Scientific Diagrams as Traces of Group-Dependent Cognition: A Brief Cognitive-Historical Analysis

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Abstract

Recent research has begun to explore the role of diagrams as cognitive tools. Here I develop new conceptual and methodological tools for exploring the sociality of cognition involving diagrams. First, I distinguish two varieties of group-dependent cognition. Second, extending Nersessian's method of *cognitive-historical analysis*, I show how a suitably-informed "literature review" of diagrams published in scientific articles offers a window into the group-dependent cognition of scientists. I end by sketching future avenues of inquiry, and how this approach may inform science education.

Keywords: chronobiology; cognitive-historical analysis; group cognition; member cognition; scientific diagrams.

Introduction

Diagrams as Cognitive and Social Tools

Cognitive scientists have recently adopted a variety of approaches to studying graphical practices ("GPs"). Tversky applies her work on embodiment, spatial cognition and navigation to study spatial graphics and spatial design more generally (2011a; 2011b; Tversky, Heiser, Lee, & Daniel 2009). Hegarty focuses on the cognitive abilities underlying the "spatial intelligence" which facilitates learning from diagrams by students in the sciences (2004; 2010; 2011). Cheng explores how suitably constrained, innovative GPs support learning the conceptual structure of highly mathematized domains (Cheng 1997; 2002; 2009; 2011).

The focus of such research has tended to be on the *consumption* of completed diagrams as a cognitive activity of individuals.[1] A few studies have also addressed the *production* of diagrams by individuals. However, constructing and reasoning with GPs are also social practices. Some researchers have recently developed ethnographic methods to study *group* cognition involving *completed* diagrams (Alač, 2008; 2011; Kirsh, 2009).

Here I take a different approach. First, I highlight social aspects of cognition in diagram *production*. GPs often integrate ideas from a variety of earlier sources, and diagrams indicate the designer's understanding of her field: GPs inform us about how individuals perceive the social and professional groups of which they are members. Second, I stress the social effects of diagram consumption: creating and disseminating diagrams is a manipulation of the social environment which helps to define boundaries between social-professional groups. To do this I develop a new strategy of inquiry: analyzing published scientific diagrams which document the history of research. My case study concerns research into the mechanisms of circadian rhythmicity in cyanobacteria (blue-green algae). One goal of the paper is to show how such a "literature review" can serve to investigate scientists' group-dependent cognition.

Extending the Cognitive-Historical Method

The present paper extends the method of cognitive-historical analysis (Nersessian, 1992; 1995; 2002; 2008). The method is historical in that it takes as data the existing record of investigative practices in the science(s) of interest. In early work, Nersessian focused on the work of notable individuals (e.g., Maxwell), highlighting specific developments in their thinking. Here, I examine a years-long record of published figures depicting multiple authors' conceptions, at various stages of inquiry, of the known and hypothesized mechanisms of circadian rhythmicity in cyanobacteria.

The cognitive aspect of the methodology is rooted in a *continuum hypothesis* – that "the cognitive practices scientists have invented and developed over the course of the history of science are […] sophisticated outgrowths of the kinds of cognitive strategies humans employ in coping with their environments and in problem solving of a more ordinary kind" (Nersessian, 2008). Scientists, like other humans, form cooperative groups to tackle large-scale tasks, and freely draw inspiration from peers when it is available.[2] I shall show that with careful attention to the field-wide context in which diagrams are developed, we can clearly identify aspects of GPs which indicate group-dependent cognition among scientists. In this initial demonstration, I focus on diagrams from review-style articles, penned by (sometimes several) well-known and respected authors in the field. The express purpose of such publications is to offer a window into the social, conceptual, and evidential context constituting the current state of play in the field.

Nersessian has always stressed that a full understanding of cognitive activities must embed them within their social context. Recently, she and her colleagues have directly studied the interplay between social and cognitive factors in scientific practice (Osbeck, Nersessian, Malone, & Newstetter, 2011). Drawing upon their insights, I hold that the lines between "individual" and "group" cognition are

[1] This is especially true of the experimental literature in which isolated subjects complete tasks involving diagrams.

[2] Scientific research is not *fully* communal and cooperative; great incentives promote individual achievement as well.

not always clear-cut, since properly attending to social context sometimes requires reconceiving an individual's cognitive activities as *group-dependent*.

