



# Experimental Philosophy of Science

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## Abstract

Experimental philosophy of science gathers empirical data on how key scientific concepts are understood by particular scientific communities. In this paper we briefly describe two recent studies in experimental philosophy of biology, one investigating the concept of the gene, the other the concept of innateness. The use of experimental methods reveals facts about these concepts that would not be accessible using the traditional method of intuitions about possible cases. It also contributes to the study of conceptual change in science, which we understand as the result of a form of conceptual ecology, in which concepts become adapted to specific epistemic niches.

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## 1. *Experimental Methods and Conceptual Analysis*

Conceptual analysis is widely regarded as not merely one way to do philosophy, but as the method that defines philosophy itself. Philosophers have traditionally analyzed concepts by appealing to their own linguistic competence with the corresponding words. Effectively, the philosopher treats him or herself as a sociolinguistic ‘sample of one’. An analysis is judged adequate if the philosopher is unable to imagine a case in which their intuitions about the application of words clash with the implications of their analysis of the corresponding concepts. This approach can be extended to technical scientific concepts, such as the concept of the gene. Any philosopher of science worth their salt should be in a position to consult his or her intuitions as a scientifically literate sample of one, and thus equivalent for this purpose to a member of the scientific community. This traditional approach to conceptual analysis faces an obvious difficulty, however, if key scientific concepts, such as the gene concept, display substantial heterogeneity between different communities of researchers. A sample of one is obviously not going to reveal the differences in ideas about the gene which arise from different training, experience, or research focus. To study these differences it is necessary to sample various different groups of biologists. This rationale for adopting experimental methods in philosophy of science is reminiscent of the way in which the introduction of experimental methods in ethics and epistemology was necessary to

reveal cultural variation in ethical and epistemic concepts (Weinberg, Nichols, and Stich; Machery et al.).

In our work we conceive scientific concepts as ongoing – and possibly ramifying – projects by scientific practitioners of deriving empirical generalizations of increasing scope and reliability. This is achieved by adjusting both the extension of those concepts, so as to encompass sets of instances with as much in common as possible, and the intension of those concepts, so that statements involving the category change their modal status in a way that reflects the centrality of those statements to current theory. For the scientific practitioner, concepts are tools which classify experience in ways that meet their specific needs and which are reshaped in the light of new empirical findings. This attitude is sometimes made explicit, but is implicit whenever scientists describe a statement as a ‘definition’ and yet regard it as hostage to future empirical findings, as they commonly do. If scientific concepts are evolving tools, it should not be the aim of philosophers of science to identify the one correct conception associated with a word or phrase. An alternative aim, and the one that we adopt, is to examine how conceptual differences reflect different scientific requirements. The needs of a particular group of investigators can be conceived as an epistemic ‘niche’ and changes in the concept over time can be seen as responses to changes in the niche. As a result of such conceptual evolution, what was originally a shared concept between two or more communities of researchers can become a range of related but distinct concepts. From this perspective, the conceptual analyst has no alternative but to examine what a range of different scientists say and do. But there are a number of ways to achieve this. One is via the history of science, an invaluable approach when a concept is changing over time. Another is by comparing published work from different scientific fields. A third is to conduct experimental studies that compare how scientists from different backgrounds respond to carefully chosen examples. This third method of ‘conceptual ecology’ has some disadvantages with respect to time, effort, and expense, and some advantages with respect to systematicity and rigor.

In the next section we will give more substance to these remarks with specific examples of experimental work on the concept of the gene and the concept of innateness. The results of the innateness study reveal another strength of experimental philosophy when compared to traditional methods of conceptual analysis. Philosophers have long realized that many concepts are not applied on the basis of a single set of necessary and sufficient criteria. The idea that the instances of a concept may be related by ‘family resemblances’ is associated with Ludwig Wittgenstein. Conceptual analyses of this type postulate a cluster of criteria, some proportion of which must be satisfied for an instance to fall under the concept. However, we are not aware of philosophical analyses that assigns different weights to the various criteria that form such a cluster, or that consider the possibility

of interaction between the criteria, so that the weight given to one criterion depends on whether some other criterion applies. The results of the innateness study suggest that both of these are important matters to bear in mind when analyzing a concept.

