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What Can Sociogenomics Learn from *Social by Nature*?

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Abstract

Social by Nature, the recent book by Catherine Bliss on the development and state of the field of sociogenomics, is far from perfect. Yet this flawed book levies a mixture of erroneous and compelling questions about the state of the field of sociogenomics, many of which we as a field would benefit from considering: How should we bring the environment back in in the post-GWAS era? How do the publication and funding incentives of our field influence the evolution of our research agenda? What role should social scientific theory play in motivating our research and interpreting our findings? How can we promote greater diversity in our research community and subjects? And how can we work to better control media and popular narratives of our research? The authors do not attempt to answer all of these questions definitively, but do argue that we as a field must grapple with them seriously to ensure that our ideals and reality as a field are more congruent.

Keywords

Sociogenomics; Gene-environment interplay

Book-length critiques of an entire field, especially ones that are sometimes controversial, are likely to provoke dual reactions, as insiders who have contributed to the field's development are prone to circle the wagons against the perceived threat, and the field's existing critics cheer on the critical effort. Furthermore, this dynamic can easily unfold without many of the interested parties having read or deeply considered the critical work in question. And of course, there is a third group, probably far larger, that is unfamiliar with the brouhaha and wants to know what all the fuss is about.

In the my¹ experience, this is the dynamic that has unfolded around *Social by Nature* (hereafter *SBN*), the 2018 book by Catherine Bliss that critiques the field of sociogenomics and is the subject of this review. Whatever camp you, the reader, are in, we believe that there is value in carefully interrogating its claims. Bliss writes that *SBN* is intended to promote a constructive dialogue. Let us have one.

To those in the insider camp: Yes, there are numerous errors in the book which seriously undermine some of its points. If you would like to learn more about those, we refer you to Jeremy Freese's recent (2018) review which partially addresses the subject. To those in the critical camp: We are attempting to construct a bridge to discuss how the field of

¹All first person pronouns refer to the first author's opinions.

sociogenomics might improve in light of some of these critiques. To those who are previously unfamiliar with this debate: We hope that you will consider contributing to the conversation – particularly those with backgrounds that have been thus far underrepresented within the field.

The goal of this review is to identify critiques and themes that may serve as fodder for productive conversations about the objectives of the field, its means of attaining them, and the congruency between the two; the warnings of its past, and the lurking challenges of the future. Whatever you think of sociogenomics, *SBN*, or whether you were previously familiar with either, this book presents those interested in sociogenomics with a chance to reexamine what the field is today and how well that matches what we want it to be.

Sociogenomics: A Brief History

To understand *SBN* and its relevance for sociogenomics today, you need to understand the era in which *SBN*'s research was conducted and how sociogenomics has subsequently evolved. The history of sociogenomics is traceable by the data available to it. In the beginning, there was twin and (less commonly) adoption data, and the purpose was to decompose phenotypic variance into bins attributed to additive genetic, shared environmental, and nonshared environmental variance. This research generally found substantial additive genetic variance, trivial shared environmental variance, and considerable nonshared environmental variance (Turkheimer 2000).

Amid concerns about the limiting assumptions of these models (e.g., Daw et al. 2015), researchers were eager to examine relationships between phenotypes and molecular genetic data, which eventually led to the dawn of the candidate gene era, in which a small number of specific genetic markers were integrated into large social science datasets such as Add Health and the Wisconsin Longitudinal Study. One strong appeal of this approach was that genes and environments were fundamentally co-equal in the modeling strategy, since in a gene-environment interaction (GEI) the effect of one is potentially dependent on the other. However, this approach had its own limitations – for instance, the genetic measures used are far from comprehensive, and subject to potential publication bias in small samples (Duncan and Keller 2010), leading to replicability concerns.

