

Issues When Applying Structuralism to Biology

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Abstract

This paper discusses some issues that arise when applying structural realism to biology. I begin by reviewing Katherine Brading's version of structural realism with a hierarchy with proliferation of models.¹ I then attempt to apply Brading's structural realism to a biological example. This biological example suggests an issue with the use of shared structure. In response, I suggest the use of relevant relations instead of shared structure. I then discuss Steven French's use of eliminativist ontic structural realism in biology. Additionally, I consider John Dupré and Maureen A. O'Malley's discussion of metagenomics and claim that biological entities are better described as self-sustaining biological processes.² These metagenomic insights suggest an eliminativist view is preferable in biology. I conclude with an attempt to combine Brading's and French's approaches into an eliminativist relevant relationalism that retains the structuralist flavor and is applicable to the fluid, constantly changing entities found in biology.

Introduction

What does it mean when science proves something? Answers to this question can be found in the realism/anti-realism debate. Briefly, scientific realism argues that it would be akin to a miracle if science made all of these empirically successful predictions without what the theory says about the world being real.³ A common critique of scientific realism argues that its dependence on continuity in science cannot account for the fact that the history of science suggests that science goes through scientific revolutions.⁴ Structuralism was purposed as a way to keep scientific realism while accounting for these scientific revolutions. The benefit

1. Katherine Brading, "Structuralist Approaches to Physics: Objects, Models and Modality," chap. 3 in *Scientific Structuralism*, ed. Alisa Bokulich and Peter Bokulich, vol. 281, Boston Studies in the Philosophy of Science (Dordrecht: Springer Netherlands, 2011), 43–65, ISBN: 9789048195978, doi:10.1007/978-90-481-9597-8_3.

2. John Dupré and Maureen A. O'Malley, "Metagenomics and biological ontology," *Studies in History and Philosophy of Biological and Biomedical Sciences* 38 (2007): 842.

3. John Worrall, "Structural Realism: The Best of Both Worlds?," *Dialectica* 43, nos. 1-2 (1989): 101.

4. Ibid., 103-105.

of structuralism is that theories can undergo content changes while still latching on to an underlying structure. This underlying structure is what accounts for the continuing empirical success of scientific theories while allowing for vast changes in content. As John Worrall points out “Einstein’s equations undeniably go over to Newton’s in certain limiting special cases. In this sense, there is ‘approximate continuity’ of *structure* in this case.”⁵ In physics, it makes sense that old equations could be considered limiting cases of new equations; but what happens for sciences where equations are less common, like in biology?

In assessing the applicability of structuralism to biology, I begin by reviewing Katherine Brading’s version of structural realism that includes a hierarchy with proliferation of models.⁶ Brading clearly describes why her version of structuralism works well with physics theories that are applicable in various models and to various data sets. However, when I try to apply Brading’s structural realism to biology, it becomes apparent that shared structure needs to be changed to shared relations. I then present one of the few structural realist views applied to biology: Steven French’s eliminativist ontic structural realism. I agree with French that John Dupré and Maureen A. O’Malley’s discussion of metagenomics points towards the need for an eliminativist version of structural realism. According to Dupré and O’Malley, “metagenomics - also called environmental genomics, community genomics, ecogenomics or microbial population genomics - consists of the genome-based analysis of entire communities of complexly interacting organisms in diverse ecological contexts.”⁷ Dupré and O’Malley argue that given the results of metagenomic studies, biological organisms are better described as self-sustaining biological processes.⁸ The influence of metagenomics suggests that a few adjustments need to be made to both French and Brading’s theories. These issues lead to my solution: eliminativist relevant relationalism.

5. Worrall, “Structural Realism: The Best of Both Worlds?,” 121.

6. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality.”

