The Dynamics of Scientific Concepts: The Relevance of Epistemic Aims and Values

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The philosophy of science that grew out of logical positivism tended to construe scientific knowledge in terms of a set of interconnected beliefs about the world, such as theories and observation statements. Confirmation was understood as a logical relation between observation statements and theoretical statements. This was dubbed the 'context of justification', to be contrasted with the 'context of discovery', where discovery was not generally deemed to be a rational process and thus not a concern for philosophy. During the last few decades this vision of philosophy of science has changed (Brigandt 2011d; Hacking 1983). Nowadays discovery (e.g., in experimental biology) is seen as intimately tied to confirmation and explanation (Bechtel 2006; Craver 2007; Darden 2006; Weber 2005). Science is conceived not merely as a set of axiomatic systems, but as a dynamic process based on the various practices of individual scientists and the institutional settings of science (Hull 1988; Longino 2002; Brigandt 2011a, sect. 4). Two features particularly influence the dynamics of scientific knowledge: epistemic standards and aims. An existing standard (be it a methodological standard, an evidential standard, or a standard of explanatory adequacy) accounts for why old beliefs had to be abandoned and new beliefs came to be accepted. At the same time, standards are subject to change. Epistemic aims (assumptions about what issues are currently in need of scientific study and explanation) likewise influence the practice and dynamic workings of science (Brigandt 2013; Love 2008). Notice that epistemic standards and aims operate on a different dimension than scientific beliefs. Whereas scientific beliefs are representations of the world, scientific standards and aims are epistemic values. Epistemic aims (e.g., explanatory problems deemed to be important) are not descriptions of the objects of science, but values held by scientists as the actors of science. Taking such epistemic aims and values into account is, in my view, key to an epistemological understanding of the dynamics of science, and past philosophical accounts that focused exclusively on various beliefs (theoretical and observational) missed a whole aspect of scientific knowledge formation.[1]

The relevance of epistemic aims and values for *belief* change has been previously recognized. My paper intends to make a similar point for scientific *concepts*, both by studying how an individual concept changes (in its semantic properties) and by viewing epistemic aims and values tied to individual concepts. In a recent publication (Brigandt 2010b), I have presented my view that a scientific concept consists of three components of content: (1) the concept's reference, (2) the concept's inferential role, and (3) the epistemic goal pursued by the concept's use. In the course of history a concept can change in any of these components (possibly with one component changing while the others are stable); and at any point in time these components of content can vary across different users of the term.

The first two components are well-known. Part of a concept's content is that it has a certain referent, such as kinds of material entities, physical properties, and natural processes. But a concept also embodies beliefs about the referent, where two coreferential concepts may represent the common referent in a different way. This is often expressed by saying that a term has a sense or an intension; sometimes it is construed as the term's inferential role, which is the way in which a term is actually used, or is properly used given the rules of language (Brandom 2000; Boghossian 1993). A concept's inferential role embodies some of one's beliefs about the referent by connecting the concept to other concepts. How a term's meaning or a concept's content (which embodies beliefs about the referent) is actually construed matters less for my purposes (as my concern is to highlight a different aspect of concepts), but in what follows I use the notion of 'inferential role'. According to my approach, a concept's inferential role consists of those beliefs that are important for the application of the concept and that underwrite the

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[1] Even when using a post-positivist framework that, in addition to statements and theories, acknowledges models and accounts of mechanisms, it is important to bear in mind that all the former are representations that must be distinguished from epistemic aims. While my discussion focuses on *epistemic* values in science, I do not rely on a distinction between epistemic and other values. In current (commercialized) biomedical research, aims and values that are intuitively epistemic and intuitively non-epistemic are so entangled in the generation of knowledge that they have to be studied together. The question is not so much whether a value is epistemic or non-epistemic but whether it is licit (including socially desirable).

term's successful scientific use. While there can be more to a term's successful use than the definitions put forward by scientists, a term's definition is a part of the term's inferential role, so that a revision of a term's definition is also a change of its inferential role and thus an instance of semantic change (for more detail, see Brigandt 2010b).[2] Despite its name, inferential role includes not only the inferences supported by a concept, but also the explanations made possible by the concept. A synonymous term found in the philosophical literature is 'conceptual role' (Block 1986, 1998; Field 1977; Harman 1987)—which is more easily seen as including explanations—but I explain below my preference for 'inferential role' (to avoid any conflation with what I call a concept's epistemic goal).

A concept's inferential role and even its reference can change in the course of history. For instance, Nancy Nersessian (1984) has studied the concept of an electromagnetic field in detail by breaking down this concept's content—inferential role in my terminology—into different parts (e.g., function, structure, and causal power) and tracking the historical change of each such part, while viewing different historical stages of each part connected by 'chain-of-reasoning connections.' While this offers a detailed study of *how* this concept's inferential role changed over time, my focus here is on a philosophical account of *why* such change occurred and why it was rational. To be sure, Nersessian (1984, 2008) views conceptual change as a problem-solving enterprise, but to fully explain the dynamic change of conceptual representations (or inferential roles) one has to make epistemic values—such as the aim of solving a *particular* problem—an additional and explicit part of one's philosophical framework. I do so by introducing the *epistemic goal* pursued by a concept's use as a third component of content in addition to reference and inferential role. It is well-known that scientists pursue various epistemic goals, such as confirming particular claims, explaining certain phenomena, or making discoveries of a certain kind. A particular epistemic goal

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[2] Due to this component of conceptual content, there is a close relation between a concept and a mental theory. It is a difficult question as to which of one's beliefs about a referent is part of the inferential role (and thus what distinguishes a concept and one's total beliefs about a referent). For some thoughts on the issue see Brigandt (2010b, sect. 2) and Brigandt (2006, sect. 3.3). I do not discuss it in this paper, as I deem my focus on epistemic aims and values to make a more fruitful contribution to understanding the use of scientific concepts than by revisiting longstanding debates about concept individuation and the analytic-synthetic distinction.