As sociogenomics applied this approach to GEI research, biological researchers were developing techniques for cheaply collecting genome-wide data. However, the techniques initially developed to analyze these data (essentially consisting of 2.5 million chi-squared tests with Bonferroni adjustments) were not especially useful for typical social science research questions, where the interplay with the environment or role as a potential confound are often the most relevant feature of genomic data. Accordingly, sociogenomics researchers developed techniques for predicting individuals' disposition for an outcome in the form of polygenic scores. Developing and validating these techniques was the primary methodological focus of sociogenomics at the time of Bliss's fieldwork.

Since the time of Bliss's fieldwork, sociogenomic methodology has continued to evolve and has begun to come more in line with the field's original goal of researching GEI.

Researchers have begun to incorporate PGSs into GEI approaches to data analysis, essentially seeking to determine how PGS's effects are environmentally mediated. However, due to a persistent concern that PGSs may select on variants that are maximally invariant in their effects, new techniques are being developed to summarize genomic data that will be most strongly oriented toward discovering GEI relationships, such as variance-based Genome-Wide Association Study (vGWAS; Yang et al. 2012).

***SBN*: A Brief Summary**

SBN was a non-trivial undertaking. Bliss attended relevant conferences and meetings; interviewed sociogenomicists and others in person and by Skype; held discussions with public health agencies, biotechnology firms, schools, and juvenile justice centers; assessed the field's reception in the media; and scoured published academic articles, grant applications, and other research-related material. In addition to Bliss's arguments and interpretations, *SBN* represents sociogenomics in its own words (oral and previously published), in those of the media, and to a lesser extent those of other interested parties such as researchers in related fields and officials in funding agencies.

Based on this original research, Bliss's central theme in *SBN* is this: Sociogenomics is a new interdisciplinary endeavor that is fundamentally driven by a nature-first approach, and thus contributes to the potential for genetic essentialism and a new, softer eugenics that is going on under our noses. Bliss argues that sociogenomics has unwittingly inherited this nature-first orientation from precursor fields such as behavioral genetics, sociobiology, and evolutionary psychology. Bliss further argues that the field's methods, foci of attention in its published articles, and treatment of gender, race, and sexuality reflect its nature-first orientation. Bliss repeatedly emphasizes that sociogenomic researchers do not believe that they subscribe to a nature-first orientation, much less a hidden eugenic agenda, so from her perspective it is completely unsurprising if those in the sociogenomics insider camp scoff at these claims – but, she argues, the practice of the field has not matched its rhetoric.

Bliss largely lays the blame for this outcome at the feet of several culprits: Funding agencies which she argues skewed the incentives and directions of the field; Academic journal editors who she argues were overeager to publish the unproven fruits of this exciting new endeavor; Media outlets who aggressively highlighted nature-oriented findings with scant mention of the environmental components (and the authors who let them); and Sociogenomics researchers themselves who responded to this environment by rapidly adopting (while barely adapting) the statistical and computational tools of the genomic sciences while leaving their work on the environmental side relatively moribund, even while they continued to reiterate that genes and environments are co-equal, inseparable determinants of human life and behavior. Bliss is sympathetic to individual researchers' motivations, but is concerned about the way they are expressed in actual research, and how they are used and interpreted in the broader discourse.

Finally, Bliss argues that these developments will have disastrous consequences unless something changes quickly, as real-world applications and public discussions of this work are ongoing and likely to accelerate in the future, with none of the nuance or caution that the

field applies to its own work. Bliss is especially concerned here with the potential of gene editing technologies like CRISPR, which, doubling down on Duster's (1990) claims, she argues has resulted in "Eugenics [entering] through the front door, [pulling] up a chair, and [plopping] down right in the middle of all the new efforts for better, fitter bodies and minds" (Bliss 2018, 221).

The remainder of this review will seek to unpack and reflect upon each of these extremely troubling claims.

Are Genes More Equal than Environments?

