



## Comments on Complexity and Experimentation in Biology

Richard M. Burian

*Philosophy of Science*, Vol. 64, Supplement. Proceedings of the 1996 Biennial Meetings of the Philosophy of Science Association. Part II: Symposia Papers. (Dec., 1997), pp. S279-S291.

Stable URL:

<http://links.jstor.org/sici?sici=0031-8248%28199712%2964%3CS279%3ACOCAEI%3E2.0.CO%3B2-2>

*Philosophy of Science* is currently published by The University of Chicago Press.

---

Your use of the JSTOR archive indicates your acceptance of JSTOR's Terms and Conditions of Use, available at <http://www.jstor.org/about/terms.html>. JSTOR's Terms and Conditions of Use provides, in part, that unless you have obtained prior permission, you may not download an entire issue of a journal or multiple copies of articles, and you may use content in the JSTOR archive only for your personal, non-commercial use.

Please contact the publisher regarding any further use of this work. Publisher contact information may be obtained at <http://www.jstor.org/journals/ucpress.html>.

Each copy of any part of a JSTOR transmission must contain the same copyright notice that appears on the screen or printed page of such transmission.

---

The JSTOR Archive is a trusted digital repository providing for long-term preservation and access to leading academic journals and scholarly literature from around the world. The Archive is supported by libraries, scholarly societies, publishers, and foundations. It is an initiative of JSTOR, a not-for-profit organization with a mission to help the scholarly community take advantage of advances in technology. For more information regarding JSTOR, please contact [support@jstor.org](mailto:support@jstor.org).

# Comments on Complexity and Experimentation in Biology

Richard M. Burian<sup>†‡</sup>

Virginia Polytechnic Institute and State University

---

Biology deals, notoriously, with complex systems. In discussing biological methodology, all three papers in this symposium honor the complexity of biological subject matter by preferring models and theories built to reflect the details of complex systems to models based on broad general principles or laws. Rheinberger's paper, the most programmatic of the three, provides a framework for the epistemology of discovery in complex systems. A fundamental problem is raised for Rheinberger's epistemology, namely, how to understand the referential continuity of the theoretical terms and concepts employed in typical case studies involving complex systems.

---

**1. Introduction.** All three papers in this symposium share the objective of achieving a coherent epistemology of detail built by use of a *patchwork methodology*, a notion Hans-Jörg Rheinberger adopted from Stuart Kauffman (1995, Ch. 11). I will focus particularly on Rheinberger's challenging paper, partly because it provides a useful framework for discussing Sylvia Culp's and Robert Richardson's contributions, partly because his is the most comprehensive and hardest of the positions to grasp, and partly to facilitate constructive criticism of some of his claims.

Let us set the stage a bit. All three symposiasts hold that philosophy of biology, like philosophy of science in general, is ill-served by an epistemology in the grand tradition, focused on laws, theories, and very general methodologies. All three also hold that sound epistemology seeks to take account of complexity in nature by employing a plurality

<sup>†</sup>Center for the Study of Science in Society and Department of Philosophy, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061-0247.

<sup>‡</sup>I am grateful to Paul Siegel for discussions regarding the interactions between MHC genotypes and resistance to Marek's disease, to Anne McNabb for help with the testosterone example, and to the symposiasts and symposium audience for discussion.

of local means for understanding and coping with particular problems and particular systems. They seek to improve our means of developing, using, and interdigitating distinct and appropriate methods and methodologies for different sciences, problem domains, and systems. Each of them follows François Jacob (1982, Ch. 2) and many others in seeing evolution as having tinkered organisms together out of the materials on hand over evolutionary time, thus providing adequate, not necessarily optimal, solutions to the problems of survival. Finally, each of them seems to hold a similar, tinkering, model of science. They agree, I think, that we have tinkered together our tools for conducting scientific investigations in a great variety of ways. Such tinkering is not only common, it is also virtuous.

Yet to say even this much suggests an obvious difficulty. Counting myself, all four symposiasts reject various old, unlamented visions of the unity of science. But if scientific puzzles and problems are to be dealt with by some sort of tinkering, we are left with an unsatisfying and epistemologically unhelpful vision of how the sciences fit together, one that treats experimental cultures as a patchwork of miscellaneous practices, a series of attempts to grapple with local problems using whatever tools lie to hand. Rheinberger's presentation is striking in that he confronts this problem directly and argues—how successfully is no small question—that a patchwork methodology actually provides a better understanding of what binds the sciences, and scientists, together into a hyper-complex enterprise than did the grand epistemologies built on the ideal of unified science. This claim, of course, does not stand alone, waiting to be attacked in splendid isolation. It is a piece of his rich account of the interaction of experimental practices, experimental systems, the epistemic things created by use of those systems, and the larger experimental cultures in which all of these are embedded (Rheinberger 1995a, 1995b, 1997).