(e. g., explaining cell-cell interaction) is specific to a scientific discipline (e. g., cell biology) in that this discipline but no others are concerned with this scientific aim. While there are often several concepts used to address a particular epistemic goal, my point here is that there are instances where an epistemic goal is tied to a specific concept insofar as the rationale for introducing the term and for continuing to use it is to pursue this epistemic goal. For instance, the epistemic goal pursued by the concept of natural selection is to account for evolutionary adaptation.

Taking this third component into philosophical consideration is essential because it accounts for *semantic change and variation*, i. e., for why a term's inferential role and possibly reference has changed in history, or why a term's inferential role and possibly reference varies across different contemporary users of the term. Among other things, the epistemic goal pursued by a term's use sets standards for when the redefinition of a term (a change in a term's inferential role) is rationally warranted. The notion of a concept's epistemic goal is thereby important for understanding the epistemic dynamics of science and how concepts figure in investigative practice. It can do so because this third component of conceptual content is not about what a concept represents (reference) or how a concept represents (inferential role), but it is an epistemic value—what scientists attempt to achieve when using a concept. For this reason, it is vital to distinguish the concept's epistemic goal from its inferential role. Both are determined by language use, and in this sense inferential role and epistemic goal are aspects of a concept's use. My approach is consistent with the common idea that 'meaning is use' (Kindi in this volume), yet use has usually been identified with how a term is used (inferential role), though what a term is used *for* (epistemic goal) is likewise to be taken into account. Most importantly, terms such as 'concept use', 'function of a concept' and 'conceptual role' could be seen as ambiguously referring to both inferential role and epistemic goal, even though the two must be clearly distinguished.[3]

My tenet that a concept consists of three components (reference, inferential role, epistemic goal) is not so much to be understood as a met-

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[3] Accounts of 'function' in biology have pointed out that there are different notions of functions used by scientists (Wouters 2003). The function of a biological trait can refer to what it does (the activity it performs), but it also can refer to what the trait is for (what it is designed to do for a larger system). These two notions of function mirror the difference between a concept's inferential role and its epistemic goal.

aphysical doctrine about what a concept is, rather it is a methodological guideline about how actual scientific concepts are to be studied—all three components, their change, and their interaction have to be considered (Brigandt 2011c). In what follows, I explain and illustrate this general approach in concrete cases by discussing three biological concepts that exhibit some interesting conceptual dynamics—the concept of evolutionary novelty, the homology concept, and the gene concept. In the final section, I will compare and contrast the three cases and draw some general conclusions.

1. The Concept of Evolutionary Novelty

An evolutionary novelty (also called evolutionary innovation) is a structure in a group of species that was not present in any ancestors of this group (Müller/Wagner 2003). An example of a novelty is the vertebrate jaw, which evolved in the transition from jawless vertebrates to jawed vertebrates (among extant vertebrates, hagfish and lampreys are jawless). The evolution of fins in fish and the transformation of fins into limbs are other examples. The origin of bird feathers is an evolutionary novelty. The concept of evolutionary novelty is central to current evolutionary biology, in particular to the emerging field of evolutionary developmental biology, typically dubbed 'evo-devo' (Hall/Olson 2003). While accounting for the evolution of novel structures is an important scientific task, evo-devo biologists contend that traditional, neo-Darwinian evolutionary biology is ill-equipped to do this. Neo-Darwinism, having population genetics at its theoretical core, can explain how the frequency of an existing trait increases within a population, but it does not provide the tools to account for the very origin of morphological structures. The explanation of evolutionary novelty is a core item on the agenda of evo-devo, and there is widespread agreement that knowledge from developmental biology is essential in explanations of novelty (Müller/Newman 2005; Wagner 2000). Despite the intimate connections of both disciplines in the second half of the 19th century, developmental biology was irrelevant to evolutionary biology for most of the 20th century. As a result, current evolutionary developmental biology is often hailed as forging a (re-)synthesis of evolutionary and developmental biology in the near future (Brigandt/Love 2010; Love 2003).

Despite the fact that, as the central item on the agenda of evo-devo, the concept of evolutionary novelty contributes to defining the intellectual identity of this new discipline, there is substantial disagreement on how to define novelty (Brigandt/Love 2010; Moczek 2008). Whereas some construals of novelty focus on the new adaptive capacities generated by some novel traits, excluding issues pertaining to adaptation and considering structure alone is important to many other accounts of novelty. Some assert that upon its evolution a novel structure qualifies as such (if it was not present in the ancestor), while others argue that novelty means new evolutionary potential, so that a structure can count as a novelty only if upon further evolution it has actually resulted in a wide array of new structural variants. Most importantly, debates about different proposals of how to define 'evolutionary novelty' stem from the difficulty of deciding which morphological changes are mere quantitative variants (and thus not novelties), and which are qualitative differences (and thus genuine novelties). Some define a novelty as a structure that is not homologous to any ancestral structure (Hall 2005; Müller/Wagner 1991), but this may be of no help given that it has been argued that 'being homologous' is not an all-or-nothing affair but a matter of degree (Minelli 2003). For any structure there are some precursors; at least some components of a novel structure (e.g., tissues, cell differentiation patterns) were already present in the ancestor. Indeed, we may be surprised by how much novelty was generated by small developmental changes and minor rearrangements of existing features (Moczek 2008). As a result, there is possibly nothing but a continuum between non-novelty and novelty. Some cynics maintain that the concept of novelty does not admit of any precise definition and does not have a real scientific significance, though it is advantageous to use the label 'novelty' in grant applications.

