Beyond the Divide:

The Conceptual Foundations of Evolutionary Developmental Biology

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Abstract

Biologists have long taken interest in the intricate mechanisms and processes that drive the evolution of species. With population genetics providing the standard framework to explain the origin of phenotypic novelty, developmental processes have often been overlooked in evolutionary explanations. Developmental processes, however, may play a bigger role in evolution than traditionally thought. Evolutionary developmental biology (evo-devo) is the field that seeks to incorporate development and evolution into a comprehensive framework. As such, evo-devo has motivated the emergence of a new research program: the Extended Evolutionary Synthesis (EES). While some contend that EES provides greater explanatory power than Standard Evolutionary Theory (SET), skeptics criticize EES on the grounds that it is superfluous. This tension has created a divide between epistemic communities within theoretical biology. The primary aim of this dissertation is to show how conceptual clarity surrounding core notions of the EES can provide fruitful ways to move beyond such theoretical divide. I begin by an assessment of two important causal notions to evo-devo: downward causation and reciprocal causation. In both cases, I argue that the debate should shift from a focus on overarching claims about the causes of evolution to focus on the ability of different epistemic communities to identify the specific causal mechanisms responsible for the salient features of evolution. I then move to analyze the concept of evolutionary novelty. A core goal of evo-devo is to explain the emergence of novel phenotypic traits. There is much controversy surrounding the concept of novelty and whether it requires an explanatory framework that is different than that of the concept of 'adaptation'. I argue that insofar as novelty is a key concept in evo-devo and foundational to EES, EES proponents are in fact committed to realism about novelty. Specifically, I argue that realism about the mechanisms responsible for the origin of phenotypic traits is necessary to ground claims by EES proponents that their framework

has an explanatory advantage over SET. The arguments about evolutionary causation and evolutionary novelty in this thesis both aim at clarifying the conceptual foundations of evo-devo and, consequently, building a more defensible version of EES.

In addition to the primary focus of this dissertation on the conceptual foundations of evo-devo, a secondary aim of this thesis is to better understand the social implications of commercializing technological advances in genetics. In the final chapter of this thesis, I argue that direct-to-consumer genetic tests and their widespread marketing can be harmful to consumers. First, I analyze a set of non-epistemic harms based on problems of bias, inaccuracy, and reproducibility of direct-to-consumer genetic tests. I then argue that two epistemic harms may emerge from the widespread marketing and consumption of such tests. First, consumers are deprived of their testimonial authority on matters related to their own identity and ethnicity. Second, the epistemic agency of individuals is undermined since in most cases, consumers lack the technical knowledge and the interpretive resources needed to resist the reduction of race and ethnicity to genetics.

Résumé

Les biologistes s'intéressent depuis longtemps aux mécanismes et processus complexes qui régissent l'évolution des espèces. La génétique des populations fournissant le cadre standard pour expliquer l'origine de la nouveauté phénotypique, les processus de développement ont souvent été négligés dans les explications de l'évolution. Pourtant, les processus de développement pourraient jouer un rôle plus important dans l'évolution qu'on ne le pense habituellement. La biologie évolutionniste-développementale (évo-dévo) est le domaine qui cherche à intégrer le développement et l'évolution dans un cadre global. À ce titre, l'évo-dévo a motivé l'émergence d'un nouveau programme de recherche : la synthèse évolutive étendue (SEE). Alors que certains affirment que la SEE offre un pouvoir explicatif supérieur à la théorie de l'évolution standard (TES), les sceptiques critiquent la SEE au motif qu'elle est superflue. Cette tension a créé un fossé entre les communautés épistémiques au sein de la biologie théorique. L'objectif principal de cette thèse est de montrer comment la clarté conceptuelle entourant les notions fondamentales de la SEE peut fournir des moyens fructueux de dépasser ce clivage théorique. En premier lieu, je présente une évaluation de deux notions causales importantes pour l'évo-dévo : la causalité descendante et la causalité réciproque. Dans les deux cas, je soutiens que le débat devrait sur la capacité des différentes communautés épistémiques à identifier les mécanismes causaux spécifiques responsables des caractéristiques saillantes de l'évolution. Je passe ensuite à l'analyse du concept de nouveauté évolutive. L'un des principaux objectifs de l'évo-dévo est d'expliquer l'émergence de nouveaux traits phénotypiques. Le concept de nouveauté est très controversé et l'on se demande s'il nécessite un cadre explicatif différent de celui du concept d’adaptation. Je soutiens que dans la mesure où la nouveauté est un concept clé de l'évo-dévo et qu'elle est à la base de la SEE, les

partisans de la SEE soutiennent une position réaliste par rapport aux nouveautés évolutives. Plus précisément, je soutiens que le réalisme sur les mécanismes responsables de l'origine des traits phénotypiques est nécessaire pour fonder les affirmations des partisans de la SEE selon lesquelles leur cadre a un avantage explicatif sur la SEE. Les arguments relatifs à la causalité évolutive et à la nouveauté évolutive présentés dans cette thèse visent tous deux à clarifier les fondements conceptuels de l'évo-dévo et, par conséquent, à construire une version plus défendable de la SEE.

