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## **Biohumanities: Rethinking the relationship between biosciences, philosophy and history of science, and society\***

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Abstract

*We argue that philosophical and historical research can constitute a 'Biohumanities' which deepens our understanding of biology itself; engages in constructive 'science criticism'; helps formulate new 'visions of biology'; and facilitates 'critical science communication'. We illustrate these ideas with two recent 'experimental philosophy' studies of the concept of the gene and of the concept of innateness conducted by ourselves and collaborators. We conclude that the complex and often troubled relations between*

*science and society are critical to both parties, and argue that the philosophy and history of science can help to make this relationship work.*

## **1. Introduction: What is 'Biohumanities'?**

Biohumanities is a view of the relationship between the humanities (especially philosophy and history of science), biology, and society<sup>1</sup>. In this vision, the humanities not only comment on the significance or implications of biological knowledge, but add to our understanding of biology itself. The history of genetics and philosophical work on the concept of the gene both enrich our understanding *of genetics*. This is perhaps most evident in classic works on the history of genetics, which not only describe how we reached our current theories but deepens our understanding of those theories through comparing and contrasting them to the alternatives which they displaced (Olby, 1974, 1985). But philosophy of science also makes claims about genetics itself in, for example, discussions of whether the Mendelian gene and the molecular gene are the same entity (Griffiths and Stotz, 2006, 2007; Kitcher, 1984; Waters, 1994).

The biohumanities label suggests a more intimate relationship between biology and the humanities than is suggested by labels such as 'biology and society' or 'ethical, legal and social implications' (ELSI). We should emphasize that we are primarily concerned with differences in the connotations of these labels, rather than differences in the actual work carried on under the labels. Much of the work conducted under 'biology and society' or 'genomics and society' is closer to biohumanities as we describe it below than to anything

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<sup>1</sup> The term 'biohumanities' was first used as the title of research grant held by Griffiths, see [http://paul.representinggenes.org/biohum\\_home.html](http://paul.representinggenes.org/biohum_home.html).

suggested by those labels. The ELSI label has a particularly strong connotation that biologists provide the facts while humanists and social scientists are confined to discussing the implications of those facts. In contrast, biohumanities research aims to feed back into our understanding of biology itself. Moreover, in the biohumanities vision, while history and philosophy of biology may provide resources for addressing 'ELSI' issues, that is not their primary aim.

We see four major aims for research in the Biohumanities: understanding biology, constructive science criticism, contributing to new visions of biology, and contributing to critical science communication. First, and most generally, biohumanities is concerned with understanding biology. Although the biohumanities are of potential value to both biology and society, this is not the sole or main justification for engaging in this research. Science is fascinating and important, and it is worth understanding science even if understanding it does not have an immediate practical payoff, just as evolution is worth understanding whether or not doing so contributes to crop improvement or drug development. As in the biosciences themselves, it is hard to imagine Biohumanities researchers doing their best work without an intrinsic interest in the material they study.

Second, biohumanities understands itself as a critical enterprise. Constructive 'science criticism' (Pigliucci and Kaplan, 2006, 8) stands back from the urgencies of actual research to reflect on the strengths and weaknesses of current approaches. Thus, as C. Kenneth Waters has remarked, the aims of philosophical analysis include "to articulate scientific concepts in ways that help reveal epistemic virtues and limitations of particular

sciences. This means an analysis of the gene concept(s) should help clarify the explanatory power and limitations of gene-based explanations, and should help account for the investigative utility and biases of gene-centered science” (Waters, 2004, 29).

Science criticism can also involve the “turning-over of stones that had hitherto held their ground” (Moss, 2006, 523). History of science points out the 'roads not taken' in science. Without calling into question the data that was gathered, it points out that other sorts of data might have been gathered, or that the data that was actually gathered could have been interpreted in different ways. Philosophy of science adds to this enterprise by critically analyzing the chains of reasoning that connect specific scientific findings to claims about the broader significance of those findings. This can lead to changes in interpretation that can potentially motivate biologists to reinterpret earlier scientific findings and to prioritize different questions for future research. Thus, ideally, critical history and philosophy of biology can contribute to our third goal, the articulation of alternative 'visions' of biology.

Finally, history and philosophy of biology can contribute to the creation of 'critical science communication' both through constructive science criticism in the sense just outlined, and by communicating to a wider audience not merely 'what has been discovered', but something of the complexity of the scientific process and the contestability of its findings. To be valuable, critical work of the sort described in the last two paragraphs must be 'bioliterate', engaging with the science at the same level as practitioners rather than via popular representations. But the broad 'visions' of science in

which its results can be expressed in a non-technical way, and can thus make a major contribution to the public understanding of science.

