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Race in the Microbiome

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Abstract

Microbiome science asserts humans are made up of more microbial cells and genes than human ones, and that each person harbors their own unique microbial population. Human microbiome studies gesture toward the post-racial aspirations of personalized medicine—characterizing states of human health and illness microbially. By viewing humans as "supraorganisms" made up of millions of microbial partners, some microbiome science seems to disrupt binding historical categories often grounded in racist biology, allowing interspeciality to supersede race. But inevitably, unexamined categories of race and ethnicity surface in a myriad of studies on microbiota. This paper approaches race as a ghost variable across microbiome research and asks, what is race *doing* in studies of the microbiome? Why is it there, and how is it functioning? I examine this research to argue that social scientists must work with biological scientists to help put microbial differences into perspective—to investigate how microbiomes *and* race are entangled embodiments of the social, environmental, and biological. Ultimately, transdisciplinary collaboration is required to address racial health disparities in microbiome research without reifying race as a straightforward biological or social designation.

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A seemingly never-ending paradox erupts around race in every new area of scientific research: race in science is commonly affirmed as a *social construct*, but not quite.[1] While some scientific research claims there is more to human diversity than race, other scientific work finds biological distinctness in race. Categories of race are used unceasingly to arrange scientific subjects and their bodily differences. Sometimes scientists invoke the "social" to avoid the unquantifiability of race in their work, while simultaneously operationalizing race to identify differences in biologies. Often, races become meaningful biological categories without any interpretation of commensurate sociomaterial factors; race in science fluctuates between solely social and simply biological. Many scholars have grappled with the critical, empirical, and everyday implications of this fraught biomedical/race relationship (Benjamin 2019; Fullwiley, Morning; Nelson 2016, Roberts, and many others).[2] Here, I will mine this analytical history to create a framework for understanding race at work in research on the human microbiome. There is no agreement (in any discipline) about what race is or where it resides, about what is considered "biological" or "social" or if those things are discrete.[3] Race becomes a ghost in the scientific work, an invisible, powerful informant that affects the categorization of bodies, how difference is scientifically made and verified, and ultimately how interventions and care are applied. But what happens as translational research is increasingly datafied and personalized? Does the ghost of race haunt these new houses?

Human microbial ecology asserts that human bodies are made up of more microbial cells and genes than human ones and that each person harbors their own unique population of microbes (Human Microbiome Project Consortium 2012; Integrative HMP [iHMP] 2019).[4] Biomedical studies of human microbiota (the ecological community of microorganisms living in and on human bodies) and the microbiome (the genomes of those microbes) gesture toward the post-racial aspirations of personalized medicine—characterizing states of human health and illness microbially, dependent on individual biosocial factors like nutrition, diet, and environment. Viewing humans as "supraorganisms" or "holobionts," assemblages of different species that form ecological units (Sekirov and Finlay 2006; Gordon et al. 2013), some microbiome science attempts to complexify the binding

historical categories of race. If humans are made mostly of microbes, which presumably don't have races, then humans' interspeciality or "becoming with" these organisms (Livingston and Paur 2011; Haraway 2008, respectively) takes precedence over old racial categories.

Inevitably, unexamined categories of race and ethnicity surface in a myriad of studies on microbiota from asthma and diabetes to colorectal cancer and bacterial vaginosis. The bodies chosen for microbiome research are explicitly raced and sexed as a central part of the scientific work. This paper approaches race as a ghost variable across different kinds of microbe research and asks, what is race *doing* in studies of the microbiome: why is it there, and how is it functioning? D. Roberts (2011) suggests that the way out of this race/science paradox is to focus on *how* race is being used as a categorizer, instead of trying to find differences in the biologies of race. I examine microbiome research to argue that social scientists and science and technology studies (STS) scholars must work with biological scientists to put microbial differences into perspective—to investigate how these differences are informed by biosocial determinants more complex than *race* alone, and how race is never alone, never an independent explanatory variable. In 2013, anthropologists at the School for Advanced Research attempted to reorient problematic anthropological perspectives on race and posited that race is recursive, "The assertion that *race is a biosocial fact*, indeed, moves us from thinking about *it* as a fixed quality, an inherent essence, or a unique causal mechanism to seeing *race as a process*, one that offers no certain line by which either 'biology' or 'society' can be starkly delineated" (Hartigan 2013, 194).[5] I have suggested similar thinking elsewhere (Benezra, DeStefano, Gordon 2012, 2018, forthcoming); regarding microbiomes as entangled embodiments of what are considered social, environmental, material, and biological elements, but requiring us to reckon with human–microbe relationships as intra-acting biosocial assemblages (Barad 2007). This paper advocates for the continual unsettling of the social/biological divide in terms of the microbiome and race. Ultimately, transdisciplinary collaboration will be required to address racial health disparities in microbiome research without reifying race as a simple designation, and to study the *biosocial intersectionality* of the human microbiome.

