Scientific kinds

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Abstract Richard Boyd's Homeostatic Property Cluster (HPC) Theory is becoming the received view of natural kinds in the philosophy of science. However, a problem with HPC Theory is that it neglects many kinds highlighted by scientific classifications while at the same time endorsing kinds rejected by science. In other words, there is a mismatch between HPC kinds and the kinds of science. An adequate account of natural kinds should accurately track the classifications of successful science. We offer an alternative account of natural kinds that better recognizes the diversity of epistemic aims scientists have for constructing classifications. That account introduces the idea of a classificatory program and provides criteria for judging whether a classificatory program identifies natural kinds.

Keywords Natural kinds · Classification · Homeostatic property clusters · Richard Boyd · Scientific kinds · Classificatory programs

1 Introduction

Richard Boyd's (1990, 1991, 1999a, b, 2000, 2003a, b) Homeostatic Property Cluster (HPC) Theory is becoming the received view of natural kinds in the philosophy of science. According to Ian Hacking, HPC Theory "is the best recent contribution to the doctrine of natural kinds" (1991b, p. 149), and Samuels and Ferreira write that "philosophers of science have, in recent years, reached a

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consensus—or as close to consensus as philosophers ever get—according to which natural kinds are *Homeostatic Property Clusters*" (2010, p. 222). Many philosophers of biology and the social sciences have adopted HPC Theory, including Griffiths (1999), Wilson (1999), Wilson et al. (2007), Brigandt (2009), and Mallon (2007). HPC Theory has even made its way into biology (for example, Wagner 2001; Keller et al. 2003; Rieppel 2005).

A major desideratum of HPC Theory is providing an account of kinds that captures the kinds of science—those kinds represented in scientific classifications. A major reason why HPC Theory has widespread appeal is that it better captures the kinds of the biological and social sciences than other theories of kinds, such as various essentialist accounts. Though HPC Theory is a more inclusive account of kinds than previous essentialist accounts, it nevertheless fails to capture many kinds highlighted by science. By its own criterion, a proper account of kinds should capture the classificatory practices of successful science. Yet, as we illustrate below, many scientific kinds fall outside the scope of HPC Theory. A further and converse problem is that HPC Theory endorses kinds not recognized by science. Putting these together, a failing of HPC Theory is that there is a mismatch between HPC kinds and the kinds of science.

Philosophy of science, we argue, needs an account of kinds that better captures the variety of classificatory practices found in science. A systematic problem with HPC Theory is that it imposes overly prescriptive constraints on what counts as a natural kind. For HPC Theory, natural kinds must be groups of entities that share a cluster of projectable properties sustained by homeostatic causal mechanisms. We do not deny that such groups are natural kinds. Our worry is that many successful research programs in science offer classifications that do not meet HPC Theory's prescriptions. Who is right: HPC Theorists or the scientists? We side with the scientists.

After critically analyzing HPC Theory, we offer a positive account of natural kinds that better captures the classificatory and epistemic practices of science. On the one hand, we aim to offer an account of kinds that is more sensitive to the classificatory practices of science. On the other hand, we do not want to offer an account of kinds that merely says that any classification offered by a scientist picks out natural kinds. Consequently, we introduce the idea of a classificatory program and offer criteria for judging whether a classificatory program identifies natural kinds. The account of kinds we propose charts a middle course between HPC Theory's overly restrictive account of kinds and promiscuous accounts such as Dupré's (1993) and Hacking's (1991a, 2007).

2 What is HPC theory?

HPC Theory is motivated by epistemological considerations. Its starting point is the observation that most kinds we refer to in inferences, explanations, and predictions are groups of entities or phenomena that are similar to one another but not perfectly the same. Only a minority of scientific kinds—perhaps only those featuring in fundamental physics—consist of entities that are indistinguishable in their relevant

traits. Most kinds used in the sciences allow for variation among their members such that there are no properties that all and only the members of a kind must exhibit. HPC Theory accommodates this observation by the intuition that for a kind to be epistemically useful, its members need not share a particular set of essential properties as long as there is a reason why they sufficiently resemble one another in relevant respects. That is, if we group entities and phenomena into kinds such that the similarity of a kind's members is due to particular causal features of the world, these causal features support inferences concerning that kind. HPC Theory thus moves away from the traditional idea that the kinds used in the sciences are natural kinds in the sense of their entirely being objective features of the world out there, toward a view of natural kinds as products of the interplay between human classificatory interests and states of affairs in nature that determines the boundaries of kinds. This is Boyd's "accommodation thesis" (Boyd 1991, pp. 138–139; 1999a, pp. 69–70; 1999b, p. 147; 2000, p. 55ff.; 2003a, p. 537). Boyd retains the notion of 'natural kind' and offers this conception of natural kinds: "Natural kinds are features, not of the world outside our practice, but of the ways in which that practice engages with the rest of the world" (2003a, p. 538). Boyd replaces the traditional conception of natural kinds as features of the world with a conception of natural kinds as products of our engagement with the world.