Admittedly, the concept of evolutionary novelty does a poor job at distinguishing novel from non-novel structural changes. But this would be a drawback *only if* the central function (epistemic goal) of this concept was to make precise distinctions, for instance, if the concept was a tool of classification. In contrast, I follow Alan Love in arguing that the primary function of the concept of novelty is to set a problem agenda, i.e., to point to a phenomenon in need of explanation (Brigandt 2010a; Brigandt/Love 2010; Love 2005, 2006, 2008).[4] In this case the problem

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[4] Some may wonder how the concept of novelty can point to a phenomenon in need of explanation (various evolutionary novelties), if it is not clear exactly which structures are novelties. However, a mechanistic explanation of a morphological transformation is an important achievement even if this structural

is the explanation of the evolutionary origin of novelty, and given the nature of this particular problem, it is clear that knowledge from different biological disciplines is required—developmental biology, paleontology, phylogeny, and evolutionary genetics, among others. As a result, the problem of novelty *motivates* intellectual integration across disciplines. Darden and Maull (1977) have already observed that the integration of fields can be effected by the existence of a problem that cannot be solved by the resources of any field in isolation. But the further philosophical point can be made that a problem agenda can *structure* intellectual integration by foreshadowing how the intellectual contributions from different fields are to be coordinated. The reason for this is twofold. First, a problem agenda is associated with criteria of explanatory adequacy (Love 2008), which specify what considerations have to be adduced to yield a satisfactory explanation. Second, a problem agenda is a complex problem, consisting of several interrelated problems (Love introduced the term problem *agenda* for this reason). A problem agenda such as the explanation of evolutionary novelty consists of component questions that stand in systematic or hierarchical relations. This problem structure indicates how the different explanatory ingredients provided by different fields (e.g., answers to particular component questions) are to be related and integrated.

To illustrate this idea in the context of evolutionary novelty, the first basic step in accounts of novelty (encompassing several smaller component questions) is to lay out a sequence of structural changes leading up to a novelty, showing that and how the novelty qualitatively differs from structures that existed earlier, what aspects or parts of the overall structure has precursors in ancestral species, and how related structures changed in this period. Apart from detailed morphological studies of the relevant structures in extant species, the field of paleontology and its fossil data is particularly important for this task. Likewise, the discipline of phylogeny (which sets up phylogenetic trees) is needed to get an idea of at which phylogenetic junctures certain morphological transitions occurred. A second basic step in the explanation of novelty is a causal-mechanistic account of how the morphological transformations came about. Here developmental biology is necessary to understand

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change does not qualify as a novelty on some definitions of ‘novelty’. The idea that the concept of novelty sets a problem agenda shifts the focus away from the identification of novelty to the more important issue of the explanation of morphological change.

how ancestral developmental systems could have been modified and reorganized so as to result in the advent of the novel morphology. Such an account has to address several levels of organizations (genes, cells, tissues, morphological structures), so that different areas of developmental biology (broadly construed) and other related fields are often involved. The need to address the activities of genes, cells, and tissues across developmental time and relevant changes in such developmental processes across evolutionary time (corresponding to particular phylogenetic junctures and structural intermediates), yields a conceptual template to relate the various explanatory inputs from different disciplines. Sometimes the novel feature to be explained is not just a single structure but an anatomical function, i. e., the relative articulation, movement, and interaction of several structures, for instance the origin of flight in birds. In this case functional morphology is another discipline whose resources are needed, and the problem agenda makes plain that the articulation and interaction of the structures involved and the evolutionary origin and change of such interactions has to be addressed. The scenario of how the novelty arose also has to be consistent with the mechanisms of genetic change in populations, and the environmental conditions and forces of natural selection that existed in this historical period, calling for an involvement of the disciplines of population genetics and paleoecology.

In my recent work, I have argued that integration in biology is not the stable theoretical unification of different fields, but the dynamic coordination of various epistemic units (explanations, models, concepts, methods) across several fields (Brigandt 2010a). Rather than several disciplines merging into a unified whole, disciplines often retain some relative autonomy (based on various intellectual and institutional factors), while at the same time engaging in various relations to other disciplines. These intellectual relations can be problem-relative: Given one problem addressed by a discipline, one set of relations to other fields is operative, for the purposes of another problem the discipline currently maintains relations to other fields.[5] Due to their internal structure, problem agen-

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[5] Kitcher (1999) argues that while genuine unification cannot be achieved (as nature is too complex), unification is still a regulative ideal. From my perspective, unification/integration is not at all an aim in itself; rather, a certain kind and degree of integration may be needed *for the aim of* solving a scientific problem (while at the same time some degree of disciplinary specialization may be required as well).

das coordinate interdisciplinary research—as discussed in the case of evolutionary novelty. A problem agenda specifies a particular *epistemic aim*, and its associated standards of explanatory adequacy are *epistemic standards*. In the introduction I have mentioned that epistemic aims and standards generally account for the epistemic dynamics of science, and the same holds in this context, where taking up a problem agenda leads to the emergence of novel epistemic relations across different ideas and fields. A change in the problems currently addressed by a discipline or in the criteria of explanatory adequacy results in further epistemic change.

To return to the *concept* of evolutionary novelty, I have suggested that the primary function of this concept is to set a particular problem agenda, so that this concept motivates interdisciplinary research and coordinates intellectual integration. In this fashion, the concept of novelty generates some epistemic dynamics, including exploratory experimental and theoretical research that is part of attempts to account for specific evolutionary novelties. Using the terminology of my framework on concepts sketched above, a major *epistemic goal* pursued by the use of the concept of evolutionary novelty is to set a problem agenda (the explanation of the evolutionary origin on novelty). Biologists clearly state that one of the aims of evolutionary developmental biology is the explanation of evolutionary novelty, though they may not *explicitly* talk about the function of scientific concepts. Yet the fact that the concept of evolutionary novelty is used to pursue a certain epistemic goal is *implicit* in the practice of many of evolutionary developmental biologists using the concept, so that philosophers can articulate this concept's epistemic goal to make the operation of scientific practice intelligible and possibly contribute to science by making the relevant scientists more aware of and reflective about the functions of their concepts.

By setting a problem agenda, the concept of evolutionary novelty fulfills an important function in science, despite definitions of novelty being contested and it being unclear exactly which structures are novel. The concept's most fruitful epistemic goal is not to classify objects or make precise distinctions. This is at odds with standard philosophical views of scientific terms, which assume that a term refers to certain objects, and that a scientifically useful term has a relatively precise definition which determines which objects fall under the term. Given disagreement on how to define novelty, the reference of the concept of evolutionary novelty is vague and what I call its inferential role (definition) may shift depending on who uses the concept. Still, by taking the epistemic goal pursued by the concept's use into account (which in this case is not to classify and make precise distinctions), one can understand its role in and positive contribution to science. By setting a problem agenda, the concept of evolutionary novelty guides the generation of an explanatory framework, which is to bring together several concepts that are needed to successfully explain the origin of novelty.

