The Causal Homology Concept

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Abstract

This presentation proposes a new account of homology, which defines homology as a correspondence of developmental or behavioral mechanisms due to common ancestry. The idea is formally presented as isomorphism of causal graphs over lineages. The formal treatment not only clears the metaphysical skepticism regarding the homology thinking, but also provides a theoretical underpinning to the concepts like constraints, evolvability, and novelty. The novel interpretation of homology suggests a general perspective that accommodates evolutionary developmental biology (Evo-Devo) and traditional population genetics as distinct but complementary approaches to understand evolution, facilitating further empirical and theoretical researches.

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1   Introduction

The homology thinking, the idea that the same anatomical structure repeatedly appears in different species or parts of the same organism, has a long history in biology (Amundson, 2005). While the existence of such anatomical similarities among or within species is now explained by the descent from a common ancestor, the conceptual issues surrounding the notion have invited philosophical as well as methodological debates and skepticism. Owen famously defined homology as "the same organ in different animals under every variety of form and function," but this definition is perplexing rather than enlightening: what characterizes and warrants the sameness of "organs," if not their form or function? What, in other words, is the unit of homology?

There are three conceptual problems. The first and foremost problem is its *definition*: what exactly is homology? Evolutionary theory tells us that homology is identity due to a common origin, but an identity of *what*? Is it morphological characters, activities, clusters of properties, or genetic networks that are regarded to be same? And what is the criterion to judge whether or not two such things are actually the "same"? The second problem is *metaphysical*. As Ghiselin (1997) points out, the homology-as-identity partitions the whole tree of life into equivalence classes. But doesn't the supposition of such universal classes, reminiscent of Aristotelian essence, commit us to an anti-evolutionary thinking? And thirdly, there is a *pragmatic* question: why do we care about homology at all? Some neo-Darwinians such

as G. C. Williams see homologs as mere "residues," i.e. a relic of the past common ancestry not yet washed out by natural selection (Amundson, 2005, pp. 237-8). If that is the case homology by itself would have no explanatory role in evolutionary theory, and the quest for its definition, however well-defined and metaphysically sound, becomes a mere armchair exercise with no scientific value.

There is at least one usage of the concept free from these issues: homology of DNA sequences. Here the "sameness" is well-defined by matching bases that can be one of the four chemical kinds, G, C, T, A. Moreover, the scientific importance of orthologs and paralogs is undeniable in reconstructing the evolutionary history and predicting gene function, to name a few. Things become different for phenotype, in particular complex phenotypes like morphological or behavioral traits. First of all, there is no clear-cut definition of "phenotypic units" as that for nucleotides. Continuous traits such as height or weight usually lack objects breakpoints by which we classify them into discrete equivalence classes. In sum, there seem to be no non-arbitrary and non-controversial units for phenotype of which we can talk about the sameness, and thus homology.

Our first task, therefore, is to identify the units on which the phenotypic homology relationship can be defined. This presentation proposes that this purpose is best served by *causal graphs* which formally represent developmental or behavioral mechanisms. Homology is thus defined as graph isomorphism over lineages, or conservation of the underlying causal structure

over evolutionary history (Section 2). I will argue in Section 3 that the formal treatment of homology (i) solves the philosophical as well as empirical puzzles and criticisms regarding the homology concept; (ii) provides clear meanings to some key but elusive concepts such as constraints, evolvability, and novelty; (iii) and suggests a broad perspective that accommodates evolutionary developmental biology (Evo-Devo) and traditional population genetics as distinct but complementary research projects. Section 4 compares the present approach to other existing accounts of homology, and discusses its relative strengths, challenge, and philosophical implication. As will be stressed there, the primary objective of this presentation is to facilitate or open up new empirical as well as theoretical questions. The last section concludes with some of these research prospects that are prompted by the new homology concept.

2   Defining homology with graphs

The idea of characterizing homology in terms of causal structures is not new. Various biologists have suggested, albeit in different fashions, that the developmental or behavioral mechanisms underlying phenotype can or should serve as a unit of homology (e.g. Riedl, 1978; Wagner, 1989, 2014; Gilbert and Bolker, 2001; Müller, 2003). These proposal, however, are mostly based on independent examples or qualitative descriptions, and the lack of a unified treatment has blurred their philosophical as well as theoretical implications.