7. Dupré and O’Malley, “Metagenomics and biological ontology,” 835.

8. Ibid., 842.

Structural realism with a hierarchy with proliferation of models

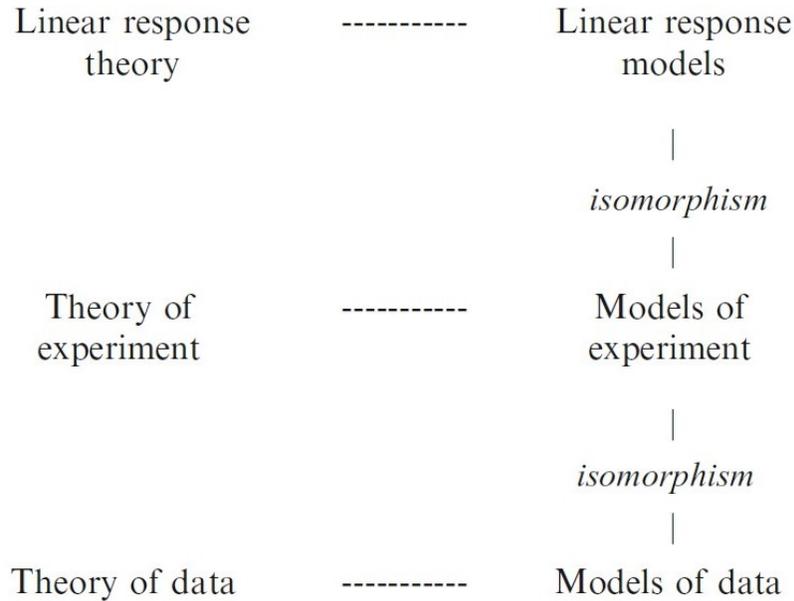


Figure 1 Brading’s Fig. 3.1 Suppesian possible hierarchy of theories

In “Chapter 3 Structuralist Approaches to Physics: Objects, Models, and Modality” of *Scientific Structuralism*, Katherine Brading, discusses issues that arise when attempting to provide a structural realist account for the domain of physics.⁹ Brading begins with a “semantic view of theories” (See Figure 1) which connects phenomena to a theory using a hierarchy of models rather than a set of rules and definitions.¹⁰ Brading’s final view of structural realism contains modifications to the original semantic view and is described as a “hierarchy with proliferation of models (II)”.¹¹ In this form of structural realism, multiple models of data and mediating models connect to a model of a high level theory through a “relationship of shared structure”.¹² It is then this entire hierarchy of models together

9. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality.”
 10. Ibid., 44.
 11. Ibid., 53.
 12. Ibid.

that is meant to represent the structure found in the world. As Brading puts it, “the realist who subscribes to the semantic view of theories believes that there is *a model of the high level theory that accurately represents the world* (or some subsystem of it), and the intermediate levels of the hierarchy become “transparent” when it comes to the *content* of the realist’s beliefs about the world.”¹³ One of the main modifications Brading makes is to include multiple mediating models and data models. This is because it is important for Brading that the mediating models are “partially independent or autonomous” in order to be consistent with scientific theorizing.¹⁴ The effect of this partial autonomy is that the mediating models may be incompatible.