As microbiome research becomes one of the most popularly publicized areas of scientific work, race functions as a ghost variable in categorizing human bodies and their corresponding microbial partners. By *ghost variable*, I mean that "race" as an operational concept in microbiome science has a ghostly presence, one that is there but not there, hiding in shadows and jumping out when least expected. M'charek, Schramm, and Skinner (2014)

have described this ephemerality as race's *absent presence,* where race is a slippery object. These authors go on to say that contemporary liberal politics of racism (and I would include neoliberal science) often means *race* but codes it as national, cultural, or religious identity. Following this, many studies of the microbiome vacillate between the terms, "ethnicity," "geography," and "genetic ancestry," but all serve as a cipher for historically and culturally saturated designations of race. In this paper, I will look at race/ethnicity-dependent areas of microbiota research: in the microbes of "uncontacted hunter-gatherers" (Fragiadakis et al. 2019), vaginal microbes across ethnicity (Ravel et al. 2011), and my own ethnographic fieldwork in a laboratory comparing guts across the globe (Yatsunenko et al. 2012).

I use this research to think about what is elided when human microbial ecologists make biological microbiomic claims presuming racial categories, and how the inclusion of social science thinking can perspectivize microbial differences within poverty, resource access, and oppression. Ethnography can be a critical first- and second-order analytical approach in investigations of how social determinants of microbiomes are also biological. Anthropologists can provide scientists with qualitative ethnographic data about living conditions, social networks, daily practices, and "local biologies" (Lock 2001), exposing how biological and social life are mutually constitutive over time in what Lock and Nguyen (2018) call *biosocial differentiation*. The conceptual and methodological tools of anthropology can account for the transnational and local realities of people embedded in global scientific research, health interventional programs, and clinical trials. This paper serves as an initiatory interrogation of race in microbiome science not only to see how race and racism function within current research, but also to think about who microbiome science is for and how to counteract the structural violence built into its technologies and aims.

What Race Means

Because race is formally designated in various ways, it is important to start with categorical clarity. How funding and regulatory agencies such as the National Institutes of Health (NIH), the National Science Foundation (NSF), and the US Census Bureau define race and ethnicity become the ways grant proposals, scientific research, and scientists use and consequently produce[6] race and ethnicity. The NIH race and ethnicity standards are set by the US Office of Management and Budget and take an ancestry/country of origin approach ("a person having origins in any of the original peoples of . . . ")[7] where races are American Indian or Alaska Native, Asian,

Black or African American, Native Hawaiian or Pacific Islander, white, and Hispanic, or Latino (ethnicity regardless of race).[8] The NSF uses the same categories but allows for respondents to choose more than one designation. The NSF also gives an explanation of the many problems with reporting race: populations change over time, self-identification is inexact, and heterogeneity in populations can be overlooked. Because nearly all of the microbiome studies discussed here (with the exception of the Gordon Lab work) are federally funded by the NIH or NSF, and all of the research takes place in US laboratories, these are the parameters for race and ethnicity that I will use throughout. Microbiome studies often conflate, confuse, and interchange ethnicity, nationality, and geography with race.

While social scientists work on constructing new research language (Yudell et al. 2016), federally funded science looks to technology to circumvent the race problem. Precision medicine's "post-racial promise" (Newkirk 2016) has the tenuous potential to make health care more data-driven and biologically accurate, though not necessarily racially equitable (Bonham, Callier, and Royal 2016; Kahn 2017). Precision medicine begets a specific type of gene-based, individualized intervention. Scientists working on the microbiome have followed suit, endeavoring to create personalized microbiomics, addressing health from a microbial perspective. Goals include microbe-based therapeutic interventions that would customize medicine/probiotics/food/health care based on proteomics, metabolomics, and genetic testing. These "inside out" approaches take the interventional form of *microbiota-directed complementary foods* and *next-generation probiotics* (human gut-derived microbial strains) designed to repair microbiomic abnormalities or deficiencies (Gehrig et al. 2019).

Looking at states of human health and illness through a microbiomic lens disarranges conventional categories of community, species, and self. Social scientists must be attuned to when the ghost variable of race begins to materialize and read microbiome studies across the grain of racial categorization and inequity. Stefan Helmreich is one of very few anthropologists beginning to speculate about race in the microbiome. In *Sounding the Limits of Life*, he comments that even though the microbiome seems to be able to create categorical havoc, ultimately, "There is nothing preventing race from manifesting in microbiome talk, in both reductionist and complex ways" (Helmreich 2016, 66). Although I agree with Helmreich's caution and show below how race does surface in microbiome work, I propose that cross-disciplinary cooperation can disrupt this seeming inevitability. I analyze three specific research areas in microbiomics and take Helmreich as an opening instead of an end point, turning statements into a series of questions:

How does race manifest microbiomically, and to what end? *What* social science interventions can help to ghostbust these manifestations of race?

Uncontacted Microbiota

Conceptually, microbiome science is race-free, but subjects of microbiome research are often placed in familiar, opposing groups: "Westerners"[9] who are primarily white and are assumed to have similar lifestyles and socioeconomic statuses, versus black and brown bodies in the global south assumed to be underdeveloped or "modernizing" (De Filippo et al. 2010; Gomez et al. 2016; Rampelli et al. 2015). Microbiome differences are sought without corresponding investigations into existing economic, political, and health vulnerabilities. Race surfaces here, as those historically biomedically exploited become ready bodies for microbiomic explorations.