Causality is an essential component of HPC Theory, as seen in Boyd's notion of "homeostatic mechanisms." Such mechanisms are the causal factors responsible for the repeated co-occurrence of clusters of properties. The members of *Canis familiaris*, for instance, tend to have four legs, two eyes, and one mouth. Various causal processes, such as shared genealogy, similar developmental mechanisms, and exposure to similar environmental conditions, cause dogs to more often than not to have such similar properties. One should not read too much into the term 'mechanism' in 'homeostatic mechanism,' however. Boyd allows the notion of homeostatic mechanism to be read metaphorically as well as literally (1990, p. 373; 1999b, p. 143); he allows all sorts of interactions and processes to underwrite kinds. A homeostatic mechanism can be anything that causes (in the broadest sense of the term) a repeated clustering of properties.

On HPC Theory, kinds are defined by two definitions. Because the key feature of kinds is their suitability for epistemic functions (inference, explanation, prediction, and generalization), the collection of similar properties found among the members of a kind is a central element of HPC kinds. Nevertheless, property clusters alone cannot individuate kinds. In many cases there is considerable variation among the members of a kind such that the relevant property cluster can only be identified after kind membership has been established comparatively well. Therefore, a second element is added to the definition, reflecting the view that kinds are individuated by causally sustained clusters of properties. This second element is the collection of homeostatic mechanisms underlying the observed property clustering (Boyd 1990, p. 373; 1991, p. 141; 1999b, 2000, p. 67). But this definition, the "explanatory definition" or "natural definition" of a kind, is only part of the story. It tells us how a given natural kind is able to play the epistemic role that it does. Kinds can play a "programmatic role" as well, before their epistemic basis for inference and explanation is established. Boyd calls such descriptions of kinds "programmatic

definitions" (1999a, pp. 70–77; 1999b, pp. 149–150). According to Boyd, an explanatory definition of a kind is "an account of the properties shared… by its members in virtue of which reference to the kind plays the role indicated by its programmatic definition" (1999a, p. 70). The programmatic definition thus precedes the explanatory definition.

Boyd takes the two-part explanatory definitions as uniquely determining kinds (Boyd 2000, p. 67). In order to accommodate the many cases in which kinds are not clear-cut, the two parts of the definition are conceived of in an open-ended manner. First, Boyd writes that "*all or part* of the homeostatic cluster … together with *some or all* of the mechanisms which underlie it provides the natural definition" of the kind's name (1990, p. 373; 1999b, p. 143; emphasis added). This openness is required as classifications are tentative. When grouping things together on the basis of observed similarities and underlying causal factors, we must remain open to the possibility that groupings may need to be modified in light of new observations or when inferences fail. Accordingly, we must remain open to the possibility that in the two-part definition of a kind some properties will need to be eliminated from the property cluster and/or some homeostatic mechanisms will have to be removed from the collection of underlying factors. The definitions of kinds thus are a posteriori (Boyd 2000, p. 54). Second, any particular entity may exhibit some but not all properties in the property cluster, or may not be affected by one or more of the underlying homeostatic mechanisms, such that its kind membership is unclear (Boyd 1990, p. 373; 1999b, p. 143; 2000, p. 67). The definitions of kinds allow for extensional vagueness and kinds with fuzzy boundaries—in accordance with the fact that nature doesn't neatly divide into well-delimited kinds of things. Third, the two parts of the explanatory definitions themselves can change: the property cluster and the collection of underlying homeostatic mechanisms are not individuated extensionally but are conceived of as historical objects or processes whose compositions can change over time (Boyd 1990, p. 374; 1999a, p. 88; 1999b, p. 144; 2000, p. 71). Here, the motivation is that nature is changeable—for example, biological species are subject to open-ended evolution—such that epistemically useful kinds should be sufficiently flexible to accommodate the changing state of nature. By conceiving of explanatory definitions as open-ended in these three ways, HPC theory aims to be an account of natural kinds that is sufficiently flexible to accommodate the various kinds in the special sciences, as well as the traditional natural kinds.

3 The mismatch between HPC kinds and scientific kinds

As we have seen, an important desideratum of HPC Theory is to offer an inclusive account of kinds that includes the traditional kinds of the physical sciences as well as the kinds of the special sciences. A central aim of HPC Theory, then, is to provide an overarching account of scientific kinds. We argue that HPC Theory does not achieve this aim because many kinds postulated by scientific classifications fall outside the scope of HPC Theory. This problem is not merely one of a philosophical theory failing to achieve its own self-imposed goals. Any adequate account of

natural kinds should capture the kinds offered by our best scientific theories. Scientific classifications highlight certain groups of entities as natural kinds, and, of course, such classifications are fallible. Nevertheless, we assume that the kinds of science have been and are epistemically superior, on the average, to those posited by ordinary language or intuition (except in cases where ordinary kinds are found to be scientific ones). This is an assumption that we believe HPC Theorists would agree with. If HPC Theory fails to capture many of the kinds offered by our best science, then HPC Theory fails as an adequate theory of natural kinds.

In what follows we highlight three types of scientific kinds that fall outside the scope of HPC Theory: non-causal kinds, functional kinds, and heterostatic kinds. We also show that HPC Theory's emphasis on similarity is inconsistent with some classificatory practices in science and leads to the positing of kinds rejected by science.