The remaining sections of the paper will give more substance to these remarks with two specific examples of research in which we have participated: the Representing Genes project and the Innateness study. Section two uses these projects to highlight the new field of experimental philosophy of science, to introduce the ideas of scientific concepts as 'tools' for research and the experimental philosopher of science as a 'conceptual ecologist'. Section three provides an example of how constructive criticism of research in molecular and developmental biology can lead to the formulation of a new vision of 'postgenomic biology'. In section four we examine biohumanities in the role of a critical communicator of scientific results and scientific practice to wider audiences. We hope that these examples all point towards a new and fruitful relationship between the humanities, biology and society.

## **2. Experimental Philosophy of Biology as Conceptual Ecology**

The new field of 'experimental philosophy' (X-phi) brings empirical work to bear on philosophical questions (Stotz, 2008). We have been involved in two X-phi projects. The first focused on changing concepts of the gene. Previous research established that it is possible to operationalize questions about the gene concept in a survey instrument completed by researchers, and hence to examine the prevalence of particular gene concepts in different biological fields (Stotz et al., 2004). The Representing Genes Project was an extension of that earlier work (Stotz and Griffiths, 2004). The next section briefly

describes the Representing Genes project, concentrating on the methods used. For our more substantive discussion of the project's findings about the gene concept, see (Griffiths and Stotz, 2006, 2007; Stotz, 2008).

The second X-phi study focused on the much-disputed concept of innateness. Griffiths, Machery and Linquist examined which features of behavior lead biologically naïve individuals to label behaviors 'innate' (Griffiths et al., Submitted). They used their findings to explain the persistent controversies over the definition of innateness. We outline this work in Section 2.2.

### **2.1 The Representing Genes Project**

This project<sup>2</sup> was an attempt to assess the impact of the on-going genomics revolution on concepts of the gene (Stotz et al., 2006; Stotz and Griffiths, 2004). The actual practice of genome annotation inspired us to design a simple, annotation-like task for part one of our survey instrument. This was used to investigate the criteria that lead biologists to annotate a particular DNA sequence as either one gene with several gene products or several genes with a single functional product. We used graphical representations and descriptions of real DNA transcription events in eukaryotic genomes to illustrate the features of genome expression that make it difficult to define a gene in a way that covers all known cases. Since common definitions of the gene are insufficient, the simplified annotation task is designed to reveal the additional implicit criteria which biologists draw upon when applying the term 'gene'.

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<sup>2</sup> <http://representinggenes.org>

Another part of the survey instrument set out to investigate whether, as Lenny Moss has argued, investigators either start with the conception of a gene defined by its predictive relationship to a particular phenotype (Gene P), or with the conception of a concrete gene with a specific molecular sequence and the template capacity to code for many different products, depending on how it is transcribed and how its initial product is later processed (Gene D) (Moss, 2003). We argued that these different starting points would affect how investigators set out to unravel the complex relationship between genes and other molecular factors with the phenotype. Hence the second task asked subjects to assess the value of different research strategies for investigating complex diseases. For each disease we offered four strategies, designed to run along a continuum from focusing on the statistical relationship between gene and phenotype to entirely giving up on such a relationship in favor of analyzing content-dependent causal pathways between gene and phenotype. We looked for differences in which strategies were favored by biologists from different backgrounds, and also at whether the choice of strategies changed for human versus animal disease, and for physiological versus psychological disease.

## **2.2 The Innateness Study**

It is a truism that the term 'innate' is vague and ambiguous. Matteo Mameli and Patrick Bateson have recently reviewed the scientific use of the term 'innate' and identified no less than twenty-six proposed definitions of the term, of which they judge eight to be both genuinely independent definitions and potentially valuable scientific constructs (Mameli and Bateson, 2006). However, the term 'innate' remains immensely popular in psychology

and cognitive science. Some philosophers have proposed that in these contexts the term means little more than 'not my department – ask a biologist' (Samuels, 2002)(Samuels, 2002). But other philosophers of science continue to propose 'analyses' of the concept of innateness, designed to show that there is a single, coherent notion of innateness that either does or should underlie the use of the term in the sciences of the mind. These analyses are typically subject to intuitively compelling counterexamples from the proponents of alternative analyses.