In June 2019, the Sonnenburg Lab at Stanford University published an opinion piece in *Nature Microbiology* entitled, "The Ancestral and Industrialized Gut Microbiota and Implications for Human Health." This essay takes a catastrophic view on the damage done to microbiomes by modern living, which the authors refer to as "industrialized microbiota"—microbiomes altered by antibiotic use, increased sanitation, caesarean sections, and industrialized food production (Sonnenburg 2019, 383). Industrialized microbiota is contrasted against microbiota collected from "traditional populations," which are reported to contain a high abundance of rare microbes. The Sonnenburgs define these microbes as *VANISH taxa*: volatile and/or associated negatively with industrialized societies of humans. They warn that the loss of these microbes is causing widespread chronic disease and dysbiosis: microbial imbalance or impairment. They propose that "healthier" diets, probiotically engineered foods, and "rewilding" (the practice of reintroducing "lost" bacterial species to the gut) can help save the industrialized gut.

What do these prescriptions have to do with race? These authors define "industrialized," but never say what they mean by "traditional populations," so the phrase becomes racially coded to mean indigenous, undeveloped, and not-white. At times they are talking about lifestyle and diet differences (foraging or rural agricultural practices, sanitation, unmedicalized births) but call those differences "nationality," "geography," and "race." Here, language matters—"rewilding" calls up racist US stereotypes of black and Native American people as wild, savage, and uncivilized.[10] Wildness is transposed from human bodies onto their microbes and back again. This is an important opening for social scientists to try to understand (and help

scientists understand) who are the participants and what categories of race do in microbiome studies.

"Salvage ethnography" refers to the recording of the languages, rituals, and so on, of "disappearing" cultures—those presumed to be under threat of extinction from modernization. Modern anthropology has eschewed this practice, and many anthropologists leveled their criticism at the same kind of work being done in the Human Genome Diversity and International HapMap Projects. These projects focused on indigenous populations as valuable to furthering genome science but fell short on equitable practices of consent, community participation, and benefit (M'charek 2005; Reardon 2005). In the 1990s, salvage ethnography became a sort of *salvage genomics* and is becoming what I would call *salvage microbiomics*, with a repeating loop of the same populations as scientific subject/objects. Salvage microbiomics wants to save valuable, vanishing microbes from modernization without acknowledging the research's own embeddedness in technoscientific systems responsible for changes in microbial populations.

In the Sonnenburgs' essay and many other studies, the racially/ethnically defined "traditional" microbiomes are compared directly against "Western" ones to establish stark contrasts—racial othering reflected in microbial difference. These papers appear in high-impact scientific journals such as *Nature*, *PNAS*, and *Current Biology* and become foundational for further studies. Without careful unpacking and recognition of colonizing scientific histories, microbiomics can racialize and discriminate. Conceiving of indigenous people as primordial, barbaric, and undeveloped has long been a driving justification for colonization, enslavement, and genocide. Hayden (2003) has described *bioprospecting* in terms of the extraction of local plants and indigenous knowledge, here, microbes from indigenous guts by US research labs and corporate partners are bioprospected. "We" have damaged our microbiomes through the overuse and abuse of medical and nutritional technologies, and our salvation will be to return to preindustrialized microbiota. To seek answers to current Western woes in the idealized purity of the past and primitive gut in turn instrumentalizes brown and black bodies in the service of white health.[11]

In the *Science Advances*[12] 2015 Clemente et al.'s study, "The Microbiome of Uncontacted Amerindians," researchers characterize the fecal, oral, and skin bacterial microbiome of members of a Yanomami Amerindian village in Venezuela and describe their subjects has having, "no documented previous contact with Western people" (p. 1). Although the Yanomami in question lived in an isolated and unmapped (to foreigners) area, "first contact" is a myth that has long occupied the imaginations of

social and biological scientists seeking "uncontaminated" study populations. Anthropology has its own an ethically violent history with the Yanomami, and microbiome science has returned to these people seeking microbiomic purity in the same ways that anthropologists sought cultural purity. The fact that the Yanomami sampled were seen as an untapped treasure trove of microbiota further reinforces the idea of salvage microbiomics. Describing Yanomami microbiota as occupying a different temporal space than modern Western microbiota[13] elicits the same othering imaginaries in which majority world populations represent the West's lost past. In "Reviving Colonial Science in Ancestral Microbiome Research," Maroney (2017) keenly analyzes the problem,

> These studies assume that peoples living so-called "hunter-gatherer" lifestyles in places like eastern Tanzania and the Venezuelan Amazon are appropriate biological proxies for humans living 10,000 years ago. This temporal collapse reduces indigenous and rural people living traditional lifestyles to mere research fodder—or "living fossils," it depoliticizes their existence in the present by writing of them as untouched and uncontacted [. . .].