3.1 Scientific kinds not captured by HPC theory

3.1.1 Non-causal kinds

Recall that for HPC Theory, kinds consist of entities with a number of co-occurring properties, where this co-occurrence is due to a kind's homeostatic mechanisms. Clearly HPC Theory requires that natural kinds are groups of entities sustained by causal mechanisms, because the theory requires "the accommodation of inferential practices to relevant causal structures" (Boyd 1999b, p. 159). There are, however, a number of kinds that do not satisfy this causal prescription—kinds that are seen as good scientific kinds by scientists even though no set of causal homeostatic mechanisms is posited as part of their ontology. The existence of such kinds in science shows that "[t]he presence of homeostatic mechanisms is not the *sine qua non* of kindhood" (Chakravartty 2007, p. 171).

Consider the *Phylo-Phenetic Species Concept* (PPSC) of microbiology. It describes the basic taxonomic kinds of microbes in the world and is the most widely accepted species concept in microbiology (Stackebrandt 2006). The PPSC highlights a number of empirical parameters that define microbial species. What is salient for our purposes is that causal mechanisms are not among those parameters. The aim of the PPSC is to capture stable kinds that have clear identity conditions, as can be seen from Rosselló-Mora and Amann's (2001) description of how the PPSC identifies microbial species. First, 16S rRNA or some other genetic marker is used to provide a phylogenetic tree of the organisms under consideration. The resultant tree is based on selected parts of their genomes and ignores other parts. Which parts are used is chosen on pragmatic grounds, namely the ubiquity and stability of a particular genetic marker. The resultant tree suffices for grouping organisms into taxa, but is insufficient for assigning a Linnaean rank to those taxa. Second, DNA:DNA hybridization is employed to identify groups that have "a high degree of genomic similarity" (*ibid.*, p. 60). A 70 % degree of genetic similarity in hybridization is normally considered the threshold for calling a taxon a 'species.' There is no theoretical reason for picking the 70 % threshold. It is merely the threshold at which phenotypic similarities and genotypic similarities tend to

coincide. Third, "a phenetic analysis of as many characters as possible is employed as a [further] practical means for ranking"—that is, for calling a taxon a 'species' (*ibid.*, p. 58).

Notice that there are no assumptions about the causal mechanisms underlying bacterial species. Parameters are chosen to provide stable and readily identifiable kinds. As Stackebrandt (2006, pp. 36–37), the former editor of the *International Journal of Systematic Bacteriology*, writes, "[b]acteriologists in particular follow guidelines and recommendations that provide stability, reproducibility, and coherence in taxonomy." The example of bacterial kinds is not a fringe example of obscure taxonomic practice. The PPSC is the most popular approach to species among microbiologists. Furthermore, most of life is microbial. HPC Theory, thus, fails to capture the most popular scientific classificatory approach to *most* of life. The HPC Theorist might respond that despite what these biologists are interested in, there must be causal structures that sustain microbial species. However, such an assertion is a philosophical overlay on scientific practice and is not part of the PPSC or the motivations biologists offer for positing it. A general lesson of this example is that though many philosophers are keen on science revealing the causal structure of the world, such enthusiasm for causality is far from universal among scientists. Note that we are not arguing that there is no causality in the world or that microbial kinds do not participate in causal relations. We are merely pointing out that the PPSC is not intended to capture the causal underpinnings of microbial species, and HPC Theory's emphasis on causality is simply irrelevant for these microbiologists.[1]

3.1.2 Functional kinds

Functional kinds are another category of kinds that is intended to fall within the scope of HPC Theory (Boyd 1999a, p. 92) but does not. Functional kinds feature in most special sciences and play important roles in explanation, prediction, and generalization (Fodor 1974; Reydon 2009). One of the long-recognized characteristics of functions is their multiple realizability: a particular function can often be realized by entities with various structures and properties. Conversely, entities tend to be multiply functional in that a particular entity can perform different functions in different contexts. Therefore, the function characterizing a functional kind can often be performed by entities with different structures and properties. Such a kind is not defined by a cluster of structures/properties and falls outside the scope of HPC Theory.

Consider kinds of genes. Genes (that is, gene tokens) are identified as members of particular kinds, such as the *Drosophila melanogaster antennapedia* gene or the *Mus Musculus PAX6* gene, based on among other things their function. The

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[1] Another example of non-causal kinds, which we will only mention in passing, is stellar kinds. These are kinds found in astrophysics, such as main sequence dwarf and pulsating variable star. According to Ruphy (2010), such kinds are not classified with the intention of capturing causal mechanisms or the causal structure of the cosmos. The aim of discovering such kinds in astrophysics is just to find stable and readily identifiable kinds (2010, p. 1118).

Molecular Gene Concept, for example, explicates how genes are conceived of in the context of molecular biology: "The fundamental concept underlying the application of "gene" in molecular biology is that of a gene for a linear sequence in a product at some stage of genetic expression…. Genes are for linear sequences in products of genetic expression" (Waters 1994, p. 178). On this concept, gene kinds are defined in part by the roles that sequences play in the production of various molecular expression products. Indeed, in order to count as a gene in the first place a sequence must perform *some* function in the production of a molecular expression product. Entirely non-functional sequences are not considered genes. However, because of the various effects that occur in the process of transcription and translation of DNA to the expression product (for example, alternative splicing, antisense reading, and frameshifting), there is no unique mapping of molecular expression products onto DNA sequences. A particular sequence can be involved in the production of several expression products and, conversely, usually several disconnected sequences are involved in the making of a particular expression product. In addition, the same sequence can count as a gene in one cellular context and not count as a gene in a different cellular context. For example, a functional sequence in the organisms of one species may be homologous to a non-functional sequence in the organisms of another species where, because of its non-functionality, it does not count as a gene in that species' genome. This makes it difficult to think of gene kinds as kinds according to HPC Theory: it is not the repeatedly co-occurring properties of a particular sequence that constitute a genetic kind, but the role that gene tokens perform in a particular cellular context.