En plus de l'objectif principal de cette thèse sur les fondements conceptuels de l'évo-dévo, un objectif secondaire de cette thèse est de mieux comprendre les implications sociales de la commercialisation des avancées technologiques en génétique. Dans le dernier chapitre de cette thèse, je soutiens que les tests génétiques directs aux consommateurs et leur commercialisation à grande échelle peuvent être préjudiciables aux consommateurs. Tout d'abord, j'analyse un ensemble de préjudices non épistémiques basés sur les problèmes d'inexactitude et de reproductibilité des tests génétiques. Je soutiens ensuite que deux préjudices épistémiques peuvent découler de la commercialisation et de la consommation généralisées de ces tests. Premièrement, les consommateurs sont privés de leur autorité testimoniale sur les questions liées à leur propre identité et ethnicité. Deuxièmement, l'agence épistémique des individus est compromise puisque, dans la plupart des cas, les consommateurs ne disposent pas des connaissances techniques et des ressources interprétatives nécessaires pour résister à la réduction de la race et de l'ethnicité à la génétique.

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EES: Extended Evolutionary Theory

SET: Standard Evolutionary Theory

DC: Downward Causation

Evo-devo: Evolutionary developmental biology.

Eco-evo-devo: Ecological evolutionary developmental biology.

DTC: Direct-to-Consumer

INTRODUCTION

> Why should similar bones have been created to form the wing and the leg of a bat, used as they are for such totally different purposes, namely flying and walking? Why should one crustacean, which has an extremely complex mouth formed of many parts, consequently always have fewer legs; or conversely, those with many legs have simpler mouths? Why should the sepals, petals, stamens, and pistils, in each flower, though fitted for such distinct purposes, be all construed on the same pattern?
> (Darwin 1859, 373)

1. Evolutionary developmental biology through the lens of philosophy

How can old forms be conserved over long periods of evolution? And how can the new emerge from the old? Why should similar bones in bats be used for such different purposes, such as walking and flying? How can a hard shell in turtles have appeared from soft-shelled ancestors? Such puzzling questions are at the heart of Darwin's *Origin of Species* (1859) and still bewilder biologist today. Indeed, current evolutionary developmental biology (evo-devo) dwells precisely on such questions when trying to understand how the conservation of old forms (such as body plans) can explain the evolution of the new (such as functions, morphologies, or even behaviors) (Nuño de la Rosa and Müller 2021).

Evolution as a discipline, in its broadest form, has been greatly informed by the paradigm of population-level thinking: the underlying idea being that evolution can be understood by measuring allele frequencies in populations to model, predict and understand evolutionary processes (Okasha 2016; Plutynski 2004; Millstein and Skipper 2008). Natural selection is the driving notion that explains how such frequencies vary over time and hence, how species evolve. Consequently, evolutionary biology became a field embedded in statistical models and assumptions. Such assumptions have proven to be fruitful in a range of domains from population genetics, ecology, eco-evolutionary dynamics, and even genetic science, broadly construed.

Research in evo-devo however, challenges the ubiquity of population-level explanations and sheds light on a plethora of developmental processes that are equally relevant to our understanding of evolution (Müller 2007; Laubichler 2009). At the genetic level, examples of such processes include developmental plasticity, developmental bias, epigenetic inheritance, modularity and gene co-option (Bolker 2000; Carroll 2008; Sultan 2017b; Nuño de la Rosa and Müller 2021). A common element of these developmental processes is that they are understood as mechanisms (Baedke 2020; DiFrisco and Jaeger 2019). More precisely, evo-devo "represents a causal mechanistic approach towards the understanding of phenotypic change in evolution" (Müller 2007, 945). Evo-devo as a mechanistic science has greatly benefitted from technical and empirical advances that enabled understanding of how ancient gene regulatory networks can be deployed to give rise to novel morphological features.

Such heterogenous insights coming from different approaches in biology have created a chasm between two ways of thinking: on the one hand, population-level explanations and, on the other, organism-centered mechanistic explanations of evolution. In theoretical biology, this chasm maps onto a debate concerning two different theoretical frameworks that mark a divide between epistemic communities. On the one hand, a group of biologists argues that an extension of standard evolutionary synthesis is much needed: the Extended Evolutionary Synthesis (henceforth EES) (Pigliucci and Müller 2010; Pigliucci and Finkelman 2014; Laland et al. 2015; Laland et al. 2014). On the other, this effort is criticized on the grounds that Standard Evolutionary Theory (henceforth SET) is unfairly depicted and sufficiently tackles developmental processes in evolution, and is therefore not in need of a significant revision or extension (Futuyma 2017; dos Reis and Araújo 2020; Dawkins 2004; Welch 2017). The debate has reached a stalemate (Wray et al. 2014; Laland et al. 2014). Biologists provide different and sometimes conflicting answers to the question of

