STEPHEN HILGARTNER, Reordering Life: Knowledge and Control in the Genomics Revolution, Cambridge Massachusetts, The MIT Press, 2017, xiv + 343 pp., May 2017

Stephen Hilgartner, *Reordering Life: Knowledge and Control in the Genomics Revolution*, Cambridge Massachusetts, The MIT Press, 2017, xiv + 343 pp., May 2017, $35.00 / £27.95.

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From 1988 to 2003 Stephen Hilgartner conducted extensive ethnographic fieldwork in and around what came to be known as the Human Genome Project. He conducted this work predominantly in the United States, but also in the United Kingdom, France, and Germany. This timing granted him, and now us, privileged access to the actors and places involved in the development of what we might call the 'official' Human Genome Project (HGP). This is of considerable value, but it also comes with the challenge of writing a book that necessarily involves historical narrative using an ethnographic approach.

The central argument of the book relies on the articulation and deployment of the concepts of 'knowledge-control regimes' and 'governing frames', by which the changes that occur over the course of the HGP are interpreted. The former is "a sociotechnical arrangement that constitutes categories of agents, spaces, objects, and relationships among them in a manner that allocates entitlements and burdens pertaining to knowledge" (p. 9). The latter is "an organized set of schemata that individuals and collectives use to interpret situations or activities as being instances of a particular kind of event or deed" (p. 11).

Hilgartner builds the case that throughout the history of the HGP, new knowledge-control regimes successively replaced previous ones that were no longer viable, for instance due to groups having sequence data poached and used in publications by others before they were able to make use of the data themselves. The knowledge-control regimes that succeeded those too burdened with problems to survive were, Hilgartner details, ones which caused the least initial disruption to the governing frames that were already in place.

This well-supported argument is partially obscured by bookending the work as a whole (and individual chapters) with an emphasis on 'revolution' and the visions of a vaguely defined 'genomics vanguard'. Rather than use these terms, Hilgartner may have served his overall argument more effectively by threading the concept of 'holdings' in tandem with his own articulation of 'perimeters' (introduced in Chapter 3) throughout the succeeding chapters. Holdings are "the knowledge objects found in the laboratory" that are "evolving assemblages" of "unequal 'strategic value'" (p. 65). Through "dynamic management of an emphatically breachable boundary"—the perimeter—the head of a laboratory has control and discretion over the selective transfer of holdings in and out of their laboratory (p. 67). These successfully characterise the control processes in individual laboratories that existed before the establishment of large-scale genome centres. However, barring a brief reappearance in the conclusion (p. 225), the concepts of holdings and perimeter and the discussion of the practices involved in their management are not used in the succeeding chapters, though there are many appropriate areas where invoking them would have been both salient and fruitful, for example in framing chapter 6 on the changes in knowledge-control regimes concerning the submission of sequence data to databases.

Hilgartner asserts rhetorical and methodological commitment to the examination of the dynamic processes underlying both the stabilisation and destabilisation of regimes. This works well in chapter 4's comparative discussion of the knowledge-control regimes exhibited by the US human genome program's approach to data submission and that of the Reference Library System initiated by Hans Lehrach at the Imperial Cancer Research Fund in the UK. The former persisted as "changes in the US program introduced at the outset of the HGP were consistent with preserving, not altering, the individualistic culture and practices of molecular biology" (p. 122). However, one was a major nationally-funded effort with the aim of completion, the

other, a smaller charitably-funded effort that did not aim at completion. This leads one to question the extent to which conclusions can be drawn from a comparison of them.

Chapter 4's engaging comparative study is told primarily through ethnographic data and extensive quotes from his anonymised interlocutors. In providing a historical account, however, people and their institutional affiliations matter. In the valuable appendix to the book where Hilgartner discusses the methodological challenges of his work, he acknowledges the problem with anonymity, but defends the use of anonymised quotes, as he is studying social structures rather than individual scientists and institutions. Nevertheless, the particularities are relevant to an understanding of social structures and processes, certainly in the more historically-oriented chapters.

Chapters 5 and 6 are the strongest. They constitute exceptional examinations of the development and adoption of expressed sequence tags (ESTs) and the changing practices, expectations, and agreements concerning the submission and publication of sequence data. In these chapters, the ethnographic data is used to detail the conceptual points against the essential background of an artfully elaborated historical narrative in which people and institutions are named. In these chapters, the concept of knowledge-control regimes has its most powerful analytical purchase in well-articulated discussions of shifts of regime.