The neglect of these obvious possibilities is still more puzzling in light of the successful experimental tradition in the psychology of concepts that was inspired by Wittgenstein's idea of family resemblance (Rosch and Mervis). Psychologists have taken the idea that a concept can consist of a prototype and a similarity metric and drawn the obvious conclusion that analyzing such a concept means specifying the mapping between the various criteria of application of the concept and the concept itself. This means considering as many mapping functions as possible and picking the one with the best fit to the data. In contrast, philosophers have restricted themselves to a small subset of the possible mappings. In addition to the two aspects of conceptual structure just highlighted, another obvious possibility is that a concept might correspond to a multi-modal similarity space with several discrete exemplars, rather than a single, central prototype. Psychologists have explored this idea, but philosophers have not. We suggest that the reason for this is simply methodological. It is hard to imagine how swapping intuitions about examples presented in narrative form could be done with sufficient rigor to test (or even to clearly characterize) analyses with anything but the crudest, qualitative version of differential weighing of criteria, let alone interaction between criteria or a multi-modal similarity space. So another reason for adopting experimental methods is that, given some widely accepted assumptions about the nature and aims of analysis, only experimental methods have much prospect of success.

A common objection to any use of experimental methods in philosophy is that by adopting experimental methods the investigator is necessarily abandoning philosophy and taking up some other discipline, such as anthropology or, as one anonymous referee alleged in our own case, sociology of science. But this objection is fundamentally mistaken. First, there is simply no definite line between philosophy and the natural sciences: the boundary is at best vague and shifting. Second, in so far as philosophy is distinguished from various natural sciences it is by the questions it asks, rather than by any restrictions on the 'proper' methods of philosophy. Experimental philosophers have not lost their identity as philosophers through their employment of methods traditionally associated with the sciences, because they employ these methods in an attempt to answer philosophical questions.

## *2. Two Studies in Experimental Philosophy of Science*

This section describes two X-phi projects. The first focuses on changing concepts of the gene. Previous research had 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 conceptualizations of the gene in particular biological fields (Stotz, Griffiths, and Knight). The Representing Genes Project was an extension of that earlier work (Stotz and Griffiths). The next subsection will briefly describe the Representing Genes project, concentrating on the methods used. For a more substantive discussion of the project's findings about the gene concept, see the works by Griffiths and Stotz ('Gene in the Postgenomic Era'; 'Gene').

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'. They used their findings to explain why a series of existing analyses of the innateness concept are subject to compelling intuitive counterexamples. We outline this work in Section 2.2.

### 2.1 THE REPRESENTING GENES PROJECT<sup>1</sup>

This project was an attempt to assess the impact of the on-going genomics revolution on concepts of the gene (Stotz, Bostanci, and Griffiths; Stotz and Griffiths). The actual practice of genome annotation inspired the investigators to design a simple, annotation-like task as one part of the 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. The survey instrument 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'.

In light of the difficulties of the classical molecular gene concept (Rheinberger; Falk, 'Gene'; Griffiths and Stotz, 'Gene in the Postgenomic Era'; 'Gene'), it has been suggested that working biologists employ a kind of *consensus gene* concept, that is, a stereotype that combines features from a number of exemplary cases (Fogle). The consensus gene concept is based on a collection of flexibly applied features of well-established genes. A stretch of DNA is considered to be a gene if it is close enough to one of the exemplars of a classical, molecular gene, e.g., it contains an open reading frame (a sequence beginning with a start codon and ending with a stop codon) of a length similar to that of known genes, it has a TATA box (a sequence within the core promoter of most eukaryotes that promotes transcriptional initiation by binding basic transcription factors), and it is known to be transcribed into an RNA molecule. Fogle has argued that by combining structural and functional features into a single stereotype

