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Geography and postgenomics: how space and place are the new DNA

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Abstract For many geographers, postgenomics is a relatively new perspective on biological causality. It is a non-dualistic way to conceptualize DNA, genes and environment. It also presents an opportunity for a broad critical engagement with biology through geography's insights into socionature and the fallacies of spatial inference. In postgenomics, mapping of the spatial and temporal contexts and circumstances surrounding DNA, rather than DNA sequence alone, has become prioritized. Consequently, scientific and economic value in postgenomics accrues through the enclosure and mapping of the 'omes'. These include the more familiar epigenome and microbiome, but also the interactome, the phenome, and the exposome among many others. The omes represent the cartographic translation of biological spatialities that modify the outcomes of DNA sequence from within as well as from outside of human bodies. In this article, we show how postgenomics leverages this omic ontologicalization of space and puts it to productive use. Drawing upon recent studies of the human microbiome, we illustrate how problematic geographies of difference arise through the way this omic mapping unfolds.

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Introduction

Genes and DNA sequence figure prominently when social scientists study biotechnology. However, molecular biologists today are not constrained to working with genes as isolated bits of DNA. Instead, they have expanded the biological boundaries of what is considered genetic. A Google image search for 'epigenome', 'proteome', or 'microbiome' yields visualizations of what could be called our other genomes. Like the Human Genome Project's (HGP) mapping of DNA, these omes are scientific endeavors to map biological phenomena relevant to understanding and improving human health.

In postgenomics, the mapping of the biological causality attributed to DNA has moved outward to the spaces around it (Richardson and Stevens 2015; Jacquez et al. 2015), The chemical environments of cells, the microbes that live in and around us, as well as psychological and physiological stress can generate biological signals and states that alter how DNA and its products function. In the post-HGP era, human DNA sequencing has become much faster, and the number of sequenced human genomes continues to expand. But accompanying these developments has been a massive investment in research to reveal how

the contexts of DNA shape our biology, from the different environments found within our individual cells to the microbial environments within and around us. Naturalists have long identified how environment shapes organisms. But where DNA was once given a central role in responding to these environmental influences, postgenomics recognizes the explicit complexity of interceding processes that shape the relationships among genotype, phenotype, and the external environment.

Scholars from a range of disciplines have articulated what constitutes postgenomic science and distilled some its implications (O'Malley et al. 2007; Rhodes et al. 2013; Meloni 2013, 2015; Rose and Rose 2012). Geographers too have recognized the relevance of postgenomics for their field (Saldanha 2006; Guthman and Mansfield 2012; Davies 2013; Mansfield and Guthman 2014). Yet geographic scholarship has focused more on the political ecology of epigenetics. There has been less emphasis on interrogating the omic spatialities of postgenomics as a whole. Rather than wide-angle assessment of the omes and their mapping, geographers have concentrated on epigenetic case studies involving specific diseases and modes of environmental exposure (Mansfield 2012a, b; but see Guthman and Mansfield 2012). Microbiota have been recognized by geographers for how they shape causality (Labban 2014; Lorimer 2016). Yet these studies similarly did not intend to examine how microbial agency is part of the larger postgenomic goal of spatializing DNA, a practice that invokes themes central to geographic thought about the relationship between humans and their relationships with environment.

Therefore, one of the aims of article is to situate the work of geographers within the broader context of postgenomics. To do so is a way to prompt geography to take a more non-dualistic view of genes and environment (e.g. Castree 2009; Eades 2012) so that we might move beyond quips about Ellen Churchill Semple and *Guns, Germs, and Steel*, the topics our conversations habitually converge upon whenever the role of genetic and environmental influences comes up. Given how molecular biologists are invoking the causal, productive capacities of space via the omes, geography should reevaluate where our lines in the sand have been drawn regarding what can be explained via genetic and environmental influences. In this way, the overview of postgenomics presented in this article is an invitation for geographers to reexamine a binary deconstructed in biology and other social science disciplines (Keller 2010; Darling et al. 2016) but lingering in our own. It is the binary that leans toward either genetic determinism (Nash 2012) or environmental determinism (Radcliffe et al. 2010; Correia 2013) whenever causality invokes biological processes.

Despite geography's relative silence for almost a century on the relevance of molecular biology and evolutionary theory as mode of explanation outside of the natural sciences, human geography's deep theorization about socionature and the productivity of space over the past few decades (Soja 1989; Harvey 1996; Massey 2005) should motivate geographers to become better informed about what postgenomics is and how the environment can exert its influence on us in more than constructivist ways (e.g. Guthman and Mansfield 2012). New materialist geographies, for example, have renewed longstanding questions about environmental causality (Shaw et al. 2010; Clark 2011). Perhaps more importantly, as with physics (O'Sullivan and Manson 2015), the increasing datafication of the world is bringing geography thought and cartography into biology as biology moves toward geography's focus on the spatiotemporal. Thus a second aim of this article is to initiate a generalist, geographical critique of how the omes, the spatial influences on DNA, are identified and represented. Through themes shared across geographic thought rather than those of a single geographic subdiscipline, our examination of postgenomics posits how omic mapping extends notions of how nature can be subsumed for economic purposes (e.g. Braun 2008, 2014; Labban 2014). As we show, nature becomes an accumulation strategy of expanded depth and pervasiveness in postgenomics (e.g. Smith 2009; Millar and Mitchell 2015). Postgenomics strives to subsume the spatial qualities of life that impinge upon our biology because isolated DNA sequences cannot account for many disease outcomes and health states. In a fundamental departure from the genomic era, and in a way different from preceding eras of scientific and economic exploration, postgenomics makes the spaces and histories of life productive. It is in this way that space and place has become the new DNA.

Our position is that although geography's theorization of space is rich and prolific, it has not yet bridged back to the new and evolving biological ideas about

the relationships among DNA, organisms and environment. In geography, space seems open to theorization in many interpretative contexts, but much less so when it involves the more mechanistic scientific content of molecular biology. DNA is not lacking for any recent critical scrutiny from geographers (Guthman and Mansfield 2012; Nash 2012). Yet even though scientific knowledge in molecular biology has expanded exponentially in the last decade, excepting the few papers on epigenetics from political ecologists, the new life science in geography has been focused more on the downstream economic implications of biotechnology (e.g. Birch and Tyfield 2013) and the big data geographies of DNA (e.g. Davies 2013; Davies et al. 2013; Leonelli 2014a) rather than upstream, where the spatial influences on DNA are first identified and cartographically translated into the omes.

We begin with a more detailed description as to how the postgenomic era differs from the biology that preceded it. Next, we illustrate how the omes invoke geography's concept of a spatial fix. We frame the way in which the spatial fixes of the omics are identified and put into productive circulation as a cartographic endeavor, subject to cartographic critiques. Lastly, we invoke the mapping and commodification of the human microbiome to illustrate the repercussions of these spatial facets of postgenomics. While offering benefits to human health and well-being, the mapping of human and microbial bodies is not entirely free of social and political issues. While there is an important role for the social production of scientific knowledge in postgenomics, the scope of our article does not allow us to characterize it in site-specific detail. In addition, we recognize that there remain different perspectives in the life sciences about the relative importance of genes and environment in their interaction (Pilpel and Rechavi 2015). Moreover, what defines the genome and how it is studied are related to philosophical positions on the value of reductionist versus holist perspectives (Morange 2002; Griffiths and Stotz 2006; Goldman and Landweber 2016). The term 'genomics' can be short hand for what biologists do in the postgenomic era, and genetics can refer to the period leading up to the Human Genome Project (Kell and Oliver 2004; Stotz et al. 2006). Genomics in this article is the practice of genetics leading up to the findings of the HGP. We consider postgenomics to be the period after, when DNA began to be more formally spatialized though the mapping of the omic influences around it. Finally, though we give examples of how postgenomics invokes cartographic generalizations and the fallacies of spatial reasoning, we remain supportive of its intellectual intent despite its sometimes overly ambitious goals.