Bliss argues the nature-first orientation of sociogenomics is present from the outset of a research project and permeates throughout, beginning with the phenotypes (outcomes) studied. Bliss argues that phenotype selection is heavily influenced by convenience, biologization, and unfounded evolutionary explanation. First, Bliss suggests that researchers often select phenotypes based on convenience from their prior social science work and availability rather than theory, taking their previous subjects of study, then "still study[ing] these matters, yet from a newly minted gene-environment perspective" (2018, 61). Second, she illustrates the biologization of complex phenotypes using an example from a press release by the Social Science Genetic Association Consortium (SSGAC) trumpeting new understanding of the "biological processes underlying learning, memory, reading disabilities and cognitive decline in the elderly." Bliss translates the press release, "Thus educational attainment was exemplarily rendered as a biological phenotype, no different from Alzheimer's or autism" (2018, 63). Third, Bliss presses the point that researchers rely on invalidated guesses about the evolutionary past of humans to justify phenotype selection, noting that, "Strikingly, social genomics researchers pride themselves on eliciting the deeper 'conserved' (throughout generations of species development) meaning of our innate nature even though they do not attempt to directly measure evolution" (2018, 64). Bliss asserts that recasting phenotypes in this manner emphasizes innate drives and contributes to the field's nature-first orientation (2018, 63).

Following phenotype selection, Bliss argues that the nature-first orientation adopted by sociogenomics filters into its research methods as well. Bliss argues that sociogenomicists inevitably adopt a nature-first orientation in their research in two key ways: (1) by focusing primarily on genetic methodological innovation over improving environment measurement; and (2) by giving far more attention to genetic considerations in articles without doing justice to the complexity of the environment and socially-constructed phenotypes. For example, rather than pushing cohort studies to collect new survey items and environmental data, researchers are more concerned with the collection of genetic data. This means that "researchers import extant survey measures as is, [and] they create new metrics that can quantitatively translate social measures into genetic ones," (Bliss 2018, 74). In Bliss's view, this is problematic since social phenomena such as educational attainment are not obviously biological in nature, yet are predicted as such.

Once it is time to present the research in the form of an article, Bliss argues that sociogenomics researchers further exhibit their nature-first orientation by belaboring the

nature side of the argument far more than the nurture side. In one example (Domingue et al. 2014), Bliss argues that the authors “do not explain the social-environmental factors that lead to assortative mating, factors such as racial stratification by neighborhoods and schools, which themselves are products of redlining and redistricting,” (2018, 89). While researchers may assume that social scientists reading their work will be familiar with these issues, *SBN* is concerned that social scientists may not be the only people reading sociogenomics research. To a wider audience, research that stratifies samples by race reinforces and “give[s] validity to unwarranted biological notions of race” (Bliss 2018, 92). Furthermore, even writing that race-specific findings cannot be generalized to all racial groups only “ends up reinforcing the notion that races are discrete and mutually opposing entities,” (2018, 91). In essence, *SBN* argues that sociogenomics is inadvertently advancing essentialist understandings of social phenomena without giving enough attention to the environmental side of the aisle – a state of affairs that Bliss labels “imbalanced interdisciplinarity” (2018, 216)

Some of these points are rooted in misunderstandings. In particular, the primary goal of sociogenomics was to bring genomic data and perspectives into the social sciences, so it makes a great deal of sense that this focus would be reflected in the field’s methodological innovations and writings. Yet I believe that *SBN* nonetheless circles around a valid point about the state of the field at the time of Bliss’s fieldwork: the vast majority of its advances were coming on the ‘G’ side of the GEI equation. Though now widely dismissed, in the candidate gene era before the time of Bliss’s fieldwork, ‘G’ and ‘E’ were probably co-equal in the focus and interpretation of this research, as much of this research directly concerned gene-environment interactions, where the effect of ‘G’ is statistically and substantively inseparable from ‘E’. At the time of Bliss’s fieldwork, sociogenomics was catching up with the GWAS era and beginning to leverage ever-expanding data consortia in the service of developing ever more predictive Polygenic Scores (PGS). As it did so, the environment in many cases receded into the background. The name of the game was more genomic data and more advanced statistical techniques for modeling it, and GEIs were rarely investigated.

