

# Biological Kinds and the Causal Theory of Reference

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## 1. Introduction

Theories of reference often invoke causal factors in quite general ways. For instance, the reference of a term may be inherited from other members of a linguistic community. In this paper, I am not concerned with and will not challenge these general causal-historical determinants of reference. The focus of my critique is on causal theories of reference for *natural kind concepts*. The original picture of how reference to a natural kind is established is given by Putnam (1975). The idea is that we pick out a sample of the kind by ostension or stereotypical description and the referent is that natural kind to which the sample belongs.

This original account had to be modified and refined. Natural kinds in science may not be observable, even though their effects are. Thus, reference to a natural kind may be established by describing its causal effects. Stanford and Kitcher (2000), however, point out that if we say that the referent is that kind which causes the observable properties, then 'cause' cannot be the *total* cause of the properties (otherwise the kind would necessarily have the stereotypical properties). They solve this problem of picking out the relevant subset of the total cause by offering a very sophisticated causal theory of natural kind concepts. On their account, reference is determined based on a set of samples of the kind and a set of foils, and a set of stereotypical properties that is shared by all members of the kind, but not by all foils. A further relevant refinement of causal theories is that they are not purely causal theories of reference. It is nowadays acknowledged that apart from causal factors descriptions also have an impact on how the reference of natural kind concepts is determined (Devitt and Sterelny 1999, Stanford and Kitcher 2000).

I criticize the causal theory based on an example from biology — the homology concept. Nowadays there are actually two distinct homology concepts used, which differ in reference. Thus, a theory of reference determination has at least to account for the difference between these two natural kind concepts. I argue that the standard tools of causal theories — samples, foils, and their properties — cannot do this job. My proposal is that even in the case of natural kind concepts, reference is determined based on other factors as well.

## 2. Phylogenetic and Developmental Homology

For the purposes of this paper, I can only give a very brief discussion of the two homology concepts; a detailed argument as to why they are actually two distinct concepts is given by Brigandt (2003) and Brigandt (n.d.). My discussion will explain why we have two natural kind concepts that differ in reference without invoking the core features of the causal theory — samples and their stereotypical properties. Instead, the difference is explained in terms of the scientific use of these two concepts and the epistemic and explanatory goals for which they are used. I start with the phylogenetic homology concept, which is the original homology concept that emerged in the 19<sup>th</sup> century and is still used in current comparative and evolutionary biology.

The phylogenetic homology concept is a relation used for the comparison of organisms and their structures. Two structures in different species are *homologous* to each other in case they are inherited from one and the same structure in the common ancestor. For example, the wing of bats is homologous to the arm of humans because they are both derived from the forelimb of the mammalian ancestor. In fact, even the individual bones of the human arm perfectly correspond to and are thus homologous to the bones of the bat wing. Homologous structures are the 'same' or the 'corresponding' structures in different species. Homology is an equivalence relation and thus the structures that are homologous to a particular structure form an equivalence class. The members of such a class of mutually homologous structures are called *homologues*. Homologues are often given the same name even if they consist of structures from very different species. For instance, we just talk about 'the' epithalamus (a part of the brain), referring to a structure that exists across the large and diverse group of vertebrates.

A class of homologues is a *natural kind*. As a class of homologues is an equivalence class of the 'is homologous to' relation, the homology concept actually defines a whole set of natural kinds. Thus homology is in fact a natural kind concept. Homologues form a natural kind for the following reason. Homologues, e.g., the forelimb of land-living vertebrates, are inherited from a particular structure in the common ancestor. The common ancestry ensures that many of the properties that hold for some homologues hold for all homologues. Morphological, histological, and developmental features can be (inductively) inferred from one homologue to the homologous structure in other species. Thus homologues are a natural kind in that we can project their properties. This is very important for comparative and evolutionary biology, and the reason why *homology individuates characters*. Individuating characters and structures by means of homology (rather than other principles) allows for unified and general descriptions of the properties of organisms that apply to large groups of organisms. By telling us what the different homologues of an organism are, homology breaks an organism down into its natural parts. Homology literally carves nature at its joints. Whether something is really a part of an organism depends on whether we can identify the same part in other organisms and species. The fact that homology is a natural kind concept is also shown by the fact that biologists were originally unclear about the 'essence' of homology that makes two structures homologous. The homology concept was introduced in pre-Darwinian comparative biology, and metaphysical notions such as Platonic ideas were sometimes invoked to explain what makes two structures homologous. With the advent of Darwinism it became clear that common ancestry is the defining feature of homology. Nowadays not only morphological structures are viewed as homologous, but also tissue types, cell types, genes, and proteins. This is the reason why homology is viewed by some biologists as the most important concept of biology.

The discussion so far was about the phylogenetic homology concept as still used in comparative and evolutionary biology. In the last few decades, however, a new homology concept emerged among biologists with a developmental perspective on evolution. Evolutionary

developmental biology is a relatively new field that tries to synthesize knowledge from the historically separate fields evolutionary and developmental biology. I call this new homology concept the *developmental homology concept*. It is a distinct concept because evolutionary developmental biology uses its homology concept for different purposes than traditional evolutionary and comparative biology. The traditional phylogenetic homology concept is used to make *inferences* and obtain unified descriptions of different species. Evolutionary developmental biology, however, is not primarily interested in the comparison and classification of organisms. Instead, the focus is on the explanation of how structures originate in development. The goal is to have a *causal-mechanistic explanation* of why the same (homologous) structures develop in different organisms such as in parent and offspring. The phylogenetic homology concept makes reference to common ancestry, but notions such as common ancestry or the inheritance of 'genetic information' do not yield any causal understanding of why and how structures emerge in subsequent generations — and the latter is what is important for a developmental approach (Wagner 1989, Roth 1991). The phylogenetic homology concept can be used to make inferences, but it does not underwrite causal-mechanistic explanations.