Delineating Group-Dependent Cognition

Classical cognitive science maintains that individuals exhibit forms of cognition which do not clearly depend upon their membership in a group. Call this *individual cognition*, or *i-cognition*. As Hutchins (1995) argued, cognition might also be *distributed* across a group of cognizers so that the group instantiates a higher-order cognitive architecture. Call this *group-level cognition*, or *g-cognition*. I emphasize that individuals exhibit a third, unique variety of cognition when they self-identify as *members* of a group (whether or not that group exhibits *g-cognition*). Call this *member cognition*, or *m-cognition*. Like *i-cognition* (and unlike *g-cognition*) *m-cognition* is attributable to (first-order) individuals, rather than to groups. However, like *g-cognition* (and unlike *i-cognition*) *m-cognition* depends upon an individual's group-membership. Osbeck et al. provide paradigmatic examples of *m-cognition* in their analysis of how scientists *position* themselves and negotiate their identity: "Identity negotiation can be considered a form of sense-making" (what they elsewhere call *seeking coherence*) "directed to the meanings one applies to oneself within social groups that include but are not limited to the particular research laboratory, one's field of practice… and science as a tradition of inquiry" (2011).

To illustrate how I conceive of *m-cognition*, consider the following objections to my proposed method. First, by looking to published diagrams, I am guaranteed to *miss* many (*i*-) *cognitive* activities involved in their production. The creator(s) of a diagram often discard a variety of "failed" versions, deploying expertise in choosing what to represent and how best to do so. Only access to the unpublished, discarded diagrams could really shed light on the process of problem-solving that led to the finished product. Second, publication requirements imposed by journals may add a layer of cognitive opacity, as the designer loses the ability to do just as they like. Published diagrams might be cognitively "whitewashed," so to speak.

While this line of thought is correct as far as it goes, it neglects one important reason for pursuing this inquiry: when authors prepare materials for publication, they *knowingly work within* the constraints imposed by "outside" powers. Publication is a *de facto* requirement for active membership in a professional science, and part of one's professionalism consists in navigating the pitfalls of publication. If part of scientists' practice involves "whitewashing" their individual cognitive products, making them ready for public consumption, the whitewashing itself depends upon interesting forms of *m-cognition* which reflect an individual's self-identification as a member of a group – e.g., awareness of professional-bureaucratic norms, and self-monitoring with respect to those norms.

More relevant, for my purposes, are the ways scientists self-monitor with respect to the empirical and evidential norms of their field. When a scientist prepares a publication for consumption by her peers, her professional reputation depends upon cognizance of: the empirical support accorded to various hypotheses; which sources of evidence have been deemed reliable; which findings have been replicated or reinterpreted, etc. These are just some of the *m-cognitive* activities which an individual engages in to negotiate her specific *expertise*, self-identifying as an able practitioner of some method(s) or authority on some topic(s).

These norms are especially relevant to the production of my source materials: authoritative review articles presenting the current state of a field. The production of diagrams is an integral part of crafting such articles. Thus, I suggest that *cognitive-historical* analysis of such published diagrams can plausibly begin with the hypothesis that these GPs, as part of the professional practice of scientists, are guided by *m-cognition* regarding empirical and evidential norms in the relevant discipline(s). It follows that such diagrams are amenable to analysis as visual traces of *m-cognition*. My task in what follows is to demonstrate that this is the case.

Three Snapshots of Cyanobacterial Chronobiology

I turn now to canvass three stages of research regarding circadian rhythms in the cyanobacterium *Synechococcus elongatus*. Here I must be selective in every aspect of my inquiry.[3] In this section I introduce the details of my case-study. Cognitive analysis occurs in the section thereafter.

Stage One: First Steps

A biological system's circadian rhythmicity ("CR") is its endogenously controlled production, once every ~24 hours, of some phenomenon (e.g., waking, onset of metabolic processes, peak transcription of a gene). For decades, while research into the CR of eukaryotes flourished, it was thought that no similar phenomena would be discovered in prokaryotic cells. Prokaryotes lack membrane-bound organelles, exhibit relatively simple metabolic activities, and frequently have lifespans of less than 24 hours. Prevailing wisdom taught that such an organism would have no use for anticipating local day-night cycles.

CR was eventually discovered in *S. elongatus* (Ishiura, Kutsuna, Aoki, Iwasaki, Andersson, Tanabe, Golden, Johnson, & Kondo, 1998). Since then this system has become a mainstay of circadian research, owing in part to its high genetic manipulability. In an early review article, Kondo & Ishiura (1999) made an explicit attempt to shoehorn cyanobacterial rhythmicity into the accepted mechanism for eukaryotic systems. Evidence from a variety of eukaryotic systems had suggested that the CR of single cells was controlled by a *Transcription-Translation*

[3] For details, cf. Johnson & Xu (2009) and Huang & Lin (2009).