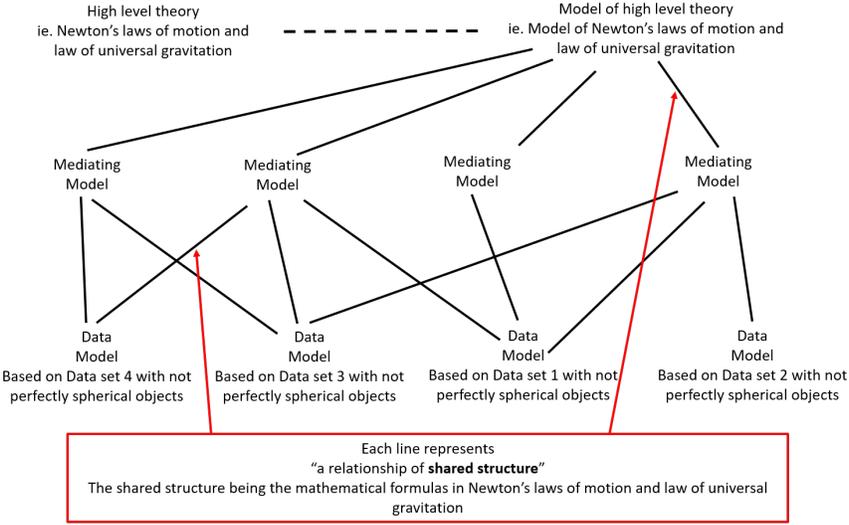


Figure 2 Applying Structural Realism to the Domain of Physics

As an example Brading considers Newton’s theories and the two-body problem in physics.¹⁵ According to Brading, a structural realist can use shared structure to explain how data models of not perfectly spherical masses, mediating models and Newton’s laws of motion and the law of universal gravitation are connected. The high-level theory includes Newton’s laws of motion and the law of universal gravitation. In experiments, the likelihood is low

13. Original italics and quotes. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality,” 54.
 14. Ibid., 45.
 15. Ibid., 48.

that any spherical mass will be considered a perfect sphere. So, the data models are the data sets collected during experiments that contain not perfectly spherical masses. Since the high level Newtonian theories can be applied in different ways and for different reasons, multiple mediating models must be created in order to account for these differences. These differences also mean that different data sets or data models could be used. The resulting picture (Figure 2) is a hierarchy with a proliferation of models that all share structure with the model of the high level theory.¹⁶

Now that we have an idea of a structural realist approach to physics, let's see if we can find an example for biology. In my view, we could consider 'the theory of evolution' a high level theory in biology. This theory is then applied to the biological world in a model of the high level theory of evolution. From there, a hierarchy of mediating models and data sets connecting biological entities to the model of the theory of evolution would be created. Considering the variety of biological entities that exist, many different data sets could be created depending on the empirical study being done. This would result in a variety of mediating models that connect all of these different data sets to the model of the high level theory of evolution. Alternatively, these mediating models could focus on different selection criteria or approaches to evolutionary theory resulting again in a variety of mediating models. For example, one mediating model could focus on a metagenomic analysis while a different mediating model could focus on a purely genetic analysis. Because the mediating models use different methods to analyze how the theory of evolution interacts with the data sets, the result may be mutually incompatible mediating models despite the fact that these models connect the data sets to the model of the high level theory of evolution. Thus, the resulting picture (Figure 3 on next page) in this case is a hierarchy with a proliferation of models that each share a structure with the model of the high level theory.