The participation of social scientists in microbiome research can change these perspectives. Included in the ELSI (ethical, legal, and social implications) section of the NIH Human Microbiome Project (HMP),[14] specific attention has been paid to the ethical challenges resulting from the inclusion of indigenous communities and the risks to historically vulnerable populations. The main issue is the lack of clinical applications that will benefit these populations in the foreseeable future. What's at stake and what's to be gained by the Yanomami participants for contributing their microbiota? The call for attention to these types of research inequities isn't new—many have speculated about how clinical research should be both ethical and responsive to the specific needs of those in resource-poor countries (Wendler, Emanuel, and Lie 2004). An extensive literature on benefit-sharing in global health research has emerged, but the conversation has taken place primarily among anthropologists, bioethicists, and public health scholars, not research scientists. Since direct, immediate intervention is unlikely, some propose an "ethics of care" that requires microbiome researchers to: attend to the current predicaments of research participants, support meaningful infrastructural changes, and remain alert to possible commercial exploitation. In 2016, researchers at University of Oklahoma published "Gut Microbiome Diversity among Cheyenne and Arapaho Individuals from Western Oklahoma" in *Current Biology* based on a study in which the scientists

established an interdisciplinary partnership between the university and Cheyenne and Arapaho Tribes. They attempted to diversify population-based microbiome knowledge (which had been limited to European Americans) to address gut microbiome–associated complex diseases that are also common health disparities among American Indians. The study focuses on how the biological interacts with the environmental and socioeconomic (Sankaranarayanan et al. 2015). The primary investigators on the study were both molecular and sociocultural anthropologists, and they employed what they called an *embedded ELSI approach*, one in which the scientific community engages in long-term relationships of mutual benefit and concern, trust, and understanding with the participants from American Indian communities. This study, while not perfect (the analysis of metagenomic data still overshadows the ethical innovation), is a good example of the social and biological science partnerships necessary for successful microbiome science.

Vaginal Sites

The influential 2011 *Proceedings of the National Academy of Sciences* paper, "Vaginal Microbiome of Reproductive-age Women," established a categorical precedent in vaginal microbiome research, claiming definitively that black and Hispanic women have different vaginal microbes than white and Asian women (Ravel et al. 2011). The study concludes that these differences in microbes have led to different disease rates; black and Hispanic women have more bacterial diversity in their vaginas which makes them more susceptible to bacterial vaginosis infections (BV). This paper is the most often cited paper on vaginal microbiota, and it laid the groundwork for every subsequent study in this area. Jacques Ravel's research was funded by the NIH, yet the study uses "ethnicity" as an umbrella term to describe three NIH-defined races and one ethnic group (black, white, Asian, and Hispanic). Race and ethnicity here are conflated and overlap, underlining colonial histories of difference. In Ravel et al.'s study, ghostly race hides within racialized ethnicity. Seeking a relationship between ethnic background and vaginal bacterial community composition is foundational to the study—race serves as an organizing research principal. With the insights made possible by ever more sophisticated biological and statistical theory, next-generation bacterial genome sequencing, and formidable computing power, we seem still trapped in Linnaeus' original race scheme, dividing the world's populations into a four-part color wheel.

The Ravel et al. paper redefines what sorts of bacterial communities are found in "healthy" women so that risk and diagnosis can be assessed

individually. However, associating black and Hispanic vaginal microbiomes with BV, which is itself associated with risk factors of multiple sexual partners, lack of condom use, and smoking, leans on racist stereotypes of hypersexualized black and Hispanic women. Setting up a different "normal" for Hispanic and black women's vaginal microbiota is a dubious use of questionably related racial identifications. As geographers Mansfield and Guthman (2015) have written, new ways of thinking of biology as plastic changes concepts of difference, normality, and abnormality. Microbiomics, just like epigenetics blurs distinctions of inside/out, biological/social in nondeterministic ways. "So while it might seem that these new epigenetic models of plastic life should eliminate race by eliminating notions of discrete kinds given in nature, it appears that epigenetics offers a new form of racialization based on processes of becoming rather than on pre-given nature" (Mansfield and Guthman 2015, 6). Similarly, since microbiota is open to intervention and optimization, making racial distinctions in microbiomes reinforces normalcy tied to race. But race itself doesn't do much work to help us understand variations in microbiota, making it harder to navigate health disparities without reifying race.

Ravel et al. conclude that the reasons different ethnic groups have these vaginal microbiota differences are unknown, but "it is tempting to speculate that the species composition of vaginal communities could be governed by genetically determined differences between hosts" (Ravel et al. 2011, 4684).[15] Complex socioenvironmental components are only briefly alluded to and considered separate from the biological/microbiomic. For example, specific sex practices have an enormous influence on microbial populations in the vagina. Yet monitoring a study subject's sexual behavior and determining what acts at what time on what bodies affect the microbiome is impossible; several sex acts can be concurrent, time of sampling hard to manage, and other variables like lubrication and hygiene confound results. So, sex practices that are instrumental in making the vaginal microbiome are hard to study. On the other hand, "race" itself cannot have an effect on vaginal microbes *alone*, but unlike investigating sex practices (difficult), race is easy to assign. BV itself is notoriously ill-defined. It would be more accurate to say that BV is more prevalent in populations of low socioeconomic status, specific reproductive age, inadequate nutrition, and so on, rather than in black and Hispanic women (Brubaker 2017). Indeed, there is an enormous public health literature substantiating that black women are at higher risk of bad maternal and reproductive health outcomes. How can ethical and effective interventions help solve these health inequities without returning to racist categories?

Although some microbial ecologists working on the vaginal microbiome focus more on how age and place within reproductive life are more influential in determining microbial communities (Cone 2014), the novelty and assumed greater precision of metagenomics has eclipsed an examination of the socioenvironmental parts of BV. Further, Ravel et al.'s study gave rise to a slew of subsequent studies, all which took the racial/ethnic groups as given, and began to place value judgments on "risky behaviors," "healthy vaginas," and "good" and "bad" vaginal microbiomes. These qualifications of vaginal microbiomes (and the vaginas they came from) correspond directly to race/ethnicity (Borgdorff et al. 2017; Fettweis et al. 2014; Srinivasan et al. 2012). What appears to be microbiota differentiated simply by race is microbiota affected by what it means to be a black or Hispanic woman in the United States.