2. The Homology Concept

The notion of homology has been crucial to the practice of comparative biology, including evolutionary biology (Brigandt 2006, 2011b; Brigandt/Griffiths 2007). Homologous structures are the corresponding structures in different species. For instance, the right arm in humans, the right wing in bats, the right forelimb of horses, and the right flipper in whales are homologous. Even some of the individual bones of the forelimb (such as the radius and ulna) reoccur in different species. Though the shape of such a homologous structure varies among different species, it is identified as the same structure and typically given the same name across species. In addition to bones, all types of anatomical structures and bodily parts can be homologous, including individual muscles, nerves, and tissues. Molecular structures such as particular genes and proteins are likewise identified as homologous across different species.

Unsurprisingly, the reason why homologous structures occur in different species is that these structures have been inherited from the species' common ancestor. This is reflected by modern definitions of homology: Two structures in two species are homologous if they have been derived from one and the same structure in the ancestor. While homology is an evolutionary phenomenon, the homology concept was actually introduced well before the advent of Darwin's theory of evolution. Up to the 18th century anatomical structures were often referred to by a description of the structure's composition, shape, position, or function, with practices varying across countries. Where shorter names were used by an anatomist, a common name was applied to structures in different species insofar as these structures were of similar shape and function, so that the same name was only used for structures in taxonomically closely related species (e.g., different mammals). The homology concept was established in early 19th century comparative anatomy and embryology, based on the recognition that the same structure can be found in taxonomically less closely related groups, such as reptiles and mammals, or even fish and mammals. This was possible due to the use of two basic criteria of homology. One was the relative position of one structure to other structures of the same organism, such as the relative position of adjacent bones, or a nerve innervating a particular muscle. A structure can substantially vary in its length and shape across species, while keeping its relative position to and articulation with other structures. The other criterion of homology was the idea that homologous structures have the same embryonic origin, i. e., develop out of the same tissues and embryonic precursors in different species.

While the homology concept was already an important part of the practice of comparative biology in this pre-Darwinian period, different non-evolutionary accounts of the nature of homology were put forward. One idea was that different species are governed by the same laws of development, resulting in corresponding structures in different species. Another account appealed to abstract geometric body plans (or possibly to blueprints in the mind of God), so that structures in actual species were defined to be homologous in case they corresponded to the same element in the abstract body plan. The fact that the advent of evolutionary theory paved the way for the later definition of homology in terms of common ancestry raises the following issue: Do the pre-Darwinian and the post-Darwinian uses of the term 'homology' amount to two different concepts, so that the Darwinian revolution led to the replacement of the pre-Darwinian concept of homology by a separate concept? The worry is that the a change in definition makes the pre-Darwinian and post-Darwinian concepts of homology incommensurable (meaning incommensurability in the sense of Kuhn 1962 and). While not addressed by other authors in the case of homology, the issue has been discussed in a related context, namely, the question of whether the pre- and post-Darwinian accounts of the nature species amount to two distinct concepts (Beatty 1986).

In the case of the homology concept, some semantic change did occur with the advent of evolutionary theory. The change in definitions and accounts of homology is what I call a change in the concept's *inferential role*. But on my philosophical framework, inferential role is only one component of a concept. The *epistemic goal* pursued by the use of the homology concept did not shift with the origin of Darwinism, so there was a major element of conceptual continuity. Before the advent of evolutionary theory, biologists used the homology concept for two epistemic aims: (1) the systematic morphological description of several species, and (2) the taxonomic classification of species. Individuating anatomical structures in terms of homology proved to be very conducive for both goals. Another possible scheme of individuating structures is in terms of analogy, where analogous structures are structures having the same function. The wings of birds and insects are analogous, but not homologous. Homologous structures need not be analogous, as the above example of the mammalian forelimb (human arm, bat wing, whale flipper) shows that the function of a homologous structure can be very different in different species.

Homology individuates structures by breaking down an organism into its natural anatomical units. What these units are is not always obvious, as what appears to be one bone can actually be several fused bones (which can be uncovered by a study of the skeletal structure's development, or by comparison with other species where the bones are not fused). Homology also individuates by relating structures across species as the same ones. First, this yields unified morphological descriptions (far more unified than other, earlier approaches permitted). Many anatomical and developmental descriptions that apply to a structure in one species also hold for the corresponding, homologous structure in other species. To the extent that a homologous structure varies substantially across species, dissimilarities (and similarities) become meaningful if they pertain to actually corresponding structures, so that homology provides a reference system to which descriptions across species have to attach. The comparative practice using the homology concept made possible a unified morphological account of the vertebrate skeleton even before the advent of Darwinian evolutionary theory (Owen 1849). Regarding the concept's second epistemic goal, pre-Darwinian taxonomists aimed at grouping species into higher taxa not in an arbitrary or artificial fashion, but in a manner that revealed the species' so-called natural affinities. Before the advent of evolutionary theory it became clear that while analogies were similarities independent of taxonomic relatedness, homologies across species reflected their natural affinities and were thus to be used as guides to taxonomic relatedness.

Despite its introduction of a new perspective for biology, the advent of Darwin's evolutionary theory did not change what comparative biologists such as anatomists and taxonomists attempted to achieve when using the homology concept—the epistemic goals were still systematic morphological description and the classification of species. Biologists gradually came to adopt the new definition of homology in terms of common ancestry precisely *because* they realized that the new construal permitted them to meet their traditional epistemic goals in an improved fashion. Once homologous structures are defined as structures inherited from an ancestral structure and taxonomic groups are seen as branches of the tree of life stemming from an ancestral species, it is clear *why* homologous structures are to be compared in the classification of species—whereas analogous structures are similarities independently of phylogenetic relatedness and for this reason are not to be used for taxonomic purposes. A phylogenetic definition of homology permitted a better resolution of controversial claims about particular homologies. A theoretically more sound morphology based on phylogenetic principles led to more adequate and unified anatomical descriptions encompassing different species, as breaking an organism down into structural units by means of homology means to pick out units of morphological evolution across species. (For more details on the history of the homology concept, see Brigandt 2006.)