**2. Some Puzzles about Rheinberger.** Robert Richardson's admirably clear account of the way in which Stuart Kauffman's higher order statistical mechanics hovers far above the details of complex systems provides a natural starting point for sharpening this puzzle about Rheinberger's paper. It is odd that Rheinberger's philosophy of epistemic detail should lead to a striking agreement with Kauffman regarding the virtues of patchwork methodology as a means of advancing science most effectively. Given a system as tinkered, complex, and devious as science must be if we accept even the barest outlines of Rheinberger's epistemology, we cannot master all of its details. Nor can we provide a general account of scientific advance based on close examination of those details across all the sciences. We must, instead, trust to a generic

claim supported in much the way that Kauffman supports his key claims: a patchwork system like that of science generates a generic class or family of results *in virtue of the abstract structure of the interactions among its patches*. The interactions will typically either fail (and very many, perhaps most, experimental systems and attempts to hybridize experimental systems *do* fail) or yield Rheinberger's conjunctures, bifurcations, or hybridizations. Putting the point as Rheinberger might: even in the most promising cases, when we shape exquisite technical systems to work on genuine unknowns to produce an unknown outcome leading to an unknown future, we cannot foresee the outcomes of our work or determine the likelihood of obtaining hybridizations, bifurcations, or conjunctures. We are not in a position to know whether such events will actually occur. Thus we cannot anticipate whether or how any particular styles or groups of specific experimental practices and experimental systems will contribute, if they do, to the resolution of conflicting claims about the diverse epistemic objects found in different experimental practices and experimental cultures. The moral seems to be that we do not have good grounds to predict anything specific about the ways in which the claims, the practices, and the disciplinary boundaries of the various sciences and scientific specialties will be reshaped. Nonetheless, just as Kauffman claims that he can derive some crucial structural features of systems about which he has no detailed knowledge, so Rheinberger claims that divergent local experimental practices will yield exchanges across boundaries, and thus produce his bifurcations, hybridizations, and conjunctures. Although each experimental practice is built to deal with the specificities of particular systems, given large numbers of experimental systems and practices and interacting in complex ways, they will (by the very nature of those interactions?) drive the sciences into new ecohistorical niches.

Perhaps it is unfair to put this strong a "generic" claim into Rheinberger's mouth. Still, unless he accepts some such claim about the likelihood of bifurcations, conjunctures, and hybridizations, I do not see how his epistemology of detail can offer much of anything to replace the claims about the unity of science which all of us in this symposium have abandoned. So I do not yet see how to interpret or justify Rheinberger's Kauffmanian optimism that the strategy of dividing up work on horrendously difficult and complex problems into a patchwork of smaller, rarely overlapping tasks will yield the bifurcations, conjunctures, and hybridizations that are at the heart of his philosophy of experiment. If the implicit basis for this optimism is not the generic kinematics of work in patches, we are owed an account of the grounds for optimism. As far as I can tell, we have not been provided with adequate grounds for either optimism or pessimism about the benefit

of working in patches until we know the details, for it is precisely the details that we are required to know according to Rheinberger's epistemology.

After addressing some issues raised in Culp's and Richardson's papers, I will bring the results of the discussion to bear on some further *problemata* for Rheinberger's philosophy of experiment.

**3. Complexities for Culp.** I turn to Sylvia Culp's excellent account of some important difficulties faced by gene targeting methods in seeking to identify the phenotypic effects of disrupted genes. On the one hand, I will argue that some of the problems she raises about identifying the phenotypes influenced by an "anonymous" gene are not as specific to gene targeting work as she suggests; they also infect classical genetic experiments. On the other hand, I will support her general point by arguing that the difficulty of getting from genes to phenes cuts very deep. In its full generality, this difficulty strengthens her point that we do not have a fully satisfactory way of delimiting the various phenotypic effects that a given gene may have until we have an adequate way of classifying phenotypes and of tracing the effects of a gene from genotype to phenotype.