There is good reason to argue, however, that this state of affairs was temporary: Bliss’s fieldwork took place at a moment in time when candidate gene studies were viewed with strong suspicion, yet the tools for appropriately operationalizing GWAS data in a co-equal GEI framework were not yet developed. Today, this appears to be shifting: in the wake of Boardman et al’s (2014) finding that Single Nucleotide Polymorphism (SNP)-by-environment models did not appear to be especially useful in standard-sized social science datasets, greater focus was applied to the development of PGSs, and in recent years these have been employed not only as an additive variable but as one interacted with environments (a PGS-by-environment model). This was an important development, but a limited one – since the most-heavily weighted SNPs in PGSs are likely to be the most environmentally-invariant, this modeling approach is most analogous to a heritability-by-environment model (c.f. Boardman and colleagues (2013)). In other words, PGS-by-environment models essentially assess the types of environments in which the underlying biology ‘shines through’ most strongly. This contrasts in its interpretation with allele-by-environment models from the candidate gene era, which were typically focused on environmental responsivity by genotype and associated patterns of predicted phenotypic convergence,

divergence, and crossover. Today, as discussed above, efforts are underway (e.g., Conley, 2018; Yang et al., 2012) to return the focus to environmental responsivity by constructing PGSs based on phenotypes' conditional variance rather than their conditional means (a variance-based GWAS, or vGWAS). In short, at least some portions of the field are working to bring E back in – and Bliss's probably accurate portrayal of the relative absence of these efforts just a few years ago should encourage researchers to continue this work.

Distortionary Dollars?

Having asserted that a nature-first orientation underlies the full sociogenomics research process, *SBN* argues that one key reason for this state of affairs is the distortionary effects of research funding. In Bliss's telling, both national and private funding agencies are seduced by interdisciplinary research and methodological innovation, and sociogenomics checks both boxes. Funders told Bliss that they view fields like sociogenomics as a bridge across a scientific chasm: “the crisis in scientific understanding, the very crisis that requires bridge builders like social genomics folks, comes from the rift in the natural and social sciences” (Bliss 2018, 152). Funders believed that sociogenomics could bring about “a holistic way to do richer inquiries,” (Bliss 2018, 153) because of their ability to do justice to both the social and biological sides of the aisle. Funders and study leaders were also excited about sociogeneticists' “greater attention to statistics” (Bliss 2018, 154) and thoroughly “believe[d] that the social science bent of the field [was] more likely to produce ethically responsible science” (Bliss 2018, 155). Funders' enthusiasm for interdisciplinary research has led them to “ignore the specific ways in which the environment factors into research so thinly” (Bliss 2018, 216) – the mere fact that social scientists are incorporating genetics into their research is often enough. Funding agencies' largesse has enabled the field to grow rapidly, but primarily through genomically-oriented innovations.

An abundance of funding for rigorous social science research is not a problem on its own – far from it! The question is whether funding has had a skewing effect on the research that sociogenomicists conduct and the findings that they disseminate. This can occur in one of two ways: it could skew the projects that are conducted compared to the full portfolio that researchers would like to conduct, or it could skew the answers that are delivered by these projects. Of course, neither of these threats are unique to sociogenomics. The first potential problem is more benign, though still potentially problematic: By effectively outsourcing decisions about what research can take place to outside decisionmakers, the field may come to inadvertently define the core questions of the field differently than it would on the basis of scientific evidence, theory, and debate alone. This potential source of skew would limit the range of questions that are investigated, but not the quality of their answers. Far more concerning would be if certain types of answers were privileged over others as a result of the skewed incentives provided by the deep well of funding available to the field. I speak here not only of scientific malfeasance or p-hacking, which would obviously be deeply disconcerting (but relatively well-guarded against in sociogenomics compared to other social science fields), but also of the interpretation of the field's evidence. Few statistical conclusions, no matter how well-founded, speak entirely for themselves – an act of interpretation and the derivation of subsequent questions for investigation are critical to the creation of a self-sustaining scientific enterprise.