Postgenomics in historical context

The ten years following the close of the Human Genome Project (HGP) in 2001 marks the transition from the genomic to the postgenomic era. Over this time, biologists began deconstructing the Central Dogma of DNA, the gene-centric paradigm that motivated the initiation of the HGP and fueled expectations about a revolution in disease treatment (Shapiro 2009; Richardson and Stevens 2015). The Central Dogma of DNA holds that there is a one-to-one unidirectional flow of information between a gene's DNA sequence and the outcome of its expression. If indeed one gene produced only one protein that controlled only a single trait among all individuals, then diseases with a genetic basis could be readily understood and potential treatments easily developed. However, postgenomics views the relationship between gene sequence and outcome as one to many. The flow of information is multidirectional. Via interactions with neighboring genes, with non-coding regions of DNA, with molecules that bind to DNA, and with many other contextual particulars, a single gene may be associated with a variety of biological outcomes.

Omes are the entities that comprise the spatial relationships between context and DNA. They diversify the potential outcomes of DNA sequence. For example, a protein coded by a single gene may actually take a range of structural configurations, functions, and effects on the human body depending upon conditions around it. To map the human 'proteome' as part of 'proteomics' is to map the entire complement of proteins inclusive of the modifications made to them as a consequence of their cellular, metabolic, or environmental contexts. The goal is to elaborate all the permutations of conditions that diversify the function of proteins originating from DNA. Similarly, because bacteria in the human microbiome can modulate gene expression, microbiomics seeks to inventory microbes in different

cultural and social contexts in order to isolate the full extent of their effects on human health. In postgenomics, DNA is no longer a set of biological instructions that will unfold deterministically irrespective of its context, the master blueprint. It is more of a script that can be performed in different ways depending upon the omic influences surrounding it.

Although this non-deterministic view of DNA was anticipated before the HGP (Waddington 1952; Levins and Lewontin 1985; Jablonka and Lamb 2005; Oyama 2000), postgenomics became formalized with recognition of the large overlap in the DNA sequence of genes in humans and chimpanzees (up to 99% depending upon what is measured). There simply was not enough information cataloged in DNA during the HGP to account for the variety of traits observable in humans. In recognition that factors exterior to DNA account for these differences, O'Malley et al. (2007) summarize the Human Genome Project by noting that "…[DNA] sequences were not the answer…but contributors to a parts list for a more integrative approach". Today, postgenomics recognizes that individuals with many shared genes can be biologically distinct in ways that are unpredictable from their DNA (Fraga et al. 2005). This malleability in DNA gene expression puts to rest binary debates over nature versus nurture or gene versus environment (Zwart 2007; Lock 2015). While space can certainly exert an influence in non-biological, constructivist ways, postgenomics foregrounds how environment diversifies the potential outcomes of DNA. What determines our individual biological uniqueness is neither environment nor DNA gene sequence alone, or their simple tit-for-tat interaction. Instead, the immense space and time contexts that surround DNA lead to a permutation of biological mechanisms that in turn diversity the outcomes DNA sequence.

As a consequence of these scientific insights, postgenomics seeks to generate value by identifying and enclosing omic influences on gene expression. Enclosure is one of capitalism's universal territorial techniques. It has a consistent logic of subsuming non-commodified, shared or common spaces (Sevilla-Buitrago 2015). Mapping of human DNA sequence was the act of enclosure in the genomic era. But in postgenomics enclosure has an outward gaze. Enclosure extends away from DNA rather than isolating itself in genes and their DNA sequence. Postgenomics thus reverses the genomic era's goal of making capital smaller. It aims to enclose and cartographically translate the permutations of biological and human environments into data. By mapping biological causality in the spaces around DNA and putting it to productive use, postgenomics subsumes another kind of commons, the combinations of space and time that shape living things.

Postgenomics as spatial fix

The spatial fix is one of the more broadly applied ideas from geography (Harvey 2001; Guthman 2015). It is invoked in general to relate how space and time are used to temporarily circumvent crises of capitalism. Postgenomics enacts a spatial fix in that space has been demonstrated to be essential for deciphering the biological causality underlying human disease. Mapping the omics has become a means to recover some of the HGP's under realized financial potential for revolutionizing medicine (Fig. 1). Despite knowledge of human DNA gene sequence pioneered by the HGP, the quest to find genes that strongly influence whether people will develop common diseases has turned out to be more difficult than expected (Kaiser 2012). Even with the capacity to map an entire DNA molecule, the markers for many diseases remain unpredictable. Studies have found genes that raise the risk of diseases such as cancer, diabetes, and heart disease. Yet even with their identification, they augment risk by a modest amount, only 20–40%, too low for predicting whether someone will develop an illness. Given it's explanatory power and potential to recoup financial investments, knowledge of the spatial and temporal contexts of DNA has become the fix for extending insights about human biology. This makes for a vastly larger biological territory exterior to DNA sequence for countries, institutions, and universities to claim and to integrate into their economies (Birch 2009; Waldby 2009).

The spatial fixes of postgenomics unfold in the way omic space is identified and partitioned to give form to the epigenome, the proteome, the microbiome, and other omic domains. One the one hand, these fixes invoke a reified notion of space. Omic knowledge is viewed as out there in the spaces of environments and bodies and awaits discovery and mapping by biologists. At the same time, these spatial fixes emerge out of situated, place-based scientific practices and

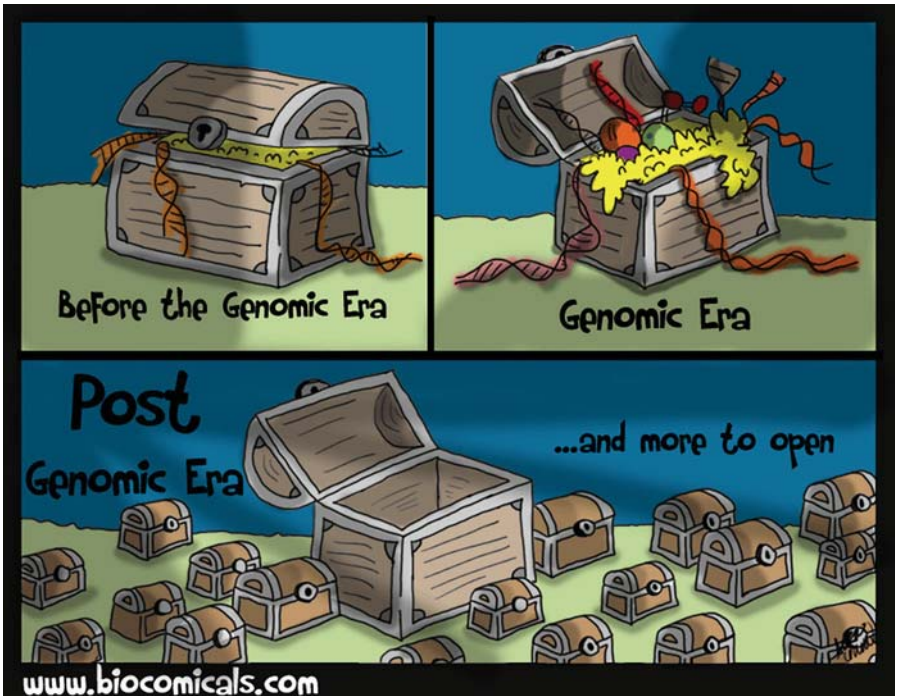

Fig. 1 Postgenomics as spatial fix Used with permission (www.biocomicals.com, Alper Uzun, Ph.D.)

economic motivations. Through these spatial strategies, postgenomics naturalizes and essentializes space when this space is also differentiated through the social. In this way, the omics reflect how the human is shaped today as much by calculus of social and economic reproduction as by the biological phenomena they study (Braun 2007). The spatial fixes of the omics are constrained by the molecules, organelles, membranes, tissues, and microbes that give dynamical texture to organisms. But they are also beholden to the scientific disciplines and individuals funded to study and commodify them.

In the traditional connotation of a spatial fix, the economic solution is temporary. The outsourcing of labor to a low wage country or the relocation of infrastructure to where resources are cheap and environmental laws lax is seen as a provisional solution. However, the spatial fix of postgenomics has a much more open-ended conception of where to relocate. Because the spaces that animate life processes are what postgenomics seeks, the postgenomic spatial fix can be seen as endless. It is a neoliberalist imagining of a boundless space for the creation and renewal of marketable scientific insights underwritten by its livingness (e.g. Thrift 2012; Labban 2014). Although there may always be decisions to relocate over issues of labor costs and the profitability of the downstream products and services of postgenomics, the resource utilized in postgenomics is the biological productivity of space. Biological properties have been recognized as integral to the neoliberalization of nature (Bridge 2008). However, under postgenomics it is the spatiotemporal character of biological processes that is neoliberalized. Commodification is no longer limited to the tangibility of a DNA sequence or a GMO. Instead, the spatiotemporality of the omics has become the source of commodification. In this way, postgenomic's recognition and utilization of the productivity of space inverts the cartographies of the HGP and the genomic era.