Here is a slightly abstract illustration of the point, allied to an example employed by Robert Brandon (1990, Ch. 3). We seek to identify the phenotypic effects of particular genes. Consider a thick stand of annual plants in which competition for light plays an important role. The plants that are taller in the stand typically spread an umbel of leaves over the plants growing next to them, thus reducing the light received by their neighbors. Eventually they choke their neighbors out, thus outreproducing them. Population genetic studies of this stand show that a particular allele has been sweeping through the population. The presumptive diagnosis is that this allele fosters rapid growth or investment in early vertical growth so as to capture the light. But this diagnosis of the phenotypic effect of the allele may well be wrong. For example, where the springtime climate has been unusually stable for a period of, say, ten years, the plants will be advantaged by a gene that does not significantly affect growth, but affects the timing of germination in such a way that, during each of those years, plants bearing the allele in question are likely to germinate at the optimal time for rapid vertical growth. The resulting advantage could well cause the plants bearing that allele to overtop their neighbors. The issue is testable in straightforward and fairly obvious ways, although pinning down whether, in context, the allele in question really affects primarily one and not the other of these traits requires some fairly sophisticated experiments. For the present point we do not need the details. Obvi-

ously, the interpretation of classical genetic experiments can yield mistaken diagnoses of the phenotypic effects (or the selectively most important effects) of any given gene. And the resolution of such questions ultimately requires not only identifying multiple phenotypes and the gene changes that have affected them, but also tracing the causal pathways from those genes to the relevant phenotypes. Many classic examples reflect this sort of complexity.

Such issues are not the invention of philosophers. Consider, for example, work done by Paul Siegel's group at Virginia Polytechnic Institute and State University on resistance to a usually fatal infection, known as Marek's disease, in chickens. Prior to development of a vaccine, this highly contagious disease was extremely costly in commercial chicken operations. Without the vaccine it is possible to produce chickens with greater resistance to Marek's by selection for a complex inherited trait and/or for specific genotypes at the major histocompatibility complex (MHC). Yet such chickens do not thrive. Although the entire picture is not clear, a good part of the problem stems from the fact that MHC genotypes interact strongly with the background genome and that individuals heterozygous at the MHC were more resistant to diseases in general than homozygotes for the most protective haplotypes against Marek's (Martin et al. 1989; for a general review see Hartmann 1989). Selection for resistance to Marek's is selection for two particular haplotypes. The reduction of population variation in haplotypes allows a number of other low-level illnesses and sensitivities to affect the flock. Reflection on this example brings out a particular point: the effects of the underlying genetics are mediated by situations at a number of different hierarchical levels. A given haplotype may be beneficial on average in a population with high haplotype variation, but disadvantageous when there are only one or two specific haplotypes (other than itself) with which it may be paired. Thus, to assess the effect of a given allele on the organisms bearing it, as this instance illustrates, one needs to understand the mediating apparatus not only of the immune system, with all its complexities, but also the effect of population-level interactions with disease organisms.

One moral I draw from these examples, hardly novel, is that the effects of a given gene or allele are often exquisitely dependent on various facets of gene interactions, enzymatic cascades, the status and roles of organelles, tissues, mediating signals, timing of developmental events, etc.—reaching all the way to population structure and environmental variance. It follows that diagnosis of the phenotypic effects of a gene requires not only tracing the pathway(s) from gene to phenotype(s), but also detailed examination of the full range of developmental and environmental conditions that pertain in the populations in which the

gene occurs. All this is required to achieve a sufficient account of the pathways between genes and phenotypes. In short, since a given gene's effects are multiply context-sensitive, unless we know how the relevant contextual factors alter the pathways by means of which differences in the gene produces differences in phenotypes, we do not know which contextual factors, if altered, would have revealed a different phenotypic effect of the gene than those we anticipated. Given this, it does not matter whether one starts from the gene's end, as gene disruption experiments do, or from the phenotypic end, as classical selection experiments do. Either way there is an enormous amount of work to be done to ensure that the relation between gene and phenotype is properly understood. Starting from either end, there are many subtle sources of major error.