In the terminology of my framework of concepts, the change in the homology concept's definition and thus its inferential role was scientifically warranted because it permitted biologists to meet the concept's epistemic goals to a greater extent (where the two epistemic goals were stable). To be sure, the continued presence of an *unchanging* epistemic goal alone cannot trigger change in a term's inferential role. Relevant are also novel empirical findings (which can lead to the endorsement of new beliefs or the abandonment of previously held beliefs), in this case the idea of the common ancestry of species and anatomical structures. But note that in addition to a change in beliefs, what philosophers have to account for in this case is a change in meaning, a change in the very definition of the term 'homology'. This is possible because the epistemic goal pursued by a concept's use provides the required standard: A change in the concepts inferential role (definition) is rationally warranted if the new inferential role meets the concept's epistemic goal to a greater degree than the previous inferential role. Some semantic change occurred with the Darwinian revolution, but there is no need to consider it as resulting in incommensurability.[6]

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[6] Given the change in definition, some may notice that I have not answered the question as to whether the term 'homology' as used by pre- and post-Darwinian biologists is the same concept or different concepts. Since on my account a term has three semantic properties (reference, inferential role, epistemic goal) and can change in each of them, I do not think that there is a unique account of concept individuation. Whether this particular instance of semantic change is

In this fashion, the epistemic goal pursued by a concept's use guides scientists to revise the definition of a term, and the notion of a concept's epistemic goal enables philosophers to account for the rationality of semantic change in the course of history. In addition to this, the notion of epistemic goal also bears on understanding semantic variation across different users of a term, if the term's epistemic goal varies. In addition to the homology concept's traditional use in comparative and evolutionary biology, in the second half of the 20th century this concept came to be used in two novel disciplines—molecular biology and evolutionary developmental biology. As I have argued earlier (Brigandt 2003), each of these two new fields came to use the homology concept for somewhat different epistemic goals. This subsequently resulted in semantic variation across fields and in conceptual divergence, where nowadays homology is construed differently in contemporary systematics / evolutionary biology, in molecular biology, and in evolutionary developmental biology. A diversification of the epistemic goals for which the term 'homology' is used (among several biological fields) led to a diversification of the term's inferential role.

In much of *molecular biology* (yet not in molecular evolution and molecular phylogeny), 'homology' simply refers to similarity of gene and protein sequences. From the point of view of evolutionary biology, this fails to distinguish similarities that are and that are not due to common ancestry, where on a phylogenetic definition only the former are instances of homology. Evolutionary biologists have criticized the construal of molecular homology as sequence similarity for this reason (Reeck et al. 1987). Yet in molecular biology, merely knowing that a gene or protein sequence (not studied yet) is similar to a sequence whose role in molecular mechanisms has been established permits an inference regarding which experimental techniques can be effectively used to investigate the new sequence. Thus, the term 'homology' as used in most of molecular biology is used for the epistemic goal of experimental discovery. The starting point for homology as approached in *evolutionary developmental biology* is that an account of homology in systematics and

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viewed as an enduring homology concept (undergoing internal change) or as one concept giving rise to a different concept, in either case the rationality of the change in the term's inferential role has to be justified. I consider it to be philosophically more important to account for change in any of a term's semantic properties than to debate whether this amount to a separate concept being used (Brigandt 2010b).

traditional evolutionary biology does not explain what makes parts of parent and offspring the corresponding (homologous) characters, and it does not explain how the same structures developmentally reappear in different generations. The epistemic goal pursued by the use of the homology concept in evolutionary developmental biology is to developmentally explain how homologues are units of morphological transformation, which can appear in different generations as the same morphological unit while being able to undergo change and structural modification. Here the epistemic goal is causal-mechanistic explanation as opposed to the unified descriptions of comparative biology.

As a result, the notion of a concept's epistemic goal also accounts for why semantic variation emerged (variation in inferential role), if the latter results from a term being used for different concrete epistemic goals by different scientific approaches. Whether or not such semantic variation creates problems depends on the particular case. If a term is used to pursue quite different epistemic goals in different fields (where a single inferential role cannot be used to meet different goals at the same time) and the scientists are not aware of this, communication across these fields can be hampered. This is, up to a point, the case for 'homology' as nowadays used, as some biologists criticize the account of homology of another field without being aware that this field pursues aims different from their own when using the same term. For example, working within the perspective of comparative biology, Cracraft (2005) rejects the approach to homology found in evolutionary developmental biology.

3. The Gene Concept

My account of the gene concept is in some ways similar to my discussion of the homology concept, involving both semantic change in the course of history (see also MacLeod in this volume), and semantic variation at present. The latter situation is of particular interest, as the use of the term 'gene' in contemporary molecular biology can vary from context to context, so most of my discussion is devoted to this issue (for my detailed treatment of the gene concept, see Brigandt 2010b).

Philosophers typically distinguish between the classical gene concept and the molecular gene concept (Waters 1994). The classical gene concept emerged around 1900 and was well-established by the 1920s. Classical genetics was concerned with the study of patterns of inheritance across generations, where phenotypic patterns of inheritance were mathematically explained based on the underlying transmission of genes. On my account, the epistemic goal pursued by the use of the classical gene concept was the prediction (and statistical explanation) of phenotypic of patterns of inheritance, i. e., distribution of phenotypes in the offspring generation. This aim was achieved by an account of classical genes—in my terminology the inferential role of the classical gene concept. Even though genes were often deemed to be concrete material entities, the classical gene concept did not embody a structural construal of the nature of genes apart from the fact that genes were tied to specific chromosomal locations (Sarkar 1998; Waters 1994). Instead, the concept's inferential role contained knowledge about how genes and chromosomes behave in processes of inheritance and sexual reproduction, including meiosis and crossing over, which sufficed for setting up chromosomal maps (showing the relative position of various genes on a chromosome) and predicting and statistically explaining patterns of genotypic and phenotypic inheritance.