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The aim of this section is to give a formal representation to the ideas of developmental sameness by using causal graphs, in view of exploring the conceptual nature of homology in the later sections.

A *causal graph* $\mathcal{G}$ is a pair $(\mathbf{V}, \mathbf{E})$, where $\mathbf{V}$ is a set of phenotypic or genetic variables of organisms and $\mathbf{E}$ is a set of edges representing causal relationships among these traits. Development is understood as a causal web connecting embryological, morphological, and behavioral traits, and the set of edges $\mathbf{E}$ characterizes these causal links. Note that such connections may remain invariant even under considerable modifications in phenotypic values or the functional form that determines the quantitative nature of each edge. The same set of $\mathbf{E}$ is consistent with a variety of phenotypic states and forms of causal production; it only defines the qualitative feature of the causal networks, i.e. which causes which.

Once modeled in this way, it becomes meaningful to compare causal structures of different organisms. A causal graph $\mathcal{G}_1 = (\mathbf{V}_1, \mathbf{E}_1)$ is *isomorphic* to another $\mathcal{G}_2 = (\mathbf{V}_2, \mathbf{E}_2)$ if they have the same structure, or more formally if there is a bijection $f : \mathbf{V}_1 \rightarrow \mathbf{V}_2$ such that if $(v, w) \in \mathbf{E}_1$ then $(f(v), f(w)) \in \mathbf{E}_2$. Likewise, isomorphism can be defined for subgraphs, which are just parts of the causal graphs restricted to a subset $\mathbf{V}' \subset \mathbf{V}$. We write $\mathcal{G}_1 \sim \mathcal{G}_2$ if two (sub)graphs are isomorphic. It is easy to see '$\sim$' is symmetric, reflexive, and transitive, and thus defines a equivalence class.

Each individual is assigned one causal graph that models a particular part of its developmental or behavioral mechanism. Let us denote the causal

structure of an organism a by $\mathcal{G}(a)$. Collectively, $\mathcal{G}(A)$ is a set of causal structures for a set of organisms A. We assume usual ancestor/descendant relationships over a set of organism Ω (which may include more than one species). If b is an ancestor of a, the *lineage* between b and a is a set of every individual between them. Given this setup homology is defined as follows.

> For two sets of organisms $A, B \subset \Omega$, let $\mathcal{G}'$ be a subgraph of all $g \in \mathcal{G}(A)$, and $\mathcal{G}''$ be a subgraph of all $g \in \mathcal{G}(B)$. Then $\mathcal{G}'$ and $\mathcal{G}''$ are homologous iff
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> 1. $\mathcal{G}' \sim \mathcal{G}''$;
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> 2. there is a set of common ancestors $C \subset \Omega$ of A and B[1]; and
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> 3. for every d in all the lineages from C to A and C to B, $\mathcal{G}(d)$ has a subgraph $\mathcal{G}'''$ such that $\mathcal{G}''' \sim \mathcal{G}' \sim \mathcal{G}''$.

The definition explicates the idea that homology is the identity between causal structures due to common ancestry. Two (sets of) organisms share a homologous causal structure if, in addition to the graph isomorphism, every individual on the lineage connecting them shares the same causal graph, capturing the idea that the structure has been conserved through the evolutionary history.

The same treatment applies to serial homology, i.e. the homology relationship among parts of the same organism, such as teeth, limbs, or tree

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[1]Note that C may be A or B themselves. Also note the condition 1 is redundant if a lineage includes the both ends. But here it is retained for clarity.

leaves. We can just set $A = B$, and compare different but isomorphic sub-parts $\mathcal{G}', \mathcal{G}''$ of the same overall structure $\mathcal{G}(A)$. Then the homology hypothesis is that there is an organism c in which the mechanism in question was duplicated, and the lineages from c to A have conserved the duplicated structures.