Feedback Loop (TTFL). A generic eukaryotic TTFL is shown at left in Figure 1. A "clock gene" (dark blue bar) is transcribed, leading to the translation of a corresponding "clock protein" (dark blue oval) outside the nucleus. After undergoing state-changes in the cytoplasm, the clock protein returns to the nucleus, where it interrupts the effect of an "activator" (red oval) at a promoter region (light blue bar). The clock protein(s) thus inhibit further transcription of the clock gene(s). By hypothesis, a TTFL constituted a cell's core circadian "clock" or "pacemaker" and the CR in the expression of other ("clock-controlled") genes was thought to be dependent upon the activity of clock proteins.

The critical functional arrangement of the TTFL is the interplay of positive and negative elements: activation at the promoter increases transcription of clock genes, but clock proteins feedback to inhibit transcription of their own genes. Such systems can instantiate a *limit cycle oscillator*. With the right time constants, the system could oscillate with a 24-hour period, giving rise to the organism's observed CR.

At right in Figure 1, the authors attempt to fit cyanobacterial CR into the same scheme. Early research (Ishiura et al., 1998) had shown (*a*) that deletion of any gene in the *kai* gene cluster (containing genes *kaiA*, *kaiB*, and *kaiC*) abolished CR in *S. elongatus*, and (*b*) that a variety of single amino acid mutations to any of the *kai* genes (resulting in the corresponding production of subtly altered Kai proteins) either disturbed or abolished CR. It was thus concluded that the core clock in *S. elongatus* involved the *kai* gene cluster and the Kai proteins working in concert.

The same study also showed that while *kaiC* overexpression resulted in rapidly *decreased* activity at the promoter ("P_{kaiBC}" in Figure 1) which controls the transcription of *kaiB* and *kaiC*, *kaiA* overexpression resulted in *increased* activity of the same promoter. Thus, the Kai proteins appeared capable of participating in a TTFL, with KaiC playing the role of a traditional "negative element" (note the re-use of the dark blue oval) which inhibits its own gene's transcription, and KaiA playing the role of a traditional "positive element" (note the re-use of the red oval) which promotes KaiC's transcription.

These initial results were consistent with a cyanobacterial TTFL, but left much underdetermined. For example, it was unknown *how* Kai proteins might influence the transcription of *kai* genes, since the Kai proteins lacked DNA binding motifs, and were thus incapable of *directly* influencing promoters (Ishiura et al., 1998). Given the success of the TTFL model in other systems, the authors of Figure 1 posited intervening entities ("x," "y," "z") to mediate between the Kai proteins and transcriptional regulation.

Stage Two: Troubles with TTFLs

A few years later, Johnson (2004) published a "minireview" in which he proposed the alternative "Oscilloid" model shown in Figure 2. The interactions between Kai proteins had by now been further determined. As shown top-right KaiC alternates between a highly phosphorylated state (with "P" attached) and an unphosphorylated state (no "P"). KaiA facilitates KaiC's phosphorylation, and inhibits its dephosphorylation. KaiB inhibits those activities of KaiA, biasing KaiC towards dephosphorylation. The result is a 24-hour rhythm in the phosphorylation state of KaiC, which is a determining factor in KaiC's downstream effects.

Meanwhile, the problem of how the Kai proteins might regulate transcription had become more pressing. It had been shown that KaiC expression not only (somehow) repressed transcription of its own gene (and of *kaiB*), but also globally repressed transcription of virtually *every* gene in *S. elongatus*' genome (Nakahira, Katayama, Miyashita, Kutsuna, Iwasaki, Oyama, & Kondo, 2004). Investigators had also shown that rhythmicity in *kaiC* expression could be attained in strains in which *kaiC* transcription was controlled by a promoter taken from another organism's genome (Xu & Johnson, 2003; Nakahira et al., 2004). These were departures from eukaryotic TTFLs, in which positive