The aim of this study was to provide some solid evidence about the pre-scientific or 'vernacular' understanding of innateness (Griffiths et al., Submitted). To determine the factors affecting judgments of innateness the authors examined the responses of biologically naïve subjects to a series of examples of the development of birdsong. Birdsong was used because it offered the best chance of finding closely comparable behaviors exhibiting every combination of the factors which earlier work had suggested would be relevant to judgments of innateness (Griffiths, 2002).

The results provided clear evidence that when people decide whether a trait is innate, they focus on two *independent* cues—whether the trait is universal and whether its development is sensitive to environmental influences, and tentative evidence that people may use a third independent cue, namely whether a trait has a designed purpose. In the light of this the authors argue that current definitions of innateness have each identified it with one of the cues, ignoring the other cues. This explains why intuitively compelling



counterexamples to each definition can so easily be found, simply by choosing examples that make the other cue(s) salient.

### **2.3. The Philosopher as Ecologist**

One motivation for the two empirical studies just described was to transcend the limitations of traditional conceptual analysis. The traditional method of devising a series of ingenious thought experiments too often ends with the 'dull thud of conflicting intuitions'. Experimental philosophy has the capacity to assess competing analyses against data and to avoid biases introduced by working with a single subdiscipline or a single school of thought in the science to be studied.

Such philosophy 'in the trenches' is in a privileged position to provide the bridge between philosophy and science, since its aim to provide biological knowledge unites it with the science itself. At least part of philosophy of science has abandoned the idea that its job is to enforce rigor and precision within science through the stabilization and disambiguation of scientific meanings. Equally gone is Paul Feyerabend's conceptual anarchism, in which the history of science is little more than a series of changes in the fashionable topics of scientific discussion (Feyerabend, 1975). In place of these two models we have come to appreciate that conceptual change in science is rationally motivated by what scientists are trying to achieve, by their accumulated experience of how to achieve it, and by changes in what they are trying to achieve. Empirical science is a powerhouse of conceptual innovation. The gene concept is a case in point: in its century of existence the gene has been redefined many times, often radically. This makes sense if

we think of concepts as tool of research, as ways of classifying the experience shaped by experimentalists to meet their specific needs. Necessarily these tools get reshaped as the demands of scientific work change. In the study of conceptual evolution, the history of genetics provides a ‘conceptual phylogeny’ of the gene. The Representing Genes project is an attempt at ‘conceptual ecology’, that is, an attempt to determine some of the pressures that caused the gene concept to diversify into a number of different epistemic niches.

In this section we have given a brief description of some experimental philosophy of biology. We hope that these concrete examples give some substance to our claim that the humanities need not be confined to discussing the social or ethical consequences of biology, but can also contribute to a better understanding of biology itself, to understanding, for example, what genes are and what it is for something to be innate.

### **3. From Science Criticism to a New Vision of Postgenomic Biology**

Biohumanities is a critical enterprise that reflects on the epistemic virtues and limitations of current approaches. For example, an analysis of the gene concept should aim to shed light on the investigative utility and biases of gene-centered explanations in molecular, developmental and evolutionary biology (Waters, 2004).

As a result of the Representing Genes project we have come to embrace a version of the widely accepted dichotomy between an abstract, statistical gene and a concrete, mechanistic gene (Falk, 2000; Gilbert, 2000; Gilbert, 2003; Moss, 2003), but have felt the

need to introduce a further distinction between a simple ‘consensus gene’, based on prototypical examples of how genome structure supports genome function, and a ‘postgenomic gene’ that embraces the messy reality of the wide range of known relationships between genome and genome product (Griffiths and Stotz, 2006, see also Gerstein et al., 2007). We believe that the nature of the postgenomic gene supports the view that phenotypes are not simply expressions of genetic information, but rather emerge from a developmental system that encompasses many aspects of what would traditionally be regarded as the environment.

Contemporary gene-centered accounts in molecular and developmental biology rest on a static, structural conception of the gene that clings as closely as the facts will allow to its starting point in the long-superseded idea that one gene corresponds to one polypeptide. In its place one of us has promoted the idea of ‘constitutive molecular epigenesis’. This replaces the metaphor of ‘gene action’ with the more apt metaphors of sequence ‘activation’, sequence ‘selection’ and sequence ‘creation’. These metaphors reflect what happens during the expression of the genome through transcriptional, co-transcriptional, and post-transcriptional processes of DNA coding sequences: genes are composed on the fly by recombining in time and tissue-specific ways the template capacity of the genome (Stotz, 2006, 2007).