Funded by the iHMP, Jennifer Fettweis has made strong claims connecting preterm birth in African American women with the specific microbial taxa in their vaginas (Fettweis et al. 2019). In subsequent work, Ravel develops novel strategies to improve women's health by *biologically* modifying the microbiome (Ravel and Brotman 2016). The Ravel Lab currently has two active NIH-funded studies, "Influence of Modifiable Factors on the Vaginal Microbiota and Preterm Birth" and "Revealing the Role of the Cervico-vaginal Microbiome in Spontaneous Preterm Birth." Millions of dollars are being used to fund studies of microbes in the vagina, trying to fix the problem of preterm birth by fixing a broken vaginal microbiome. These studies enact what Duster (2006) has called the *molecular reinscription of race* and Fullwiley's (2007) *molecularization of race,* but on a microbial level. This science seeks probiotic interventions to prevent adverse outcomes while failing to account for the well-documented evidence that racial discrimination, chronic stress, and other disparities contribute to preterm birth (Braveman et al. 2017; Gavin et al. 2018; Kramer and Hogue 2009). Following this, the inclusion of perspectives from a social science expert in public/sexual health, epidemiology, or medical anthropology in vaginal microbiome studies is crucial to foregrounding the biosocial entanglements like structural racism that can affect microbial populations.

Global Guts

In 2010-11, I conducted fourteen months of ethnographic fieldwork at the Gordon Lab at the Washington University Center for Genome Sciences and Systems Biology, a leading US microbiome laboratory. During that time, I served as the lab anthropologist while doing my own research. This lab is at the forefront of studying how human microbiota is constituted, changed,

and its role in health and disease. The lab's research aims to treat metabolic dysfunction and nutritional deficiencies through microbes. Much of the work is done in the service of a philanthropically funded global health project, and study subjects are primarily from resource-poor, globally south countries. One of the central Gordon Lab projects is to seek microbiomic solutions to the problem of malnutrition.

When I was in the Gordon lab, one postdoctoral researcher had a project known colloquially around the lab as the "global gut study"; analyzing children in different areas of the world, looking at the establishment of their first gut microbial communities through the first three years of life. The postdoc was interested in the interplay of host genotype, environment (culture, diet, climate), and early childhood development (interaction with caregiver, transition from breast milk) with the gut microbiota of different geographical populations. Because she was comparing African, South American, and US subjects, she asked, how does gut microbiota react to "Westernization?"[16]

The global gut study (actually titled, "Human gut microbiome viewed across age and geography") collected thousands of fecal samples, over years, from hundreds of people in different parts of the world,

> To examine how gut microbiomes differ between human populations when viewed from the perspective of component microbial lineages, encoded metabolic functions, stage of postnatal development, and environmental exposures [. . .]. (Yatsunenko et al. 2012, 222)

Yatsunenko struggled with the great variation in her data and was challenged to find group effects, "Each sample is only representative of that one person on that one day. There are no features of significant association with malnutrition across all families. All families have to be looked at individually. There is little overlap of ages where kids became malnourished."[17] When she stopped looking for similarities and instead started looking at the diversity of microbiota, her results started to take shape. In the data, she was seeing the effect of antibiotics and the introduction of new foods on the microbial populations. She published this work in *Nature* (Yatsunenko et al. 2012), and it radically impacted scientific understandings of how the microbiome is constituted in early life, and how the microbiome differs in relationship to worldly populations. Yatsunenko's study established that children's microbiomes develop relatively the same everywhere and was the first study comparing the gut communities of humans living different kinds of lives in different places.

This paper had several significant and entangled outcomes regarding how microbial populations are established as a factor of age, geography/cultural traditions, and diet. Yatsunenko and her colleagues recognized that these elements are not separable from human lives, nor from what microbes dominate the gut and what functions they perform. Here, the global gut study takes a different trajectory from the vaginal microbiome research. Whereas in the vaginal studies, racial/ethnic groups are the starting point of finding difference in microbes, in the global gut study, people were categorized by diet and lifestyle. More consequentially, socioenvironmental factors were determined to be the most important to microbial constitutions, not presumed race. Diet, birth, and nursing practices; how many people slept in a house; and what they ate contributed to the makeup of microbiomes.

The subjects of the global gut study were divided into three "geographical" groups: Malawian, Amerindian, and US. The Malawians were identified through their nationality, but from four distinct rural communities, the Amerindians were ethnically Guahibo Indians living in two villages in Venezuela, and the US subjects were from urban populations in the cities of Boulder, Philadelphia, and St. Louis. Yatsunenko found out that the "Malawian" and "Amerindian" microbiomes were good at breaking down starches, while the "US" microbiome specialized in the degradation of glutamine and other amino acids. This made sense from a digestion point of view, since these Malawians and Amerindians ate mostly corn and cassava, and subjects from the US ate a lot of animal protein. Other research has shown that rather than designating human microbiomes as "indigenous," "traditional," or "modernized," it would be more precise to divide into meat and plant eaters.[18] A global gut contains all of these chemical particularities and microbial gene representations, which were the result of where people lived and consequently what they ate.