The explanatory definition of a kind on HPC Theory (the combination of clustering properties and underlying causal factors) thus does not successfully individuate gene kinds because it does not capture their functional element. While this functional element might be incorporated in the programmatic definition of a kind, such a maneuver will not yield a unitary kind because of the multiple realizability of functions. A programmatic definition in terms of a function performed within a particular organismic context will not necessarily pick out one property cluster: it may pick out different property clusters, all of which can perform the same defining function.

This problem also occurs with kinds found in various biomedical ontologies (Bodenreider and Stevens 2006). There, kinds are defined by those aspects of entities that are epistemically relevant for researchers in a particular domain. In the Gene Ontology, for example, three such aspects determine kinds: molecular function, biological process (in which this function is realized), and cellular component (the cellular and organismic context in which this process occurs) (*ibid.*, p. 258). The material/structural properties of the kind's members are secondary and do not enter into the definition of a kind. Because the same epistemically relevant features are often multiply realizable and, conversely, the same material entity can be epistemologically relevant for different reasons in different research contexts, groupings based on epistemic relevance do not necessarily map onto single clusters

of material/structural properties. It is thus difficult to see how HPC Theory can be applied to kinds in biomedical ontologies.[2]

3.1.3 Heterostatic kinds

A third type of kind that HPC Theory fails to capture is heterostatic kinds. HPC Theory focuses on kinds of entities that have a number of similar properties, but many kinds in science also consist of entities with persistent differences. Examples of such heterostatic kinds are biological taxa (species, genera, families, and so on), which proponents of HPC Theory cite as paradigmatic examples of HPC kinds (Boyd 1991, 1999a, 1999b; Griffiths 1999; Wilson et al. 2007). The problem is that while the organisms of a taxon often have a number of similarities, they also usually display persistent differences that are characteristic of a taxon. Because HPC Theory only focuses on similarities, it fails to account for such diversity.

Biologists call persistent differences among the members of a taxon 'stable polymorphisms.' Polymorphism occurs in virtually every biological taxon, from species to families to kingdoms (Ereshefsky and Matthen 2005). Among sexual species, for example, males and females have pronounced physiological and behavioral differences. Within mammals, females have ovaries, have eggs, and lactate. Males have testes, produce sperm, and do not lactate. Alternatively, consider the different life stages of some insects, for example, the metamorphosis from caterpillar to butterfly. A dramatic example of polymorphism is the different stages of a slime mold. At one stage, a slime mold consists of disconnected amoebas that independently forage for food. At another life stage, the different parts of a slime mold come together and form a slug-like vertical stalk capable of reproduction. Examples of polymorphism are easily multiplied.

HPC Theory focuses on the similarities among the members of a taxon and the homeostatic mechanisms that cause those similarities. Yet a proper account of taxa also needs to capture stable polymorphisms and their heterostatic mechanisms. Proponents of HPC Theory do recognize the existence of such heterogeneity, and some HPC theorists have suggested how HPC Theory can explain stable variation among the members of a kind. Boyd suggests that species can contain "lots of conditionally specified dispositional properties for which canonical descriptions might be something like, "if male and in the first molt, P"…" (1999b, p. 165). Wilson et al. (2007) offer the same suggestion. However, as Ereshefsky and Matthen (2005) and Magnus (2011) argue, such fixes do not adequately capture variation within a kind. Using Magnus' (2011) example, we could say that if a female duck were a male it would have a green head, but no biological mechanism underwrites such a conditional. We could equally state that if the Eiffel Tower were a male duck it would be green. Clearly, such conditionals are outside the realm of science. Stepping back from these details, stable heterogeneity is a salient aspect of

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[2] Elliott Sober suggests that the ecological kind predator is a functional kind not associated with a particular property cluster; hence the kind predator fails to be an HPC kind. While there may be some functional properties common to all predators, that cluster of properties is too slim to be the sort of cluster required by HPC Theory.

many scientific kinds, yet HPC Theory offers no adequate account of this feature of kinds.

3.2 When similarity is misleading

The preceding examples show that HPC Theory's focus on similarities and homeostatic mechanisms causes that theory to leave out many kinds in science. The opposite also occurs: HPC Theory posits kinds that science does not recognize as kinds. Examples of the latter are found in biological taxonomy. An overriding aim of contemporary biological taxonomy is to identify and classify branches on the Tree of Life (Hull 1988). Taxa are considered groups of organisms each with their own common and unique ancestry. The problem for HPC Theory is that being a similarity cluster and having a common ancestry can part company. When similarity and ancestry come into conflict, HPC Theory sides with similarity, whereas the two major schools of biological taxonomy—Cladism and Evolutionary Taxonomy—side with ancestry. In such cases, HPC Theory conflicts with scientific practice.