Mapping the omes

The omics attempt to chart and represent the position, distribution, and movement of biological objects and processes across volumes spanning the DNA molecule out to the sum of our environmental influences, some of which start before birth. The way these circumstances and contexts external to DNA sequence are

mapped and visualized as omics invokes a formalization of space and time as in GIScience (Pavlopoulos et al. 2015; Jacquez et al. 2015). Through the omics, postgenomics performs subjective ontologicalizations of molecular configurations, chemical pathways, and interaction networks. These are then given a highly distributable digital form. Postgenomics has developed elaborate metadata standards to allow different researchers to work with these data (Schuurman and Leszczynski 2008). Analogous to the history of raster and vector representations in GIS, postgenomic research often involves finding ways to integrate omic representations (Leonelli et al. 2011).

This mapping of omic space stands in sharp contrast to what was considered mapping in the genomic era. Then, space was an obstacle or barrier to be circumvented. It was to be decontextualized down to infinitely recomposable DNA base pair code. The tools for sequencing DNA and transferring genes from one organism to another were to allow production to circumvent the costly and unpredictable spatial externalities of running a traditional boots-on-the-ground factory (Cooper 2008). In this way, the genomic era's spatial fix was molecularization. Surplus value could be gained by taking production down to the scale of DNA, where it was assumed that DNA sequences could to be transferrable from one organism to another. Space in the genomic era was a container rather than explicitly involved in the production of life.

DNA sequence is still essential to the postgenomic project. However, space intercedes and redirects the assembly of life in concert with DNA rather than as a replacement for it in postgenomics. In this way, postgenomics extends mapping from DNA sequence outward, going so far as to envision, as some biologists have, of omic maps of all of an individual's health-impacting environmental exposures, or of all the microbial DNA found on humans. In this way, postgenomics should be considered a far more ambitious and distinctively geographic expansion of genomics. It is a territorialization of the volumes of life more analogous to Google Earth than the Human Genome Project in the scope of its mapping. What is key to recognize about the territorial ambitions of the omics is that in moving outward from DNA – all the way out in the case of the exposome, the cataloging of environmental exposures—there are vastly greater degrees of freedom in potential biological outcomes compared to those from DNA sequence alone. Then, these immense and contingent permutations of biological interaction become bound to the highly differentiated gazes of scientific disciplines and their particular goals, motivations, and scales of inquiry. Consequently, the number of omic mapping projects has proliferated. Where there was initially the Human Genome Project, there is now the Human Epigenome Project, the Human Proteome Project, and the Human Microbiome Project. Because of the enormity of what postgenomics maps, countries, governments, institutions, and private industry are dividing up omics by their types (e.g. phenomics, transcriptomics), by location (e.g. chromosome, protein), or in the case of the microbiome, by parts of the human body. These mappings in turn necessitate their reintegration and exploratory analysis via bioinformatics and computational biology. This makes it possible to translate how DNA sequence, proteins, cellular conditions, and environment integrate, not entirely unproblematically, to generate a mechanistic outcome useful for medicine (Leonelli 2014b; Levin 2014a).

As this suggests, through the enclosure of space by the omes life can be made to respond to other social, economic, and scientific motivations. Haraway (1997) was among the first to describe this repurposing of life through gene mapping. She conveyed that the genomic era's grail, DNA sequence, was just a map, a model, by nature incomplete, indicative of the world imagined by the mapper, and constitutive of the world we imagine. Yet Haraway's concerns, and others (Lippman 1992; Hall 2003) about the representations of molecular biology are exponentially more relevant for postgenomics. The mapping of human biology via the omics extends well beyond DNA sequence and into the spaces in us, around us, and even into our ancestry (Holmes et al. 2016). Consequently, as O'Malley et al. 2007) observed, "genome sequencing [was the] barest beginnings of socioethical concerns" regarding the way in which biological processes and social identities become represented.

A cartographic critique of the omics

Like all maps, omic maps reflect the spatial and temporal scales of intellectual inquiry of their life science cartographers and their imperatives to make their spatial knowledge useful. Yet there may be no

privileged level of omic causation now that DNA's centrality has been questioned. Microbiologists have microbiomics and molecular biologists who study proteins have proteomics. Each can make fair claims that their omic levels mediate the products of DNA. With the incorporation of space in postgenomics, an ome becomes a matter of the map maker selecting influences on human biology from a much larger number of possibilities. As a result what counts as postgenomic knowledge creation is not just the mapping that gives coherence to an individual new ome. It is also the way in which omes are invented and delineated.

This dividing up of omic space reflects the concept of individuation, the act of splitting up complex entities to simplify them into legally definable and economically tradable property rights (Castree 2003; Robertson 2011). Because this categorical stabilization of space via the omics creates another form of capital (Rajan 2006), there has been an ever growing number of omes since the end of the Human Genome Project, like the microgenderome, the ecosystome, the phenome, the secretome, the responsome, and the diseasome to name just a few (Lederberg and Mccray 2001; Eisen 2012). Some are recognized as useful ('goodomics'), others have been judged less so ('badomics') by scientists (Baker 2013). Like the postmodern generator that preceded it, there is now an online omics generator (http://www.ark-genomics.org/badomics-generator) coded by biologists to poke fun at the profundity of omes. At this web page, postgenomic terms are randomly combined to give title to yet another omic to map and commodify out of the immense spatial volumes of human biology and the intellectual fields that have divided them up. While tongue in cheek, the omics generator does capture an attitude voiced from within biology that the identification of omics has become an industry unto itself. Proposing a new ome has become a way of validating the importance, relevance, and financial promise of a research program. But this web page is more than humorous cynicism about the way in which scientists have to construct their niche and compete in the marketplace of ideas. It reflects how space has become neoliberalized in postgenomics. Through the omics, biologists open up vast planetary spaces and histories to mapping.

Once identified and enclosed, omic maps are like any other type of map in that they construct and shape our perceptions of the world instead of just merely reproducing it. Postgenomic mappings impose order, connectivity, and predictability. However, this is amid a highly context-dependent biological world. For postgenomics, this tidying up nature boils down to its goal of seamlessly integrating omic information, and creating a "…new cartography of epistemological coalitions" (Lewis 2012, p. 181) in the way that one omic begets another and integrates smoothly with it. For example, mapping the epigenome depends upon comprehension of information from the DNA sequence below it as well as the transcriptome and the proteome above it. Similarly, understanding how the human microbiome shapes health requires insight into how bacteria modulate not just DNA, but also the epigenome and the transcriptome. In a game of who has the more inclusive omic, larger and more inclusive omes and omics have been proposed, with each nesting around the others. At the largest extent, the human exposome intends to catalog the environmental exposures that shape health (Borrell 2011; Richardson et al. 2013). Other scholars have considered scaling up the microbiome to sequence all of life on earth (Gewin 2012). There is also the interactome, an inventorying of all the interactions in a cell, and the integrome, the integration of all omic knowledge. Lastly there is the omnisciome, the entirety of knowledge about a cell, organism or system (Baker 2013), or more whimsically, the ome–ome, the collection of all omes (Eisen 2012). There is even an 'unknome' for functions that are not yet claimed (Greenbaum et al. 2001). A rejection of them all encompasses the personome, the narrative and stories that comprise a person (Ziegelstein 2015).