Postgenomic biology has brought with it a new conception of the ‘reactive genome’ that is not only activated and regulated, but in which sequences are actively selected and newly created during the expression process that include signals from the internal and

external environment. Therefore, alleged explanatory categories such as ‘genetic’ versus ‘environmental’, instead of explaining the origin of a phenotype, preclude further investigation into its real causes.

The concept of a genetic trait, and the related idea of innateness, are often defended by pointing to the allegedly unique role of DNA in heredity. Transgenerational stability of form, however, requires more than faithful transmission of DNA. Genome sequences depend on the context for their differential expression. Natural selection selects adaptive phenotypes, which are always derived from non-linear interactions among a range of diverse developmental resources. Their organization frequently exhibits phenotypic plasticity, a capacity that allows the organism to react adaptively to different environmental conditions (Pigliucci, 2001; West-Eberhard, 2003). The stable but sufficiently plastic inheritance of an adaptive developmental system results from the reliable transmission of all the necessary developmental factors across generations. In other words, heredity relies on a stable ‘developmental niche’ which is faithfully reconstructed by various combinations of the population, the parent and the organism itself. The unit of evolution is the whole developmental system (Schlichting and Pigliucci, 1998; Waddington, 1952).

To understand heredity and development we should “Ask not what’s inside the genes you inherited, but what your genes are inside of” (West and King, 1987, 552). What counts is not only the particular gene you inherit but also when, where and how it is expressed by a time- and tissue dependent regulatory network. Given the vulnerability of the genome to

environmental influences, it was simply a matter of time before most systems found ways to manage aspects of their developmental niche. Cytoplasmic chemical gradients, mRNAs, transcription factors together with the necessary cellular organelles and structures that are inherited with the ovum, give this process a head start, and maternal control over the fetus' environment extend to the uterus or pre-hatchling state. Postnatal factors, such as the licking of pups by rat mothers, continue to influence gene expression levels. The protein packaging of DNA provides an imprinting system, often called the histone or chromatin code, which gives parents pre- and postnatal control over the offspring's gene expression (Meaney, 2004). Parental effects also include differential provisioning of resources, preference induction (oviposition, imprinting on food, habitat, and mates), and social learning (Jablonka and Lamb, 2005; Mousseau and Fox, 2003).

There have been repeated attempts to reduce all of these mechanisms of extended inheritance to the action of inherited or parent-of-origin genes, so that ultimately the real causes are all genetic. This special pleading fails in the light of the discovery that development relies not only on the presence of particular genes in an organism but at least as much on the regulated expression of genomes, which ultimately depends on environmental, as well as genomic, factors. Wherever there are genes there are extragenetic factors necessary for their regulated expression.

The sketch just given shows how science criticism can lead to changes in interpretation of known facts to give rise to a different – in this case radically different – vision of biology. One aim of constructing such a new vision is to potentially motivate biologists to

reinterpret earlier scientific findings and to prioritize different questions for future research. Another, as we now go on to discuss, is to contribute to a more adequate form of science communication.

#### **4. Biohumanities and Critical Science Communication**

If the history and philosophy of biology has something to offer to the public understanding of science, it is to contribute to the creation of a critical science communication process, one aimed at making expert understanding accessible whilst simultaneously revealing it as contestable. Historians of science have often tried to achieve this by emphasizing the contingency of the intellectual frameworks within which science accommodates data, and which in turn influences the kinds of data that are collected. By documenting the historical influences that led scientists to adopt a particular intellectual framework, they suggest that different choices might have led science to develop in a different manner. Discussions of the origin of the informational framework for understanding genetics make a case for historical contingency of this kind (Kay, 2000; Keller, 1995). This is not to suggest that the currently dominant intellectual framework does not accommodate the data that has been gathered, or even that it was not (or is not) a fruitful source of discoveries. The point is rather that there are other ways to look at that data, and that there are other kinds of data that might be gathered.

Philosophers of science have been less concerned than historians with the contestability of science. Their main contribution to science criticism has been to analyze the chains of reasoning that connect specific scientific findings to claims about the broad significance of those findings. There is a very direct connection between this work and the public

understanding of science, since it is just these broader claims about the wider significance of some class of scientific findings that tend to be the focus of popular science writing. Thus, for example, following the popularization of post-Hamiltonian evolutionary genetics by *The Selfish Gene* (Dawkins, 1976) and similar works, philosophers of science discussed whether the developments in evolutionary genetics in the 1960s and 1970s really implied that the individual gene is the unit of evolutionary change. Some argued that this model of the evolutionary process was simply equivalent to more traditional models. Others argued that there were substantial scientific reasons to prefer more traditional models in at least some cases. Rather than being straightforward empirical matters, these questions were shown to turn on philosophical issues such as the nature of theory reduction, or the relationship between prediction and explanation (Sterelny and Griffiths, 1999, Chapters 3-4). The work of a number of philosophers and biologists gradually established that the most socially prominent claim made on the basis of mid-twentieth century genetics – that the fundamental principle of evolution is selfishness – is at least as much a matter of semantics as a scientific discovery (Sober and Wilson, 1998). Given the long history of attempts to draw lessons for society from the nature of the evolutionary process, this conclusion is of obvious value.

