Chapter 23
Introduction to "Re-situations of Scientific Knowledge: A Case Study of a Skirmish Over Clusters vs Clines in Human Population Genomics"

Carlos Andrés Barragán

The analysis in this chapter focuses on how life scientists working in the field of human population genomics ancestry studies (HPGA) produce and re-use scientific knowledge (see Griesemer and Barragán 2022, Chap. 24 in this volume). We understand *re-situation* as a process of accommodating the direct or indirect transfer of objects of knowledge from one site/situation to (one or many) other sites/situations. Our take on the concept borrows from Mary S. Morgan's work on the traveling of scientific facts and the re-situation of knowledge (Howlett and Morgan 2010; Morgan 2014) while expanding it to include other objects of knowledge such as models, data, software, findings, and visualizations. We structured a specific case study by tracking the use of the objects above between research laboratories/projects studying human population diversity and reported in three articles in *Science*, *Genome Research*, and *PLoS Genetics* between 2002 and 2005. These articles reflect on whether *clines* (geographic gradients of genetic variation) rather than *clusters* (discrete genetic populations) best characterize the distribution of human genetic variation at a global scale through time and space. We portrayed these three engagements as a unit of analysis, a "skirmish," in order to compare the divergence of interests in how life scientists answer comparable research questions, and to track the challenging transformation of workflows in their research laboratories as these scientific objects are re-situated individually or in bundles.

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C. A. Barragán (✉)
University of California, Davis, CA, USA
e-mail: cabarragan@ucdavis.edu

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Our analysis of the case study shows that an accurate understanding of re-situation requires tracking the whole bundle of objects in a project because they interact in particular and strategic ways. The absence or dismissal of these interactions for practitioners, consumers, and observers opens the door to unforeseen trade-offs, misunderstandings, and misrepresentations about research design(s) and workflow(s) and what these say about the questions asked and the findings produced. The skirmish reported in our case study contributed to continued controversy over the Human Genome Diversity Project, and the emergence of several advanced initiatives within HPGA, including: (*a*) technically advanced approaches to ancient DNA for ancestry studies and, (*b*) a shift toward explicit geographic modeling in genetic ancestry studies involving new software development to model human genomic variation.

Another interesting contribution of this chapter was highlighting the fundamental role of software development for HPGA studies, such as STRUCTURE. Life scientists have developed multiple software packages and experiment with them to explore theoretical models and answer old and new research questions. Sometimes tools *within* their workflow, sometimes a workflow in itself that encompasses other objects of knowledge (e.g., models, datasets, findings), software packages are crucial means for the detection of population structure and the number of subpopulations in a given DNA sample/dataset(s), the definition of ancestral populations for non-admixed and admixed populations, and the assignment of ancestral population proportions to sample tissue donors—whether from ancient specimens or contemporary populations.

Nonetheless, despite the mathematical complexity and analytical sophistication behind population genomic software, single packages are not equally useful for answering all the questions being asked for the types of problems already mentioned. Such particularity leaves life scientists—in both their roles as *developers* and *users* of algorithms—with the need to identify strengths and weaknesses of available software. Likewise, with the need to evaluate their comparative potential for answering specific research problems, questions, and their pitfalls for producing misleading or problematic results. Such evaluations have also been used to gesture at the potential for combining uses and/or the need to develop new algorithms that adjust to the particular interests of a research laboratory. Furthermore, there are major differences in how each package *models* certain human genomic population structures, making them an interesting case for scientists and social scientists for understanding how such nuances have powerful implications for the robustness assessment, reproducibility, and comparability of research findings. In addition to emerging as scientific objects in their own right, we show that human population genomic software packages are not just tools applied at specific steps in analytical research workflows, they are sites for the re-situation of a variety of kinds of objects involved (e.g., models, datasets, metadata, findings) and means of fitting such objects into the coherent workflows needed to produce new models, findings, and software enhancements.

The arguments in this chapter are part of a larger research agenda that seeks to understand the re-situation of scientific knowledge, focusing on ancestry studies

and biomedicine (Griesemer and Barragán 2018). These human genomic studies range in scope from (*a*) global comparative studies of genotype and sequence distributions across many populations to infer ancestry and historical relationships as well as putative migration patterns, to (*b*) regional studies within continental areas of complex ancestry and migration histories, to (*c*) local studies unraveling fine-grained ancestry and population relationships. Knowledge, generalizations, and understandings produced at these scales, when re-situated to other scales and across specialties (e.g., studies comparing contemporary DNA samples to ancient DNA samples from fossils), often creates novel challenges in the "translation," of research findings across contexts. Furthermore, it creates novel technical challenges to sampling methodologies, modeling assumptions, data analysis and inference techniques, empirical findings, and interpretations (see Griesemer 2020; Barragán et al. 2025; Barragán and Griesemer Submitted).