As the unknome exemplifies, maps are by nature incomplete. But if postgenomics aims to map biological spatial causality in a useful manner, postgenomic mapping must be not only comprehensive but also ubiquitous because the processes and entities defining the omes are biologically transitory and less conserved than DNA sequence. Aspects of them may perpetually perish and form anew. Thus, it is unlikely that no one exposome could be finalized and applicable to a single person much less to everyone. Nor is it likely that the human microbiome could ever be pinned down to a static composition. As a result, idiographic, or local knowledge becomes necessary to generate value in postgenomics. Making omic maps and putting them to use as medical interventions has to be tied to specific

people embedded in particular places (Niewöhner 2011, 2015; Levin 2014b). One of the major challenges in postgenomics is defining how to map the contours of a given ome. Short of characterizing all of humanity's epigenome, microbiome or exposome, what groups of people should be used to define it? Under what environmental or cultural contexts should these people be sampled? The underacknowledged caveat about mapping the omes is that they in theory encompass all possible biological interactions, but in practice they are mapped and related to particular bodies, places, and times. It is in this way that the 'big biology' postgenomics has come to signify does not necessarily mean that the local and the contextual does not matter (Davies et al. 2013; Lezaun 2013; Rajan 2013).

As geographers have also long recognized, map boundaries can be imagined, contingent or arbitrary. The overriding boundary issue in postgenomics is whether the mapping of the omes has a limiting horizon, a map border, or whether it is limitless now that the causal role of space has been formally integrated into biology. In human proteomics, for example, the possible one-on-one interactions for 20,000 or so proteins generates 200 million possibilities to map (Baker 2013). The huge quantities of bacteria on humans and their near constant reproduction and plasticity also alludes to a limitlessness of their mapping, notably so given how quickly bacteria evolve and how microbiomes change in tandem with the varieties of human environments (Gillings and Stokes 2012). The varieties of individual human activity, behavior, and interactions with other life forms become part of the generation of novelty that is captured and commodified in postgenomics. Bodies everywhere can even be thought of as potential clinical sites or postgenomic mapping experiments (e.g. Goodchild 2007; Cooper 2012; Wyatt et al. 2013).

When one considers where the boundaries of the more encompassing omes like the interactome, the exposome or the integrome might be drawn, one begins to see again the speculative, expansionary neoliberal zeal of the mappings of postgenomics, another biotechnological "production of promise" (Pickersgill et al. 2013). Yet the construction of tangible, finite boundaries is ultimately required of omic mapping. Causal linkages must paradoxically be parsed out and made stable for capitalization. Despite the openness of postgenomic causality, the marketization of omes contradictorily depends upon a reductionist closure similar to what fueled the Human Genome Project (McAfee 2003; Wynne 2005). By proposing to identify and map the omes, postgenomics retains an obsession with limits and isolation of causation (Rajan and Leonelli 2013; Jacquez et al. 2015). In this sense, the cartographic strategy of postgenomics may be one of simplifying complexity and downplaying its heterogeneity and relationality in the interest of having a stable map (Fujimura 2005). More pragmatically though, postgenomics represents an attempt to engage with and enact this complexity (Levin 2014c). Even so, stabilizing the omics is intimately dependent upon comparisons of people and places. As we show in the next section, these comparisons invoke potentially problematic geographies of difference. The mapping of the human microbiome is one area of postgenomics where this is becoming increasingly apparent.

The promise and peril of mapping the human microbiome

Microbes are pointers to a biology full of yet-to-be explored possibility regarding how we understand the human body and eco-evolutionary processes (Hird 2010; Paxson and Helmreich 2013). One reason for this view is that we carry around a little over a kilogram of bacterial biomass in our bodies. The amount of information from bacterial DNA in our body is greater than that contained in our own DNA. However, accounting of this human 'metagenome' is more than a clinical observation. It is one intimately tied to the locations of our bodies. The human body is a host to a variety of bacteria because of the configurations of space, place and time in which these human-bacterial relationships unfold. The fundamental insight emerging out of the mapping of the human microbiome is that is has a geography.

Relatively recent and rapid cultural changes in human diet, hygiene, exposure to pathogens, and contact with animals have been identified as the major influences on the composition of the human microbiome (Velasquez-Manoff 2012). Which bacteria live within and on humans varies with our age, ethnicity, race, diet, and health status (Lozupone et al. 2012; Yatsunenko et al. 2012; Huttenhower et al. 2012). Our microbiome links our physiology with the history of our cultural and natural surroundings. We obtain

whole microbes as well as parts of their genome from family members, friends, nearby surfaces, and the local water supply. Consequently, an individual's microbiome can be unique. It can provide detailed information about the social, economic, and environmental contexts of their lives (Smillie et al. 2011; McDonald et al. 2013). It also changes according to where we travel (David et al. 2014).

In this way, accumulation in microbiomics is based on acquiring knowledge of geographical and historical differences in human microbiomes. Bodies-in-places have become fundamental to mapping the microbiome. The distinction between present-day developed versus undeveloped economies is the most pronounced geographic contrast shaping the mapping of the human microbiome (Parker et al. 2012; Rook et al. 2014; Ursell et al. 2013). Contrasts in the microbiomes between individuals in developed and developing countries have been associated with their dissimilar frequencies of obesity, diabetes, autoimmune disease, and some types of cancer.

These geographic comparisons play a role in their commodification of the microbiome. Fecal microbiota transplantation (FMT) and helminthic therapy are two recent medical treatments that derive their efficacy from the underlying geographies of the human microbiome. FMT is a remedy for a range of digestive autoimmune diseases, most of which are more prevalent in developed societies (De Vrieze 2013; Ettinger et al. 2013). In this procedure, feces are transplanted from a person whose diet and environmental exposures are associated with a healthy, diverse bacterial flora to a patient whose microbiome is disrupted. FMT has been shown to dramatically restore microbiomes damaged by heavy antibiotic use and colonization by *Clostridium difficile*, a pathogenic bacteria associated with modern hospitals. In helminthic therapy, parasitic nematodes like hookworm or whipworm are self-introduced in order to counter autoimmune diseases that occur almost exclusively with living conditions in developed countries. These include Crohn's disease, multiple sclerosis, asthma, eczema, dermatitis, and food and pollen allergies. The general explanation for the effectiveness of these parasite and bacterial therapies is that individuals in the developed world have impaired immune systems and dysfunctional microbiomes due to evolutionarily novel standards of hygiene, overreliance on antibiotics, and the industrialization of food and diet (Parker et al. 2012).

The point to recognize in these two examples of evolution-based medicine (Nesse et al. 2010), the characterization of our microbiota and how it matters for health relies not just upon a geography, but a geography of difference. Where people are, their place, becomes the basis for making inferences about the quality and value of their microbiota. In a deepening of uneven development, human microbiomes from poor, agrarian cultures may be judged as beneficial by those working to address public health concerns of developed countries. By seeking to restore our bodies to an ideal fixed in some place or other body, microbiomic therapies aim to ameliorate changes accelerated by capitalism in one location—historically unprecedented standards of hygiene, new types of environmental exposures, shifts in diet, alteration of our encounters with non-human microbe-shedding organisms—while simultaneously promoting another intensification of uneven development and the production of nature in another. Any commodification of the microbiome based on knowledge from rural agrarian cultures reflects a problematic dependency upon ecological and economic contrasts fostered upon particular places and bodies.

Such views of the microbiome may strengthen the illusionary nature of a quest for purity and a return to a bodily Eden. However, in this case Eden is not entirely metaphorical but an actual place where contrasts in the human microbiome and health can be referenced. Microbiomes affixed to other countries, places, and people—agrarian cultures, affluent health-obsessed foodies, or locations where people live closer to nature—can become fetishized, as already apparent in the marketization for probiotics (Slashinski et al. 2012) and soon, prebiotics. For the affluent, a healthier non-western microbiome could become a matter of buying these bacterial cultures or facsimiles of them to complement life style choreographies of food choice and environmental exposure to dirt, animals or other fashionable inoculants. The food scholar Michael Pollan (2013) has already gone on the record of registering his satisfaction with the non-Western character of his own gut microbiota. This kind of microbiomic fetishization sidesteps the issue of how the less than desirable environmental and economic contexts that produce microbiomic knowledge can be perpetuated or ignored. As a prominent example, even though parasitic hookworms are now a new and potentially lucrative source of drugs to treat

autoimmune diseases in developed countries, these parasites remain an under addressed scourge across many parts of the developing world.