whether a new theory of evolution is needed. There are disagreements as to the standard of proof required to accept and incorporate relevant developmental mechanisms as evidence for evolution. For example, EES proponents argue that plasticity is an essential feature of evolution (Laland et al. 2014; Sultan 2017b). EES critics, on the other hand, question whether plasticity 'leads' genetic variation during adaptation (Wray et al. 2014). This stalemate can be exemplified by other controversies over questions such as: the role of reciprocal causation in evolution, the importance of niche construction vis à vis natural selection or whether evolutionary novelties are distinct from adaptations. Such crucial questions are answered differently by members of the two epistemic communities in question. For example, for EES proponents, reciprocal causation is a distinctive feature of the extension, niche construction is on par with natural selection and novelties deserve their own explanatory framework (Laland et al. 2015; Müller 2017). For EES critics, reciprocal causation is well-acknowledged in SET and not a novel feature of EES (Svensson 2018; Dickins and Barton 2013), niche construction is simply a consequence of natural selection (Gupta et al. 2017; Dawkins 2004) and evolutionary novelties can be explained within the same framework as adaptations (Charlesworth, Barton, and Charlesworth 2017). Moreover, it has proven difficult to reconcile the two sides of the debate over either a novel, unified framework, the merging of the two frameworks, or even the acceptance that the two frameworks can coexist.

2. Philosophy of biology through the lens of evolutionary biology

Philosophers of science have been active in the debate by providing conceptual contributions that clarify SET. For example, Sober (1984) presents a philosophical analysis of the concept of natural selection. Walsh has proposed a statisticalist theory of natural selection (Walsh, Ariew, and Matthen 2017) to describe and explain evolutionary change. Many other examples of

how population-level thinking has informed philosophical investigation of evolution can be found in the literature (Bouchard 2007; Brigandt 2013; 2010a; Godfrey-Smith 2009; Walsh 2019). One hypothesis is that explaining evolution in terms of changes in allele frequencies can lead to genetic reductionism (Sarkar 1998). For example, Love (2008) argues that most evolutionary explanations have been dominated by models from evolutionary genetics and that in turn "these models reductively explain evolution in terms of changes in genetic properties, such as allele frequencies" (2008, 875). Philosophical inquiry surrounding this view of evolution has been useful in untangling conceptual questions from empirical matters. Because the paradigm of population genetics is a well-established and widely endorsed field of evolution, philosophers had ample opportunity to scrutinize such models and consensus practices in the field. The richness of accounts of the philosophy of standard evolutionary biology, however, is not matched by an equally rich account of a philosophy of evolutionary developmental biology.

While scholars have long been interested in discussions about evolutionary theory from the perspective of population genetics, less attention has been given to the philosophical concerns raised by evo-devo as an independent research field. Only recently has discussion about SET and EES been assessed from a philosophical perspective (Buskell 2019; 2020; Baedke, Fábregas-Tejeda, and Vergara-Silva 2020; dos Reis and Araújo 2020; Fábregas-Tejeda and Vergara-Silva 2018; Gefaell and Saborido 2022; Lewens 2019; Marchesini and Celentano 2021). However, a comprehensive conceptual analysis of the central notions of EES and the implications of such philosophical scrutiny for theory-construction in biology is not yet available and is precisely the object of this thesis. Accordingly, the aim of this thesis is to provide a conceptual framework that sheds light on some divisive notions in philosophy of biology, as well as in biology itself. Specifically, the key notions I assess in this thesis are downward causation, evolutionary novelties,

reciprocal causation and niche construction. My overarching argument is that greater conceptual clarity is needed on such foundational notions for the debate between two ways of seeing evolution to move forward. My investigation shows that conceptual precision surrounding such core notions of evo-devo is important and necessary to overcome the current stalemate. It is precisely the lack of conceptual clarity that has ignited unfruitful disagreements and controversies that led to a divide between EES critics and its proponents. The direct contribution of evo-devo to EES should be grounded on solid empirical and philosophical foundations. Namely, for the debate to become constructive, philosophers of biology and biologists need to converge on standards of adjudication between EES proponents and critics. Such standards can then be used to specify which empirical work to pursue to make progress in theoretical matters. The standards may include criteria that delimitate: the scope of the respective research programs, the role of concepts within each framework, the characteristics of the respective explanatory targets of concepts such as novelty, and the causal models supporting theories. To settle on the relevant standards of adjudication, a first step is to clarify core concepts within each theoretical framework. This is a philosophical task.