Underlying this discussion, there is a puzzle about the proper analysis of complexity. Time of germination, height, and perhaps even resistance to Marek's disease are not, as such, complex properties. In each of these instances, what is complex is the causal network in virtue of which an organism has these properties. In general, the pathway from gene to phenotype is extremely complex. Even in fairly straightforward cases, it is a mistake to identify the protein produced by a coding segment of DNA as *the* (or even *a*) phenone associated with that gene. What the protein *does* is the issue. And the protein may do different things in different contexts and according to what happens to it after it is produced. For one thing, a protein may be modified post-transcriptionally or, thanks to alternative splicing, may be only one of many proteins produced by the gene, depending on the physiological state of the organism or cell. For another thing, until one understands the metabolic or (often multiple) developmental or enzymatic pathways into which that protein enters, the effects that methylation at various sites has on the behavior of the protein, and so on, one does not properly know what its phenotypic effects are.

The difficulty of proceeding from biochemistry and genetics to characterize the phenotypic effects of different enzymatic actions in different bodily compartments is strikingly illustrated by the differential pathways by means of which sex steroids affect development in birds and mammals. The various enzymatic conversions of the single hormone testosterone illustrate the point (for mammals, see Hadley 1996, 378 ff., esp. the diagram on p. 380; for more technical accounts for birds, see Elbrecht and Smith 1992 and Schlinger and Arnold 1992). During a critical early postnatal period, testosterone (normally present only in males) triggers differentiation of male internal genital ducts and various secondary sexual characteristics. However, testosterone has no such effect in the brain; there the enzyme *aromatase* converts testos-

terone into estradiol, where this *estrogenic* hormone serves to *masculinize* the brain.<sup>1</sup> Nor does testosterone trigger the differentiation of all external male genitalia; in some other tissues (e.g., the scrotum) it is enzymatically converted into dihydrotestosterone, which triggers the differentiation into masculine tissues. Thus, thanks to differing enzyme-controlled conversions, testosterone yields at least three different active products in different parts of the body (in fact more when one pursues the matter in detail). The effects of the products that result from these enzymatic conversions of testosterone depend on the presence of the specific receptors for those products in the different body compartments; in the absence of estradiol receptors in the brain, estradiol produced from testosterone cannot have masculinizing effects. Thus the phenotypic effects of an enzyme and the compounds whose production it facilitates cannot be predicted simply from the biochemical characteristics of the enzyme or the products.

This illustrates a crucial grain of truth in Vance's (1996) argument that molecular genetics cannot do without the concepts of classical genetics. My suspicion is that whether we are tempted to consider many phenes of interest—for example, height or masculinized brains—as simple or complex depends on what issues we are considering. For the plants of our example, relative height is a simple property affecting which plants survive in their particular ecological setting, but relative height is complex with respect to the causal networks that bring it about. Until we are clear about the level at which a trait is being considered, there is no basis for considering it simple or complex. We need to be clear about the grounds for such classifications; until we are clearer than we usually are, we will also be unclear about what we mean by complexity.

**4. Richardson and Choice of Models for Complex Systems.** Richardson's paper mainly extends some work that he and I did together (Burian and Richardson 1992). I have no bones to pick with the general lines of his argument. But it will be useful to focus on the way he distinguishes between 'abstract' modeling in Stuart Kauffman's style and detailed, qualitative, rule-based 'expert system' modeling that seeks to mimic the behavior of some specific system or group of bounded interactions. The key point is straightforward. To undertake modeling of the detailed sort is to be committed to a certain degree of 'realism' in the model. Although there is no general formula for exactly what

1. In female embryos, estradiol, plentifully present, is prevented from reaching the brain by an  $\alpha$ -fetoprotein (fetoneonatal estrogen-binding protein), which binds the circulating estradiol during the critical period and prevents it from masculinizing the brain.

detailed modeling requires, it puts fairly straightforward constraints on models. Depending on the purposes to hand and our knowledge of the things, processes, or systems being modeled, the behavior of the simulacra in the model must follow rules analogous to those governing the behavior of the entities modeled to a contextually-reasonable standard. In general, when the behavior of the experimental system is reasonably well understood there is considerable 'local' consensus among experts about the standard of realism (here meaning only fidelity to the relevant behaviors or patterns of behavior) required, but there is considerably less consensus about the generality of the models. This is precisely as it should be if, to use Goethe's phrase, God is in the details. To the extent that the details of the system matter, generality obtained by abstracting from the details comes at a high price. Many developmental biologists have a well-informed hunch that the historical accidents that affected particular lineages over evolutionary time are reflected in the ontogeny of their descendants. If such intuitions are correct (a matter which I am incompetent to judge, though my Wimsattian prejudices [see Schank and Wimsatt 1986, Wimsatt 1986] make me sympathetic to them), detailed modeling will be more useful in helping us to understand development, even in general, than abstract modeling à la Kauffman. This is just another way of stating the basic reason that Richardson offers for preferring detailed to abstract models for many of the biological contexts in which, by and large, the details *do* matter. Because the interest in biology so often turns on the historically contingent differences of detail from one system to another, the specific information in detailed models makes those models more likely to be useful than the abstract ones. Of course major successes with abstract models might make converts of us, but until we are forced to recognize that the generic assumptions on which abstract models are built have unexpected purchasing power, background considerations of this sort leave the balance of the argument in favor of detailed modeling.