Of course, due to the expense required to collect and genotype molecular samples and the specialized training that is required that is not typically available in established academic training programs, sociogenomics could not exist in anything resembling its current form without the support of outside funders. However, this reliance on funding to collect data and train scholars opens the field, to an unusual degree for a social science, to being shaped by the priorities of these funders rather than the researchers themselves. Research funding in this sense has the potential to become a double-edged sword. No easy solutions are possible here, but the contrast between the field's stated goals as well-summarized by *SBN* (full and co-equal synthesis of genetic and environmental models of behavior, oriented toward equitably unlocking human potential) and the research largely produced by the field is stark. As a field, we should pay close heed to the negative space in the set of potential explanations for human behavior that we address, and ask ourselves why we take some more seriously than others.

Undertheorized and Underrepresented Social Differences

SBN is not complimentary of the field's approach to the study of social differences by race/ethnicity, gender, and sexuality, nor of its inclusiveness in the researcher pool. Bliss explains that populations that differ by key axes of structural inequality are often essentialized and undertheorized in sociogenomic research and the broader media narrative around it. Bliss buttresses (and qualifies) this claim through a review of how sociogenomics deals with race, gender, and sexuality. In her telling, researchers regard race as a nuisance parameter best dealt with through population stratification adjustments or restrictions to respondents of European descent; render gender metonymous with sex; and relatively rarely study sexuality but often address it with more complete accounts when it is.

On the subject of race, Bliss argues that sociogenomicists have failed both to adequately define and measure race in their research and push back against the media's frequently essentialized depictions of race. Bliss summarizes her qualitative data on this matter as follows: "While my conversations with social genomics researchers and analysis of social genomics publications generated hundreds of statements on race (over three hundred, to be more precise), only a handful include definitions or conceptualizations that challenge the media's status quo" (2018, 86). Rather, Bliss argues that statements about race are typically very rote, used with little explanation and hardly any reference to the systems of inequality that define it (2018, 89). At other times, research is whitewashed entirely: "A common strategy that study teams have adopted is to simply work with people of European descent" (2018, 90). Therefore, researchers more typically treat race as a nuisance parameter or natural category rather than a socially-constructed, fundamental axis of structural inequality, as she would have us do.

Turning to gender, Bliss's core claim is that it is nearly always treated as equivalent to biological sex, and thus severely undertheorized in her view. In sociogenomics' typical account of gender differences, "There is no acknowledgement of social circumstances informed by experiences of stratification or categorization" (Bliss 2018, 97), nor any "acknowledgement of social outcomes informing gender roles, and gender roles informing biology" (Bliss 2018, 98). Rather, researchers treat gender as an axis of analytical (rather

than social) stratification, or a nuisance parameter influencing the analysis of X-linked traits. To the degree that researchers consider gender inequality, it is in the interest of protecting the nascent field from accusations of sexism, as illustrated by one researcher who said “that publishing work that could have sexist repercussions only ‘tends to harm the science’” (Bliss 2018, 102).

Finally, Bliss argues that sociogenomicists offer a mixture of research using lax definitions of sexuality and underdeveloped theory with some work that addresses the topic in a deeper manner by covering issues such as sexual plasticity and the potential benefits of sociogenomics research for public discourse around sexual orientation (2018,108-12). This stands in sharp relief to her views on the field’s treatment of race and gender, which in Bliss’s view shows “that the political context of how a trait has been debated in the larger culture makes for its presentation as more or less overtly deterministic” (2018, 112). However, she argues that the broader rhetoric of essentialism inadvertently buttressed by sociogenomics research will likely erode the sometimes more appropriately complex treatments of sexuality, as well.