The molecular gene concept grew gradually out of the classical gene concept in the 1950s and 1960s. Despite this historical continuity, the classical concept (of the 1920s) and the molecular concept (of the 1970s) differ in important respects. Molecular genetics is not in the business of studying patterns of inheritance across generations; instead, it addresses processes taking place within organisms, in fact within single cells. The epistemic goal pursued with the molecular gene concept is to account for how a gene codes for a specific molecular product, usually a protein. For this reason, a structural characterization of genes is essential. The inferential role of the molecular gene concept includes the idea that a gene is a so-called open reading frame, which is a stretch of DNA bounded by a start and a stop codon and preceded by a promoter sequence. In combination with knowledge about how genes as structural units figure in molecular processes, this explains gene function, i. e., the production of gene products. Molecular entities bind to the promoter and thereby initiate the transcription of a gene's DNA sequence into an RNA sequence. In a second step, this RNA sequence is translated into a protein as a sequence of amino acids, where the particular amino acid sequence is determined by the gene's DNA sequence. (Three adjacent DNA nucleotides code for one amino acid, and the nucleotide-amino acid mapping is called the genetic code.) In contrast to the classical gene concept, whose function is to predict (and offer statistical explanations), the molecular gene concept is a tool of causal-mechanistic explanation.

As a result, all three components of content (reference, inferential role, epistemic goal) changed in the transition from the classical to the molecular gene concept. The inferential role of the term 'gene' changed since only the molecular gene concept offers a structural account of genes. This led even to a change in reference. Since classical genes are individuated in terms of their phenotypic effects and molecular genes are defined as particular structural units coding for proteins, these two concepts may offer a different account of how many genes there are at a genetic region in the case of regions with a complex organization (Weber 2005, ch. 7).[7] A change in reference has traditionally been seen as threatening incommensurability of meaning, and the causal theory of reference has been invoked by philosophers of science to show how a term's reference can be stable despite major theory change. However, the gene concept is one of the cases where a scientific concept underwent rational change in meaning despite a change in reference (Brigandt 2010b; Burian et al. 1996; Kitcher 1982). In the case of the homology concept, I have accounted for the redefinition of this concept based on the concept's stable epistemic goal, which sets standards for when a change in inferential role and possibly correlated change in reference is rationally warranted. However, this option does not seem to be available in the present context, as in the transition from the classical to the molecular gene concept the very epistemic goal pursued by the use of the term 'gene' changed. Still, a philosophical account is possible, based on the fact that the change in epistemic goal was gradual. The reader is referred to Brigandt (2010b, sect. 3) on this issue.[8]

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[7] While detailed classical studies carried out in the 1970s had suggested five classical genes at the *achaete-scute* gene complex, molecular research of the 1980s instead revealed four molecular genes that are responsible for the phenomena observed by prior classical studies. Weber (2005) argues that what geneticists were tracking when studying 'genes' was not a single structural kind, but that there are several kinds with overlapping extensions, to which biologists can and did refer. He introduces the useful notion of 'floating reference' for the idea that the reference of the gene concept has changed constantly during its history, though in a gradual fashion from one category to another category overlapping with the former.

[8] Another complication is that the advent of the molecular gene concept did not eliminate the classical gene concept. Even though both concepts are still in use, it is important to account for how the molecular concept growing out of and

In this section I want to devote more discussion to how the molecular gene concept has changed in the last few decades, and the associated origin of substantial semantic variation. While the molecular gene concept was well-established by the 1970s, novel findings in molecular genetics and genomics have led to semantic change. Originally, it was assumed that all genes have the same structure (a stretch of DNA delineated by a start and stop codon and preceded by a promoter sequence), where one such structural unit codes for a single product and every gene product results from one such DNA unit. However, it has been discovered that gene structure and function is incredibly more complicated in non-bacterial eukaryotes (Griffiths/Stotz 2007; Stotz 2006a, 2006b). It turns out that genes form a structurally heterogeneous kind and that the relation between DNA elements and their products is many–many. This led to revised construals of what molecular genes are, resulting in a historical change of both the inferential role and reference of the molecular gene concept. At the same time, the molecular gene concept's epistemic goal has been stable—the concept is still used to explain how genes code for their products (but see the refined account below). The new use of the molecular gene concept came about through those findings about gene structure that bear on gene function. Thereby it was an instance of rational semantic change, as current construals of what molecular genes are provide an improved account of how DNA elements function by coding for gene products—meeting the molecular gene concept's epistemic goal to a higher degree.

This semantic change in the last few decades has also led to a significant degree of *semantic variation*. Nowadays, different molecular biologists may offer different of genes. These scientific developments have recently triggered philosophical discussions of the molecular gene concept, addressing such questions as whether there is a unified concept underlying the varying uses of 'gene' or whether there are two or more distinct gene concepts used in molecular biology (Beurton et al. 2000; Griffiths/Stotz 2007; Moss 2003; Stotz/Griffiths 2004; Waters 2000). In my study of the homology concept, I have pointed out that nowadays the term 'homology' is used for different scientific purposes (epistemic goals) in different three biological fields (systematics / traditional evolutionary biology, molecular biology, and evolutionary developmental biology), so that one could argue that these three are different,

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largely replacing the classical concept was an instance of rational semantic change.

though related concepts. In the case of the term 'gene' as employed across molecular biology, the situation is that there is still a shared epistemic goal underlying different uses of the term. Its usage is context-sensitive, where the term is used in slightly different ways by different molecular researchers (or by the same person in different scientific contexts). In any case, rather than trying to determine whether semantic variation corresponds to one shared or several distinct concepts, I view it as philosophically more fruitful to study and explain the presence of semantic variation (as an instance of conceptual dynamics), in particular showing why a context-sensitive use of a term can be beneficial to scientific practice.