The above definition is illustrated with a case of special homology in figure 1, which depicts a particular region of the tree of life for (groups of) organisms A to G. Two mutations M_1, M_2 on the developmental mechanism occurred in the lineage leading to F, in which one causal edge $V_1 \to V_3$ was first removed and then restored. In this example, the causal structure $\mathcal{G}(D)$ of population D is homologous to $\mathcal{G}(E)$, for they are both inherited from the ancestral graph $\mathcal{G}(B)$ and $\mathcal{G}(A)$. In contrast, it is not homologous to $\mathcal{G}(F)$ even though they are graph-isomorphic. This is because the lineages connecting D and F do not conserve the causal structure in question: particularly it is not shared by C.

The example, though too simplistic to capture any real biological phenomena, makes explicit the idea that homology is a concordance of developmental mechanisms due to common ancestry. Note the criterion makes no reference to the resulting phenotype represented by particular values or distributions of variables. It does not require or forbid that, for example, two populations E and D show similar morphological distributions. Nor does it assume the graphs consist of the variables of the same nature. If the causal graphs in figure 1 represent a genetic network, kinds of genes/variables that
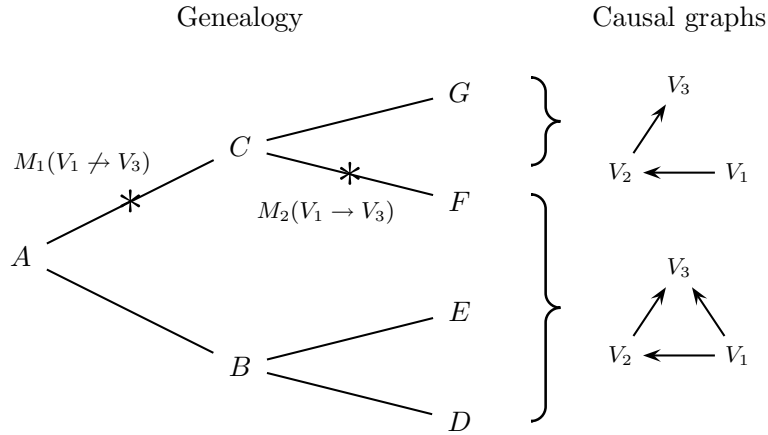
Figure 1: Illustration of graph homology. On the left is a genealogy tree for hypothetical populations A, B, C, D, E, F, G, while the graphs on the right describe causal structures of these populations over three characters, V_1, V_2, and V_3. Two asterisks ($*$) on the tree denote mutation events on the causal structure. See text for explanation.

constitute the network may vary across populations, as long as they serve the same causal roles within the overall structure. It is structural, rather than material, identity that defines homology. Theoretical as well as philosophical implications of this view will be explored in the following sections.

3 Conceptual advantages of the view

The above account is intended to provide a theoretical platform to formulate and evaluate hypotheses or explanations regarding homology. This section explicates the conceptual benefits of thinking homology in terms of causal graphs. Discussions on the empirical adequacy are differed to the next sec-

tion.

As discussed in the introduction, the major obstacle in defining homology is the absence of definite phenotypic units. Homology is an identity rather than similarity relationship (e.g. Ghiselin, 1997; Müller, 2003; Wagner, 2014), whereas no two or more phenotypic characters are identical in a strict sense — there are always subtle differences in, say, shape or size. The problem could be solved if we could find a natural and non-arbitrary way to factorize the phenotypic space into discrete regions so that two phenotypes within the same region are regarded "identical" despite their apparent differences. This is a difficult task, especially because we do not know the topological feature of the phenotypic space (Wagner and Stadler, 2003). To solve this issue the present analysis adopts a different strategy: instead of trying to impose a certain structure on the phenotypic space, it takes the generative mechanisms as basic units. Once these mechanisms are represented by causal graphs, which by nature are discrete mathematical entities, the desired identity relationship is given by graph isomorphism regardless of differences in the resulting morphology/phenotype. The graphical representation thus provides natural units prerequisite to define homology.