A similar issue of relevance to geographers is how the human microbiota can be physically acquired. The recognition of the potential value of FMT and helminthic therapies points toward the possibility of the bioprospecting of individuals (Yatsunenko et al. 2012; Obregon-Tito 2013). Raced, classed, and other types of geographically and environmentally profiled human bodies may be sought for their potential to provide insights into disease treatments. The microbiomes of agrarians, from hunter-gatherer populations and from human remains in archaeological sites provide a reference point to hypothesize about how lifestyles in developed countries alter the microbiome and cause disease (Tito et al. 2012; Blaser et al. 2013; De Vrieze 2014; Clemente et al. 2015). Knowledge of the chemicals produced by these and other microbiomes could be used to design molecules for use as pharmaceuticals. However, the cultural groups, populations, and individuals that create the geographic contrasts that allow postgenomic knowledge and products to develop may not necessarily benefit from their development and application. At first glance, such practices may seem identical to the bioprospecting of human genomic diversity or of molecular compounds from rainforest plants (Parry 2004). However, postgenomic bioprospecting encompasses the agency of space and the interacting organisms within it rather than DNA sequence alone. It is the spatial and temporal contexts of biology that create novel microbiomes, not just a relatively stable and discrete DNA sequence.

The omics also construct ideas of what is normal and abnormal, as Mansfield and Guthman (2014) has shown with epigenetics. Although there are crowdsourced web-driven initiatives to map broad swaths of human microbiomes in developed countries (for example, the American Gut Project), the scientific literature reporting on the composition of the human microbiome often relies upon a small sampling of human donors relative to total human population numbers. Consequently, there is the potential for these initial snapshots to become a standard and lock in a conception of what defines a normal human microbiome. Donors may be selected to match categories of healthy versus non-healthy in ways that limit the full spectrum of human socio-spatial microbiological diversity. Optimistically, knowledge of our microbiome and other omic markers could provide opportunities for personalized medicine (Schloissnig et al. 2013). The composition and functionality of any individual's microbiome may track or predict disease states since it may be a better reflection of our immediate health than our DNA. However, personalized microbiomics raises questions about who controls and benefits from this information. Although the identification of a single person out of large sample of microbiome 'gut' prints is not yet perfected, preliminary research indicates it is feasible (Callaway 2015; Franzosa et al. 2015). Concerns have been raised about how our microbiome could be commodified without our permission (Hawkins and O'Doherty 2011; Wolf et al. 2013).

The mapping of the microbiome draws the external environment into bodies and then defines bodies according to these environments. This cartographic translation, and who does it, to whom, and for what ends is germane to issues of sociospatial justice. Postgenomics could, on the one hand, encourage a greater awareness on how microbial environments matter and how they might be altered to address health disparities related to malnutrition, physiological and psychological stress, and pollutant exposure (Calvert 2008; Landecker 2011; Relton and Smith 2012). On the other hand, postgenomic's emphasis on the contextual environmental plasticity of humans creates the potential for its misappropriation (Landecker and Panofsky 2013; Meloni 2015). For instance, epigenetic logic implies that social structure can be causally linked to biology. Once epigenetic, as well as microbiomic or other omic signatures are detected, they become biomarkers. They are indicators of the socio-environmental quality of our upbringing, of the potential for disease, and thus they may reinforce stereotypes related to race and class. As a form of 'epi-eugenics', the memory of the environmental exposures recorded in your microbiome or epigenome could be used to judge your social and economic background. Microbiomic and epigenetic markers would become another form of geographic profiling. A snapshot of your epigenetic markers and microbes might provide health insurers with information of your immediate as well as your past environments, and contribute more deeply to ecology-driven stereotyping (Williams et al. 2016). In this new form of environmental determinism, who you are is not just where you

are at present, but where you have been. Thus DNA sequence may not be the only issue for privacy given the information contained in the microbiome and the epigenome. Postgenomics may eventually become another form of surveillance, idealistic in intent, but prone to the fallacies of spatial inference.

The social and political implications of microbiomics and the other omics have drawn the attention of scholars in and outside of geography (Guthman and Mansfield 2012; Mansfield and Guthman 2014; Waggoner and Uller 2015; Meloni 2015). Political ecologists (Mansfield 2012a, b) have shown how epigenetics can be turned around by polluting industries. Rather than responsibility residing with the polluters, it could become our personal responsibility for avoiding spaces and circumstances where epigenetic and microbial exposures are less likely to promote health. Debates about race-based medicine also invoke epigenetic mechanisms and the potential for making fallacies of spatial inference (Gravlee 2009; McGuinness et al. 2012; Duster 2015). Social-environmental exposures have been shown to provide a more parsimonious explanation than genetics for the persistence of some health disparities between members of socially-imposed racial categories (Kuzawa and Sweet 2009). However, postgenomics can problematically construct homogenous gene-environment groupings that downplay the heterogeneity underlying the causes and treatment of complex diseases (Shim et al. 2014; Santos et al. 2015). The details of behavioral and social risk factors can be smoothed over when there is a need to integrate them into bodies and then 'harmonize' these data generalizations to meet research goals (Duster 2015; Ackerman et al. 2016).

Closing

This article has framed postgenomics as a multifaceted spatial fix and critiqued its suppositions about space and representation. We examined several outcomes and conundrums of these spatial inferences originating from biology, including those already articulated by geographers. Their work in political ecology shows how epigenetics, as one of the many omes of the omic revolution, can result in new problems related to social and environmental justice. But we have emphasized that it is geography's broader theorization of space, representation, and the production of nature that also undergirds a framework to examine postgenomic biology (e.g. Guthman and Mansfield 2012; Labban 2014; Hird 2017). From the perspective of geography, postgenomics is a form of ubiquitous mapping more like Google Earth than the Human Genome Project. Postgenomic maps are processural and relational (e.g. Kitchin and Dodge 2007). There is an inseparability between mapper and map that insures the need for constant map revisions. In seeking the production of life not just in DNA code but in the evolved and evolving spaces of the cell, in microbes, and in external landscapes, postgenomics utilizes mapping as a way to neoliberalize the production of postgenomic space. Bodies, because of their livingness and mobility will need to be constantly remapped and thus make new rounds of postgenomic knowledge accumulation possible. In this way, postgenomics might be considered a form of autoproduction, a culturally framed practice of how space reproduces us (Franklin 2014).

Geographers should not be reticent to speak up about what other disciplines can claim to do with space. For one, postgenomic's dependency on the productivity of space conveys how medicine may not be moving toward such an idealized end-of-disease kind of future. As Hinchliffe and Lavau (2013) point out, there are limits to how "… knowledge practices can be responsive to the mutable world". Moreover, humans are continuing to evolve, more so with the advent of culture (Hawks et al. 2007; Pennisi 2016; Beauchamp 2016) Expecting that the spatial fixes of evolutionary medicine and the environments of traditional people closer to the land will yield uncomplicated and permanent revelations to stabilize first-world health has been criticized as a kind of paleofantasy (Zuk 2013). If postgenomic knowledge is to end preventable disease, it would require constant surveillance, a near instantaneous mapping of human bodies and their space–time contexts. Because life has an emergent, unpredictable inventiveness (Braun 2008), the omics are best thought of as temporary security mechanisms. They are an imposition of limits needed to bring stability to random elements in order to improve, but never perfect, human health. The proliferation of omic spaces and their capitalization can be understood, in part, as a containment of this biological inventiveness. While we have not overtly discussed Foucaultian

biopolitics here out of an aim to avoid specialized subdisciplinary discourses, they have application to the way in which postgenomics attempts to extend control over life processes.

But still, in closing, is postgenomic science a good investment, for understanding human well-being? The Human Genome Project invested financially in DNA. DNA can also be considered a biological, non-monetary investment. Over billions of years, organisms have invested in DNA sequence to promote their persistence. But DNA provides a return on investment only when enacted in a spatial context, through contact with other organisms, and with chemicals and conditions in cell as well as outside of the body. The spatial fix of postgenomics, the shift of mapping outward from DNA and into the surrounding environments, may be worth the investment because it reflects more of the spatial dynamism of life (Stallins 2012). And life has been remarkably successful. But for the human macrobe, with its propensity for their institutions to become parasitic on the convolutions of space and time that animate ecology and evolution, the returns remain more complex and unpredictable. As Braun (2014, p 1) notes, we must "distinguish between nature's innovative force and the mechanisms that seek to capture this force". The neoliberalization of biological space and time that defines the omic projects should be comprehended as a response to the inventiveness of life, and not its origin. It is tempting to cast postgenomics as a final subsumption of nature, but it is only a small slice of space and time that science and its benefactors can grasp. Then, and without fail, the biological fills in around our extraction and ultimately diminishes any expectation of our having harnessed nature with any permanence.