Boyd, for instance, states that "[s]pecies are defined, according to the HPC conception, by those shared properties and by the mechanisms … which sustain homeostasis" (1999b, p. 81). He also writes: "I do not … hold that HPC kinds are defined by historical relations rather than shared properties" (1999b, p. 80). Boyd suggests that species can be non-historical entities and offers hypothetical examples to that effect (*ibid.*). Nevertheless, both Cladism and Evolutionary Taxonomy require that taxa be historically continuous entities (Ereshefsky 2001). There is, then, a clear conflict between HPC Theory and scientific practice. For biological taxonomy, two historically disconnected lineages are different species regardless of how similar their organisms are; yet from the perspective of HPC Theory such lineages belong to a single species if their member organisms are sufficiently similar. In such cases, HPC Theory recognizes kinds that successful science rejects.

This problem also occurs when applying HPC Theory to speciation events. When a population branches off from its ancestor species, the member organisms of both the isolated population and the ancestral branch continue for awhile to have the same family of properties: splitting need not be accompanied by immediate changes in traits and often traits remain conserved over considerable evolutionary time scales (Reydon 2006). In such cases, two different branches on the Tree of Life contain organisms that are overwhelmingly similar. Following HPC Theory, we should consider the branched-off population and the ancestral branch as constituting one species, given that their organisms share a robust cluster of similar properties. Yet, generally recognized models of speciation hold that when an isolated population branches off from its ancestral species speciation occurs (Coyne and Orr 2004). A supporter of HPC Theory might respond that such branching events are vague and no new species should be recognized until there are a significant number of dissimilarities between the organisms of those two branches. However, this response misses the aim of biological taxonomy, which is to classify distinct branches on the Tree of Life rather than clusters of similar organisms. The root of the problem is that HPC Theory assumes that *all* scientific classification should capture similarity clusters that can support inferential and explanatory practices.

This assumption fails to acknowledge that classification in science can have different aims.[3]

4 Towards a more adequate account of kinds

HPC Theory aims to be a naturalistic account of natural kinds, as evidenced by Boyd's "accommodation thesis." In brief, HPC kinds figure in the inductive and explanatory practices of a discipline and are supported by relevant causal structures. For Boyd, such disciplines are primarily scientific ones, but he allows that there may be relevant "practical disciplines" (1999b, pp. 160–161). Whatever the source of kinds, HPC Theory is intended *at least* to capture the kinds offered by successful science. We wholeheartedly agree with this naturalistic approach to natural kinds. As mentioned earlier, we assume that the kinds of science have been, and are, epistemically more productive on the average, than those posted by ordinary language or intuition (except in cases where ordinary kinds are found to correspond to scientific ones). This is not an overly controversial assumption and we believe Boyd and other HPC theorists would agree with it.

Yet, as we saw in the previous section, a major problem with HPC theory is that it fails to include many kinds offered by various scientific classifications. HPC Theory, in other words, is not naturalistic enough. Scientists not only posit kinds whose members have many similarities and an underlying causal basis, they also posit non-causal kinds, functional kinds, and heterostatic kinds. HPC theory fails to capture such kinds. Moreover, its focus on similarity clusters causes it to posit classifications that conflict with those of scientists. In sum, a failing of HPC theory is that the kinds it posits do not map well onto the kinds of the various sciences. An appropriate account of natural kinds should capture the different kinds posited by successful scientific classifications, while at the same time not positing kinds that scientists reject.[4]

As a project in descriptive, naturalistic philosophy of science—one that accurately describes scientific practice—HPC theory is flawed and should be rejected. But what is the alternative? If we believe that an adequate theory of kinds should capture the classificatory practices of science, does that mean we should subscribe to an account of kinds on which natural kinds are just those groups of

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[3] A reader might worry that many of our counterexamples to HPC Theory involve biological taxa, yet according to the species-are-individuals thesis (Hull 1978) such taxa are not kinds but individuals and hence not counterexamples to HPC Theory. Such a defense, however, is not available to the HPC theorist because Boyd and other HPC Theory proponents believe that the distinction between individuals and kinds is "merely pragmatic" (Boyd 1999b, p. 163; also see Wilson et al. 2007 and Brigandt 2009).

[4] A defender of HPC Theory might respond that HPC Theory was never intended to capture all of the kinds offered by successful science. After all, HPC Theory is not intended to capture those scientific kinds that lack sufficient similarities to sustain induction. However, a thesis of this paper is that to limit natural kinds to those kinds that feature in successful inferential practices, as Boyd does (for example 1999b, p. 147; 2000, p. 57), is an *a priori* approach to natural kinds that does not do justice to the epistemic practices of scientists, as illustrated by the examples in the previous section. Tellingly, Boyd (1999b, p. 146) calls this limitation on natural kinds a "truism".

entities that scientists say are kinds? We think that an adequate account of natural kinds should do more than that. In what follows we chart a middle course between a purely descriptive and an overly normative account of kinds. On the one hand, we desire an account of kinds that more accurately captures the classificatory practices of science than does HPC theory. On the other hand, we want a moderately normative account of kinds that places constraints on what counts as a natural kind. After all, scientists are not perfect beings and their classificatory decisions may sometimes be flawed. In what follows we suggest criteria for determining which classifications represent natural kinds.