While the microbes of babies in all three geographic areas underwent transformations through the first three years of life, the assemblages of bacterial species, as well as their functional genomics (what those bacteria did in the gut), were strikingly different in the US samples. Malawian and Amerindian baby microbiomes had more genes for utilizing the readily available sugars in breast milk, and more genes for making vitamin B2, possibly because US babies get more B2 from their mothers who eat more meat and dairy. Although it appears that conventional categories of global north and south contrast the "developed" American microbes against the "underdeveloped" African and Amerindian ones, reifying them through

studies of microbes, human microbial ecology can contribute to a more complicated view of humans. Yatsunenko told me,

> I think it's too early to identify populations by their microbiomes. I guess you can do that, but the boundaries between populations probably would fluctuate and remain fuzzy given the lability of the microbiome due to dietary changes, along with exposure to antibiotics and disease. I'm not sure how much geography contributes to the identity of the microbiome because we have globalization.

Here, the geography of the microbial begins to displace worldly continents. For Yatsunenko and her colleagues, the ways of life that contribute to the establishment and alteration of the microbiome supersede physical location or conventional ideas of population. "Continent of origin" genomic hap-mapping tells very little of the story of diversity compared to human microbiomes, which conclude there are more similarities by diet—and potentially food economies than by "race." Yet it is complicated; this research still deals heavily in the currency of racial–national identities by designating microbiomes as "US," "Malawian," and "Amerindian." And though the microbiome scientists I worked with view malnutrition as a complex, multifaceted problem with contributing economic, biological, genetic, and social factors, they still hope to treat it with probiotic intervention. *Fixing* a malnourished microbiota with food or bacterial supplements circumvents sociomaterial vulnerabilities, the very daily dilemmas of sewage, food, population density, and poverty that bring these microbiomes into being.

Microbiomes are amalgamations of practices of everyday life, the small details of human existence, with the evolutionary co-histories and genomes of humans and microbes. One of Dr. Gordon's favorite phrases to repeat around the lab was, "We are human DOINGS, not just human beings." The global gut study found that when people eat mostly plants, when they breastfeed for several years and live in small dwellings with lots of extended family members, their gut microbes adapt to those very specific circumstances. These are domains, small and big, in which the forms of individual and collective existence are at stake.

Biosocial Intersectionality

Physician and epidemiologist J. Dennis Fortenberry (2013) states that oppressive categories of race continue to manifest in medicine because of

demands for social "inclusion" in biomedical studies (Epstein 2007). As long as clinical research sees categories of race as preformed and rigid, and social/biological effects as separate and exclusive, the biomedical knowledge produced will incorporate these binary reifications.

In that vein, Helmreich asks, "Would it make sense to take a more sophisticated approach and ask how social categories like race and processes like racism—and its attendant stresses and deprivations (and, in some cases, privilege)—can reach into people's biologies and reshape their microbiomes?" (2016, 67). But he warns that to molecularize the environmental influences on race is as problematic as the molecularization of race itself. I suggest something different than reductive biologizing: interpret microbiomes as biosocial relationships in process rather than reinforcing the separation of biological and social influences. Warning against molecularizing the social implicitly affirms the distinction between a "social" and a "biological." Instead of insisting on a division between the biological body and its social environments, I follow Lock and Nguyen (2018) to examine the dynamic process of embodiment, "also informed by the body, itself contingent on evolutionary, environmental, social, economic, political and individual variables that have impinged on it over time and in space" (p. 3). Instead of asking scientists to do qualitative analyses of the "social" categories and processes at work in the microbiome (for which they are not trained), what if social scientists brought critical expertise to microbiomic partnerships, helping to expand the parameters of *what a microbiome is*?

Helmreich is concerned about complicated social practices being reduced to simplistic environmental influences, and worries the "microbiome" is an object taken for granted, separate from the technologies that produce it. Certainly, microbiome science has emerged as a direct result of next-generation shotgun sequencing, which has produced what we think of as microbiomes. Acknowledging that the technoscientific apparatuses, systems, and legacies of knowledge[19] make up "microbiomes" as much as the microbial organisms themselves, I suggest an ontological trajectory of feminist science studies that takes seriously the sociomaterial as one (multiple) object. New materialism and feminist STS are pushing social analysis to reevaluate relationships with science, nonhumans, and our own disciplinary commitments. These turns have faced criticisms; there is unease about the foreclosure of the political, the social, and the human. In a special issue of *Catalyst: Feminism, Theory, Technoscience* on "Feminism's Science" editors Subramaniam and Willey (2017) address these issues,

> We—feminist science studies scholars—must learn to think of ourselves not only as critics or students of science, but as makers of scientific knowledge. What sciences would we put on our proverbial boots to march for? (p. 12)

