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Data graphs and mechanistic explanation

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ABSTRACT

It is a widespread assumption in philosophy of science that representations of data are not explanatory—that they are mere stepping stones towards an explanation, such as a representation of a mechanism. I draw on instances of representational and explanatory practice from mammalian chronobiology to suggest that this assumption is unsustainable. In many instances, biologists employ representations of data in explanatory ways that are not reducible to constraints on or evidence for representations of mechanisms. Data graphs are used to represent relationships between quantities across conditions, and often these representations are necessary for explaining particular aspects of the phenomena under study. The benefit of the analysis is two-fold. First, it provides a more accurate account of explanatory practice in broadly mechanistic investigation in biology. Second, it suggests that there is not an explanatorily "fundamental" type of representation in biology. Rather, the practice of explanation consists in the construction of different types of representations and their employment for distinct explanatory purposes.

> *"To be able to look behind the mask of rhetoric requires an understanding of the esoteric language of a science as well as a knowledge of the immense body of phenomenology that is assumed by the current literature of a scientific subject. … In biology, as in history, the distinction to be made in understanding the role of 'fact' is between assertions about particular sample paths and general assertions about types of events."*
>
> *—————R. C. Lewontin*
>
> *"And all that I know*
> *Is blowing like tumbleweed"*
>
> *—————Joanna Newsom*

1. Introduction

Explanation in biology consists in showing how a biological system produces a phenomenon of interest. According to the new mechanistic philosophers of science (Bechtel & Richardson, 1993; Machamer, Darden, & Craver, 2000), explanations are couched as descriptions of mechanisms—organized systems of biological parts performing specific operations, which interact causally to produce the phenomenon. This perspective is a major departure from traditional, deductive-nomological views of explanation, and some mechanists (among others less directly concerned with mechanisms) make a further departure in arguing that visual representations can be a key vehicle for explanation (Bechtel & Abrahamsen, 2005; Griesemer, 1991; Machamer et al., 2000; Perini, 2005; Ruse, 1990; Sheredos, Burnston, Abrahamsen, & Bechtel, 2013). Generally, mechanists have focused on "mechanism diagrams," which show the parts, operations, and organization of the mechanism. Indeed, biologists often present explanations in mechanism diagrams.

I claim that mechanism diagrams, while important for explaining biological phenomena, are not the only kind of visualization serving this goal. Often, in initial decomposition of a system, biologists pursue the kinds of epistemic activities that mechanists have rightly characterized as positing parts and operations, and that culminate in mechanism diagrams. However, mechanists have not paid attention to some other common explanatory practices, which more frequently employ data graphs

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in explanatory ways, and which biologists often pursue following initial division of a system into parts and operations. In particular, data graphs show relations between quantities over time and/or across conditions, and representing these relations is often required to show how some aspect of the phenomenon is produced. Even if the parts, operations, and organization of the mechanism are known, an explanation is often insufficient unless quantitative relationships are also represented. When quantitative relationships are represented in an explanatory way, I call them "explanatory relations." Looking at how data graphs are employed in active biological research highlights these elements of practice.

Mechanists, with few exceptions (Burnston et al., 2014), have missed or misconstrued the explanatory import of data graphs. It is not obvious why this has been the case, since there is relatively little overall discussion of data representation in the mechanist literature. It may be due in part to an overreliance on textbook accounts of biological discovery, which often paint an accepted mechanism diagram as the end-stage of explanation. Another possible reason is a tendency towards a kind of explanatory fundamentalism—the assumption that some particular kind of description, representation, or entity is the fundamentally explanatory kind, and that all epistemic work in research must be geared towards establishing the type that does the explaining. Some mechanists argue that mechanistic models are explanatorily fundamental, and that representations other than those describing mechanisms, be they verbal descriptions, computational models, network models, or whathave-you, are explanatory only to the extent that they map directly to a mechanistic explanation (for examples, see Craver, 2006; Kaplan & Craver, 2011). There is resistance to explanatory fundamentalism—Bechtel and Abrahamsen (2010), for instance, suggest in several places that mechanistic models must be conjoined with models representing the mechanism as a dynamical system. Pluralists of different stripes suggest that multiple models are necessary for explanation (e.g., Green, 2013).