Two terminological clarifications are imperative at this point. First, the choice of the term Standard Evolutionary Theory (SET) over Modern Synthesis is deliberate. Modern Synthesis is a narrower term that encompasses the early 20th century reconciling of Darwin's findings and Mendel's experiments to explain all of the long term features of evolution (Huxley 1942). SET is a broader term that includes the Modern Synthesis as well as the developments in population genetics and molecular biology during the second part of the 20th century. In its most general formulation, SET focuses on understanding phenotypic variation through genotypic variation. As such, focus on genes and population genetics is key to SET. The choice of the term SET is consistent with the terminology used in the field of philosophy of biology to address similar

debates. Second, throughout this thesis, referring to EES is not equivalent to referring to an altogether *new* theory of evolution (even if this is sometimes how critics portray it). While EES is a research program that aims at extending the "scope and practice of evolutionary biology" (Pigliucci and Müller 2010, vii), it is not, per se, the proposal of a novel theory. Instead, EES refers to the research project that claims an emendation of SET is necessary in light of recent developments in biology. This means that EES is an effort to build on and extend SET into a more comprehensive framework that is aligned with current empirical research that was not yet available at the time of the Modern Synthesis. The debate surrounding the EES has created two epistemic communities: those who argue that the EES is an urgent and much needed framework and those who are satisfied with SET and are critics or skeptics with respect to EES. In sum, even if EES is consistent with the standard framework, its proponents emphasize that it is not a *part* of it (Pigliucci and Müller 2010a).

The EES proposal is founded on two core commitments. First and foremost is an empirical commitment to investigate evolutionary trajectories by highlighting the role of constructive development. Constructive development is a term that contrasts with the standard view according to which development follows a blueprint, or a genetic program. Instead, the EES provides the empirically adequate tools to conceptualize development in terms of both genetics *and* plasticity (i.e., the organism's potential to respond to changing environments). The best example of a 'plasticity-first' view of evolution is perhaps West-Eberhard's (2003) work on developmental plasticity and evolution. Second, the EES is theoretically committed to the notion of reciprocal causation as a foundation for evolutionary explanations. Reciprocal causation entails that organisms are both causes and effects of evolution. This concept is presented as an alternative to Mayr's proximate-ultimate distinction (1961) whereby natural selection is the cause that best

captures evolutionary trajectories. Mayr's distinction has been criticized for being an overly bottom-up approach to evolutionary change. As such, reciprocal causation supports the view according to which organisms can also influence their selective pressures through processes such as niche construction, playing an active role in their evolutionary trajectories. Such pressures in turn shape how organisms evolve showing there is reciprocity between organisms and their environments. According to the EES proposal, focusing on constructive development and reciprocal causation yields a *better* picture of evolution where explanations are more adequate than those typically available in SET through bottom-up approaches.

Another important point brought forth by the proponents of EES is that many of the notions central to the extension are simply not seriously taken into consideration in SET. Examples include phenotypic plasticity, niche construction, developmental bias and evolvability (Müller 2017). Such notions are well discussed and studied in contemporary biology but remain underexplored in current philosophy of biology. Since such concepts play a central role in the EES framework, it seems beneficial to analyze them from a philosophical standpoint. Indeed, some of the research questions I address in this thesis surfaced from the realization of the underexplored potential of a philosophy specific to evo-devo. And last, while not all evo-devo biologists support the EES project, EES proponents draw most of their claims from findings in evo-devo. Moreover, evo-devo is said to be the discipline motivating the claims that an extension is needed (Müller 2007; 2021).

An underlying theme of the four chapters of this thesis is to tackle different philosophical problems raised by reductionist thinking about the role of genes. This underlying criticism is clearly expressed in the criticism that EES proponents direct at SET as being too gene-centric and placing excessive focus on unidirectional causation running from genotype to phenotype. While SET advocates will typically reject this criticism, SET research programs have expanded mostly

thanks to the advances in population genetics and molecular biology that followed the Modern Synthesis. With such underlying theme in mind, the fourth chapter of this thesis addresses reductionist thinking about the role of genes from a new perspective: an applied ethical problem resulting from new genetic technologies.

Consequently, in addition to the primary focus of this dissertation on the conceptual foundations of evo-devo, a secondary aim of this thesis is to better understand the social implications of commercializing technological advances in genetics. Namely, in the final chapter of this thesis, I argue that direct-to-consumer genetic tests and their widespread marketing can be harmful to consumers. I outline two kinds of harms that emerge from the widespread commoditization of direct-to-consumer genetic tests (such as those sold by companies such as 23andMe). First, I analyze a set of non-epistemic harms based on problems of inaccuracy and reproducibility of direct-to-consumer genetic tests. I show in detail why results of direct-to-consumer genetic tests may not be as accurate and meaningful as they are marketed to be. I then argue that even if the non-epistemic harms were to be mitigated, two epistemic harms persist from the widespread marketing and consumption of such tests. First, consumers are deprived of their testimonial authority on matters related to their own identity and ethnicity. Second, the epistemic agency of individuals is undermined since in most cases, consumers lack the technical knowledge and the interpretive resources needed to resist the reduction of race and ethnicity to genetics.