A consequence of this conceptual difference is that the two homology concepts have a different extension. Developmental homology has a larger extension in that it includes so-called *serial homologues*. Sometimes an organism has a structure that occurs repeatedly, for instance hair in mammals, leafs in plants, the vertebrae in vertebrates, or the segments in segmented animals. This multiple occurrence of the same structure is called serial homology. Thus structures within one and the same individual (rather than structures of different species) are serially homologous. Biologists using a developmental homology concept acknowledge the existence of serial homologues (Wagner 1989, Roth 1991). The existence of a repeated pattern is an important starting point for developmental research. The question is whether this pattern is due to some underlying developmental commonality, e.g., something like a duplication of genes or a duplication of a developmental program (at work in different parts of an organism). The developmental homology concept is intended to give a causal-mechanistic account of why the same structures develop and re-appear *within* and *between* organisms. Serial homologues are one instance where the 'same' structure re-occurs and call for a developmental explanation. The traditional phylogenetic homology concept, however, does not include serial homologues. The reason is that phylogenetic homology is used for the comparison of *different species*, and comparative biologists sometimes reject the very idea of serial homology on this ground (Ax 1989).

### 3. Toward a Broader Account of Reference Determination

My brief discussion of the phylogenetic and developmental homology concept explained their difference—including the difference in reference—based on how these concepts are embedded in the conceptual practices of these fields and for what scientific purposes they are used. The phylogenetic homology concept supports inferences and is used to obtain unified comparative knowledge of different species. The developmental homology concept underwrites causal-mechanistic explanations and is used to explain why structures reappear in subsequent generations and sometimes several times within an individual. My

claim is that these pragmatic and epistemic aspects of concepts are a crucial factor of reference determination, and that standard causal theories of natural kind concepts do not address these factors adequately. To be sure, causal theories can acknowledge that these factors have *some* influence on reference determination. Epistemic and pragmatic aspects can be claimed to influence which samples and stereotypical properties are used, while the latter are the real determinants of reference. However, my point is that samples and stereotypical properties *alone* do not determine the reference of natural kind concepts, and that instead the epistemic and pragmatic aspects of concepts have a *direct* influence on reference that goes beyond picking out certain samples and properties.

Sophisticated causal theories such as Stanford and Kitcher (2000) view samples, foils, and some of their properties as the core determinants of the reference of natural kind concepts. While samples surely played a role when the phylogenetic homology concept emerged, samples, foils, and properties alone cannot account for reference. In fact, these factors are not even sufficient to account for the *difference of reference* between the phylogenetic and the developmental homology concept. Proponents of the causal theory might try to argue that the reference of developmental homology is fixed by means of samples (and properties) that actually include serial homologues, while phylogenetic homology is defined using (besides standard homologues as samples) alleged serial homologues as foils. However, this does not fit biological practice. Labeling alleged serial homologues as foils was of no importance for 19<sup>th</sup> century comparative and evolutionary biologists, but their comparative research agenda determines the extension of 'homology'. The current debate with developmental biologists about the existence of serial homologues is not the *origin* but the *consequence* of the existence of two different homology concepts. When nowadays an evolutionary biologist insists that there are no such things as serial homologues, then this is not a statement that fixes the reference of her homology concept, but it is just the expression of the previously established fact that her homology concept does not refer to serial homologues.

One could point out that current causal theories allow for descriptive factors as determinants of reference. So the difference between phylogenetic and developmental homology could be explained by using theoretical statements about the referents of these two concepts. Maybe this is the case. Some descriptions of homologues surely have an impact on the reference of 'homology'. But if by descriptive elements one has some necessary or sufficient properties in mind that the user associates with the concept or that are analytically linked to the concept, then it is not clear whether this can really yield a satisfactory account. The discussion of the last section tried to make clear that there are actually two distinct concepts of homology in use, but it did this neither by relying on samples and foils, nor by invoking any special descriptions of homologues. Our best evidence for there being two concepts that differ in reference is the fact that these two concepts are used for different epistemic and theoretical goals. And my claim is that the reference of these concepts is determined by the way these concepts are embedded in different conceptual practices.

My critique of standard causal theories of the reference of natural kind concepts was based on one example—the phylogenetic and the developmental homology concept. But I think that the same point applies to other natural kind concepts as well. Another likely candidate is the species concept, which has figured prominently in philosophical

discussion as an example of a natural kind concept. My assumption is that a close look at how reference is actually determined by scientists and their practice in the case of species and other examples reveals that real cases cannot be adequately accounted for by current causal theories of reference. My proposal is that even in the case of natural kind concepts we need a broader account of reference fixing. Apart from samples, stereotypical properties, and descriptions of a kind, there are other factors that have a crucial influence on reference. These are aspects of how concepts are scientifically used and for what epistemic purposes they are used.

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# Experience and Analysis

Papers of the 27th International  
Wittgenstein Symposium

August 8 – 14, 2004  
Kirchberg am Wechsel

Volume XII

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## Editors

Johann Christian Marek  
Maria Elisabeth Reicher



Printed in cooperation with the  
Department for Culture and Science  
of the County of Lower Austria

Kirchberg am Wechsel, 2004  
Austrian Ludwig Wittgenstein Society

**Distributors**

Die Österreichische Ludwig Wittgenstein Gesellschaft  
The Austrian Ludwig Wittgenstein Society

Markt 63, A-2880 Kirchberg am Wechsel  
Österreich/Austria

ISSN 1022 - 3398

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Visuelle Gestaltung: Sascha Windholz

Druck: Druckwerker, 1110 Wien