**5. Rheinberger Again.** It is time to return to Rheinberger and an issue about which he and I have a long-standing friendly disagreement (e.g., Rheinberger 1995a, Burian 1995; see also Rheinberger 1997). I am not yet sure that I understand correctly what he means by 'epistemic entities', but if I have him right, I think he gives away a key part of the machinery he needs to rescue himself from his surprising alliance with Kauffman. Let me put it as simply as I can. Rheinberger's toolkit contains tools falling in two rather different classes. One class contains tools to investigate the material practices and physically-constructed experimental systems that are part of the residue left by scientists. These material practices and experimental systems have a life of their own;

they are to be studied with all of the techniques of physical and conceptual archeology so that they can be understood not as dead remains but as situated in a certain context. In archeology, *in situ* is as critical as it is in biology. Rheinberger's other class of tools contains a battery of devices for understanding discourse—tools exploiting the linguistic and interpretative practices of the relevant communities to interpret their understandings of the traces of material systems. What he calls 'epistemic things', 'epistemic objects', 'epistemic entities' are poised somewhere on the cusp between material objects and processes on the one hand, and interpreted traces (that is, *signs* that *may* reflect the presence of objects or processes) and linguistic or conceptual products on the other. These entities hover at the edge of the unknown; they are the material/conceptual products (or artefacts) of the practices, work, interpretative apparatus, and experimental system(s) of group(s) working on the forefront of the unknown, trying to produce new knowledge.

If we are to understand such key concepts as *bifurcation*, *conjunction*, and *hybridization*, we must understand what epistemic objects are and what happens to them as we develop new knowledge. We know something about how Rheinberger conceives of these objects. They are the focal target of investigation, they are what it is that scientists are trying to grasp, to understand, to capture. Thus *genes* count, the *process of protein synthesis* counts, the *entity causing Rous sarcoma* counts.

At this stage of Rheinberger's research, he is not terribly clear about how to understand or delimit epistemic objects. They are closely connected to material objects or traces, though, of course, these may include what we later recognize as artefacts. Thus, in earlier work on the causes of Rous sarcoma (e.g., Rheinberger 1995b), he traces the particles found in a specific layer of ultracentrifuge tubes from putative causes of the sarcoma to microsomes to ribosomes. But the dominant tendency of his approach to epistemic objects, if I understand him rightly, is to place them on the linguistic/conceptual side rather than on the material side, a choice which, I will argue, is a mistake. Epistemic objects, as he treats them, are what scientists conceive of as the sort of thing that they expect (or hope) to find by use of their experimental systems. Thus, when the particles in the ultracentrifuge tube turn out to be microsomes, an epistemic object—the particles that cause Rous' sarcoma—disappears from the history of the experimental system and from the line of research that leads on, after much strenuous work, to ribosomes. And if the moral of the story about genes turns out as Rheinberger clearly expects (a view with which I am in sympathy), the gene will soon no longer be a significant epistemic thing in molecular genetics.

My worry with this line is, in the end, very simple. If Rheinberger

holds the position just described, it will be extremely difficult for him to achieve the robust contact he seeks with the material traces produced in experimental systems and the practices of detailed modeling. If genes as epistemic objects are replaced by variations in the genetic material plus pre-transcriptional, post-transcriptional, and even post-translational processing, the contact between new work in genetics with what went on in the pre-molecular past will be fragile indeed. The complexity of our current models and our current technically and technologically generated traces must be connected in some intelligible way with the previous work that led us to produce those traces. With all of the complexities of contemporary molecular work, we still must connect the material traces we produce to those produced by the Morgan group and perhaps even those produced by De Vries and Mendel. To that extent, at least, to forge the linkages with previous work, we must situate genes not only in their earlier contexts, but also in ours.