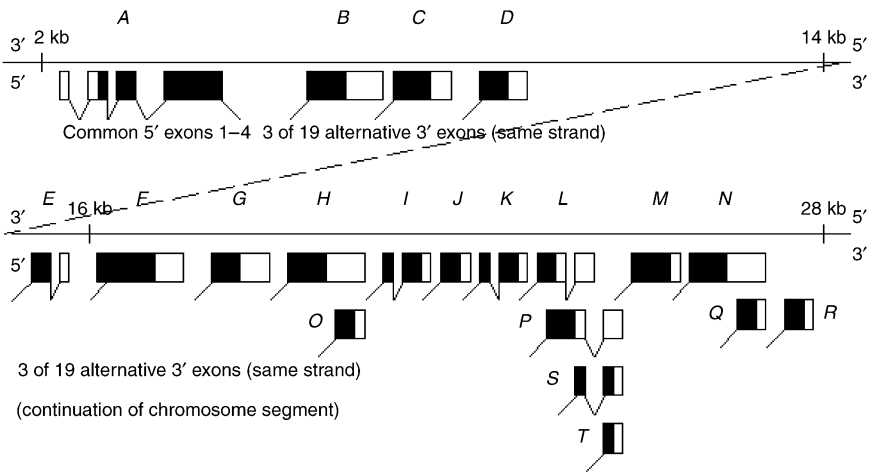


Fig. 1. A case used in the Representing Genes survey instrument (see text for discussion).

the consensus gene concept hides both the diversity of DNA sequences that can perform the same function and the diverse functions of particular DNA sequences. In other words, the consensus gene concept inherently distracts from conceptually problematic cases. As with stereotypes more generally, even when biologists have been exposed to cases that violate the rule, they tend to revert to the stereotype in future work.<sup>2</sup> Complex genetic elements are consequently often presented as spectacular but isolated discoveries, rather than a platform for questioning current conceptualizations of the gene.

Prototype-based cognition can be seen at work in biologists' responses to two closely related cases. The *Drosophila* locus *mod* (*mdg4*) contains a fairly conventional gene from which the larger part of a molecule is transcribed. The final section of the molecule, however, comes in several variations, located some distance away on the chromosome. Some of these are on the same strand of the DNA as the main part of the molecule (Fig. 1). Others are on the opposite (antisense) strand, so that when they are transcribed they are read in the 'opposite direction' (Fig. 2).<sup>3</sup> The mechanisms that make the smaller part of the molecule and which 'trans-splice' it to the larger part are identical whether it is transcribed 'in sense' or 'antisense'. However, when we presented these two cases to biologists there was a substantial difference in their responses, with the first case more likely to be treated as a single gene than the second case (Figs. 3 and 4). We are not aware of any substantive theoretical reason to treat these two cases differently. The difference seems to be that a single gene with parts on both strands and hence running in opposite directions – 'head to head' – is just too far away in the similarity space from the exemplars of the gene that feature in the education of biologists.

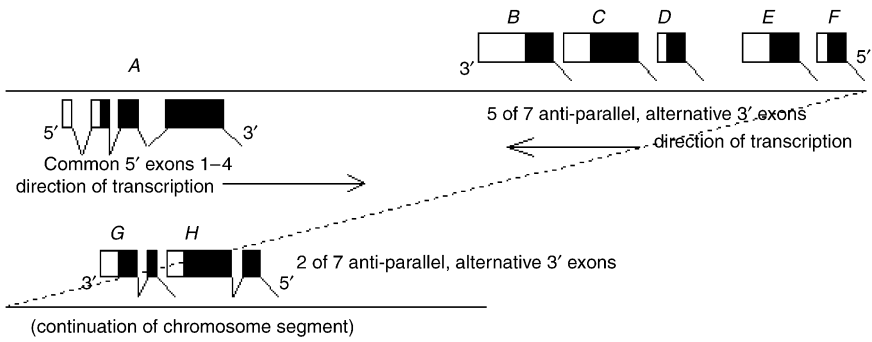


Fig. 2. A case used in the Representing Genes survey instrument (see text for discussion).

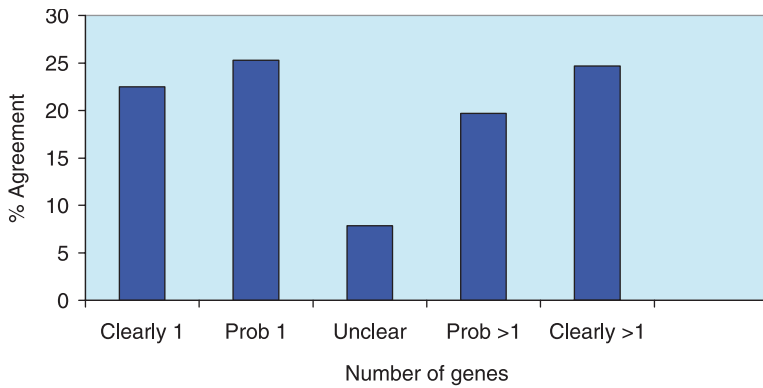


Fig. 3. Responses of c.150 biologists to the case shown in Fig. 1. Note the bimodal distribution of responses (see text for discussion).