In the earliest stages of various initiatives to sequence the human genome on a systematic basis, there were proponents of sequencing cDNA—DNA reverse transcribed from mRNA that thus represented the coding portion of the genome. Advocates of this approach emphasised that functional or coding DNA should be a priority for sequencing due to its likely relevance to research concerning the role of genes in particular diseases. Those who argued for a project aiming to sequence the full genome feared that a partial approach based on a problematic division of the genome into important and irrelevant parts would undermine support for whole-genome sequencing. The NIH-led programme in the United States opted for the whole genome approach (with some cDNA sequencing as a minor part), whereas other projects such as the UK's Human Genome Mapping Project were based on the cDNA approach.

At this time, Craig Venter was still at the NIH's National Institute of Neurological Diseases and Stroke. Frustrated with the slow pace of the overall HGP, he pioneered an approach towards partial sequencing of cDNAs, producing ESTs. He and his group then used the partial sequence data to search the sequence database GenBank for corresponding sequences associated with genes that had already been found, for example in other species. Through this, partial cDNA sequencing was repackaged by Venter as tools for finding and indexing genes. As Hilgartner observes, "Venter transformed the job to match the tool" (p. 130). Work centred on the sequencing of ESTs and indexing genes circumvented the problem faced by more systematic efforts. ESTs here have a role as intermediaries, valued for what they can help find rather than in themselves. For Venter it wasn't all about finishing the genome but finding areas of the genome with potential use in biomedical research.

The prospect of patenting ESTs led to a crisis within the NIH-funded initiative, mistrust from international partners, and a debate about the epistemic as well as potential commercial value of ESTs (p. 135). Fearing the consequences of allowing ESTs and data concerning them to be held privately by biotechnology companies, a coalition of HGP scientists and the pharmaceutical company Merck (who funded the initiative) came together and established an open, publicly-accessible EST database, the Merck Gene Index. Merck also funded a programme to generate huge numbers of ESTs for deposition into GenBank's EST database. These moves transformed the EST into an "ordinary tool" and deflated their commercial value, forcing the companies that were built around them to explore alternative strategies (p. 150-151).

Hilgartner's argument is that "between the late 1980s and roughly 1996 […] a series of distinct knowledge objects took shape: namely, the cDNA strategy, the EST, the EST patent, the proprietary EST database, the public EST database, and finally the EST as an ordinary tool." These changes constitute for Hilgartner "transformations of strategic objectives, material practices, organizational structures, and, not least,

knowledge-control regimes." (p. 152). The focus on cDNA and ESTs provides a welcome alternative approach to the predominant narratives of the HGP. Particularly intriguing is the discussion of the change in epistemic status and valuation of ESTs.

After discussing earlier challenges of getting sequence data onto public databases, he describes the advent of a regime based on progressively brisker submission of sequence data and open public access to that data. The consequence was the progressive separation of producer and user, which culminated in sequencing increasingly taking place on a large-scale at a small number of centres—the so-called G5. While Hilgartner's focus is on the advent of the knowledge-control regime associated with the publicly and charitably funded G5, alternative approaches to sequencing and the use of sequence data existed. These included smaller-scale sequencing activities that have not yet been fully captured by historical accounts of sequencing and genomics, and Venter's private-sector effort. Hilgartner hints at the incompatibility of the knowledge-control regimes of the public HGP and the Venter-led programme. I would have liked to see this developed further and the potential consequences explored.

Overall, Hilgartner's discussions of the regimes associated with the cDNA and ESTs break significant new ground, and present a strikingly original and compelling perspective on the HGP and its development. The central argument concerning the succession of knowledge-control regimes and the implications of this provides a fertile basis for further research, including how the increasing abstraction of the domains of the production of sequence data and the use of sequence data took place, what its consequences were for translation, and how smaller-scale sequencing operations fit into and around the knowledge-control regimes and governing frames that emerged thereafter.

More broadly, the book offers a well-written and engaging discussion of the HGP that will be interesting and enriching for general readers. The technical descriptions and illustrations are clear, concise, and precise. To those who work on genomics from historical, philosophical, social scientific, and anthropological approaches, it offers this as well as considerable resources, perspectives, and plenty of empirical detail to provoke new insights and lines of investigation.