It is granted that a graph representation is not determined uniquely, because the same developmental mechanism can be modeled in various levels of abstraction, yielding causal graphs of different complexities. However, I take this to be a strength rather than weakness of my view, because homology too is often treated as description-dependent. Teleost fins and tetrapod limbs

are said to be homologous *as* paired vertebrate appendages, but *not as* fins or limbs. In contrast, our hands and pectoral fins of the whale are homologous not only as appendages but also as limbs. One tempting hypothesis is that such degrees of homology relationship correspond to isomorphisms of causal structures described at different granularities. In the above example, it is hypothesized that teleost fins and tetrapod limbs are represented by the same, but rather course-grained, causal graph, while tetrapod species share the causal structure to much finer details.

Fixing the level of abstraction determines not only the equivalent classes but also the degree of similarity between these classes. Two distinct causal graphs may be closer or further depending on the number of changes required to obtain one from the other. If $\mathcal{G}''$ is obtained by removing one edge from $\mathcal{G}'$ which in turn lacks one of the edges of $\mathcal{G}$, $\mathcal{G}''$ is one step further than $\mathcal{G}'$ from the original $\mathcal{G}$. Each such deletion or addition of causal connection is called *novelty*. Novelty in this framework is a modification of the causal graph, and as such creates a new equivalence class of causal graphs, namely homology. Evolutionary novelty also comes in different degrees. In general, a single modification in abstract graphs will correspond to multiple edge additions or deletions in detailed ones, and thus is weighted more. In this regard a change in the causal graph shared both by teleosts and tetrapods will count as a significant novelty and possibly a creation of a new "bauplan."

This brings us to one of the central contentions in today's evolutionary biology, namely the alleged inadequacy of the Modern Synthesis framework,

in particular population genetics, to incorporate macro-scale evolutionary phenomena uncovered by evolutionary developmental biology (e.g. Pigliucci and Müller, 2010). It has been claimed that homology (macro-scale conservatism) and novelty (a large phenotypic change) not only resist explanations by the Neo-Darwinian gradualism, but also constrain evolutionary trajectories as modeled in population genetics (e.g Amundson, 2005; Brigandt, 2007). The theoretical relationship between Evo-Devo and population genetics, however, remains elusive, which makes difficult to evaluate the call for the "new synthesis."

The present approach, by expressing homolgy and novelty in terms of graph equivalence and modification, suggests a perspective on this connection and a way to turn these claims into empirical hypotheses. Because causal models induce evolutionary changes as studied in population and quantitative genetics (Otsuka, 2015, 2016), the graphical representation allows one to analyze how developmental structures generate and constrain evolutionary dynamics. In particular, topological features of the graph such as modularity yield, via the so-called Markov condition, patterns of probabilistic independence on the phenotypic distribution and determine possible evolutionary trajectories or *evolvability*. The causal graph approach thus supports the view that a homolog constitutes a unit of morphological evolvability (Brigandt, 2007).

The graph structures that yield population dynamics are usually not study objects of population genetics. They rather serve as background frame-

works in which evolutionary models are build to study changes in genetic or phenotypic frequencies. These frameworks, however, must come from somewhere, and this evolutionary process is a primary interest of Evo-Devo. Studies on homology and novelty — graph stasis and change — amount to "higher order" evolutionary analyses that deal with changes in the theoretical framework used in population genetics to predict local population dynamics. The graphical conception of homology thus suggests a broad perspective that accommodates these different, and sometimes seen antagonistic, research fields as complementary approaches to understand evolution.

Finally, let us turn to the metaphysical problem. As seen above, homology is defined as an equivalence class over a set of causal graphs. But to what do such classes correspond, if not some ideal types or essences? Homology thinking has been criticized as anti-evolutionary due to its alleged commitment to essentialism. These critics thus re-interpret homology as a lineage that connects individual parts, rather than as a universal class to be instantiated by its members/homologs (e.g. Ghiselin, 1997). A detailed examination of this criticism must await another occasion, but here I just want to propose a different way to look at the issue. A metaphysical implication from the present study is that homology stands to concrete parts of organisms not as a universal to individuals, nor as a whole to parts, but rather as a model to phenomena to be modeled. A homology hypothesis is based on an observation that two or more individuals or parts thereof can be modeled by

the same causal graph.[2] Hence the proper relationship is not instantiation or mereology, but representation (Suppes, 2002). Once conceived in this way, the metaphysical ghost of essentialism vanishes away. Just like the same oscillator model characterizes various kinds of pendulum clocks, homology-as-model is a mathematical entity (directed graph) that may represent more than one actual individual, but that does not force us to commit to any form of essentialism.