3. Research questions

The first three chapters of this thesis therefore provide answers to the following questions:

1. Is the EES is sufficiently novel or distinct from SET?

1.1. What notions or concepts are central to EES and is it a better framework than SET to address them?

1.2. What is the epistemic advantage of EES over SET?

2. What causal notions underlie evolutionary developmental explanations?

2.1. Is downward causation a coherent notion in evo-devo, and if so, what are the commitments needed to ensure this notion can be used in biological explanations?

2.2. What role should niche construction play in evolutionary explanations?

2.3. Is the EES better equipped to explain niche construction when compared to SET?

2.4. Is reciprocal causation a concept special to EES, or is it already incorporated in SET?

3. What are evolutionary novelties?

3.1. How can we provide a casual mechanistic explanation of the appearance of novelties, such as turtle shells, over the course of evolution?

3.2. Are novelties and adaptations two different kinds of phenomenon? Can one be explained by the other?

3.3. What is the role of the concept of novelty in the EES?

3.4. What is the importance of mechanisms such as gene co-option in explanations of the origin of novelty?

From these research questions in the philosophy of evo-devo emerged a new set of questions dealing with the data processing techniques in biology and how they can contribute to knowledge,

which is the secondary aim of this thesis and the topic of the fourth chapter. Hence, I address the following research questions in chapter 4:

4. What are the social and epistemic implications of the widespread consumption of direct-to-consumer genetic tests?
    4.1. What are the social implications of direct-to-consumer genetic tests?
    4.2. What harms and risks do such tests pose to their consumers?
    4.3. Can an ethical evaluation of direct-to-consumer genetic tests help shed light onto broader issues in genetic science?

In understanding the problems of bias, accuracy, and reproducibility in the use of genetic data, I developed a general framework to assess current techniques in genetic science (broadly construed) and sought to bring a new philosophical perspective on the ethical problems and harms that ensue from these techniques. This more applied aspect of my thesis provides insights to applied problems in contemporary philosophy of biology and data ethics.

4. Central theses

The overarching goal of the first three chapters of this thesis is to provide greater conceptual clarity around contentious notions in biology. My aim is to show how, once such clarity is achieved, it is possible to move beyond the present divide between two distinct views surrounding evolutionary theory, namely EES and SET. To overcome the current stalemate, I argue that there is a constructive way to re-orient the debate such that the conversation becomes fruitful to the epistemic communities in question. By clarifying important concepts at the source of disagreements this thesis provides reasonable standards of adjudication with respect to concepts and causal claims at the center of the debate. Specifically, alongside conceptual clarity, this thesis

lays out the metaphysical, causal, and ontological commitments of notions such as downward causation, reciprocal causation, niche construction and evolutionary novelty. Insofar as concepts are supporting pillars of scientific systems, this thesis re-examines some of the foundational concepts of evolutionary developmental biology that are also core tenets to the EES.

The overarching theses presented here can be outlined as follows:

i. <u>The conceptual foundations of EES are sound.</u>

I argue that the conceptual foundations of EES are sound even when putting contentious concepts like evolutionary novelties and reciprocal causation to test its consistency as well as its empirical adequacy. In fact, such notions are coherent and fruitful and should be explored in greater precision.

ii. <u>Some of the controversies that emerge between EES proponents and skeptics are a question of a misportrayal or a misinterpretation of SET.</u>

I argue that such misinterpretation is often at the origin of the quarrels between the different epistemic communities in question. I show that both approaches are sufficiently theoretically sophisticated to potentially account for the salient features of evolution. It is often the case that the explanations within each theory differ in their scope. Once the scope of research programs is clarified, it becomes clearer which causal models support each respective research program.

iii. To reach a constructive stage, the debate between EES and SET should focus on their ability to support research programs that identify the specific causal mechanisms responsible for salient features of evolution.

I show that some underlying assumptions about causation (coming both from metaphysics and the biological sciences) are misguided, and that once specific examples of downward or reciprocal causation are analyzed more closely, it becomes possible to strip them away from common misconceptions to arrive at causal notions that can be applied in practice while accurately describing and explaining the relevant empirical cases.

The cumulative effect of the first three chapters of this thesis is a vindication of a practice-centered philosophy of evolutionary developmental biology: an approach that starts from the way biologists use such concepts and notions *in practice* to evaluate how philosophical investigation can bring greater conceptual clarity. Instead of starting from metaphysical assumptions about causes and about the meaning of concepts, I propose to investigate central concepts in evo-devo by (i) extracting the meanings of terms and concepts as well as the assumptions that guide scientific practice from the practice itself, and (ii) analyzing contemporary and historical scientific literature, through conversations with practicing scientists and through observation of laboratory work. Moving beyond the divide means clarifying standards of adjudication. Such standards can be achieved by elucidating concepts, causal assumptions, and the scope of research programs. This move entails greater awareness as to the scope of research programs and their ability to identify the relevant causal mechanisms that support their findings. Disagreements are still likely to persist but would no longer focus on which explanatory framework is more epistemically advantageous. Rather, the debate should, ideally, focus on which empirical evidence should be pursued to better

support different research programs in their different scopes. Moving beyond the divide also means providing the tools to avoid confusion over the meaning of terms and concepts such as 'novelty' or 'reciprocal causation'. By placing core EES concepts in philosophical focus, I diagnose some areas where such claims remain unclear and show a way to clarify them. My hope is to widen the field for philosophical discussion by providing sound conceptual clarity and arguments that sharpen the difference between issues that remain unsettled allowing the debate to reach a new stage.