Since human microbiomes entangle microbial processes with intimate human social practices, tools for understanding human microbial ecology also entangle the life and social sciences. Slowly, the collaborative needs of human microbial ecology are resulting in real-world research projects. In 2019, a group including a microbial ecologist, a biological anthropologist, and an anthropologist-historian (who have been working on a cross-disciplinarily project called "Afrobiota") proposed that, "Microbiome research should integrate multiple scales, levels of variability, and other disciplinary approaches to tackle questions spanning conditions from the laboratory to the field" (Amato et al. 2019). Another team consisting of scholars across disciplines suggests, "We come to understand that social and political barriers to the resources required to maintain our microbiome also become an issue of social equity" (Ishaq et al. 2019, 6). An immunobiologist and public health scholar published a paper in *Nature Reviews Immunology* about how poverty affects diet, diet affects the microbiome, and the microbiome affects chronic disease (C. A. Harrison and Taren 2018). In 2020 an international working group I am a member of put out a paper attempting to set the agenda for social science research on the microbiome (Greenhough et al., 2020). This trend is an acknowledgment by biological and social scientists working together that microbes are essential to all multifarious forms of health, and thus biosocial causes and outcomes must be studied by biosocial teams.

Instead of enforcing the biological and social binary, this new thinking enacts Barad's ethico-onto-epistem-ology. In *Meeting the Universe Halfway*, Barad (2007) points to the inseparability of ethics, ontology, and epistemology when engaging in knowledge production, that knowing is a material practice of engagement, and that boundary production between disciplines is itself materially discursive (p. 90). I see this enacted as microbiomes coming into being through biosocial relationships across disciplines, across microbial and human bodies. Focusing on a mutable biology (inextricable from the social and technological) has been a significant inroad for social science (Landecker and Panofsky 2013; Meloni et al. 2018; Niewöhner 2011). Palsson argues that biological–social–human–microbe assemblages affect how social scientists conduct research, and thus, "a radical separation between social and biological anthropology seems theoretically indefensible" (Ingold and Palsson 2013, 39). For these

reasons, transdisciplinary collaboration is essential. The enormity and complexity of microbiome networks and all their interactions need biosocial intersectionality to intervene at different scales, into structures, lives, bodies, and microbiomes.

In his article, "Evidentiary Symbiosis: On Paraethnography in Human-microbe Relations," Nading (2016) asks: "How might one do a social study of the microbiome in places where it does not (yet) exist as a category of expert practice or public discourse? Strictly speaking, the microbiome, as a category of scientific and public interest, has been limited to the Global North" (p. 561). To attempt this kind of intercession, I worked in the Gordon Lab and at the lab's field research site in Bangladesh, adding ethnographic data that corresponded to the biological samples. My observations on ways of living, caring for children, and feeding families tried to help evolve the scientific view of study subjects. I tried to "un-North" the microbiome by having conversations with study subjects about their experiences, with careful attention to how responsibility and compliance are assigned to the most vulnerable actors, attempting to reroute scientific health interventions. It was unprecedented for the lab scientists I worked with to hear the voices of their subjects and to learn how they felt being part of the study and what was at stake for them. They had never confronted the qualitative face of malnutrition, nor seen photos of the mothers and children and what their homes and communities looked like. When I asked Gordon Lab members to ask themselves, why these communities, why these bodies? I was trying to un-ghost race by making racial and ethnic thinking explicit. My work in Dhaka consisted of collecting and contributing ethnographic data to analyses of the microbial genomes of Bangladeshi children suffering from severe acute malnutrition. During my time in Bangladesh, I interviewed field research assistants, senior scientific staff, and families across four community camps in Mirpur, Dhaka, conducting intensive interviews and participant observation. I spoke primarily with mothers, but I also interviewed other extended family and household members about being enrolled in the study, how they understood microbes, and what they cared about most. Fieldwork in Dhaka consisted of visiting each family every day, accompanying mothers as they cooked, cleaned, and traveled to market and to hospital nutrition centers. On the other end of my field network, I spent eight hours a day in the Gordon Lab for one year: attending lab meetings; observing diet experiments in progress; watching DNA and RNA extraction, sequencing runs, and data analysis. On a daily basis, I spoke informally with scientists about their work and the larger scientific and philosophical issues surrounding human microbial ecology and also conducted formal

interviews with the lab members individually and in groups. At times I was required to present my own work to the lab, explaining and accounting for what anthropology had to contribute both to the scientific work and to the world-at-large. Together with Dr. Gordon and my anthropological collaborator, I wrote and published a paper in *PNAS* about how to coevolve anthropology and human microbial ecology to create an "Anthropology of Microbes" (Benezra, DeStefano, and Gordon 2012). With the lab scientists, I tried to hold microbiome science accountable to the sociomaterial conditions of life, while working out tactics for integrating ethnographic information into the design and implementation of microbiome studies. This didn't always work. I was a PhD candidate doing fieldwork for the first time in the lab of a prominent scientist, and sometimes the disciplinary power imbalances were too great. It was frustrating, hard, and exhilarating with potential.[20]

For microbiome scientists, a biosocial partnership emphasizes that there are relationships between and beyond humans that need to be considered in designing and interpreting observational and interventional microbiome studies. And for social scientists, a focus on human–microbe relationships may push us to "reimagine health and well-being as more than human concerns" (Brown and Nading 2019), perhaps even reorienting an analysis of race that goes beyond fixed, stable categories of biology, culture, and human (Hartigan 2013, 2017).[21] Feminist scholars give us a good starting place: what Yates-Doerr (2019) calls *careful equivocation*, attuning ourselves to disparate bio/social binaries but working together to shape global health imperatives or E. F. S Roberts' (2015) "bioethnography": combining biological data with ethnographic details to produce new knowledge, where neither type of information is privileged or discrete.