The individual-universal distinction has also cast a shadow on the pragmatic issue regarding the epistemic role and significance of the concept of homology. It has been argued that the study of homology cannot be any more than a historiography since there is no such thing as a law for individuals (Ghiselin, 1997). A very different picture, however, emerges from the present thesis. A homology statement is a historical hypothesis regarding causal isomorphism — that two or more (sets of) organismal parts can be represented by the same causal model — and as such makes various predictions. For example, it supports extrapolations from model organisms, predicting that homologous organs will respond in the same or similar fashion to physiological, chemical, or genetic interventions. In addition, since isomorphic developmental structures will generate similar patterns of phenotypic variation (see above), their evolutionary changes are expected to follow similar trajectories. Establishing homologous relationships therefore is not a mere

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[2]This, in turn, implies these individuals would respond in a more or less same fashion to hypothetical interventions (Woodward, 2003). Hence homology statements eventually boil down to counterfactual claims.

historical description, but has predictive implications both on physiological and evolutionary studies.

4   Comparisons and possible objections

This section compares the present proposal with some of the existing accounts of homology and also discusses possible objections. A number of philosophers and biologists have recently proposed to define homology as a *homeostatic property cluster*, a cluster of correlated properties maintained by "homeostatic mechanisms" (e.g. Boyd, 1991; Rieppel, 2005; Brigandt, 2009; Love, 2009). Since clustering and correlations are a matter of degree, homology according to this view is not an identity but a similarity relationship. It thus confronts with the boundary problem — to what extent properties must be clustered to form a homolog? The underlying "homeostatic mechanism" is supposed to clarify this boundary, but without a clear definition of what it is such an attempt only leads to a circularity. In particular, if it is defined as "those causal processes that determine the boundary and integrity of the kind (Brigandt, 2009, p.82)," the charge of circularity cannot be avoided.

This kind of problem will not arise if the generative mechanisms are defined explicitly in terms of causal graphs. While my approach proposes a formal framework to represent these mechanisms, it does not make any assumption or restriction on their structure: in particular it does not require the mechanism to be homeostatic, circumventing the criticism that a home-

ostatic mechanism by definition cannot evolve (Kluge, 2003). Moreover, the reference to "clusters" or even properties becomes superfluous, because the variational properties of phenotype are mere derivatives of the underlying causal graph. Of course, covarying traits suggest some ontogenetic connections, and thus may serve as a useful heuristics for finding homologs. They are, however, only "symptoms" — what *define* homology are not properties, clustered or homeostatic, but rather generative mechanisms.

The present approach has a closer affinity to the so-called *biological homology concept* that attempts to explain the phenomena of homology on the basis of a particular feature of the underlying causal structure, such as gene regulatory networks (e.g. Wagner, 1989, 2014). Indeed, one motivation of this presentation is to give a formal platform for these empirical hypotheses to elucidate their theoretical as well as philosophical implications. An important empirical challenge to the biological homology concept, and any other attempts to identify a homolog with a certain developmental structure, is the well-known fact that morphological similarity does not entail developmental sameness (Wagner and Misof, 1993). It has been reported that apparently homologous characters in related species may develop from different genes, cell populations, or pathways — the phenomena called *developmental system drift* (True and Haag, 2001). Although these phenomena present a challenge to my account as well, not all of them count as counter evidence. If, for example, "drift" concerns only genetic or cell materials, topological features of the causal network may remain invariant. Descriptive levels also matter.

