today. Sampling strategies must be subjectively relevant, biosocially relevant *and* governmentally relevant in order to succeed. Furthermore, as Epstein (2007) and this research cogently show, government racial policies and genomic power/knowledge continue to normalize and individualize in important ways.

Still, Rose points to an important aspect of contemporary biopower that must be further addressed: the apparatus of state racism in the new genomic era. Foucault's articulation of racism in terms of eugenics and Nazi *Rassenhygiene* has limited relevance today, as the subject's relation to science and the state changes. Moreover, the relationship between global projects and the U.S. government, and between large-scale biology and the state, indicate that structures of governmentality are rapidly transforming. It remains to be seen how global biomedical development will affect domestic race policies. Finally, we must watch as genomics moves from a populations framework to individualized medicine. Will OMB continue to play a role in this new science of the self?

As of today, there are five new international human genome projects underway and many corollary projects being devised. Genomics continues to gain ground in the biological sciences across the world. My investigation shows that the links between state notions of race, ethical envisionings, and genomic practice are critical aspects of the evolution of biopower in the 21st century.

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