Of course, there are serious methodological impediments to conducting GWAS work in samples marked with population stratification and differential linkage disequilibrium, and available GWAS data to date has been primarily concentrated in European and Asian populations. Researchers are actively working to address this – for instance, *The Genome Factor* (Conley and Fletcher 2017, hereafter referred to as *TGF*) contains an entire section documenting and lamenting these difficulties, and they are not alone in their efforts to overcome this barrier. Studying race and ancestry from a biodemographic framework also raises theoretical issues that complicate the nature/nurture divide to which we are accustomed – for instance, as *TGF* points out, when genetic variation is expressed in visible traits to which differential social value is attached, these genetic variations may well be linked to differential outcomes through socially-mediated pathways. Thus, *TGF* argues, even if data were available to construct ancestry-group-specific PGSs or even if we could conduct sibling comparisons of genetic principal components linked to ancestry, these would not be straightforwardly interpretable in a nature/nurture framework. Taking better care to confront and discuss such statistical, inferential, and theoretical limitations as Conley and Fletcher do is an important step in the right direction which may help address some of Bliss’s concerns. Similarly, ongoing work seeks to bridge or interrogate the divide between genetically-based approaches to bio-ancestry and socially-constructed race (e.g., Guo et al. 2014; Frank 2014; Shiao et al. 2012; Nelson 2016). Continuing this debate while integrating the insights of sociogenomics and enormous, increasingly diverse DNA databases should produce valuable insights.

However, these cautionary steps will not address Bliss’s critiques concerning the undertheorization of racial/ethnic inequality, nor do we lack the ability to address gender beyond sex-stratified analysis – as indeed, more recent research demonstrates (e.g., Short, Yang, and Jenkins 2013, Perry 2016). While many of Bliss’s critiques would hold almost as much water if Bliss had reviewed the field of demography as it does for sociogenomics, a full synthesis of genetics and the social sciences should do better justice to the systems of inequality that produce racial/ethnic, gender, and sexuality inequalities, and seek to

understand how more fully theorized matrices of social inequality structure the environments, health, and potentially genetic expression of a wider range of humanity.

Relatedly, Bliss highlights that the limited diversity of our research subjects is mirrored in the limited diversity of sociogenomics researchers, as “Less than a quarter of the field comprises women” (2018, 54) and “Almost 90 percent of the field self-identifies as white” with “The remaining 10 percent self-identify[ing] as Asian” (2018, 55), with only one respondent self-identifying as black (who had considered leaving the field). Lest you think that this is a selective product of her ethnographic investigation, section-specific demographic data from the American Sociological Association² does largely conform to this claim: the section on Evolution, Biology, and Society (EBS; N=125) included 30.3% individuals who identify as something other than cisgendered male and 0 members who identified as something other than White or Asian.³ Figure 1 compares this composition to other ASA sections, depicting the percentage of each section’s membership that identifies as something other than White or Asian against the percentage that identifies as something other than cisgendered male. These data show that EBS is part of a cluster of four sections (including Mathematical Sociology, Rationality & Society, and Methodology) that rates especially low on both racial/ethnic and gender diversity. However, it should be noted that a substantial percentage of this gap can be explained by the member type composition of the EBS section – graduate students (who are less likely to be white and cisgendered males) are only 20% of EBS membership (the second-lowest figure of all sections), and retired members (who are more likely to be white and cisgendered males) are 13.6% (the second-highest figure). On the whole, however, while sociogenomics does not align perfectly with EBS section membership by any means, these data do largely lend credence to her claims. Our field would do well to redouble our student recruitment efforts, especially among underrepresented groups.

Though *SBN* does not explicitly link the field’s composition to the field’s undertheorizing of important social differences, researchers cannot ignore that a researcher’s identity is often associated with the types of questions that they study, the strategies they use to study them, the process of interpretation that they apply, and the pathways of researcher recruitment they open into the field. Perhaps a field comprised of more women and racial and sexual minorities would defend better against undertheorizing gender, sexuality, and racial/ethnic inequality. However, I argue that in order to attract a more diverse set of researchers to the field, those of us already in the field should redouble our efforts to make the field something that a more diverse group of researchers would like to take part in – in part, by broadening the range of lived experience that our research can address. But regardless of the success of these efforts, our scientific practice would better match our rhetoric.

²<http://www.asanet.org/research-and-publications/research-sociology/trends-sociology/asa-membership>. Accessed 9/21/18.