Accordingly, the challenge to Rheinberger is how his account of the epistemic objects of contemporary molecular genetics can be understood so that those objects remain in contact with the earlier material traces of genes as epistemic objects. The many conceptions of the gene that Rheinberger rehearsed for us—the conceptions of biochemists, crystallographers, developmental biologists, evolutionary geneticists, molecular geneticists, and so on—must be adequately connected back to the material traces of genes in the appropriate historical contexts.<sup>2</sup> Unless we can reconnect to those traces within contemporary biology, we will not have a historically sound account of what geneticists are doing now because we will not be able to situate the current conceptions with respect to the distant, but primary ancestors from which they stem. Indeed, I take a central part of Rheinberger's historicist program to seek to establish connections *within biology* between the situated understanding of epistemic objects at different historical periods through the material/conceptual (“graphematic”) traces that are left behind in each well developed experimental system. This move seems to be the key to his epistemology. I believe that his epistemology of detail will be able to handle the historical continuities of research adequately only when he can solve the problem of connecting the traces in different experimental systems that end up counting as traces of ‘the same’ objects. Without a solution to that problem, we will not be

2. This does *not* mean that *all* conceptions of the gene, or candidates for successor concepts to the gene concept, must connect properly to prior gene concepts. Some of them rest on artefacts or turn out to miss their target. One of the delicate tasks to be faced in ‘situated epistemologies’ such as Rheinberger’s is to evaluate which conceptual refinements genuinely connect back to prior concepts and which move in a new direction.

able to capture the complexity of the practices of scientific research adequately.

The best available answer to this challenge (and the one Rheinberger gave to this query at the symposium) is that we can work backward all the way to the ancestral epistemic objects via the historical chain(s) of descent that led, via a complex series of practices and work with specific experimental systems. Recent enough conceptions, built in part by working with experimental systems in current use, show strong continuities with current and recent conceptions, but if one takes Morgan's *gene* (say, as of seventy years ago), there is a strong appearance of discontinuity that can only be overcome by examining the use of the experimental systems produced in the interim and working one's way through a significant proportion of the bifurcations, conjunctures, and hybridizations that took place in the intervening time. In this way, we can follow the connections from one epistemic object to the next and, in the process, (re)situate the whole series of epistemic entities relating to the gene. The long lineage of connections here always provides *local* continuity, and (according to Rheinberger) it is simply an error to expect that any of the local continuities can remain intact in a chain as long as that from Morgan to, say, Christiane Nüsslein-Volhard, who recently received a Nobel Prize for her work on the role of mutations affecting early development in *Drosophila* (see e.g., Nüsslein-Volhard 1991, Nüsslein-Volhard and Wieschaus 1980). There is a fundamental disagreement between us here, but one that must be argued out in detail on another occasion.

**6. Conclusion: A Constraint on Epistemologies of Detail?** What is ultimately unsatisfactory about Rheinberger's treatment of conceptual continuity is that it cannot capture a feature that goes right to the heart of the problem of epistemic objects. As Hilary Putnam argued long ago for electrons (Putnam 1973), concepts like *gene* and *electron* are *trans-theoretical* in the sense that we have devices for referring to them in ways that do not depend on the particulars of the relevant theories of genes or electrons. This transtheoretical character of key theoretical concepts can be extended in important ways. Just as genes (and electrons) can be described quite differently by competing theories without loss of common reference, so, too, their traces can be captured by different experimental systems without loss of common reference. Indeed, Rheinberger's own list of various theoretical and experimental approaches to the gene serves to demonstrate that quite different experimental systems and conceptions of the gene still overlap sufficiently to allow spatiotemporal location of *common* epistemic objects and 'triangulation' on the properties of those objects. The means we employ

to characterize such epistemic objects may be vague and may change enormously, but, at least at times, the whole process of seeking conjunctures, etc. depends on the adequacy of the devices we employ to ensure that the different conceptions and experimental systems involved are being used to treat entities as the same spatiotemporally localized entities and that those entities (although they are characterized differently in our differing experimental systems) cannot be properly understood except as different aspects of *the same* entity. With proper coordination, we *can* learn that the extremely different properties captured in different experimental systems are different features of the elephant—or of the genetic material. The challenge to Rheinberger is to show how he can accommodate this fundamental fact in his philosophy of discovery.