For the purpose of this essay I mention only one major reason for the current semantic variation, namely, the many–many relation between DNA elements and gene products. A continuous DNA segment can give rise to an RNA transcript, where in a process called splicing only some chunks of the RNA are selected and fused to be translated into the protein product (so that only certain chunks of the DNA segment actually code for the product). In the case of alternative splicing, different parts of a gene's RNA transcripts can be selected in different cells of an organism or in one cell at different points in time, leading to the situation where one DNA element produces many protein products with distinct amino acid sequences. One could consider this DNA element to be a gene, which happens to code for many distinct products. On the other hand, one could postulate a gene for each product, where these genes happen to physically overlap or be identical. There is also a many–one relation between DNA elements and gene products. In the case of trans-splicing, several non-contiguous DNA elements (possibly located on different chromosomes) are independently transcribed to RNAs, which are then fused together to generate a single protein product. This raises the question of whether each of these non-contiguous DNA elements is a separate gene (though each such gene does not code for a protein in isolation), or whether they jointly form a gene (that happens to be physically spread out over the genome). Due to such many–many relations between DNA elements and gene products, it is unclear which DNA elements (and their mereological sums) count as a gene, as a mere part of a gene, or as a collection of several genes. As a result, different scientists may use different criteria for individuating genes, which also entail a different reference of the term 'gene'. This is aggravated by the fact that the relation from DNA elements to RNA products is largely one–one, but the relation between DNA elements and protein products is many–many (due to alternative splicing and trans-splicing of RNA transcripts). Nowadays it is clear that both RNAs (originally assumed to be mere intermediates) and enzyme-forming proteins fulfill important cellular functions. Researchers focusing on RNAs or rather on proteins as the molecular gene products of interest are likely to individuate different DNA elements as independent genes.

Both the use and the reference of the term 'gene' in contemporary molecular biology can vary across utterances, which is determined by two basic factors. First, genes form a heterogeneous kind, so that different structural and functional features can be used to characterize genes. Some geneticists assume that only DNA elements with distinct promoters can count as distinct genes; others do not make this requirement. Some permit that a gene may have different products, yet count genetic elements that are trans-spliced together as distinct genes. Other relevant considerations are whether all separable genetic elements are translated, whether a genetic element that forms a product in conjunction with other DNA elements (trans-splicing) also produces another product on its own in other cellular contexts, how far apart the different DNA segments involved are, and how chemically diverse the different products are. Several such considerations can be combined to various specific characterizations of what a gene is. Each way of individuating genes picks out a different category (though the categories overlap extensionally), so that genes are not a unique kind, but a set of several overlapping categories. Second, when using the gene concept on a certain occasion, a biologist has particular investigative or explanatory aims in mind. A geneticist is typically interested in quite specific aspects of gene structure or gene function in her research. The research question that is pursued when using the term 'gene' influences which of the possible structural or functional features of genes are relevant for this instance of term use. As a result, two biologists may employ different construals of precisely what defines a gene when addressing one and the same complex genetic region. For example, one scientist may be interested in the RNA produced from a DNA segment, while another may focus on the protein as the gene product of interest. Usually, this semantic variation is pronounced across different branches of molecular biology (RNA researchers as opposed to protein biochemists), but occasionally one and the same person can use the term 'gene' differently in different scientific contexts.

On my philosophical account, there is a common *generic* epistemic goal pursued with the use of the molecular gene concept, namely, to account for gene function. Yet in concrete contexts this can be spelled out in different ways, resulting in different *specific* epistemic goals underlying actual uses of the term, e. g., focusing on RNA or protein as the gene product of interest. The variation in the (specific) epistemic goal pursued explains why there is semantic variation (i. e., variation in inferential role and reference), and why a context-sensitive use of the term 'gene' is conducive to scientific practice. For different epistemic goals are legitimate, and a unique construal of what genes are cannot do justice to various epistemic goals and the complexities of genetic structure. This semantic variation does not lead to communication failure, as the variation is small and the particular context disambiguates the particular use in play. In this fashion, small and context-dependent variation in the epistemic goal pursued with a term's use accounts for conceptual dynamics across utterances.

4. Conclusions

A theme common to all three case studies was that scientific concepts are used to pursue particular epistemic goals, and that these epistemic goals influence the epistemic dynamics of science. One basic difference between the concept of evolutionary novelty, on the one hand, and the homology concept and the gene concept, on the other, is that it is only in the latter two cases that the very concept under consideration is meant to meet the epistemic goal specified by this concept. The molecular gene concept, for instance, is used to account for how DNA segments produce their molecular products—the epistemic goal pursued by the concept's use. This concept sets out a phenomenon to be explained, *and* its inferential role (as one part of the concept's content) ideally offers an explanation of this phenomenon.[9] The concept of evolutionary novelty, in contrast, sets out a problem agenda; however, it is not the concept of novelty, but several other biological concepts, that are assumed to account for the origin of novelty. Some such concepts are notions pertaining to the structure of gene regulatory networks, the concepts of epigenetic interaction, thresholds in morphogenesis, de-

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[9] Other terms pertaining to gene structure and function (such as 'exon', 'transcription unit', and 'splicing') are involved in explanations of how genes produce their products, so that the term 'gene' is not the only one tied to the goal of explaining gene function. But the term 'gene' is central in this context and the other terms are tied to it as part of the gene concept's inferential role.

velopmental reprogramming, and heterochrony—a successful explanatory framework is a task yet to be achieved in the future. As a result, the epistemic dynamics that is at stake in this case is not a change of the concept of evolutionary novelty.[10] The concept fulfills a stable function by setting out a problem agenda, but as argued above, this substantially influences the operation of evolutionary biology, as this particular problem agenda (consisting of hierarchicallyrelated component questions and associated criteria of explanatory adequacy) coordinates research across several biological subdisciplines, foreshadowing how various intellectual resources (models, explanations, concepts, and methods) are to be related and integrated. Thereby, the concept of evolutionary novelty influences the epistemic dynamics of several biological fields in general, and the behavior of *other* concepts in particular.

In the case of the homology concept and the gene concept, the dynamic behavior of these very concepts was concerned (even though other concepts related to them have changed as well). The definition of 'homology' changed during the 19th century in the transition from pre-evolutionary biology to evolutionary theory. Likewise, basic accounts of what a molecular gene is have changed since the advent of the molecular gene concept in the late 1960s. Both are changes in inferential role on my account, and the stable epistemic goal of the respective concept motivated biologists to revise its definition (once new empirical knowledge became available), and furthermore, the notion of epistemic goal philosophically justifies why the redefinition was legitimate. Nowadays, the terms 'homology' and 'gene' also exhibit semantic variation, as a consequence of variation in the precise epistemic goal pursued by different users of the respective term. The homology concept came to be used within different branches of biology, and used for different epistemic purposes and aims among these branches. The molecular gene concept is universally used for a generic epistemic goal (accounting for how DNA segments produce their products), but this generic goal can be spelled out differently by different researchers and in different research contexts (e. g., focusing on RNAs or rather proteins

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[10] This leaves out the fact that traditional evolutionary biology did not see the explanation of novelty as a distinct challenge for evolutionary theory, so that historically with the advent of evolutionary developmental biology the concept of novelty has exhibited some change, and likewise its dynamic behavior across different parts of evolutionary biology is contingent upon how seriously this concept is taken.

as the gene product of interest); thus, there is a variation in the specific epistemic goal tied to the use of term ‘gene’, resulting in context-dependent construals of what genes are.