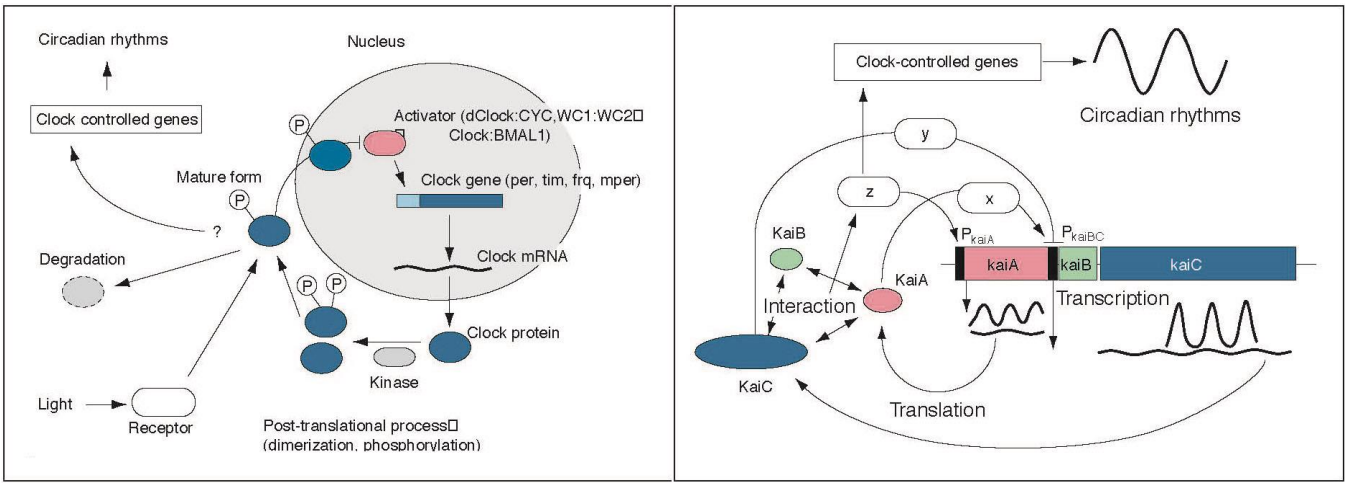

Figure 1: Kondo & Ishiura's (1999) Figures 3 (left) & 4 (right). At left is the TTFL model of rhythmicity in eukaryotic cells. At right, available data in *S. elongatus* are fitted into a similar scheme. See text for discussion.

and negative feedback loops compete for dominance in the activation and inhibition of specific, native promoters.

The same researchers recommended an elegant solution. KaiC had been shown to be part of a large family of DNA recombinases (Leipe, Aravind, Grishin, Koonin, 2000). KaiC was thus hypothesized to be capable of altering the shape and structure of cyanobacterial chromosomes in a rhythmic fashion, thereby globally affecting gene transcription (including, as just one example, the *kaiABC* cluster). At middle-left in Figure 2, Johnson added this to the hypothetical model of CR in *S. elongatus*.

Stage Three: Surviving 2005

Not long after Johnson's minireview, a pair of momentous reports showed conclusively that cyanobacterial CR was not dependent upon a TTFL. An initial report showed that CR in KaiC's phosphorylation state persists even when both transcription and translation are globally inhibited (Tomita, Nakajima, Kondo, & Iwasaki, 2005). Shortly thereafter, it was reported that KaiC's phosphorylation rhythm could be reconstituted *in vitro*, using a mixture containing only the three Kai proteins and ATP (Nakajima, Imai, Ito, Nishiwaki, Murayama, Iwasaki, Oyama, & Kondo, 2005). The core clock in cyanobacteria, it seemed, was instantiated entirely in post-translational entities and processes, and required no transcriptional regulation whatsoever. Transcriptional and translational regulation were reconceived as *effects* of clock functioning, not operations *constitutive* for clock function.[4]

After 2005, researchers pursued the molecular details of KaiC phosphorylation rhythms. Here I cannot discuss this research in detail. Figure 3, a representative example of the period, displays no details concerning chromosomes, transcriptional regulation, or transcriptional rhythms.