The other way in which the Biohumanities can contribute to critical science communication is through creating and criticizing broad visions of biology in the sense described in Section 3. Take, for example, the claim by ethologists such as Patrick Bateson (1976) and Richard Dawkins (1986) that biological development is more like the execution of a recipe than the execution of a blueprint. Communication theorists have criticized this proposal on the grounds that many audiences do not understand these

metaphors in the way their creators intended (Condit, 1999a, 1999b). But this assumes that Bateson and Dawkins' aim was to find a good metaphor to communicate the (known) content of science. Instead, at the level of this broad summary of what we have learnt from a century of genetics, the content of science is contested. The two metaphors embody different, competing visions of that content. The recipe metaphor is an attempt to communicate the vision that morphogenesis is less like the workings of a computer than like a chemical reaction. Developmental biologist H. Frederick Nijhout writes, "The simplest and also the only strictly correct view of the function of genes is that they supply cells, and ultimately organisms, with chemical materials." (Nijhout, 1990, 444) While Nijhout does not use the r-word, it is on the tip of his tongue: the protein-coding sequences in the genome are a list of ingredients. So at the deepest level, the recipe metaphor was intended, not as a device for popularization, but as a vision of developmental biology, and one intended to be taken as seriously as 17th century life-scientists like Stephen Hales took the idea that the body is a machine. Critics of the blueprint metaphor have written of the need for a 'gestalt-switch' - a change in scientific vision - so that without necessarily questioning any specific findings of past research, biologists will come to see those findings differently and perhaps prioritize different questions for future research. In the same way, those who defend metaphors like that of the genetic program are usually convinced that the analogy between the genome and some aspect of computer technology is very close indeed. For example, someone who believes that small RNAs are the real key to the control of development will emphasize the 'digital', combinatorial nature of the specificity of these sequences for the regions of DNA which they bind (Mattick, 2004). For such authors, a computational vision of the



genome embodies in a diffuse way a set of expectations, research emphases, tactical decisions about what to build into artificial experimental systems, and so forth.

Authors in the biohumanities are in an excellent position to contribute to discussions of this kind. The broad interpretations of biology which they offer are founded in the best cases on an extensive knowledge of the biology itself and an extensive historical knowledge of how current intellectual formations came into being, as well as of the 'roads not taken'. This puts them in a position to break out of conventional representations of biology and create new visions. For example, one of the most striking new metaphors of recent years has been philosopher and former cell-biologist Lenny Moss's description of the regulation of gene expression as the work of 'ad hoc committees' of molecules assembled not on the basis of some plan to be found in the fertilized egg, but on the basis of the particular molecular 'expertise' available in a cell as a result of its actual history of transactions with other cells/tissues and with influences derived from the wider environment (Moss, 2003). This is a metaphorical expression of the sort of 'postgenomic biology' that we sketched in Section three. Moss's new figurative landscape has been taken up by a major contributor to the literature on the public understanding of genetics (Turney, 2005).

## **5. Conclusion**

This paper described a conception of the role of history, philosophy and social studies of biology in relation to biology itself, a conception which we termed 'biohumanities'.

Biohumanities research has four related aims: deepening our understanding of biology itself, engaging in constructive science criticism, creating alternative visions of biology,

and achieving critical science communication. In Section two we outlined how the new 'experimental philosophy' methods can contribute to the first of these aims. Section three and four demonstrated the potential of biohumanities research to further the other three aims.

Physicist Richard Feynman is supposed to have said that philosophy of science is no more use to science than ornithology is to birds. In this paper we have tried to show that this is very far from the truth. The complex and often troubled relations between science and society are critical to both parties, and the philosophy and history of science can help to make this relationship work. They may be as valuable to science as conservation biology is to birds<sup>3</sup>.

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<sup>3</sup> This analogy is due to Griffiths' colleague John Wilkins: <http://scienceblogs.com/evolvingthoughts/>

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