Before discussing those criteria, we need to introduce some concepts. A *classificatory program* is that part of a discipline that produces a classification. A classificatory program has three parts: *sorting principles*, *motivating principles*, and *classifications* (Ereshefsky 2001). Sorting principles sort entities into kinds within a classification. Motivating principles justify the use of sorting principles and in doing so embody a program's aims for positing a classification. Consider the Biological Species Concept (Mayr 1940). Its sorting principles tell us to sort organisms of populations that interbreed into the same species, to sort organisms of populations that do not interbreed into different species, and to sort organisms that reproduce asexually into no species. The motivating principle for the Biological Species Concept is the hypothesis that interbreeding and the existence of relatively closed gene pools cause the existence of stable and distinct evolutionary groups of organisms.

Note two things about classificatory programs. First, different classificatory programs have different principles. Sorting and motivating principles are program-specific. That is clearly seen in the classificatory programs that sort organisms into species. The Phylo-Phenetic Species Concept's sorting principles employ genetic markers, overall genetic similarity, and phenetic traits, while the Biological Species Concept's sorting principles focus on reproduction. The motivating principle of the PPSC is to highlight stable kinds with clear identity conditions, whereas the Biological Species Concept aims to capture groups of organisms that evolve as a unit.

The other thing to note is that the central problem with HPC Theory can be described using the terminology of classificatory programs. HPC Theory is too restrictive concerning both the sorting and the motivating principles of a classificatory program. HPC Theory requires that classificatory programs have two primary sorting principles: sort things into kinds on the basis of similarities, and select similarities that reflect shared causal structures. These principles constitute the elements of the explanatory definitions of kinds on HPC Theory. Yet as we have seen, many kinds offered by science do not satisfy these sorting principles. The motivating principle behind these sorting principles is that kinds should be useful for inferential and generalizing practices. Recall that according to Boyd's accommodation thesis, kinds are construed in order to realize "the accommodation of inferential practices to relevant causal structures" (1999b, p. 159). Although Boyd asserts that kinds have programmatic definitions in addition to explanatory definitions (Sect. 2), he does not further specify what such programmatic definitions can consist in. Given the emphasis HPC Theory places on inferential practices it

seems clear that HPC Theory sees the possible motivational principles behind scientific classifications as quite limited: classifying is *primarily* about making inferences, and any sorting suitable for this purpose must be based on clusters of similarities sustained by common causal structures. As the examples discussed above have shown, this is a too restrictive view of the aims of scientific classification. An approach to kinds that is less restrictive than HPC Theory and better reflects the reasons scientists posit classifications should allow a broader scope of sorting and motivating principles. At the same time, it should place constraints on which classificatory programs produce classifications that pick out natural kinds. Here are three such constraints.

Internal coherence: This first criterion comes from Laudan's (1987, 1990) "Normative Naturalism." Laudan suggests that scientific disciplines have three components: overall aims (such as the desire for reliable knowledge), methodological rules (for example, prefer simpler or more unified theories), and theories. Overall aims and methodological rules may vary from discipline to discipline, and Laudan suggests that we choose methodological rules in relation to the aims of a discipline. More precisely, Normative Naturalism requires a type of internal methodological consistency: for a given scientific discipline, we should choose those methodological rules that best promote the aims of that discipline.[5] The first constraint we place on classificatory programs takes a similar tact: the sorting principles of a classificatory program should promote the program's motivating principles. For if they do not, the kinds obtained by those sorting principles will be arbitrary with respect to the aims of the classification. A minimal requirement for a kind to be natural is non-arbitrariness. Thus, internal coherence in the sense described here is a necessary criterion for a classificatory program to involve natural kinds.

An example of a classificatory program that satisfies this requirement is the PPSC discussed earlier. Its motivating principle is to produce stable and identifiable taxonomic units. It does not aim to give the single right classification of microbes, nor does it attempt to construct classifications that capture causal structure. Its sorting principles (using genetic markers, DNA hybridization, and phenetic traits) satisfy the program's aims—they result in stable and easily identifiable taxa. The PPSC meets the requirement that a classificatory program's sorting principles promote its motivating principles. Contrast this case with the Phenetic school of biological taxonomy (Sneath and Sokal 1973). That school of taxonomy aims to produce classifications that make no theoretical assumptions. Its primary sorting principle is to sort organisms according to overall similarity. In brief, pheneticists construct multi-dimensional graphs where each dimension represents an observed trait and points represent sample organisms. The densest clusters of points represent species; clusters of species that are closer together on the graph represent genera, and so on. The problem for Phenetics is that its motivating principle cannot be satisfied using its sorting principle. Organisms have an indefinite number of similarities, so some similarities must be selected for constructing a classification

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[5] See Sober (2000, pp. 169–172) for similar considerations.

(Sober 2000, pp. 170–171). As Hull (1970) argues, pheneticists must employ theoretical considerations to choose which traits to use for constructing classifications, which, in fact, they do (Ereshefsky 2001). Consequently, Phenetics is a classificatory program whose sorting principles prevent the satisfaction of its central motivating principle. Phenetics is not an internally coherent classificatory program and not one that highlights natural kinds.

Empirical testability: Internal coherence is a necessary but insufficient criterion for determining which classifications describe natural kinds. An additional criterion is that the motivating or sorting principles of a classificatory program should be empirically testable. For if they are not, we have no way of discerning whether they make any connection with the empirical world. This criterion elaborates the long-standing view that natural kinds are at least to some extent grounded in nature—that natural kinds are kinds in the empirical world that are to some degree independent of our classificatory practices (a view that is also embodied in Boyd's accommodation thesis). Following Popper (1963), empirical testability does not require that we currently have the technology for performing such tests but that such tests are possible.