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). The investigators argued that these different starting points would affect how scientists set out to unravel the complex relationship between genes or other molecular factors and the phenotype. Hence the second task asked subjects to assess the value of different research strategies for investigating complex diseases. For each disease four strategies were offered, 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. The study looked for

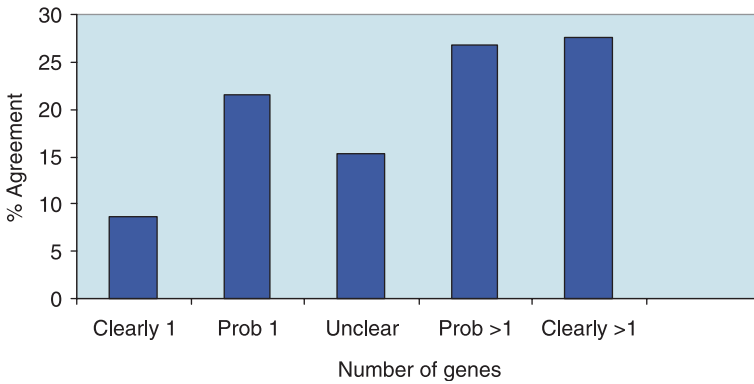


Fig. 4. Responses of c.150 biologists to the case shown in Fig. 2. Note that the responses are skewed towards the right of the graph (e.g., more than one gene. See text for discussion).

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). 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’. But other philosophers 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, Machery, and Linquist). 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 (Fig. 5). 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, ‘What is Innateness?’). These features are:

Birdsong is one of the most intensively studied aspects of animal behaviour. Since the 1950s scientists have used recordings and sound spectograms to uncover the structure and function of birdsong. Neuroscientists have investigated in great detail the areas of the brain that allow birds to develop and produce their songs. Other scientists have done ecological fieldwork to study what role song plays in the lives of different birds.

The Alder Flycatcher (*Empidonax alnorum*) is a migratory neo-tropical bird which breeds in southern Canada and the northern USA. Studies on the Alder Flycatcher show that the song an adult male produces does not depend on which songs they hear when they are young. Studies also show that different males in this species sing different songs. Furthermore, close observations of these birds reveal that the males' song attracts mates and helps to defend their territory. Scientists therefore agree that the bird's song has a real function, like the heart in humans.

On a 7-point scale, 1 meaning strongly disagree and 7 meaning strongly agree, how would you respond to the following statement?

'The song of the male Alder Flycatcher is innate.'

Fig. 5. One of the probes used in a study of the innateness concept by Griffiths, Machery, and Linquist. In the second paragraph of this particular probe, subjects are encouraged to think that this song is developmentally fixed, varies between individuals, and serves a purpose. The order of presentation of these three items of information was randomized in the actual study.

1. Fixity – the trait is hard to change; its development is insensitive to environmental inputs in development; its development appears goal-directed, or resistant to perturbation.
2. Typicality – the trait is part of what it is to be an organism *of that kind*; every individual has it, or every individual that is not malformed, or every individual of a certain age, sex or other natural subcategory.
3. Teleology – this is how the organism is *meant* to develop; to lack the innate trait is to be malformed; environments that disrupt the development of this trait are themselves abnormal.

By systematically varying information about Fixity, Typicality, and Teleology in a set of cases presented to nearly 250 undergraduate students, Griffiths, Machery, and Linquist were able to determine the statistical relationship between the presence of each of these three features and subjects' willingness to describe a song as innate.