³We did not have access to individual-level data – only tabular data separately summarizing the gender and racial/ethnic diversity of each section. The response categories for gender included: female, male, genderqueer/gender non-conforming, transgender, other, and missing. EBS members included 85 males, 37 females, and 3 individuals with missing gender data. Response categories for race/ethnic included African American, Asian/Asian American, Hispanic/Latino(a), Native American, White, Other, Multiple Selected, and missing. We excluded those with missing (N=13 in EBS) or multiple categories (N=5 in EBS) from these calculations.

The Media Megaphone

Another key claim of *SBN* is that sociogenomicists are collectively failing to critically engage with the media and general public in a manner that promotes thoughtful, complete interpretations of the field's findings. Bliss is careful to distinguish media representations from those of sociogenomic researchers themselves, which are often different: she depicts a media with a significantly more nature-first portrayal of these factors than most researchers advocate, which researchers fail to effectively counter. In Bliss's account, researchers' relative emphasis on the genetic aspects of their analysis and attendant inattention to the environment leaves non-specialist readers with a nature-first interpretation of the findings. Bliss provides one example of this media distortion in a *Good Morning America* special in 2012. The program reports on a Rockefeller University study linking maternal instincts to genes. But in the reporting of this study, genes were discussed as if they were "innately gendered," and the program bore the title, "Is There a Gene for Motherhood?" (2012). Bliss argues that this program left viewers "with the takeaway that intensive parenting is something bred in women, not men" (2018, 94). In another example, Bliss draws on an article from *The Economist* (2010) that summarizes the underlying research as follows: "Businesswomen, it seems, are born. But businessmen are made." Bliss argues that this sort of pat summary "feeds folk beliefs that men and women are interminably distinct down to their cellular core," (2018, 93-94).

Thus, in *SBN*'s telling, sociogenomicists have done a poor job of shepherding their research from the ivory tower to the public, leading to a reproduction of past cycles of scientifically-buttressed essentialist dialogue. Obviously we should, as a field, be deeply concerned about this claim - and indeed we are, as Bliss acknowledges: "It's not that individual scientists - the geno- poli-, socio-, and econ folks who are leading the way - buy into genetic determinism. Far from it, they want nothing more than to complicate oversimplistic notions of genetic supremacy. They want to show the sciences and the world that the environment matters to our biology, health, and life outcomes" (Bliss 2018, 216). Thus the claim that sociogenomics researchers are "CRISPR's Willing Executioners" (Comfort 2018) does not pass the sniff test at the conscious level, even in *SBN*'s telling. In the end, it is our responsibility as a field to determine how to avoid the mistakes of the past, and indeed what they were. To date, the field has primarily done so by acknowledging and disavowing the scientific errors and maliciousness of prior fields with similar aims. But is disavowal enough? How would sociogenomicists know?

Again, I do not come armed with a ready answer. But it strikes me that this is a general problem of social science - sociogenomics is far from alone in its need to confront these sorts of issues. For instance, in 1904 the *American Journal of Sociology*, then the flagship journal of the American Sociological Association, published an entire symposium on eugenics featuring extensive commentary by Francis Galton and others sympathetic to his cause (Galton 1904). Stephen Jay Gould's *The Mismeasure of Man* (1996) documents other examples in anthropology and psychology - for instance, Cyril Burt and others' use of anthropological skull measurements to justify racial hierarchies, and how Alfred Binet's IQ scale was deployed to label racialized immigrants as 'feeble-minded' individuals. In short, many social science fields were founded or brought into their modern form in the late 19th

and early 20th centuries, and many of their sometimes overtly racist founders encouraged terrible practices. Despite this legacy, presumably most readers of this article agree that social science is a worthy undertaking that ought not be wholly shuttered. What then is a field to do? When should the sins of the past be visited upon the present, and what can those of us now doing the work do about them?

Beyond explicit disavowal, which we should surely do as often as needed, another path is illustrated by *TGF*—identify damaging, lightly supported claims inherited from that past and directly test them. After all, sociogenomicists have the data to test many of the claims made by the worst actors of the past and present. Frequently we as a field seem to assume that even asking these questions is damaging, and perhaps in some cases it is. But when damaging ideas have taken hold in our area of expertise, a major part of our job should be not only to disavow them, but to refute them where scientifically appropriate. Conley and Fletcher make an excellent example of this path in their data-driven dismantling of the arguments of *The Bell Curve* (Hernnstein and Murray 1994). We as a field would do well to follow suit, often.