The theoretical aims of the larger project behind this chapter substantiate Griesemer's long-term commitment with interdisciplinary work toward the understanding of biological sciences *in practice*. His historical, philosophical, and STS analysis of the work of well-known evolutionary biologists, developmental biologists, ecologists, and geneticists (see Chap. 25 in this volume) have expanded our understanding of life sciences beyond the narratives and representations produced by scientists about their own disciplinary work, and beyond traditional and popular histories produced by social scientists and/or journalists. If I were to map out Griesemer's oeuvre on how scientists understand life and how they use such views to intervene it, I would gesture grouping them around (*a*) material models in biology, (*b*) the tracking, mapping and representation of causal processes, and (*c*) the conceptual integration of heredity, development, evolution, and ecology. Our research agendas on the re-situation of knowledge draw heavily from the first two.

Methodologically, our ongoing archival, ethnographic, and conceptual scaffolds structuring the larger project behind this chapter have been articulated by Griesemer's subtle but powerful take on *tracking* the tracking of phenomena pursued by life scientists. Ethnographically, I have been inspired by his conceptualization of biological theories as tracking devices (Griesemer 2006, 2007). For Griesemer, much of the work of scientists in areas like biological inheritance is "tracking work" of *causal processes* that involves abstracting, marking, and visually representing traces, among other activities, to produce theoretical models and empirical work. He says, "[…] whatever mix of theoretical, experimental, and observational techniques biologists proceed, their activity always involves tracking: following genes, cells, organisms, mathematical quantities, light spots on film, phenotypes in genetic hybrids, and so on" (Griesemer 2006: 6; see also Gannett and Griesemer 2004). His argument and framework allowed us to prioritize and articulate historical and ethnographic insights gathered about the materiality of HPGA studies and thus formalize concepts needed to develop models of re-situation phenomena such as: problem, situation, setting, workflow, task, project, and program —all in dialogue with the objects of knowledge already mentioned. For example, *situations* are usefully distinguished from *settings* in analyzing contexts of production of scientific knowledge and their re-situation into other contexts of work. A *situation* is a problem arising in

a setting that must be resolved in order to get research work done, while a *setting* is a semiotic and material context in which research workflows are carried out. Sometimes these problems are research questions scientists seek to articulate and answer, but other times problems are challenges to methodology, practice, or procedure faced by the re-situation of objects of knowledge into different settings. We argue that the re-situation of an object of knowledge changes the problem structure of scientific work—in the new setting compared to the old—, including research questions asked and methods/analytical approaches deployed to answer them.

Lastly, I would like to emphasize that behind the content of the following chapter—and the project that made it possible—there has been a priceless and incredibly generous mentoring endeavour in which I have inherited from Jim Griesemer many of his *disciplinary* and *boundary* issues! More than ever, I am more than comfortable experimenting with any standpoints that enhance and critique my anthropological, historical, and STS repertoire as I inhabit and seek for insights into life scientists' practices through space and time. Thus, the questions I now pursue require most of the time the crossing of disciplinary boundaries—sometimes gently, other times forcefully—to facilitate the tracking of the material-semiotic aspects of how scientists think, talk, and do while tracking phenomena. It is not about me impersonating a philosopher of biology or for that matter a human geneticist, or a biostatistician. It is about using philosophy of biology or human genetics and genomics to identify blind spots in my field of attention and then—as Griesemer likes to say—start coloring *outside the lines*.

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References

Barragán, Carlos Andrés, and James R. Griesemer. Under review. "Problem Agenda, Platform, and Research Environment: Tracking Workflow Disruptions in Svante Pääbo's aDNA Research Program."

Barragán, Carlos Andrés, Sivan Yair, and James R. Griesemer. 2025. "Eventualizing Human Diversity Dynamics: Admixture Modeling through Time and Space." In *DNA, Race, and Reproduction*, edited by Emily Merchant and Meaghan O'Keefe. University of California Press.

Gannett, Lisa, and James R. Griesemer. 2004. "Classical Genetics and the Geography of Genes." In *Classical Genetic Research and its Legacy. The Mapping Cultures of Twentieth-Century Genetics*, edited by Hans-Jörg Rheinberger and Jean-Paul Gaudillière. Routledge.

Griesemer, James R. 2006. "Theoretical Integration, Cooperation, and Theories as Tracking Devices." *Biological Theory* 1 (1): 4–7.

———. 2007. "Tracking Organic Processes: Representations and Research Styles in Classical Embryology and Genetics." In *From Embryology to Evo–Devo: A History of Developmental Evolution*, edited by Jane Maienschein and Manfred D. Laubichler. MIT Press.

———. 2020. "A Data Journey through Dataset-Centric Population Genomics." In *Data journeys in the sciences*, edited by Sabina Leonelli and Niccolò Tempini. Springer.

Griesemer, James R., and Carlos Andrés Barragán. 2018. "Standard Grant: A Case Study of How Re-Situation of Scientific Knowledge from Human Population Genomics Works." Science & Technology Studies Program (STS)/Department of Philosophy, UC Davis. NSF grant SES-1849307, 2019–25.

———. 2022. "Re-situations of Scientific Knowledge: A Case Study of a Skirmish over Clusters vs Clines in Human Population Genomics." *History and Philosophy of the Life Sciences* 44: 16.

Howlett, Peter, and Mary S. Morgan, eds. 2010. *How Well Do Facts Travel? The Dissemination of Reliable Knowledge*. Cambridge University Press.

Morgan, Mary S. 2014. "Resituating Knowledge: Generic Strategies and Case Studies." *Philosophy of Science* 81 (5): 1012–24.