16. Brading, "Structuralist Approaches to Physics: Objects, Models and Modality," 48.

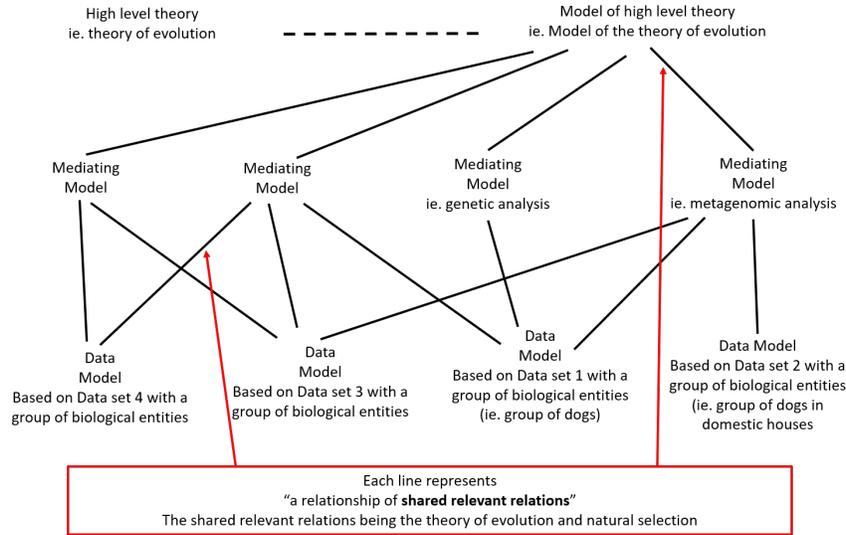


Figure 3 Applying Structural Realism to the Domain of Biology

Changing to shared relevant relations

In this example, it seems odd to discuss shared structure when talking about how the theory of evolution relates to biological entities. The theory of evolution is not a mathematical formulaic law like Newton’s laws of motion or law of universal gravitation. The theory of evolution is about the dynamic relationship between biological data sets as impacted by the environment or not. Thus, it seems more appropriate to discuss the connection between models as one of shared relations and not shared mathematical or law-like structure. Characterizing something as a shared relation, however, does not discount the possibility of a mathematical or law-like relation. By changing to a hierarchy with proliferation of models connected by shared relations, structural realism can more clearly be applied to disciplines like biology that focus less on mathematical law-like relationships while still being applicable to disciplines that do.

Unfortunately, changing to shared relations comes with the problem of relevance. If we consider the biological example, we are not concerned with *any* shared relation. The goal is to pick out a specific shared relation that is *relevant* to connecting biological entities and the theory of evolution. Thus, I agree with Katherine Brading and Elaine Landry that

we need a “methodological strategy of seeking out, exploring, and exploiting the notion of the *appropriate* kind of shared structure”¹⁷¹⁸ For example, it is accurate to say that the model of the theory of evolution, the mediating models, and the data models all share a relation in which all biological entities are living. However, this relation is true of many things and not just the theory of evolution; this is likely not the relation that evolutionary biologists are concerned with. Instead, it is the relation of natural selection functioning in a particular way in particular environments that relates different data sets and models to the theory of evolution. Therefore, I argue that in order to be as clear and accurate as possible when describing what is important and real, structural realism should be a hierarchy with proliferation of models connected by a relationship of *shared relevant relations*.

The problem of incompatible mediating models

Brading notes that this version of structural realism has both benefits and drawbacks. The benefit is demonstrated in this biological example where incompatible mediating models can still explain the relationship of the data to the model of the high level theory through shared structure. Brading’s use of multiple mediating models separates it from other structural realism theories that use one particular isomorphism of the same structure connecting all levels of the hierarchy resulting in a “cascade effect”.¹⁹ In other theories, this cascade effect explains how the structure is maintained throughout the hierarchy. Brading, however, moves away from isomorphism in an effort to better match how scientific theorizing is done and recognize the fact that most mediating models “share features with both the data models and the high level theory, but are also partially independent or autonomous”.²⁰

The drawback to allowing incompatible mediating models is that “it is no longer clear

17. My italics. Katherine Brading and Elaine Landry, “Scientific Structuralism: Presentation and Representation,” *Philosophy of Science* 73 (December 2006): 577, <https://www.jstor.org/stable/10.1086/518327>.

18. It should also be noted that in the same quotation, Brading and Landry also point out that this structure should be consistent across all directions of the hierarchy.

19. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality,” 44.

20. Ibid., 45.

what it means to say that our higher level theory accurately represents *the* structure of the world.”²¹ Because there are incompatible mediating models that are supposed to be transparent and show how the model of the high level theory connects to the data, there is a question as to how incompatible models can ultimately represent the *one* structure of the world. If we consider our theory of evolution example, the problem of incompatible mediating models remains despite changing from a shared structure to a shared relevant relation. For example, how is it possible that both the purely genetic model and the metagenomic model represent only one relation? It seems possible that the two models can present the same structure in different ways and the difference is based on viewpoint. The problem is then justifying the connection between these different and incompatible presentations with one underlying relation. Saying that there are different viewpoints could equally mean that there are different underlying relations being represented. Thus, even when extended to biology, consideration must be given to how to justify a transparent hierarchy; that is how to justify a notion of a shared relevant relation that results in incompatible mediating models.

Eliminativist ontic structural realism

As an alternative Steven French supports an eliminativist ontic structural realism for biology. When considering the nature of biological entities, French accepts that there may be multiple models within one hierarchy. In part this could be a practical consideration in order to make computations plausible given our resources.²² For French even these idealized models may still present an underlying structure.²³ Another possible reason for there being multiple models in one hierarchy could be “the different modeling traditions of different communities (geneticists and theoretical biologist).”²⁴ Different goals may also require the combination

21. Original italics. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality,” 57.

22. Steven French, “Shifting to Structures in Biology and Beyond: Metaphysics and Representation,” chap. 12 in *The Structure of the World* (Oxford: Oxford University Press, 2014), 335, ISBN: 978-0-19-968484-7.