## REFERENCES

- Brandon, R. (1990), *Adaptation and Environment*. Princeton: Princeton University Press.
- Burian, R. M. (1995), "Comments on Rheinberger's 'From Experimental Systems to Cultures of Experimentation'", in G. Wolters and J. Lennox, in collaboration with P. McLaughlin (eds.), *Concepts, Theories, and Rationality in the Biological Sciences: The Second Pittsburgh-Konstanz Colloquium in the Philosophy of Science*. Konstanz and Pittsburgh: UKV-Universitätsverlag Konstanz and University of Pittsburgh Press, pp. 123–136.
- Burian, R. M. and R. C. Richardson (1992), "Form and Order in Evolutionary Biology: Stuart Kauffman's Transformation of Theoretical Biology", in A. Fine, M. Forbes, and L. Wessels (eds.), *PSA 1990*, v. 2. East Lansing, MI: Philosophy of Science Association, pp. 267–287.
- Elbrecht, A. and R. G. Smith (1992), "Aromatase Enzyme Activity and Sex Determination in Chickens", *Science* 255: 467–470.
- Hadley, M. E. (1996), *Endocrinology*, 4th ed. Upper Saddle River, NJ: Prentice Hall.
- Hartmann, W. (1989), "Evaluation of 'Major Genes' Affecting Disease Resistance in Poultry in Respect to their Potential for Commercial Breeding", in B. S. Bhogal and G. Koch (eds.), *Recent Advances in Avian Immunology Research, Progress in Clinical and Biological Research*, v. 307. New York: Alan R. Liss, pp. 221–231.
- Jacob, F. (1982), "Evolutionary Tinkering", in F. Jacob, *The Possible and the Actual*. Seattle: University of Washington Press, pp. 25–46.
- Kauffman, S. (1995), *At Home in the Universe: The Search for the Laws of Self-Organization and Complexity*. New York: Oxford University Press.
- Martin, A., E. A. Dunnington, W. E. Briles, R. W. Briles, and P. B. Siegel (1989), "Marek's Disease and Major Histocompatibility Complex Haplotypes in Chickens Selected for High or Low Antibody Response", *Animal Genetics* 20: 407–414.
- Nüsslein-Volhard, C. (1991), "Determination of the Embryonic Axes of *Drosophila*", *Development* (Supplement) 1: 1–10.
- Nüsslein-Volhard, C. and Wieschaus, E. (1980), "Mutations Affecting Segment Number and Polarity in *Drosophila*" *Nature* 287: 795–801.
- Putnam, H. (1973), "Explanation and Reference", in G. Pearce and P. Maynard (eds.), *Conceptual Change*. Dordrecht: Reidel, pp. 199–221.
- Rheinberger, H.-J. (1995a), "From Experimental Systems to Cultures of Experimentation", in G. Wolters and J. Lennox, in collaboration with P. McLaughlin (eds.), *Concepts, Theories, and Rationality in the Biological Sciences: The Second Pittsburgh-Konstanz Colloquium in the Philosophy of Science*. Konstanz and Pittsburgh: UKV-Universitätsverlag Konstanz and University of Pittsburgh Press, pp. 107–122.

- . (1995b), “From Microsomes to Ribosomes: ‘Strategies’ of ‘Representation’”, *Journal of the History of Biology* 28: 49–89.
- . (1997), *Toward a History of Epistemic Things. Synthesizing Proteins in the Test Tube*. Stanford: Stanford University Press.
- Schank, J. C. and W. C. Wimsatt (1987), “Generative Entrenchment and Evolution”, in A. Fine and P. Machamer (eds.), *PSA 1986*, v. 2. East Lansing, MI: Philosophy of Science Association, pp. 33–60.
- Schlinger, B. A. and A. P. Arnold (1992), “Plasma Sex Steroids and Tissue Aromatization in Hatchling Zebra Finches: Implications for the Sexual Differentiation of Singing Behavior”, *Endocrinology* 130: 289–299.
- Vance, R. (1996), “Heroic Antireductionism and Genetics: A Tale of One Science”, *Philosophy of Science*, 63 (Proceedings): S36-S45.
- Wimsatt, W. C. (1986), “Developmental Constraints, Generative Entrenchment, and the Innate-Acquired Distinction”, in W. Bechtel (ed.), *Integrating Scientific Disciplines*. Dordrecht: Nijhoff, pp. 185–208.