An additional, critical step that has recently been extensively undertaken by groups like the SSGAC is to provide a detailed, accessible FAQ with every landmark study, so that journalists and members of the public can readily understand what a given set of results do and do not mean.⁴ This practice, if more widely adopted, could well help address a dynamic that *SBN* decries wherein researchers fill their research papers with subtlety and myriad qualifications, only for journalists to reduce them to “Gene for X Discovered” headlines for the consumption of the general public. In addition to widely imitating these laudable efforts, sociogenomics would likely greatly benefit from more widespread media training, to help further ensure that these misleading dynamics between academia and the general public are ameliorated, if not eliminated.

Conclusion: Good Questions in Need of Better Answers

In the face of the provocative claims of *SBN*, sociogenomicists’ primary responses have been to either ignore it or circle the wagons. This is an entirely understandable reaction. Bliss is an outsider to the field that many sociogenomicists nonetheless agreed to talk to for the book, so her more aggressive claims can be experienced as a kind of betrayal. For those who, like the authors of this review, were not interviewed for this book, academics still tend to identify with their research pretty closely, so being told that sociogenomicists have unwittingly contributed to the very agenda that sociogenomics is avowedly aligned against will nonetheless feel very personal. And it is easy to convert these feelings of defensiveness into a damning critique: Because she is an outsider, any errors in the book, and there are plenty to choose from, can readily be used as the basis to counterclaim that Bliss is misguided or biased in her critiques.

However, I argue that it is important for sociogenomics insiders to resist this temptation in this case. Personally, I disagree with or would heavily qualify many of Bliss’s conclusions,

⁴<https://www.thessgac.org/faqs>. Accessed 9/21/18.

as noted in a few instances above. However, reading and especially re-reading this book has led me to wrestle with several questions that Bliss raises, that I believe the field would benefit from reconsidering as well.

For outsiders to this debate who have read this far, I invite you to convert your curiosity to contributions to this scientific endeavor – particularly if scientists like you are underrepresented in this subfield. Training programs such as the Russell Sage Foundation's Summer Institute in Social Science Genomics,⁵ the National Institutes on Aging's Genomics for Social Scientists workshop⁶ are available to aid you, alongside more limited dataset- or method-specific sessions that are frequently offered at conferences such as the Population Association of America and the Integrating Genetics and the Social Sciences conference.⁷

Whoever you are and whether or not you agree with my reflections on the questions presented above, I hope that you will take the time to consider and discuss the following questions, on which this review will conclude:

- Are the environment and social theory adequately represented in current sociogenomic research? If not, what is the appropriate balance?
- What should gene-environment interplay research look like in the GWAS/PGS era, and moving forward?
- What, if any, sorts of research questions are sociogenomicists no longer asking, perhaps influenced by funding availability?
- How can sociogenomicists more fully interpret findings to better reflect the complex social processes underlying them?
- How can sociogenomicists better incorporate evidence and theory on the socially constructed axes of inequality by race/ethnicity, gender, and sexuality into the treatment of the social environment?
- What steps can sociogenomicists take to better diversify the pool of researchers pursuing sociogenomics, and how can sociogenomicists better empower more diverse researchers to influence its agenda?
- How can sociogenomicists conduct and disseminate our research in a way that builds off current efforts to guide the media narratives and public interpretations of the implications of this research?

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⁵<https://www.rsfgenicsschool.com/>. Accessed 2/2/2019.

⁶<https://hrs.isr.umich.edu/genomics-workshop>. Accessed 2/2/2019.

⁷https://cupc.colorado.edu/IGSS_conference.html. Accessed 2/2/2019.

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Figure 1: Composition of Member Sections of the American Sociological Association, by Race and Gender