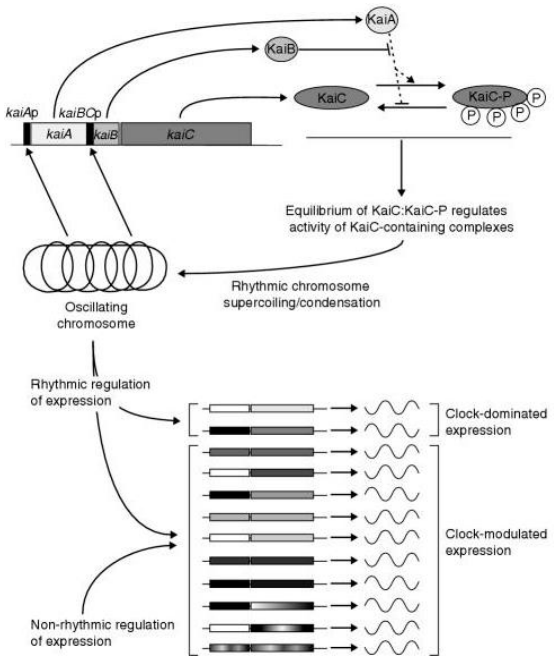

Figure 2: Johnson's (2004) Oscilloid model.

[4] Transcriptional regulation was later seen as stabilizing or supporting the Kai-based clock (Johnson, Mori, & Xu 2008).

Analysis

By attending to the social and evidential contexts surrounding the production of Figures 1-3, we gain insight into the *m-cognition* of these diagrams' designers. In this way we can provide cognitive answers to questions about scientists' GPs. We simultaneously gain insight into how GPs helped shape the social environment of chronobiology.

Consider Figure 1. A pertinent question to ask regarding this figure is: Why did the authors construct this diagram as they did, drawing an analogy between eukaryotic and prokaryotic CR?

At the time of publication, no data substantively confirmed the presence of a TTFL in *S. elongatus*. Available data were merely consistent with such a model. What drove Kondo & Ishiura to produce this diagram was a broader awareness of hypotheses accepted elsewhere in chronobiology. Eukaryotic TTFLs were then considered the sole concrete examples of circadian *limit cycle oscillators* in living systems. The group of "chronobiologists" was *de facto* defined by an interest in such mechanisms. By hypothesizing that the newly discovered CR in cyanobacteria fit the same model, the authors explicitly positioned themselves in the broader theoretical community of chronobiologists.

The text of the article supports this interpretation. Kondo& Ishiura aim to show how cyanobacteria could fit the "basic circadian model" of a limit-cycle oscillator, and explicitly recommend strategies for further-extending this model to CR in plants (1999, p. 171). Kondo & Ishiura also stress the importance of assimilating cyanobacteria to the TTFL model, forming a theoretically unified chronobiology: "Cyanobacteria could be a model system for molecular approaches to the circadian clock, because it is the simplest organism that has a clock" (1999, p.172). The subsumption of cyanobacterial CR to the TTFL model would lend credence and generality to the working assumptions of chronobiologists at large.

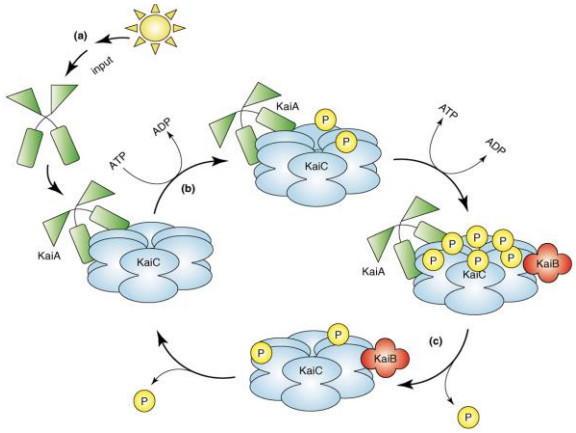

Figure 3: Mackey & Golden's (2007) visual summary of the stages of the core Kai-based oscillator in *S. elongatus*.

Figure 1 is the visual depiction of this shared theoretical framework: the authors literally *drew* the analogy between the models of CR in eukaryotes and prokaryotes which unified the theoretical framework of chronobiology. Kondo & Ishiura were positioning themselves as (and encouraging other researchers to recognize themselves as) members of a single, theoretically-unified group of "chronobiologists." Their GP is (partly) explained by appeal to this *m-cognition*; the graphic itself is a trace of that *m-cognition*.

Consider next Figure 2. A pertinent question to ask regarding this diagram is: Why did the author depart from earlier GPs in the field, especially by including a novel depiction of the entire chromosome of cyanobacteria?