23. Ibid.

24. Ibid., 336.

of different elements into one model from say a model organism and a mathematical model in order to create ‘synthetic’ models.²⁵ Thus, it is not surprising to French that a structural realist view of something like the theory of evolution may involve multiple mediating models and multiple data models. For example, we noted earlier that there could be multiple mediating models based on the selection criteria used. For French, this would represent both a practical and community issue. The mediating model created would depend on the data set selected by the community and the selection criteria. Thus, geneticists may use genetic coding as selection criteria while evolutionary biologists may use a metagenomic approach where they consider both the genetic coding and the environmental effects.

According to French, the fact that ‘biological structures are evolutionarily contingent’ leads to two options for structural realists.²⁶ The first option is to situate “spatio-temporally limited and evolving structures” in a version of “the principles of natural selection, understood as globally invariant nomological generalizations as in physics.”²⁷ So, there would be a high level theory that stipulates these principles of natural selection. These principles are then applied to a model of the high level theory which then connects to evolving and various data sets through evolving and various mediating models. The second option for French is a reductionism to a more fundamental non-contingent physical structure.²⁸

French takes the second option and abandons the idea of biological objects because of “the ‘Problem of Biological Individuality’ and the heterogeneity of biological objects in general.”²⁹ For French there is convincing evidence, particularly when considering definitions of concepts like ‘the gene’, that it is difficult to come up with a clear outline of what constitutes the biological object’s identity.³⁰ There is a problem when defining biological individuals because no such definition can be produced given the current usage of biological terms. This problem becomes particularly salient when looking at metagenomics as described by John Dupré

25. French, “Shifting to Structures in Biology and Beyond,” 336.

26. *Ibid.*, 337.

27. *Ibid.*

28. *Ibid.*

29. *Ibid.*, 338-339.

30. *Ibid.*, 339-342.

and Maureen A. O'Malley where the definitions of individuals relies on the marrying of the genetics and the particular environment within which that genetic code is found. Not to mention the fact, that these environments are constantly changing resulting in likewise, constantly changing definitions.³¹ The issue of the heterogeneity of biological objects involves the fluidity of biological entities due to consideration of the symbiotic nature of many entities considered individual organisms or the fact that what is considered 'one' organism becomes difficult to define spatially.³² What this all means for French is that a biological object is best viewed as being "dependent upon the appropriate structures ('nodes') and from the realist perspective, eliminable, or, at best, regarded as secondary in ontological priority."³³

The effect of metagenomics on structuralism

For French it is eliminativist ontic structural realism that can accommodate the challenge metagenomics makes to the notion of an individual organism.³⁴ According to Dupré and O'Malley, metagenomics involves analysis of not just the genetics of the entity but also the community and environmental context of this entity.³⁵ Thus, for Dupré and O'Malley, "life is in fact a hierarchy of processes (e.g.: metabolic, developmental, ecological, evolutionary) and ... any abstraction of an ontology of fixed entities must do some violence to this dynamic reality."³⁶ In "Metagenomics and biological ontology" Dupré and O'Malley discuss various types of metagenomic fields³⁷ including consideration of interdisciplinary efforts to combine different organisms, networks, and conceptual levels of analysis in what is called "metaorganismal metagenomics, or microbial systems biology."³⁸ For structural realists the

31. French, "Shifting to Structures in Biology and Beyond," 344.

32. Ibid., 348-350.

33. Ibid., 350.

34. Ibid., 345.

35. Dupré and O'Malley, "Metagenomics and biological ontology," 835.

36. Ibid.

37. These fields include studies of biodiversity metagenomics, evolutionary metagenomics, and functional metagenomics, all of which combine analysis of the genome of the organism with analysis of the environment these organisms are found in.