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Even if two causal structures differ at a fine-grained description, they may coincide at a more abstract level. Finally, my view does not require the entire developmental system to be conserved: if causal graphs share *some* part, they may still be homologous *in that aspect.* Indeed, it would be surprising if two apparent homologs turn out to share no developmental underpinnings at all. Some degree of flexibility may be expected, but so is inflexibility. Representing and comparing homologs in terms of the underlying causal graphs will serve as a heuristics to identify which part of the overall developmental system is responsible for generating similar morphological patterns.

From a philosophical perspective, a distinguishing feature of my account is its explicit reference to *models.* Homology has traditionally considered to be a relationship among concrete biological entities or properties thereof: it is organs or phenotypic features that are said to be homologous. In contrast, homology in my view is a relationship among abstract entities, i.e. causal graphs. How and why does such an abstract relationship reveal anything interesting about the concrete evolutionary history? That scientific theories and concepts should directly describe actual phenomena is a predominant view of science both in lay and scholarly circles. Under this conception logical positivists made it their primary task to define theoretical terms by the observable. In the same vein philosophers of biology have tried (not successfully in my view) to justify the concepts like homology or species by identifying necessary and sufficient conditions in terms of visible or directly verifiable features of organisms.

This apparently intuitive picture, however, has been criticized to be an overly simplistic view on the relationship between a scientific theory and reality (e.g. Suppes, 1967; Cartwright, 1983; Suppe, 1989). According to the critics the primary referents of scientific theories, concepts, and laws are not actual phenomena but idealized models. These models are not exact replicas of reality, but extract only certain features that are supposed to play essential roles in the scientific problem at hand. The present analysis is in line with this tradition. Causal graphs are highly idealized and thus possibly incomplete representations of complex causal interactions in living systems, but it is this idealization that affords explanatory power and general applicability. That is, on the condition that a model extracts the common causal structure of a population can it be used to predict the population's evolutionary trajectory or consequences of hypothetical interventions.

Most of these models, however, are still idiosyncratic to particular populations — e.g. population geneticists usually build, customize, or parameterize their model for each study object.[3] Homology thinking aims at even higher generality: its core idea is that some distinct species or organs allow for the same treatment/model in the analyses of their evolutionary fate or physiological performance. A homology statement is a historical hypothesis as to why such a unified explanation is possible at all. That is, it justifies the use of the same causal model based on evolutionary history, i.e. by the descent of the

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[3]Models of adaptive evolution, however, may be extrapolated to the same or similar environmental conditions. In this regard, the analogical thinking and homological thinking represent two distinct ways to generalize evolutionary models.

causal graph from common ancestry. Hence homology is far from "residual," but has a significant explanatory value in biology — it allows an extrapolation of an evolutionary or physiological model to other contexts, and thus provides a basis for the highest-level generality in biological sciences.

5 Conclusion

The concept of homology presupposes phenotypic units on which identity relationships can be defined. The present analysis identified these units with causal graphs representing developmental or behavioral mechanisms and defined homology as graph isomorphism over lineages. The advantage of this formal concept is that it acknowledges the distinctive role of the study of homology while suggesting its connection to the traditional population genetics framework. That is, it not only provides definite meanings to such concepts like constraints, evolvability, and novelty, but also presents homology as a historical account or justification of the generalizability of evolutionary or physiological models. This is paralleled with the shift in the ontological nature of what can be said to be homologous: homology is a relationship between theoretical models, rather than concrete biological entities such as organs. Hence the proper relationship between homology to actual biological phenomena is not instantiation, but representation. Once conceived in this way the metaphysical problem of the alleged essentialism fades away.

The new account of homology prompts empirical, theoretical, and philo-

sophical researches on various topics, including the study of novelty and evolvability, the interplay between Evo-Devo and population genetics, implications of developmental flexibility, and the generalizability of biological models, to name a few. Another interesting philosophical question not mentioned above is the possibility of extending the current approach to another vexing concept in evolutionary biology, namely *species*. If homology is a partial matching of the causal structures between distinct species, it is tempting to define species by the whole causal structure — so that two organisms belong to the same species if their entire ontogeny and life history are represented by the same causal graph. This is a big question that requires an independent analysis, but will be briefly discussed in the presentation if time permitted.

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