New data showed that circadian transcriptional regulation in *S. elongatus* was not specific to individual promoters, in contrast to eukaryotic TTFLs. Since previous data had been consistent with a cyanobacterial TTFL and had shown that Kai proteins *do* (somehow) participate in regulating transcription, it was a "surprise" to find these discrepancies with the eukaryotic model (Johnson 2004, p.217.2). It is these data, plus the persisting field-wide theoretical assumption that transcriptional regulation is *somehow* constitutive for clock function, which "suggests a broadly global mechanism for the cyanobacterial clock system" (Johnson, 2004, p.217.3). It is within these constraints that he appeals to the broader literature regarding chromosome topology in cyanobacteria, and articulates the Oscilloid model to provide a novel hypothesis regarding *transcription-translation feedback* in cyanobacterial CR.

Thus in Figure 2, Johnson breaks the struct visual analogy with eukaryotic, as was demanded by evidence showing that "the clock system in cyanobacteria is different from that in eukaryotes" (2004, p.217.4). Despite this, the view of transcriptional regulation as a process constitutive for clock function remained part of the shared theoretical framework of a still-unified chronobiology. For this reason, Johnson stresses that the cyanobacterial data might lead us to consider the hypothesis that eukaryotic clocks themselves involve chromosomal topology as a mechanism of transcriptional regulation. He writes that "If this proves to be the case, the investigations of the cyanobacterial clock may lead to fundamental insights that are broadly applicable to all organisms" (2004, 217.4). In either case a unified chronobiology would need to refine its theoretical framework to incorporate cyanobacterial data.

Figure 2 is the visual depiction of the new model for cyanobacterial *transcription-translation feedback*. The graphical disparity from earlier depictions of the cyanobacterial clock reflects the conceptual departure from the TTFL model. Johnson positioned himself as (and encouraged other cyanobacterial researchers to recognize themselves as) a member of a distinct sub-group of chronobiologists which was helping to refine the general theoretical framework of chronobiology. Johnson's GP is (partly) explained by appeal to this *m-cognition*; the graphic is itself a trace of this *m-cognition*.

Finally, consider Figure 3. A pertinent question to ask regarding this diagram is: Why have the authors departed from earlier GPs, especially by excluding all reference to transcriptional regulation?

The core clock in *S. elongatus* had been identified as a post-translational oscillation in the phosphorylation state of KaiC (involving interactions with other proteins). The data showed that "transcriptional regulation is apparently a dispensable layer of reinforcement on a post-translational clock in the cyanobacterium" (Mackey & Golden 2007, p.382). Transcriptional regulation (local or global) was no longer considered part of the core clock in *S. elongatus*.

Figure 3 above is the visual depiction of the new model of the cyanobacterial clock. By excluding any depiction of genes, chromosomes, transcriptional feedback, and the like, Mackey and Golden underscore the distinction between cyanobacterial and eukaryotic clocks. Cyanobacterial chronobiology was no longer theoretically yoked to molecular hypotheses drawn from eukaryotic systems: the hypothesis that *some form* of transcriptional regulation would be constitutive for the function of every circadian *limit-cycle* oscillator had been excised from the general theoretical framework of chronobiology. Cyanobacterial chronobiologists had distinguished themselves as a unique subgroup of chronobiologists. Mackey and Golden's GP can be (partly) explained by appeal to this *m-cognition*, and the diagram itself is a trace of this *m-cognition*.

Concluding Remarks

In this brief case study, I have demonstrated that the method of cognitive-historical analysis may be fruitfully extended to reveal scientific diagrams as visual traces of group-dependent cognition (*m-cognition*). In doing so, I have sketched how scientists' GPs help demarcate the boundaries between groups of researchers. It is hoped that with the benefit of future elaboration, this approach can take its place as a compliment to other empirical methods of examining the cognitive activities involved in GPs.

With this initial demonstration completed, I suggest that inquiry into diagrams may be especially well-suited for investigating the *m-cognition* of scientists. As in the cases above, published diagrams frequently offer "at a glance" a window into authors' construal of the state of the art in their field. While I have not emphasized it, the examples also hint at the extent to which authors recycle old formats (often citing their original designers), positioning themselves as members of a persisting group and building extended "lineages" of GPs. Further research might fruitfully explore the "cognitive" lineages of which these are visual traces.

Finally, I suggest that such analyses might fruitfully inform science education. The foregoing demonstrates how published figures provide a visual record of the empirical and theoretical developments which fuel scientific fields' growth and subdivision, and how they can serve as a window into researchers' conception of their own field. As I hope to have shown, when such graphics are presented with appropriate context, and when they are queried in a suitable

manner, they can serve as intuitive scaffolds to help novices gain a rich understanding of the course of expert thinking in a field of study.

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