Finally, the fourth thesis defended in this dissertation can be found in the fourth chapter:

iv. <u>The widespread commoditization of direct-to-consumer genetic tests is the source of non-epistemic as well as epistemic harms.</u>

Through an in-depth study of how direct-to-consumer genetic tests are marketed, sold, and consumed, I defend that they can be a source of both non-epistemic and epistemic harms. Namely, I show that even when the non-epistemic harms are mitigated, at least two epistemic harms remain that are tied to the use of reductionist rhetoric and the assimilation of race and ethnicity to DNA information.

4.1.Evolutionary causation

> The multiplicity of causal chains, all of weak individual influence in their normal condition, presents a special difficulty for the attempt to understand life processes.
> (Lewontin 2000, 95)

In recent years, significant attention has been given in biology to the general notion of "evolutionary causation" (Uller and Laland 2019). Interest in causation from the evolutionary standpoint, however, pre-dates recent discussions. In biology, for example, Mayr's famous distinction between proximate and ultimate causes has greatly shaped causal reasoning in evolutionary studies. In fact, Mayr's distinction sets apart two research fields that focus on different causal accounts. On the one hand, the functional biologist is "vitally concerned with the operation and interaction of structural elements, from molecules up to organs and whole individuals" (Mayr 1961, 1502). On the other, the evolutionary biologist's key preoccupation is to "find the causes for the existing characteristics, and particularly adaptations, of organisms" (Mayr 1961, 1502). Hence, the functional biologist is concerned with proximate causes: the immediate conditions responsible for a certain change or behavior in the organism in question, while the evolutionary biologist is interested in "the causes that have a history and that have been incorporated into the system through many thousands of generations of natural selection" (Mayr 1961, 1503). While Mayr's distinction is a key starting point to thinking about evolutionary causation, it has been argued that the proximate-ultimate distinction is insufficient to capture the plethora of causes at play in evolution (Laland et al. 2011; Laland et al. 2013).

Biologists use causal language in explanatory capacity in several sub-fields. For example, in population-level thinking, natural selection is seen as a causal process (Millstein 2006). In evo-devo, development is said to be understood in causal-mechanistic terms (Baedke 2020). While scientists are interested in causality, it is often seen as a metaphysical and, more generally, philosophical problem whose treatment is delegated to philosophers (Pigliucci 2019). One problem is that the metaphysics of causation has often been described as too out of touch with scientific practice (Ibid). A practice-centered epistemology of causation, as I suggest in Chapter 1, can

contribute to bridging the gap between abstract theorizing about causation and its pragmatic use in science. The underlying strategy of a practice-centred approach is to begin by an assessment of what kinds of processes biologists describe as cases of downward causation. From there, analyzing different cases such as weak and strong compositionality provides useful information as to how to conceptualize downward causation in accordance with how biologists use the notion in explanatory capacity. In fact, a starting point of my arguments in Chapters 1 and 2 is that purely theoretical and metaphysical claims about causation can sometimes obscure the usefulness of causal notions as used by biologists, such as downward causation and reciprocal causation.

Causal assumptions in biology are not only used in explanatory capacity, but also for the purpose of theory construction. In Chapter 1, I challenge metaphysical views that deem the notion of downward causation incoherent and find that most objections to downward causation take issue at the problem of compositionality (i.e., that downward causation cannot be coherent because wholes are composed of parts and it is a compositional, rather than a causal relation). I have found that in some cases, compositionality is not a nuisance to the coherence of downward causation. In fact, it is possible to arrive at a coherent notion of downward causation even in the strongest cases of compositionality. This is especially fruitful for understanding the causal models at play in evo-devo. Environmental effects on phenotypic change are often labeled as cases of 'top-down' causation and downward causation seems to be used unproblematically by biologists. Hence, by clarifying and defending the coherence of downward causation I show that it can adequately be a part of causal explanations in evo-devo (research question 2.1). Additionally, if biologists use the notion of downward causation in their descriptions, embracing compositionality and defending downward causation in the strongest cases of compositionality can be fruitful to make such explanations more defensible. While the criterion of adjudication of claims about downward

causation I propose in Chapter 1 is not specific to EES, it is nonetheless crucial for causal assumptions in evo-devo. Namely, in this chapter I defend that there are two criteria that decide whether dependencies among causal variables at different levels satisfy the conditions for interlevel causation. First, conditional independence holds when fixing variables at an upper level while changing those at the lower level yields the same effect. When conditional independence is satisfied, the upper level is causally efficacious: only when it is intervened upon, the lower-level effect changes. Second, the condition of independent fixability establishes that it is possible, at least in principle, to intervene on and manipulate variables at different levels separately. Both conditions are met in the cases of strong compositionality, showing that downward causation is a coherent notion even in the cases where it is thought to be most problematic.