The results provided clear evidence that when people decide whether a trait is innate, they focus on two *independent* cues – Typicality and Fixity, and tentative evidence that people may respond to a third independent cue, namely whether a trait has a purpose (Teleology). The results also showed that Fixity is weighted substantially more heavily than Typicality. The more features of innateness something has, the more likely people are to call it 'innate'. The fact that the effects of each of the three features on the application of the innateness concept are *statistically independent* is the

most important result of the analysis. Griffiths, Machery and Linquist hypothesized that people implicitly believe that animals have inherited inner natures. These natures cause animals to have the distinctive observable traits of their species (genus, family, etc.). The three features of innateness are the properties that mark something as an expression of an animal's inner nature, as opposed to a trait that the animal has because of the impact of its environment. A common reply to the claim that innateness is a combination of several different properties is that only one of these properties is actually part of the meaning of 'innate'. On this view, the fact that other properties influence judgments of innateness can be explained by saying that people believe that a behavior with those other properties is also likely to be innate, although those properties are not part of what it means to be innate. Hence, it is argued, accounts like that of Griffiths, Machery, and Linquist simply fail to distinguish between innateness itself and evidence for innateness. But if this objection were correct, then information about those other properties should be discounted when subjects are told that a behavior lacks the key property that is actually part of the meaning of 'innate'. This would show up as an interaction effect in the experiment.

These results can be used to explain some of the problems facing existing philosophical analyses of the concept of innateness. Griffiths, Machery, and Linquist argue that each popular analysis fixes on one aspect of the vernacular concept of innateness, leaving itself open to counterexamples which appeal to intuitions derived from the other aspects. This explains why intuitively compelling counterexamples to each analysis can readily be found, by choosing examples that make the other feature(s) salient. For example, an analysis which identifies innateness with insensitivity to the developmental environment (Fixity) will appear compelling if it is presented using examples which either combine Fixity with the other two features, or give no information about those other features, or do not make salient the fact that those features are absent. But the analysis is vulnerable to a counterexample which, for example, presents a trait that is clearly an evolved adaptation (Teleology) and found in every normal individual (Typicality), but which depends for its development on the details of parental care (~Fixity). As luck would have it, the ability of laboratory rats to use their penis in copulation provides just such a counterexample.

The traditional approach to conceptual analysis could in principle have discovered that the concept of innateness has more than one criterion of application. It is also possible in principle to imagine a series of well-chosen examples providing positive evidence of an interaction effect. However, it is much harder to imagine how a series of examples could convincingly eliminate the possibility of an interaction effect. The issue of differential weighting also poses a challenge to traditional methods, as noted above. Discussing how strongly one feels the pull of a certain aspect of an

example seems unduly subjective, to say the least. Nor is it clear how intuitions about an unsystematic set of examples can be used to address the question of whether different criteria interact with one another.

### *3. Experimental Philosophy of Science as Conceptual Ecology*

We claimed in section one that because experimental philosophy of science is well-suited to study conceptual differences between research communities, it has the potential to throw new light on the nature and cause of conceptual change in science. We have come to believe 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 was in part 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. Newly discovered phenomena have necessitated new conceptions of the gene, but the new conceptions have not displaced earlier conceptions, which often remain best adapted to the classes of genetic phenomena which they were devised to handle. As a result, multiple conceptions of the gene have come to coexist (Griffiths and Stotz, ‘Gene in the Postgenomic Era’; ‘Gene’).

The gene was originally defined functionally in terms of the results of the whole-organism hybridization techniques available to early geneticists. In the absence of knowledge about the biochemical basis of Mendelian inheritance this early ‘instrumental gene’ was a hypothetical entity, an intervening variable between the phenotypes of the parental generation and the distribution of phenotypes in following generations (Falk, ‘What is a Gene?’). As new techniques became available and new questions about the structural nature of the gene became pressing, the gene was redefined in molecular terms, as we discuss below. However, just as old techniques can survive alongside newer ones, old concepts can remain the best tool for the work for which they were originally designed. For example, when a medical geneticist is seeking the ‘genes for’ a disorder she is looking for traditional Mendelian genes – sections of chromosome whose pattern of inheritance explains the phenotypic differences observed in patients. Translated into molecular terms these sections may turn out not to be molecular genes. Some abnormalities in human limb development, for example, have been tracked down to mutations in a gene on chromosome 7. But

recent research suggests that the gene in which the mutation is located plays no role in the development of these abnormalities (Lettice et al.). Instead, embedded in that gene is a sequence which acts to regulate the use of the gene ‘sonic hedgehog’, about one million DNA nucleotides away on the same chromosome, which is involved in the relevant aspects of limb development. Nothing has gone wrong in either piece of research. It is simply that the molecular gene concept is not a good tool for some kinds of research. The instrumental, Mendelian gene remains the best tool in fields like medical genetics and population genetics. Hence we need to go beyond the insight that changes in a scientific concept reflect changes in scientific knowledge: this cannot explain the parallel use of several different concepts at a single time. An adequate understanding of conceptual change requires the recognition that scientific concepts are tools for research, as much as glassware, microscopes, and automated sequencers. When multiple tasks are carried on in parallel, different conceptualizations derived from some common conceptual origin may coexist at one time.