My case studies mentioned various kinds of epistemic goals tied to concept use. The homology concept used in molecular biology is purely a tool of discovery. The homology concept in comparative biology (and traditional evolutionary biology) is used to yield unified descriptions, and the classical gene concept aims at predictions. Beyond inference, prediction, and classification, causal-mechanistic explanation can be an epistemic goal, as witnessed by the homology concept used in evolutionary developmental biology, the molecular gene concept, and the concept of evolutionary novelty. Even if the epistemic goal pursued by a concept is to arrive at a scientific explanation (rather than to discover certain phenomena), this may influence investigative practice in an essential way. The molecular gene concept clearly guides discovery in molecular biology, and the concept of evolutionary novelty motivates and structures exploratory experimental and theoretical research.

Concepts refer to the world and represent the world in a certain fashion. Consequently, concepts have usually been construed as consisting of some beliefs about the concept’s referent: an intension, an inferential role, a definition, or an analytic statement. However, note that the *epistemic goal* pursued by a concept’s use operates on a different dimension than reference and inferential role. For the epistemic goal does not consist in a belief *about states of the world*—not even in a desire as to how aspects of the world studied by science should be like. Instead, it is a goal *for scientific practice*, or a desire as to what a scientific community should achieve. Such goals have to be taken into account to understand the dynamic operation of science, including the epistemology of scientific concepts. It has been observed that a tentative definition of a term can be revised once a new definition becomes available which is explanatorily more fundamental (Bloch in this volume). However, in order to adjudicate whether one definition is explanatorily more fundamental than another, one has to know what particular issues are in need of explanation in the context of *this* concept, which is provided by the concept’s epistemic goal. Some concepts are used to pursue several explanatory aims; some are not used for the purpose of explanation, so that other considerations apart from explanatory fundamentality determine the appropriateness of a definition. Scientific concepts are open-ended in that scientists are never hostage to the definitions they once favored and free to change their concepts (MacLeod in this volume). Nevertheless, to understand this phenomenon it is not enough to point to the fact that the meaning (inferential role) of some terms is not clearly delineated, as in the case of a Wittgensteinian family resemblance, and thus easier to change. Apart from a flexible inferential role one needs an independent standard that motivates the inferential role's change, and thus has to consider a property on a different dimension than inferential role, namely the epistemic goal of a concept.

It is for this reason that my claim that the epistemic goal pursued by a concept's use is a part of this concept's content is controversial. Reference and inferential role (or some equivalent property) have generally been deemed to constitute mental content, and reference (extension) and inferential role (intension) are semantic properties of terms.[11] But many will resist my suggestion that the epistemic goal pursued by a term's use is also a semantic property of a scientific term, as it is not part of the 'what is said' (the truth-conditional meaning of an expression containing terms). Still, I maintain that the epistemic goal pursued by a concept's use is a component of this concept, because this component accounts for the rationality of semantic change and variation, and thus fulfills a semantic task—even if this task has not been recognized by traditional accounts of concepts. In fact, all three components of conceptual content have to be studied together. A stable epistemic goal causally determines and rationally justifies historical change in inferential role and reference, and variation in a concept's epistemic goal (across different persons) accounts for variation in inferential role and reference. Likewise, changes in inferential roles and scientific beliefs can transform epistemic goals that scientists deem worth pursuing.

My framework of concepts is not so much to be construed as a metaphysical account (or the only account) of what a concept is, but as a methodological guideline for how philosophers should study scientific concepts. Such a methodological framework is to be defended in terms of its fruitfulness for understanding the behavior of actual concepts (Brigandt 2011c). Ascribing a certain reference, inferential role, and epistemic goal to a term is justified if it sheds light on the use of this term and the change and variation in use. One may wonder whether every concept (or at least every scientific concept) has an epistemic goal. While there are very generic epistemic goals common to most

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[11] The exception is conceptual atomists (and direct reference theorists), who claim that concepts are individuated in terms of reference only (Fodor 2004; Laurence/Margolis 1999).

concepts, for instance referring to a referent or ensuring cognitive economy, more specific epistemic goals that are particular to a concept may exist only for scientifically central concepts, as the ones discussed above. Nonetheless, this is unproblematic as a unique epistemic goal has to be ascribed to a concept only if the concept exhibits semantic change or variation, which needs to be philosophically explained.

Associated with epistemic goals are standards of adequacy that specify what would count as meeting the epistemic goal—what method is suitable for an investigative goal, what evidential standards obtain for an inferential or inductive aim, or what criteria of explanatory adequacy underlie an explanatory goal. Both epistemic goals and standards are *epistemic values*. Values are not beliefs about the object of scientific study and are thus not part of scientific theories and models—they operate on a quite different dimension. Yet epistemic aims and values are part of scientific practice and essential determinants of the epistemic dynamics of science, including scientific discovery and belief change. The central purpose of this essay has been to argue that (1) not only do epistemic aims and values influence theory change, but more specifically they influence the dynamic behavior of individual concepts, and (2) epistemic aims and values can be *embodied* by specific scientific concepts, so that such concepts influence the dynamics of science. As a result, the epistemic aims and values underlying the use of individual concepts have to be taken into account by any epistemology of science.[12]

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[12] In Brigandt (2011c), I suggest that also philosophical concepts should be related to aims. Against the armchair method of analyzing philosophical concepts by using intuitions, I argue that in analogy to scientific concepts, philosophical concepts should be viewed as being tied to philosophical goals. The specific goal pursued by a philosophical term's use determines what philosophical account of the term is the most adequate one.

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