It is easy to see how this constraint applies to a program's motivating principles when such principles make claims about the empirical world, such as the motivating principle of the Biological Species Concept. Its motivating principle—that an interbreeding population reproductively isolated from other such groups is a stable evolutionary unit—is empirically testable and has been substantially tested. There are also classificatory programs whose motivating principles make no particular claims about the empirical world. In such cases at least the sorting principles of a classificatory program should be empirically testable. The PPSC of microbiology, for example, merely aims to find stable and easily identifiable kinds, an aim that rests on no assumptions about the nature of microbes. Still, the question of empirical testability arises concerning this program's sorting principles. When microbiologists sort organisms according to a particular genetic marker, they should be able to test whether the information they have gathered is about that genetic marker. Sorting principles, thus, should be empirically testable in that the parameters they employ are measurable and the accuracy of those measurements can be tested.

Progressiveness: While internal coherence and empirical testability are necessary conditions for classificatory programs that describe natural kinds, they are insufficient, even when taken jointly. Consider classificatory programs that meet these criteria but turned out to be failures. The classificatory program of phlogiston theory, for example, is a failed but empirically testable program. In fact, it is through empirical testing that we learned that phlogiston is not a kind. Given such cases, another constraint on which classificatory programs highlight natural kinds is needed.

To obtain such a criterion we turn to Lakatos' (1970) distinction between progressive and degenerating research programs. For Lakatos, a progressive research program must be both theoretically and empirically progressive. It is theoretically progressive if it predicts novel facts—facts not predicted by other theories. It is empirically progressive if those predictions are corroborated. A research program is degenerative if it fails one of those requirements: that is, it fails

to generate novel predictions or the predictions it generates remain unconfirmed. An important aspect of Lakatos' schema is that the progressiveness of a research program is comparative. The issue is not whether a research program is progressive *simpliciter*, but whether it is more progressive than its rivals. If one research program is more progressive than a competing research program, then the latter program is degenerative and should be discarded. If there is no rival program, then there is no requirement to discard a research program even if that research program is stagnant. This is the thrust of Lakatos' critique of Popper's falsifiability criterion: scientists retain problematic research programs (falsified theories) until a more progressive replacement comes on the scene.

Lakatos' ideas about progressive and degenerative research programs can, with some adjustment, be applied to classificatory programs. A classificatory program is progressive if it provides principles that produce additional classifications or extend existing classifications (relative to competing classificatory programs) and those classifications are empirically successful. An example of a progressive classificatory program is the Biological Species Concept when compared to its principal rival of the first half of the twentieth century, the Morphological Species Concept. Supporters of the Biological Species Concept believe that sexual compatibility and the ability to produce fertile offspring are better indicators of evolutionary unity than morphology. A famous case confirming this belief is the discovery that fruit flies thought to belong to a single species because of their morphological similarity in fact belong to two evolutionary units (species), *Drosophila persimilis* and *Drosophila pseudoobscura* (Ridley 1996, p. 404). The Biological Species Concept was, and continues to be, better at detecting evolutionary units than the Morphological Species Concept.

Two other examples of progressive classificatory programs are the Phylo-Phenetic Species Concept and the Cladistic school of biological taxonomy. The sorting rules of the PPSC allow microbiologists to construct more stable and readily identifiable classifications of microbes than approaches that employ one genetic marker or just phenetic similarity (Stackebrandt 2006). Cladism, or Phylogenetic Taxonomy, is also a progressive research program when compared to its rivals, Phenetics and Evolutionary Taxonomy. Cladism assumes that common ancestry is the ultimate sorting principle for organisms, and it posits that all biological taxa are clades or branches on the Tree of Life (Ereshefsky 2001). Without going into detail, the sorting and motivating principles of Cladism have led to the positing of countless successful classifications, as well as contributed to the extinction of the Phenetics school and the near extinction of Evolutionary Taxonomy (Hull 1988).

Turning to examples of degenerative classificatory programs, the Morphological Species Concept, popular in the nineteenth and early twentieth centuries, is a degenerative classificatory program. As just mentioned, the Morphological Species Concept does not track evolutionary units (groups of organisms that evolve as a unit) as well as its chief rival, the Biological Species Concept. Recent Phylogenetic Species Concepts also outpace the Morphological Species Concept (Ridley 1996). Phylogenetic Species Concepts are part of Cladism and focus on species as the smallest recognizable branches on the Tree of Life. Another example of a degenerative classificatory program is Macleay's Quinarianism (Hull 1988; Mayr

[1982](#)). Introduced early in the nineteenth century, Macleay argued that the appropriate way to construct classifications of the biological world is not with linear relations but with groups of circles. For Macleay, Animalia is represented by a circle consisting of five smaller circles that represent subgroups within Animalia, such as Vertebrata. Vertebrata itself consists of five smaller circles that represent subgroups within Vertebrata. And so on. Huxley and others pursued Quinarianism and attempted to arrange higher taxa in groups of nested circles of five. However, the taxonomic patterns predicted by Quinarianism were not found in nature: Quinarianism was never empirically corroborated. Moreover, classificatory programs based on genealogical (linear) relations and evolutionary ideas were more successful. Quinarianism is a degenerative classificatory program and its classifications do not highlight natural kinds.