In this review we have summarized postgenomics and outlined how it gives rise to a range of opportunities for geographic scholarship. It calls for geography to take a deeper and more explicitly spatial engagement with the biological than what began in the genomic era. The potentially more embarrassing intellectual response to postgenomics may be to ignore it.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

References

Ackerman, S. L., Darling, K. W., Lee, S. S.-J., Hiatt, R. A., & Shim, J. K. (2016). Accounting for complexity: Gene–environment interaction research and the moral economy of quantification. *Science, Technology and Human Values, 41*(2), 194–218.

Baker, M. (2013). Big biology: The 'omes' puzzle. *Nature, 494*(7438), 416–419.

Beauchamp, J. P. (2016). Genetic evidence for natural selection in humans in the contemporary United States. *Proceedings of the National Academy of Sciences, 113*(28), 7774–7779. doi:10.1073/pnas.1600398113.

Birch, K. (2009). The knowledge-space dynamic in the UK bioeconomy. *Area, 41*(3), 273–284.

Birch, K., & Tyfield, D. (2013). Theorizing the bioeconomy biovalue, biocapital, bioeconomics or…what? *Science, Technology and Human Values, 38*(3), 299–327.

Blaser, M. J., Dominguez-Bello, M. G., Contreras, M., Magris, M., Hidalgo, G., Estrada, I., et al. (2013). Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. *The ISME Journal: Multidisciplinary Journal of Microbial Ecology, 7*(1), 85–95.

Borrell, B. (2011). Epidemiology: Every bite you take. *Nature, 470*(7334), 320–322.

Braun, B. (2007). Biopolitics and the molecularization of life. *Cultural Geographies, 14*(1), 6–28.

Braun, B. (2008). Environmental issues: Inventive life. *Progress in Human Geography, 32*(5), 667–679.

Braun, B. (2014). New materialisms and neoliberal natures. *Antipode, 47*(1), 1–14.

Bridge, G. (2008). Environmental economic geography: A sympathetic critique. *Geoforum, 39*(1), 76–81.

Callaway, E. (2015). Microbiome privacy risk. *Nature, 521*(7551), 136.

Calvert, J. (2008). The commodification of emergence: Systems biology, synthetic biology and intellectual property. *Biosocieties, 3*(4), 383–398.

Castree, N. (2003). Commodifying what nature? *Progress in Human Geography, 27*(3), 273–297.

Castree, N. (2009). Who's afraid of Charles Darwin? *Geoforum, 40*(6), 941–944.

Clark, N. (2011). *Inhuman nature: Sociable life on a dynamic planet*. London: Sage Publications.

Clemente, J. C., Pehrsson, E. C., Blaser, M. J., Sandhu, K., Gao, Z., Wang, B., et al. (2015). The microbiome of uncontacted Amerindians. *Science Advances, 1*(3), e1500183.

Cooper, M. (2008). *Life as surplus: Biotechnology and capitalism in the neoliberal era*. Seattle: University of Washington Press.

Cooper, M. (2012). The pharmacology of distributed experiment—User-generated drug innovation. *Body & Society, 18*(3–4), 18–43.

Correia, D. (2013). F** k Jared diamond. *Capitalism Nature Socialism, 24*(4), 1–6.

Darling, K. W., Ackerman, S. L., Hiatt, R. H., Lee, S. S. J., & Shim, J. K. (2016). Enacting the molecular imperative: How gene–environment interaction research links bodies

and environments in the post-genomic age. *Social Science and Medicine, 155,* 51–60.
David, L. A., Materna, A. C., Friedman, J., Campos-Baptista, M. I., Blackburn, M. C., Perrotta, A., et al. (2014). Host lifestyle affects human microbiota on daily timescales. *Genome Biology, 15*(7), R89.
Davies, G. (2013). Arguably big biology: Sociology, spatiality and the knockout mouse project. *Biosocieties, 8*(4), 417–431.
Davies, G., Frow, E., & Leonelli, S. (2013). Bigger, faster, better? Rhetorics and practices of large-scale research in contemporary bioscience. *Biosocieties, 8*(4), 386–396.
de Vrieze, J. (2013). The promise of poop. *Science, 341*(6149), 954–957.
de Vrieze, J. (2014). Gut instinct. *Science, 343*(6168), 241–243.
Duster, T. (2015). A post-genomic surprise. The molecular reinscription of race in science, law and medicine. *The British Journal of Sociology, 66*(1), 1–27.
Eades, G. L. (2012). Determining environmental determinism. *Progress in Human Geography, 36*(3), 423–427.
Eisen, J. (2012). Badomics words and the power and peril of the ome-meme. *GigaScience, 1*(1), 6.
Ettinger, G., Burton, J. P., & Reid, G. (2013). If microbial ecosystem therapy can change your life, what's the problem? *BioEssays, 35*(6), 508–512.
Fraga, M. F., Ballestar, E., Paz, M. F., Ropero, S., Setien, F., Ballestar, M. L., et al. (2005). Epigenetic differences arise during the lifetime of monozygotic twins. *Proceedings of the National Academy of Sciences, 102*(30), 10604–10609.
Franklin, S. (2014). Analogic return: The reproductive life of conceptuality. *Theory, Culture & Society, 31*(2–3), 243–261.
Franzosa, E. A., Huang, K., Meadow, J. F., Gevers, D., Lemon, K. P., Bohannan, B. J., et al. (2015). Identifying personal microbiomes using metagenomic codes. *Proceedings of the National Academy of Sciences, 112*(22), 2930–2938.
Fujimura, J. H. (2005). Postgenomic futures: Translations across the machine-nature border in systems biology. *New Genetics and Society, 24*(2), 195–225.
Gewin, V. (2012). The sequencing machine. *Nature, 487*(7406), 156–158.
Gillings, M. R., & Stokes, H. W. (2012). Are humans increasing bacterial evolvability? *Trends in Ecology & Evolution, 27*(6), 346–352.
Goldman, A. D., & Landweber, L. F. (2016). What is a genome? *PLoS Genetics, 12*(7), e1006181.
Goodchild, M. (2007). Citizens as sensors: The world of volunteered geography. *GeoJournal, 69*(4), 211–221.
Gravlee, C. C. (2009). How race becomes biology: Embodiment of social inequality. *American Journal of Physical Anthropology, 139*(1), 47–57.
Greenbaum, D., Luscombe, N. M., Jansen, R., Qian, J., & Gerstein, M. (2001). Interrelating different types of genomic data, from proteome to secretome: 'oming in on function. *Genome Research, 11*(9), 1463–1468.
Griffiths, P. E., & Stotz, K. (2006). Genes in the postgenomic era. *Theoretical Medicine and Bioethics, 27*(6), 499–521.
Guthman, J. (2015). Binging and purging: Agrofood capitalism and the body as socioecological fix. *Environment and Planning A, 47*(12), 2522–2536.
Guthman, J., & Mansfield, B. (2012). The implications of environmental epigenetics: A new direction for geographic inquiry on health, space, and nature-society relations. *Progress in Human Geography, 37*(4), 486–504.
Hall, E. (2003). Reading maps of the genes: Interpreting the spatiality of genetic knowledge. *Health & Place, 9*(2), 151–161.
Haraway, D. J. (1997). *Modest witness at second millennium: Female man meets oncomouse: Feminism and technoscience*. London: Routledge.
Harvey, D. (1996). *Justice, nature, and the geography of difference*. Cambridge: Blackwell Publishers.
Harvey, D. (2001). Globalization and the spatial fix. *Geographische Revue*, *2*(3), 23–31.
Hawkins, A. K., & O'Doherty, K. C. (2011). Who owns your poop? Insights regarding the intersection of human microbiome research and the ELSI aspects of biobanking and related studies. *BMC Medical Genomics, 4*(1), 1.
Hawks, J., Wang, E. T., Cochran, G. M., Harpending, H. C., & Moyzis, R. K. (2007). Recent acceleration of human adaptive evolution. *Proceedings of the National Academy of Sciences of the United States of America, 104*(52), 20753–20758.
Hinchliffe, S., & Lavau, S. (2013). Differentiated circuits: The ecologies of knowing and securing life. *Environment and Planning D-Society & Space, 31*(2), 259–274.
Hird, M. J. (2010). Meeting with the microcosmos. *Environment and Planning D: Society and Space, 28*(1), 36–39.
Hird, M. (2017). Burial and resurrection in the Anthropocene: Infrastructures of waste. In P. Harvey, C. B. Jensen, & A. Morita (Eds.), *Infrastructures and social complexity a companion*. Oxford: Routledge.
Holmes, C., Carlson, S. M., McDonald, F., Jones, M., & Graham, J. (2016). Exploring the post-genomic world: Differing explanatory and manipulatory functions of post-genomic sciences. *New Genetics and Society, 35*(1), 49–68.
Huttenhower, C., Gevers, D., Knight, R., Abubucker, S., Badger, J. H., Chinwalla, A. T., et al. (2012). Structure, function and diversity of the healthy human microbiome. *Nature, 486*(7402), 207–214.
Jablonka, E., & Lamb, M. J. (2005). *Evolution in four dimensions: Genetic, epigenetic, behavioral, and symbolic variation in the history of life*. Cambridge, MA: MIT Press.
Jacquez, G. M., Sabel, C. E., & Shi, C. (2015). Genetic GIScience: Toward a place-based synthesis of the genome, exposome, and behavome. *Annals of the Association of American Geographers, 105*(3), 454–472.
Kaiser, J. (2012). Genetic influences on disease remain hidden. *Science, 338*(6110), 1016–1017.
Kell, D. B., & Oliver, S. G. (2004). Here is the evidence, now what is the hypothesis? The complementary roles of inductive and hypothesis-driven science in the post-genomic era. *BioEssays, 26*(1), 99–105.
Keller, E. F. (2010). *The mirage of a space between nature and nurture*. Durham: Duke University Press.
Kitchin, R., & Dodge, M. (2007). Rethinking maps. *Progress in Human Geography, 31*(3), 331–344.
Kuzawa, C. W., & Sweet, E. (2009). Epigenetics and the embodiment of race: Developmental origins of US racial disparities in cardiovascular health. *American Journal of Human Biology, 21*(1), 2–15.