Clearly, there are some complex issues at foot here. This is largely because these debates often discuss, in one go, the representations that scientists use to explain, the role of models in the explanation, and/or the metaphysics underlying the explanation. Here, I am only interested in representation (see Section 4 for a discussion of how the representational question relates to the others). Explanatory fundamentalism vis-à-vis the question of representation argues that there is a type of representation that is fundamentally explanatory, and that other kinds of representation play subsidiary roles in establishing the genuinely explanatory kind. This kind of "representational fundamentalism" would explain the relationship that mechanists have posited between data representation and representation of a mechanism—data graphs are thought to provide *evidence for* or to *constrain* mechanistic hypotheses, but are not thought to themselves be explanatory. I argue that these views underdescribe the use of data graphs in mechanistic research, and that in some cases data graphs serve genuinely explanatory roles.

As mentioned, it is difficult to pin representational fundamentalism on anyone directly. As such, I have articulated it more as a foil than in an attempt to criticize any particular theorist. Arguing against representational fundamentalism points the way to a positive view of how representations are employed in explanation. The view I propose claims that giving an explanation in a given case consists in coordinating distinct representations with distinct explanatory roles. My account is thoroughly pragmatic—I am not offering an analysis of either "representation" or "explanation" as such. However, I think we can learn something deep about the nature of explanation by understanding the relative roles that distinct representations play in accounting for phenomena.

I will discuss a detailed case study from mammalian chronobiology, which I claim can only be adequately described if data graphs are taken to be playing a key explanatory role in the investigation. I will argue that the role of the data graphs is *dissociable* from those played by those of mechanism diagrams and causal graphs in the investigation. That is, the specific content of the data graphs serves an explanatory role that is needed for the explanation, not present in other representations, and not dependent on their specific content for fulfilling its role.

I will pursue only one case study in order to thoroughly distinguish the representations and the relationships between them. However, I take the case to be exemplary of a wide range of explanatory uses of data representations, and I discuss other examples elsewhere (Burnston, submitted for publication). I will start in Section 2 by describing the representational differences between data graphs and mechanism diagrams in the context of mammalian chronobiology. I will then give the case study in Section 3 and argue for the distinctive explanatory role of data graphs. In Section 4, I will give a general view of the relative explanatory roles of data graphs and mechanism diagrams, and situate the view amongst the related debates in the mechanist literature. Section 5 concludes.

2. Diagrammatic representation

Mechanistic explanation consists in describing the physical system responsible for an *explanandum* phenomenon (Craver, 2007). In a successful explanation, standardly construed, the system is decomposed into parts and operations, and the explanation shows how those parts and operations are organized to produce the phenomenon in question. A part is an entity or type of entity. An operation is a type of interaction between entities—standard examples include *binding*, *activating*, *regulating*, and *inhibiting*. Organization includes both the spatial locations of parts and operations, and the temporal ordering of operations. It is often important, for instance, that one operation occur before another, at a certain place, so that the second operation can occur. I will use the phrase "mechanistic posits" to refer to hypotheses about and representations of parts, operations, and organization in these traditional senses.

Mechanistic understanding in the field of chronobiology has advanced rapidly in the last 15 years. One of the field's primary explanandum phenomena is circadian rhythms—roughly 24 hour, endogenously generated physiological rhythms occurring in a wide range of organisms, which regulate an array of processes ranging from sleep and activity patterns, to metabolism, to gene transcription across the entire genome. Rhythmicity, in mammals and many other organisms, is due to internal "clock" mechanisms, which in eukaryotes operate at several mechanistic levels. The most basic timekeeping mechanisms are molecular clocks within individual cells, which are composed of interlocking feedback loops amongst gene products (mRNAs and proteins). Circadian "time" is kept in the oscillating quantities of gene products—when the clock is working properly, these oscillate over a roughly 24 hour period, thus providing a timing signal that can regulate other processes.

In abstract terms, the basic mechanism works as follows: proteins from the "positive loop" cause transcriptional activation of the "negative loop" genes, leading to increasing quantities of negative loop gene products. The negative loop proteins then feed back and inhibit their own transcription. When negative loop proteins degrade, the inhibition is released, and activation can resume, causing levels to increase again. With the appropriate rates of transcription, translation, and degradation, the mechanism can produce oscillations of roughly 24 hours. In mammals, the positive loop genes are *Bmal1* and *Clock*, and the negative loop genes are *Cryptochrome (Cry)* and *Period (Per)*. The standard "mechanism