In Chapter 2 I clarify claims made about reciprocal causation and the role of this notion in the strengthening of EES (research question 2.4). If causation is crucial for theory-construction in biology, and, more specifically to evaluate the scope of reciprocal causation in the EES, then it is a timely philosophical task to scrutinize such causal concepts at play in biology. I found that part of the controversies surrounding reciprocal causation stem from a misportrayal of how the notion is deployed in SET (research questions 1.1 and 1.2). Additionally, the way in which reciprocal causation is used in explanatory capacity in the EES may not be as innovative as its proponents state. Instead of a focus on the overarching causal claims in each framework, I found that delimitating the scope of explanations that make use of reciprocal causation is an important step in understanding and clarifying the role that reciprocal causation plays within each epistemic community in question. Namely, reciprocal causation is a term used to *structure inquiry* in relation to the kinds of mechanisms each community seeks to explain. Niche construction (i.e., the process by which organisms modify their environments, thereby creating additional selective pressures) is

a useful empirical example to delve deeper into the role of reciprocal causation in SET and EES and analyzing a case of niche construction from each perspective provides evidence for the claims I make about the scope of reciprocal causation (research questions 2.2 and 2.3). Once the scope of reciprocal causation is clarified, the epistemic advantage of the EES when making use of this notion becomes clearer. While both frameworks are well-equipped to explain niche construction the scope of explanations making use of reciprocal causation is different in each framework with regards to time scales and the fine-graininess of explanations. Clarifying the scope of reciprocal causation allows the debate to move forward insofar as it specifies the explanatory goals of the two different research programs in question. The debate is no longer about *whether* reciprocal causation is a feature of SET, but rather, about what is the scope of explanations making use of reciprocal causation explain within SET and EES respectively. Therefore, the criterion of adjudication I propose in the case of reciprocal causation is whether the reciprocity of causes on a fine-grained, shorter time scale explains evolutionary processes that the reciprocity of causes on a more coarse-grained, longer time scale does not.

In this thesis I have therefore zoomed in on two important causal notions that underlie evolutionary developmental explanations: downward causation and reciprocal causation. Chapters 1 and 2 aim at answering research questions 1 (and sub-questions 1.1 and 1.2) and 2 (and sub-questions 2.1 – 2.4). Since biologists tend to make use of such notions rather loosely to describe and explain processes such as feedback loops, social interactions, and ecological processes such as niche construction, the two chapters dedicated to causation in biology develop a pragmatic approach to causation compatible with its use within epistemic communities in evolutionary biology.

4.2. Conceptual clarity and bridging gaps between theory and practice

Investigating evolutionary causation in evo-devo also means understanding the emergence of key concepts in the discipline. Conceptual issues in evo-devo arise not only at the causal level, but also at the level of scientific concepts and definitions. Such is the case, for example, with a central notion in evo-devo: evolutionary novelty. The work of Brigandt and Love (2012; 2010) is a key framework I build on to argue for a stronger epistemic goal of the concept of novelty (Chapter 3 of this thesis). Research question 3 is a question that goes back to Darwin's (1859) question about the deployment of the same bone structures for such different purposes such as flying and walking. In fact, this question is fundamental to understand the difference between two different concepts: novelty and adaptation. While adaptation captures the *modification* of existing features, novelty usually refers to the *origination* of phenotypic characters. The legitimacy and distinctness of a concept of novelty, as I argue, depends on a realist commitment to the existence of a definite set of mechanisms that explain the origin of phenotypic traits. This epistemic goal of the concept of novelty is much stronger than the one proposed by Brigandt and Love (2012; 2010) and is better-suited for the role that the concept plays in EES. That is, novelty is a kind of phenomenon that biologists seek to explain in mechanistic terms by identifying specific developmental processes that account for the origin of phenotypic traits. The concept of novelty therefore has a stronger epistemic goal than the one described in Brigandt and Love's account. In addition to structuring research agendas, the concept of novelty is meant to encompass all and only those phenotypic traits whose emergence is explained by a certain set of mechanisms. Mechanisms in that set are hypothesized to be distinct from the mechanisms that give rise to adaptations. My discussion of

novelties is also framed within the SET and EES discussion. EES proponents argue that novelty is a core concept of the extension that was too often enmeshed with adaptation under SET. If novelty is to play a central role in claims defending the need for an extension, my hypothesis is that a stronger epistemic goal is already in place when biologists use the concept in practice. It follows that the criterion of adjudication I propose for EES claims about novelties is whether a distinct set of mechanisms is identified that explains the origination of phenotypic characters.