Collaborations create an opportunity to use ethnography as a "crucial methodological tool for achieving better comprehension of health services at all levels of analysis" (Biehl and Petryna 2013, 4). A microbe-expanded view of humans will necessitate partnerships where social scientists are active participants in reformulating categorizations of people, while accounting for the biosocial effects of living within structural violence of racism. Race is meaningful as a category if the designation can be seen as an ethico-onto-epistem-ological one and not biologically a priori: race as the sum, not the addend. Poverty, resources, social inequities, and race are not peripheral to how the microbiome is understood, nor are they singularly explanatory. Race as a process and all its attendant biosocial outcomes are important to study along with microbiomes, especially as growing knowledge shows that diet, toxic exposures, housing, and health-care access affect

what microbial populations we have. It will take the careful cooperation of those in the social and biological sciences to navigate the labyrinthine biosociality of human–microbe relationships in order to make interventions that matter. There is no easy formula for collaboration, but that doesn't mean it isn't worthwhile to share our expertise, to chase the ghosts of biomedical race into the light.

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Notes

1. Morning (2007) shows ethnographically that despite that common belief that constructivism ruled, much of the scientific literature of the early 2000s was premised upon race, "grounded in and reflective of human biology" (p. 438).
2. Between the 1970s and 2000s, there seemed to be broad cross-disciplinary agreement about the social construction of race (see above). After the genomic revolution of the late 1990s made claims about the genetic diversity of humans, a clear debate around race and science ensued—not only between scientists but also among anthropologists, sociologists, and bioethicists.
3. The introduction to *Anthropology of Race* (2013) describes two different anthropological interpretations to how genetic science approaches race. One perspective (F. Harrison 1998; Mullings 2005; Koening, Lee, and Richardson 2008) presupposes the social constructionist view and forces a focus on *racism* rather than *race*, leaving the biological out entirely. The other perspective, seen

elsewhere (Whitmarsh and Jones 2010), sees new genomic science as a revival of historical race science. Neither view proposes that it is possible to eliminate race from scientific research.

4. PubMed shows 55,266 human microbiome papers published between 2009 and 2019. I use the findings of the National Institutes of Health-funded Human Microbiome Project as the baseline of accepted microbiome knowledge. While being mindful of reductive generalizations, there are a series of tenets in human microbial ecology which are undisputed in the field.
5. Following the work of Mukhopadhyay and Moses (unified biocultural approach, 1997) and Jackson (ethnogenetic layering, 2008), they strongly emphasize turning anthropological attention to sociocultural *and* biological data on race.
6. As M'charek (2005) discusses, the conclusions drawn about genetic (racial) difference and the technologies created and used to define those differences are epistemologically entangled.
7. What is meant by "origins" and "original peoples of" is not well defined.
8. https://grants.nih.gov/grants/funding/inclusion-basis-on-sex-gender-race-ethnicityfaq.htm#5549
9. The "American Gut" project, based out of the Knight Lab at the UCSD School of Medicine is a citizen science, crowd-sourced attempt to create a massive public microbiome data set. The first 2018 results show participants have been overwhelmingly (87 percent) white, 47 percent with a graduate or professional degree, and mostly in the above $100,000/year income range; speaking volumes about who represents the Western gut.
10. Rewilding also speaks to a nostalgic return to a mythologized "wild" nature.
11. Interventions to save the Western gut function differently than those focused on addressing the health crises of American indigenous populations or people in the majority world, as discussed below.
12. The publication of the American Association for the Advancement of Science.
13. The idea of "Yanomami microbiota" or "modern Western microbiota" that are definable and homogenous also deserves analysis.
14. The 2009 Human Microbiome Project (HMP) attempted to map a "normal" microbiome to draw correlations to health and disease. When it became clear no such normal microbiome was identifiable, the 2012 iHMP emerged. The iHMP reported results in 2019 showing how microbial disturbance in disease is linked to host processes (Lloréns-Rico and Raes 2019).
15. In a personal communication, a senior microbiome scientist told me that Ravel's connection between microbial communities and "ethnicity" was unsubstantiated—that when the study was replicated among undergraduate women across race and ethnicity, it showed the subjects had mostly the same

microbiota. This scientist concluded that class and age were more influential factors than race in determining microbial populations in the vagina.

16. In the Gordon Lab, "Westernization" meant new forms of food acquisition and availability that accompany economic development. Lab scientists described a "Westernized" diet as access to nonindigenous, processed food, or foods with a novel nutritional makeup.
17. All quotes taken from personal interviews, lab meeting presentations, or lab group discussions I attended.
18. Ruth Ley and collaborators studied the fecal microbiota of humans and other animals and found that host diet influences bacterial diversity (Ley et al. 2008).
19. Legacies of knowledge including anthropological ones.
20. My collaboration with the Gordon Lab is at the center of my imminent book from University of Minnesota Press, and I write about it extensively there (Benezra forthcoming).
21. Hartigan (2017) makes a captivating point in *Care of the Species* that, "race is not uniquely about people" (p. xv), concluding that how racial thinking is applied to nonhumans is crucial to understanding race.

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