5 Summary and concluding remarks

Let us step back and summarize the account of kinds offered. The classifications of a discipline's classificatory program pick out natural kinds when:

1. The sorting principles of a classificatory program promote that program's motivating principles;
2. The motivating or sorting principles of a program are empirically testable; and
3. A classificatory program is not degenerate relative to competing classificatory programs.

This approach to natural kinds is more inclusive than HPC Theory because it allows more types of scientific kinds than HPC Theory. Recall our motivation for developing an alternative account of kinds. HPC Theory is advertised as a naturalist approach to natural kinds—one that, according to Boyd's accommodation thesis, says that natural kinds accommodate the explanatory and inductive practices of a discipline. However, HPC theory is not naturalistic enough. It leaves out various sorts of natural kinds posited by successful science, such as non-causal, functional, and heterostatic kinds. Because HPC theory is too restrictive in recognizing which groups of entities are natural kinds, we offered an account of kinds that is more inclusive.

The account of kinds we offer is also more precise than HPC Theory. According to HPC theory, scientific and perhaps some practical disciplines offer classifications that track natural kinds. But which disciplines are those? HPC is silent on how to determine which disciplines highlight natural kinds. Maybe this is taken as obvious, or perhaps guidelines for recognizing which disciplines highlight natural kinds can be derived from HPC Theory's requirement that kinds are groups of objects that share clusters of projectable properties maintained by homeostatic causal mechanisms. That may be so, but proponents of HPC Theory have not yet specified such guidelines. In the meantime, the criteria we offer for determining which classificatory programs highlight natural kinds are more precise than HPC Theory.

One might worry that the criteria we suggest look a lot like demarcation criteria. While we have dipped into the rich philosophical literature on demarcating science from non-science, we are not trying to define 'science.' The status of 'science' is not of interest to us: we judge a classificatory program by its epistemic merits, not by whether a particular classificatory program is called 'scientific.' To be sure, some classificatory programs proposed by scientists may fail to meet our suggested criteria and, conversely, some classificatory programs outside science may meet them and have good potential to pick out natural kinds. This brings to the fore an important aspect of our account: our criteria do not constitute infallible guidelines for finding natural kinds. They explicate the assumption that our best scientific theories and classificatory programs are the best place to learn about natural kinds; though, of course, our current theories and programs may turn out wrong. Natural kinds on our account are not necessarily eternal ontological categories; they are foremost groupings picked out by our best scientific theories and classificatory programs.

The account of kinds offered here is more inclusive than HPC Theory, and it is also more restrictive than the promiscuous accounts of Dupré (1993, 1999) and Hacking (1991a, 2007). Dupré and Hacking allow that scientific, practical, and ordinary language classifications trace natural kinds. Moreover, they allow that there are cases where scientific and practical classification conflict yet both types of classifications equally offer natural kinds. For example, Dupré (1993) allows that conflicting classifications developed by evolutionary biologists and culinary experts equally represent divisions in the world. Hacking (1991a) similarly believes that the kinds of geologists and artisans are on a par epistemically. We do not deny that both scientific and practical classifications can, in principle, reflect natural kinds. The crucial question is whether a classification meets the criteria we have suggested for judging if a classification highlights natural kinds, not whether it is scientific or 'merely' practical. Furthermore, if there is a conflict between kinds, the question becomes whether one classification has better epistemic credentials than the other.

Dupré (1999), for instance, believes that a folk biology classification that sorts whales into the category fish (rather than into Mammalia) is legitimate. Fish is an ordinary language category and Mammalia is a technical one from biological taxonomy, nevertheless for Dupré fish and Mammalia are equally natural kinds. We beg to differ. In this case, folk biology and scientific biology provide competing classificatory programs. Yet Mammalia is a category offered by Cladistics, which, as we have seen, is a progressive classificatory program. In the past, fish was a taxonomic category of science, but it is no longer.[6] The category fish is not part of any current progressive classificatory program. Consequently, when comparing the two, the scientific classification wins out and we have reason to be restrictive when sorting whales into a larger kind. Stepping back from this example, the point is that the approach to natural kinds we offer is more inclusive than HPC theory, but at the same time it is not overly liberal concerning which groupings should be recognized as natural kinds.

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[6] Fish is a paraphyletic taxon and as such does not include all of the descendants of a common ancestor. Cladistics requires that a taxon include all of the descendants of a common ancestor.

In conclusion, we believe that the account of natural kinds offered here has three virtues. First, it better recognizes the diversity of epistemic aims found among classificatory programs in science. Unlike HPC theory, there is no metaphysical overlay such as the requirement that natural kinds involve causal structure or causal structure of a certain sort. Nor is there the limiting assumption that all scientific classifications ought to support inductive practices. In this regard, our account of natural kinds is more naturalistic than HPC theory. Second, the account of kinds offered here is more precise than HPC Theory. Our account provides specific criteria for determining which classificatory programs highlight natural kinds. Third, the account of kinds offered here is more discerning than Dupré's and Hacking's promiscuous accounts. While an account of kinds needs to be more sensitive to the epistemic aims of science than HPC Theory, we also believe that an account of kinds should be more restrictive than recent promiscuous proposals. We have endeavoured to give such an account. Our suggested approach to kinds may need further refinement; nevertheless, we think it is a step in the right direction and an improvement over HPC Theory.

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