38. Dupré and O'Malley, "Metagenomics and biological ontology," 839.

important take away is that

In system-level understandings of microbial communities, the metaorganism is conceived of as deriving causal powers from the interactions of the individual components from which it is constituted. At the same time, however, those components are themselves understood to be controlled and coordinated in various ways by the causal capacities of the metaorganism.³⁹

Further, these organisms, as described earlier need to be considered within the context of the environment. This means that what might actually be considered the ‘real’ component of the world that these studies represent is a system, relation, or structure, rather than individual things.

Dupré and O’Malley’s view has informed French’s reasoning for moving towards an eliminativist view of ontic structural realism.⁴⁰ The metagenomic view of organisms leads to a picture of a dynamic organism that is the result of influences both within and outside the organism. Because metagenomics views biological entities as not just their features but dynamic processes, the notion of one individual organism becomes difficult to define. Thus, having an eliminativist view is fine because “*there are no biological objects (as metaphysically robust entities)*. All there is are biological structures, interrelated in various ways and causally informed.”⁴¹ So, how does one define something like a dog or human? According to Dupré and O’Malley, what we consider a biological organism is a stable biological process that does not remain stable because of durable parts “but rather the dynamic stability of processes that constantly recreate or maintain their essential constituents.” To me, a dog would need to be defined as an idealized model of a collection of self-maintaining processes that creates a system that interacts with its environment in a specific way we have chosen to call ‘dog’. Then in order to study the ways in which ‘a dog’ interacts with its environment, we have used a sort of short-hand in the form of ‘dog’ instead of saying ‘a collection of

39. Dupré and O’Malley, “Metagenomics and biological ontology,” 841.

40. French, “Shifting to Structures in Biology and Beyond.”

41. *Ibid.*, 345.

self-maintaining processes that creates a dog system.’

This characterization of biological entities as metaorganisms could be helpful to Brading when it comes to the problem of incompatible models. As we noted earlier, Brading was trying to explain how the presentation of the structure could result in incompatible models while still representing accurately *the one* structure found in the world. Brading notes that unlike a scientific realist, a structural realist cannot rely on objects to ground the structure in question.⁴² For the scientific realist, what connects the shared structure in the hierarchy is how it connects similar versions of an object within incompatible mediating models. The incompatibility of the mediating models in this case can result from incompatible features “of the same *fundamental kind* of object” that is described in the high level theory.⁴³ For Brading, who sees the kind of biological object as a function of the shared structure, relying on objects to connect the incompatible mediating models is unacceptable.⁴⁴ It is the structure, not the kinds of object, that is shared at all the levels connecting the model of the high level theory to the mediating models and data models. There is a transparent hierarchy connected by shared structure that is supposed to represent a real world structure and at the same time present various incompatible models.⁴⁵

If a metagenomic view is taken then the definition of the ‘object’ will depend on the interactions this object has with the environment. Thus, multiple models will need to be created in order to take into consideration the different kinds of environmental influences. The one structure represented in the hierarchy will be presented differently depending on the environment within which this structure is observed. Taking this a step further, one might even be able to say that because there *are* different environments and therefore different influences on the relation represented in the model, there *are* different mediating models of this interaction and these mediating models may be incompatible depending on the combination of environmental influences. This use of metagenomics may be too eliminativist

42. Brading, “Structuralist Approaches to Physics: Objects, Models and Modality,” 54.

43. *Ibid.*, 55.

44. *Ibid.*, 49.

45. *Ibid.*, 56-57.

for Brading though. Ultimately, it will depend on if Brading is willing to accept a notion of biological kinds that are “in constant interactive flux: subtly different in every iteration, but similar enough to constitute a distinctive process.”⁴⁶ This line of argument would only be useful to Brading if a self-sustaining type process can acceptably be defined as a kind of biological object. For example, Brading would need to accept kinds of dogs as a shorthand for kinds of ‘a collection of self-maintaining processes that creates a dog system.’