In the 1960s molecular biologists devised a single, unified concept of the gene, which united its structural and functional aspects. The molecular gene is a *structure* in the DNA whose *function* is to specify the linear order of elements in a gene product (RNA or polypeptide). This is reflected in the Central Dogma of Molecular Genetics, which claims that the genetic ‘information’, meaning the linear sequence of nucleic acid bases, specifies the linear order of the gene product (Crick, ‘Central Dogma’; ‘On Protein Synthesis’). In the light of today’s knowledge about the ways in which a limited number of DNA sequences is used to create a vastly greater ‘transcriptome’ of gene products, the sequences we count to arrive at the claim that there are about 21,000 human or 14,000 *Drosophila* genes are best regarded as ‘nominal genes’ (Burian) – sequences that fit a stereotype of how DNA plays the gene-role, as we described above. The cases that inspire the stereotype are the simple cases of bacterial transcription and translation that were used to derive our basic understanding of molecular genetics in the 1960s.

Over the past twenty years, and particularly in the ‘postgenomic era’ in which massive amounts of sequence data have become readily available, it has become clear that the relationship between DNA sequences and gene products is not one to one, but many to many. Stotz, Griffiths, and their collaborators have argued that in some areas of the molecular biosciences a new, ‘postgenomic’ conception of the gene is emerging. Genes are ‘things an organism can do with its genome’: they are ways in which cells utilize available template resources to create the biomolecules that are needed in a specific place at a specific time (Stotz, Bostanci, and Griffiths; Griffiths and Stotz, ‘Genes in the Postgenomic Era’). The same DNA sequence potentially leads to a large number of different gene products and the need for a rare product calls for the assembly of novel mRNA sequences.

Certain coding sequences, plus regulatory and intronic sequences, are targeted by transcription, splicing, and editing factors (proteins and functional RNAs), which in turn are cued by specific environmental signals. Regulatory mechanisms determine not only whether a sequence is transcribed, but where transcription starts and ends, how much of the sequence will be transcribed, which coding and noncoding regions will be spliced out, how and in which order the remaining coding sequences will be reassembled, which nucleotides will be substituted, deleted, or inserted, and if and how the remaining sequence will be translated. Many of these mechanisms do not simply produce alternative protein-coding transcripts on different occasions. A sequence may be transcribed into several parallel, coding and noncoding transcripts on a single occasion. The factors that interactively regulate genomic expression are far from mere background condition or supportive environment; rather they are on a par with genetic information since they *co-specify* the linear sequence of the gene product together with the target DNA sequence. Networks of genome regulation, including several different kinds of gene products and instructional environmental resources, specify a range of products from a gene through the selective use of nucleotide sequence information and, more radically, the creation of nucleotide sequence information that is not present in the base sequence of DNA (Stotz).

The idea that ‘gene’ must be defined top-down, starting from the gene product and working backwards, has been explicitly proposed by some leading molecular biologists (Gerstein et al.). One pragmatic, technological reason that today’s biologists are prepared to consider such radical options is that the challenge of automated genome annotation has turned the apparently semantic issue of the definition of ‘gene’ into a pressing and practical one as the limitations of a purely structural, sequenced-based definition of the gene have become apparent. This is, of course, a fine example of what we have described above as the demands made on concepts by a changing epistemic niche.

#### 4. Conclusion

Experimental philosophy of science is not the rejection of the traditional *goals* of philosophy, but the adoption of new and powerful *methods* to achieve those goals. It allows philosophers to consider accounts of conceptual structure that cannot be assessed – or even clearly stated – using the traditional method of individual intuition. It allows philosophers to embrace and study conceptual diversity, and hence to gain new insights into the process of science, as we argued in section three. It can provide insights for *normative* work in philosophy of science – scientists may be using conceptual tools that are not well suited to the job in hand.