Labban, M. (2014). Deterritorializing extraction: Bioaccumulation and the planetary mine. *Annals of the Association of American Geographers, 104*(3), 560–576.

Landecker, H. (2011). Food as exposure: Nutritional epigenetics and the new metabolism. *Biosocieties, 6*(2), 167–194.

Landecker, H., & Panofsky, A. (2013). From social structure to gene regulation, and back: A critical introduction to environmental epigenetics for sociology. *Annual Review of Sociology, 39,* 333–357.

Lederberg, J., & Mccray, A. (2001). Ome sweet omics—A genealogical treasury of words. *The Scientist, 17*(7), 8.

Leonelli, S. (2014a). What difference does quantity make? On the epistemology of Big Data in biology. *Big Data & Society, 1*(1), 2053951714534395.

Leonelli, S. (2014b). Data interpretation in the digital age. *Perspectives on Science, 22*(3), 397–417.

Leonelli, S., Diehl, A. D., Christie, K. R., Harris, M. A., & Lomax, J. (2011). How the gene ontology evolves. *BMC Bioinformatics, 12*(1), 325.

Levin, N. (2014a). What's being translated in translational research? Making and making sense of data between the laboratory and the clinic. *Technoscienza: Italian Journal of Science & Technology Studies, 5*(1), 91–114.

Levin, N. (2014b). Making up "persons" in personalized medicine with metabolomics. *Somatosphere*. http://somatosphere.net/2014/02/making-up-persons-in-personalized-medicine-with-metabolomics.html. Accessed 17 March 2015.

Levin, N. (2014c). Multivariate statistics and the enactment of metabolic complexity. *Social Studies of Science, 44*(4), 555–578.

Levins, R., & Lewontin, R. (1985). *The dialectical biologist*. Cambridge: Harvard University Press.

Lewis, J. N. (2012). Matchmaking mechanisms: Collaborative arrangements in proteomics and bioinformatics. In J. N. Parker, B. Penders, & N. Vermeulen (Eds.), *Collaboration in the new life sciences* (pp. 180–199). Farnham: Ashgate Publishing.

Lezaun, J. (2013). The escalating politics of 'Big Biology'. *Biosocieties, 8*(4), 480–485.

Lippman, A. (1992). Led (astray) by genetic maps: The cartography of the human genome and health care. *Social Science and Medicine, 35*(12), 1469–1476.

Lock, M. (2015). Comprehending the body in the era of the epigenome. *Current Anthropology, 56*(2), 151–177.

Lorimer, J. (2016). Gut buddies: Multispecies studies and the microbiome. *Environmental Humanities, 8*(1), 57–76.

Lozupone, C. A., Stombaugh, J. I., Gordon, J. I., Jansson, J. K., & Knight, R. (2012). Diversity, stability and resilience of the human gut microbiota. *Nature, 489*(7415), 220–230.

Mansfield, B. (2012a). Environmental health as biosecurity: "Seafood choices," risk, and the pregnant woman as threshold. *Annals of the Association of American Geographers, 102*(5), 969–976.

Mansfield, B. (2012b). Race and the new epigenetic biopolitics of environmental health. *BioSocieties, 7*(4), 352–372.

Mansfield, B., & Guthman, J. (2014). Epigenetic life: Biological plasticity, abnormality, and new configurations of race and reproduction. *Cultural Geographies, 22*(1), 3–20.

Massey, D. (2005). *For space*. London: Sage Publications.

McAfee, K. (2003). Neoliberalism on the molecular scale. Economic and genetic reductionism in biotechnology battles. *Geoforum, 34*(2), 203–219.

McDonald, D., Vazquez-Baeza, Y., Walters, W. A., Caporaso, J. G., & Knight, R. (2013). From molecules to dynamic biological communities. *Biology and Philosophy, 28*(2), 241–259.

McGuinness, D., McGlynn, L. M., Johnson, P. C., MacIntyre, A., Batty, D. G., Burns, H., et al. (2012). Socio-economic status is associated with epigenetic differences in the pSoBid cohort. *International Journal of Epidemiology, 41*(1), 151–160.

Meloni, M. (2013). Biology without biologism: Social theory in a postgenomic age. *Sociology, 48*(4), 731–746.

Meloni, M. (2015). Epigenetics for the social sciences: Justice, embodiment, and inheritance in the postgenomic age. *New Genetics and Society, 34*(2), 125–151.

Millar, S. W., & Mitchell, D. (2015). The tight dialectic: The anthropocene and the capitalist production of nature. *Antipode*. doi:10.1111/anti.12188.

Morange, M. (2002). The relations between genetics and epigenetics. *Annals of the New York Academy of Sciences, 981*(1), 50–60.

Nash, C. (2012). Genetics, race, and relatedness: Human mobility and human diversity in the genographic project. *Annals of the Association of American Geographers, 102*(3), 667–684.

Nesse, R. M., Bergstrom, C. T., Ellison, P. T., Flier, J. S., Gluckman, P., Govindaraju, D. R., et al. (2010). Making evolutionary biology a basic science for medicine. *Proceedings of the National Academy of Sciences of the United States of America, 1079*(Suppl 1), 1800–1807.

Niewöhner, J. (2011). Epigenetics: Embedded bodies and the molecularisation of biography and milieu. *Biosocieties, 6*(3), 279–298.

Niewöhner, J. (2015). Epigenetics: Localizing biology through co-laboration. *New Genetics and Society, 34*(2), 219–242.

O'Sullivan, D., & Manson, S. M. (2015). Do physicists have geography envy? And what can geographers learn from it? *Annals of the Association of American Geographers, 105*(4), 704–722.

Obregon-Tito, A. J. (2013). *Metagenomics and social inclusion in Peru*. Norman: University of Oklahoma.

O'Malley, M. A., Calvert, J., & Dupre, J. (2007). The study of socioethical issues in systems biology. *American Journal of Bioethics, 7*(4), 67–78.

Oyama, S. (2000). *Evolution's eye: A systems view of the biology-culture divide*. Durham: Duke University Press.

Parker, W., Perkins, S. E., Harker, M., & Muehlenbein, M. P. (2012). A prescription for clinical immunology: The pills are available and ready for testing. A review. *Current Medical Research and Opinion, 28*(7), 1193–1202.