Eliminativist Relevant Relationalism

Dupré and O’Malley’s characterization of biological organisms fits well with my own view that biological entities must be considered fluid and constantly changing. Like water in a river, no matter where you dunk a bucket in to collect a sample, the next sample will be of a slightly different water source. Similarly, human bodies seem to be constantly changing; cells in the body are destroyed and new ones are created to replace them. Further, if we consider that the gut contains bacteria that breakdown the food we eat, it is hard to say that a human body contains only one organism. It does not. It contains at least two, namely the human and the bacteria within the human gut. Without the bacteria the ‘human’ is unable to process food and therefore will no longer be able to sustain itself and likely perish. Thus, it is not entirely accurate to say that a human is just one self-sustaining process. It is in fact multiple self-sustaining processes put together.

Given my view of biological entities, it would be preferable to move to a version of structural realism that represents a world of interacting processes, some self-sustaining and some not. In order to capture both formula-like and organizational connections, I would use a relationship of shared relevant relations. I further suggest that understanding what becomes the ‘relevant relation’ would be dependent on the context including the goal and situation within which the high level theory is being applied (See figure 4)

46. Dupré and O’Malley, “Metagenomics and biological ontology,” 841.

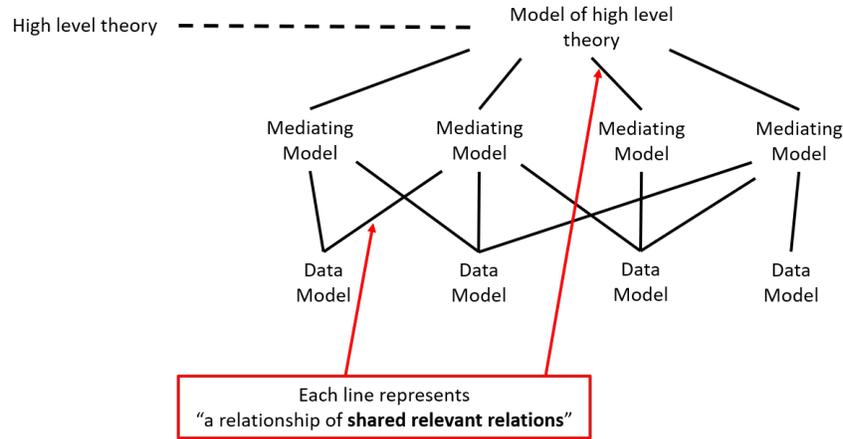


Figure 4 Eliminativist Relevant Relationalism

For example, what part of the biological world do we want to look at? Imagine the question is about humans and what foods they eat. In this case the relevant relation could be natural selection but one model may include natural selection that impacted which gastrointestinal organisms developed while a different model may not. Thus, we would need two separate mediating models and possibly multiple data models.

My contextual approach allows consideration of specific relations for specific theories while still being open to incompatible mediating models. This approach also considers the fact that the biological processes that create the data sets include an element of randomization meaning that any two processes may have different results. Further, my contextual approach can account for the fluid and dynamic view of organisms that Dupré and O'Malley argue for which has an eliminativist flavor. Thus, I have named this approach Eliminativist Relevant Relationalism.⁴⁷

Concluding Summary

In this paper, I discussed two options for extending structural realism to the domain of biology before presenting my own view. I first discussed Katherine Brading's version of

⁴⁷ I have not included "realism" in this name because I am still concerned that this view is consistent with both empiricism as well as realism. A longer version of this paper will discuss the possibility of this view maintaining a good argument for realism.

structural realism with a hierarchy with proliferation of models. With a few modifications, it seemed possible to use this form of structural realism as long as the relationship within the hierarchy is one of shared relevant relations rather than shared structure. However, the problem of incompatible mediating models still persisted. I discussed Steven French's eliminativist ontic structural realism as an alternative way to apply structural realism to biology. I agreed with French that moving to an eliminativist version of ontic structural realism makes sense particularly given the effect of metagenomics as described by John Dupré and Maureen A. O'Malley. Metagenomics was then discussed as a possible way to assist Brading with the problem of incompatible mediating models. However, this move is only useful if it is acceptable to include dynamic, self-sustaining processes as kinds of objects. Finally, I described my own contextualist view: eliminativist relevant relationalism.

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