Experimental methods do not seek to *replace* more traditional philosophical methods, but rather to *supplement* them. The impression that experimental

philosophy is out to displace the rest of the discipline can only come from an extraordinarily narrow identification of philosophy with what we might call 'descriptive conceptual analysis'. If the only aim of philosophy was to accurately characterize how some topic is conceptualized by 'the folk' or by some more specific discursive community, then philosophy would be frighteningly close to sociolinguistics and might, indeed, be best served by a predominantly experimental approach. But philosophers have not traditionally contented themselves with documenting the way a subject is conceptualized and waiting for science or society to change the subject. Philosophers have tried to understand why things are conceptualized in a particular way. They have suggested how they might usefully be conceptualized in other ways. Philosophers have documented a range of ways of conceptualizing something and tried to place these alternatives into a broader theoretical framework. Intellectual history has traditionally made as large a contribution to these efforts as the elicitation of intuitions about possible cases. All this is part of philosophy, and of conceptual analysis properly understood.

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### *Short Biographies*

Paul Griffiths is a philosopher of science with a primary focus on the life sciences. He is the author of an influential book on the sciences of emotion, *What Emotions Really Are* (Chicago, 1997) and with Kim Sterelny of a widely used textbook in the philosophy of biology, *Sex and Death* (Chicago, 1999). He has published extensively on philosophical issues in the study of developmental biology and psychobiology as well as on the concept of the gene, the nature of biological categories, and the philosophy and history of animal behavior research <<http://paul.representinggenes.org>>. Together with Karola Stotz he pioneered the use of 'experimental philosophy' methods in the field of philosophy of science, analyzing the diversification of the gene concept in different research communities within contemporary biology <<http://representinggenes.org>>. More recently he and his collaborators have turned their attention to the concepts of innateness, and human nature. Paul was educated at Cambridge and the Australian National University. He taught at Otago University in New Zealand and the University of Sydney, before joining the Department of History and Philosophy of Science at the University of Pittsburgh. He returned to Australia in 2004,

first as an Australian Research Council Federation Fellow and then as University Professorial Research Fellow at the University of Sydney. He is also Professor of Philosophy of Science at the ESRC Centre for Genomics in Society at the University of Exeter, where he spends part of each academic year. In 2006 he was elected to the Australian Academy of the Humanities.

Karola Stotz's research contributes to a reconciliation of nature and nurture, a dualism that stands in the way of a full understanding of development, evolution, and heredity. She has been instrumental in importing this debate into cognitive science and psychology <<http://nanu.dynalias.org>>. An important pillar in such a new theory of development is molecular postgenomic biology, where she has argued for the idea of distributed agency in the regulation of gene expression and cellular processes in general. She has used examples from this field of research to argue for an integrative explanatory strategy that involves reductionist and holistic research methods. Other research areas that inform her approach are embodied, distributed and extended cognition, and animal minds <<http://mypage.iu.edu/~kstotz/>>. Together with Paul Griffiths she pioneered the use of 'experimental philosophy' methods in the field of philosophy of science, analyzing the diversification of the gene concept in different research communities within contemporary biology <<http://representinggenes.org>>. This work has received significant attention from biologists and was discussed in *Nature* 441 (2006): 398–401. More recently, she and her collaborators have turned their attention to the concepts of innateness and human nature. Karola Stotz received her Masters in physical and cultural anthropology from the University of Mainz and her Ph.D. in philosophy from the University of Ghent. She has worked at the Konrad Lorenz Institute for Evolution and Cognition Research in Austria, the Unit for History and Philosophy of Science at the University of Sydney, the Department of HPS at the University of Pittsburgh, and the Cognitive Science Program at Indiana University. In 2008 she will return to Australia as an Australian Research Fellow to work at the University of Sydney in the project 'Postgenomic Perspectives on Human Nature'.

### Notes

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<sup>1</sup> <<http://representinggenes.org>>.

<sup>2</sup> We owe this point to Rob D. Knight.

<sup>3</sup> Both strands of the double-stranded DNA can only be transcribed from the 5' end to the 3' end (the chemical convention of naming different carbon atoms in a nucleotide sugar-ring). Since the sense and antisense strand lie head to toe, both get transcribed from opposite ends.

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