Parry, B. (2004). *Trading the genome: Investigating the commodification of bio-information*. New York: Columbia University Press.

Pavlopoulos, G. A., Malliarakis, D., Papanikolaou, N., Theodosiou, T., Enright, A. J., & Iliopoulos, I. (2015). Visualizing genome and systems biology: Technologies, tools, implementation techniques and trends, past, present and future. *GigaScience, 4*(1), 1–27.

Paxson, H., & Helmreich, S. (2013). The perils and promises of microbial abundance: Novel natures and model ecosystems, from artisanal cheese to alien seas. *Social Studies of Science, 44*(2), 165–193.

Pennisi, E. (2016). Tracking how humans evolve in real time. *Science, 352*(6288), 876–877.

Pickersgill, M., Niewohner, J., Muller, R., Martin, P., & Cunningham-Burley, S. (2013). Mapping the new molecular landscape: Social dimensions of epigenetics. *New Genetics and Society, 32*(4), 429–447.

Pilpel, Y., & Rechavi, O. (2015). The Lamarckian chicken and the Darwinian egg. *Biology Direct, 10*(1), 1.

Pollan, M. (2013). Say hello to the 100 trillion bacteria that make up your microbiome. *The New York Times*, May 15.

Radcliffe, S. A., Watson, E. E., Simmons, I., Fernández-Armesto, F., & Sluyter, A. (2010). Environmentalist thinking and/in geography. *Progress in Human Geography, 34*(1), 98–116.

Rajan, S. K. (2006). *Biocapital: The constitution of postgenomic life*. Durham, NC: Duke University Press.

Rajan, K. S. (2013). Questions of critique for big biology: Conjuncture, agency and the global postcolonial. *Biosocieties, 8*(4), 486–490.

Rajan, K. S., & Leonelli, S. (2013). Introduction: biomedical trans-actions, postgenomics, and knowledge/value. *Public Culture, 25*(3), 463–475.

Relton, C. L., & Smith, G. D. (2012). Is epidemiology ready for epigenetics? *International Journal of Epidemiology, 41*(1), 5–9.

Rhodes, R., Gligorov, N., & Schwab, A. P. (2013). *The human microbiome: Ethical, legal and social concerns*. New York: Oxford University Press.

Richardson, S. S., & Stevens, H. (2015). *Postgenomics: Perspectives on biology after the genome*. Durham: Duke University Press.

Richardson, D. B., Volkow, N. D., Kwan, M. P., Kaplan, R. M., Goodchild, M. F., & Croyle, R. T. (2013). Spatial turn in health research. *Science, 339*(6126), 1390–1392.

Robertson, M. (2011). Measurement and alienation: Making a world of ecosystem services. *Transactions of the Institute of British Geographers, 37*(3), 386–401.

Rook, G. A. W., Raison, C. L., & Lowry, C. A. (2014). Microbial "old friends", immunoregulation and socioeconomic status. *Clinical and Experimental Immunology, 177*(1), 1–12.

Rose, H., & Rose, S. P. R. (2012). *Genes, cells, and brains: The promethean promises of the new biology*. London: Verso.

Saldanha, A. (2006). Reontologising race: The machinic geography of phenotype. *Environment and Planning D, 24*(1), 9–24.

Santos, R. V., da Silva, G. O., & Gibbon, S. (2015). Pharmacogenomics, human genetic diversity and the incorporation and rejection of color/race in Brazil. *Biosocieties., 10*(1), 48–69.

Schloissnig, S., Arumugam, M., Sunagawa, S., Mitreva, M., Tap, J., Zhu, A., et al. (2013). Genomic variation landscape of the human gut microbiome. *Nature, 493*(7430), 45–50.

Schuurman, N., & Leszczynski, A. (2008). Ontologies for Bioinformatics. *Bioinformatics and Biology Insights, 2,* 187–200.

Sevilla-Buitrago, A. (2015). Capitalist formations of enclosure: Space and the extinction of the commons. *Antipode*. doi:10.1111/anti.12143.

Shapiro, J. A. (2009). Revisiting the central dogma in the 21st century. *Annals of the New York Academy of Sciences, 1178*(1), 6–28.

Shaw, I. G. R., Robbins, P. F., & Jones, J. P., III. (2010). A bug's life and the spatial ontologies of mosquito management. *Annals of the Association of American Geographers, 100*(2), 373–392.

Shim, J. K., Darling, K. W., Lappe, M. D., Thomson, L. K., Lee, S. S.-J., Hiatt, R. A., et al. (2014). Homogeneity and heterogeneity as situational properties: Producing-and moving beyond?—Race in post-genomic science. *Social Studies of Science, 44*(4), 579–599.

Slashinski, M. J., McCurdy, S. A., Achenbaum, L. S., Whitney, S. N., & McGuire, A. L. (2012). "Snake-oil," "quack medicine," and "industrially cultured organisms:" Biovalue and the commercialization of human microbiome research. *BMC Medical Ethics, 13*(1), 28.

Smillie, C. S., Smith, M. B., Friedman, J., Cordero, O. X., David, L. A., & Alm, E. J. (2011). Ecology drives a global network of gene exchange connecting the human microbiome. *Nature, 480*(7376), 241–244.

Smith, N. (2009). Nature as accumulation strategy *Socialist Register, 43*. http://socialistregister.com/index.php/srv/article/view/5856#.UdJTB5y3a4Y.

Soja, E. W. (1989). *Postmodern geographies: The reassertion of space in critical social theory*. London: Verso.

Stallins, J. A. (2012). Scale, causality, and the new organism–environment interaction. *Geoforum, 43*(3), 427–441.

Stotz, K. C., Bostanci, A., & Griffiths, P. E. (2006). Tracking the shift to 'postgenomics'. *Public Health Genomics, 9*(3), 190–196.

Thrift, N. (2012). The insubstantial pageant: Producing an untoward land. *Cultural Geographies, 19*(2), 141–168.

Tito, R. Y., Knights, D., Metcalf, J., Obregon-Tito, A. J., Cleeland, L., Najar, F., et al. (2012). Insights from characterizing extinct human gut microbiomes. *PLoS ONE, 7*(12), e51146.

Ursell, L. K., Van Treuren, W., Metcalf, J. L., Pirrung, M., Gewirtz, A., & Knight, R. (2013). Replenishing our defensive microbes. *BioEssays, 35*(9), 810–817.

Velasquez-Manoff, M. (2012). *An epidemic of absence: A new way of understanding allergies and autoimmune diseases*. New York: Simon and Schuster.

Waddington, C. H. (1952). *The epigenetics of birds*. Cambridge England: University Press.

Waggoner, M. R., & Uller, T. (2015). Epigenetic determinism in science and society. *New Genetics and Society, 34*(2), 177–195.

Waldby, C. (2009). Biobanking in Singapore: Post-developmental state, experimental population. *New Genetics and Society, 28*(3), 253–265.

Williams, K. E., Sng, O., & Neuberg, S. L. (2016). Ecology-driven stereotypes override race stereotypes. *Proceedings of the National Academy of Sciences, 113*(2), 310–315.

Wolf, S. M., Annas, G. J., & Elias, S. (2013). Patient autonomy and incidental findings in clinical genomics. *Science, 340*(6136), 1049–1050.

Wyatt, S., Harris, A., Adams, S., & Kelly, S. E. (2013). Illness online: Self-reported data and questions of trust in medical and social research. *Theory Culture & Society, 30*(4), 131–150.

Wynne, B. (2005). Reflexing complexity: Post-genomic knowledge and reductionist returns in public science. *Theory Culture & Society, 22*(5), 67–94.

Yatsunenko, T., Rey, F. E., Manary, M. J., Trehan, I., Dominguez-Bello, M. G., Contreras, M., et al. (2012). Human gut microbiome viewed across age and geography. *Nature, 486*(7402), 222–227.

Ziegelstein, R. C. (2015). Personomics. *JAMA Internal Medicine, 175*(6), 888–889.

Zuk, M. (2013). *Paleofantasy: What evolution really tells us about sex, diet, and how we live*. New York: W.W. Norton & Company.

Zwart, N. H. (2007). Genomics and self-knowledge: Implications for societal research and debate. *New Genetics and Society, 26*(2), 181–202.