Hence, in Chapter 3, I show that to provide a causal mechanistic explanation of the origination of novelty, biologists have a realist commitment to the underlying mechanisms responsible for the origination of phenotypic traits (research questions 3.1 – 3.4). Their goal is to identify such mechanisms and research on gene co-option (i.e., when new functions for existing genotypic traits occur, generating developmental or morphological novelties) is a good example of one candidate mechanism. I framed my discussion of novelties within the context of Brigandt and Love's (2010; 2012) extensive work on the epistemic goal of evolutionary novelty. Realism about novelty helps the debate move forward in at least two ways. First, it moves away from terminological and definitional quarrels by specifying the epistemic goal in place. Second, it shows that different relevant mechanisms should be empirically pursued to explain novelties and adaptations respectively.

4.3. The epistemic harms of direct-to-consumer genetic tests: perspectives from the philosophy of biology and genetics

In Chapter 4, I analyze a practical dimension of current biological practice: the implications of the widespread sales and consumption of genetic tests that allegedly provide information on

ancestry as well as information about the risk of developing certain diseases (research question 4.1). Through an in-depth study of how such tests work and from reading consumers' testimonials, I show that there are serious problems of bias and inaccuracy in the data processing techniques meant to extract genetic information and establish predictions about ancestry and health risks. I contend that beyond problems of bias, accuracy, reproducibility, there are also epistemic harms that should be addressed and mitigated (research question 4.2). I frame my discussion of epistemic harms within the literature of epistemic trust between laypersons and scientific communities (Grasswick 2010; Hardwig 1991) as well as within the literature on epistemic injustices (Fricker 2007). This more applied section of the present thesis sheds light onto a larger set of questions in genetic science that should be addressed from a philosophical point of view. Namely, the question of Euro-centric bias of databases means that predictions are a lot more accurate for consumers who have DNA that is similar to the majority of samples in a database (research question 4.3). This should be made clear in the marketing of direct-to-consumer tests so that consumers are aware that results might not be as exact as they are marketed to be. Additionally, Chapter 4 also raises questions about the use of reductionist rhetoric on matters related to ancestry, race, and genetic information. Such investigation of the use of reductionist rhetoric is related to one of the common themes of this thesis, which is to encompass different philosophical problems raised by reductionist thinking about genes. This especially relevant nowadays with a growing number of companies obtaining personal genetic data and selling it as information to consumers who provide DNA samples.

5. Methodology

5.1. A toolbox view of models of evolution

Kenneth Waters (2014) has identified an important shift in how theorizing in the philosophy of biology has changed from being theory-focused to a practice-centered epistemology. Similarly, Pigliucci (2019) argues that a productive model of scientific and philosophical enquiry is to approach both disciplines as mutually beneficial areas of overlap. What marks this shift is specifically a focus on pluralistic approaches replacing dogmatic philosophical assumptions. I adopt a similar methodological move in my thesis to show how a philosophy of evolutionary biology that is practice-centered, rather than proceeding from a fixed set of metaphysical assumptions, can bring conceptual clarity to problems that remain unclear to biologists simply because they cannot be settled empirically. This practice-centered focus is a necessary condition for disciplinary integration to occur and for the debate to move beyond the divide. Hence, in the arguments presented in this thesis, the same underlying methodology can be found: an approach to evo-devo as a toolbox rather than a one-size-fits-all analysis of the structure of theories. The toolbox metaphor is useful here. As Waters explains, the toolbox view "emerges from centering attention on practices of theorizing: one aim of scientific theorizing is to construct causal models that explain aspects of the process in a domain", which "entails articulating a multiplicity of theoretical concepts and causal principles that can be drawn upon to construct models that might decompose the causes of different processes in different ways and the causes of some processes in a multiplicity of ways" (Waters 2014, 130). Against a purely theory-driven understanding of evolution, this thesis draws on the toolbox metaphor whereby the relevant biological models are the tools being used to assess the success of theoretical commitments (Cartwright, Shomar, and

Suárez 1995; Suárez and Cartwright 2008). Examples of the causal models of the processes discussed include the models explaining the origination of phenotypic traits (such as gene co-option), or models of feedback loops (such as in reciprocal causation and niche construction). This toolbox view of evo-devo articulates scientific notions and concepts integrating a multiplicity of views and sub-domains in evo-devo. Such a view is also compatible with process ontology (*sensu* Dupré 2012), whereby biological processes are the relevant units for analyzing theoretical claims in biology.

5.2. Philosophy of science in practice and evo-devo

The history of theory-construction in biology is a valuable source of information that provides knowledge about the historical reasons for theory change as well as the sources of theoretical disagreements. It does not, however, provide the tools needed to move forward in discussions between different epistemic communities. My hypothesis is that a project that seeks to provide the necessary tools to move beyond the divide must address two aspects: the empirical challenges that emerge in scientific practice as well as the conceptual lack of clarity in theoretical biology. Hence, philosophy is indispensable to bring to light the epistemic significance of empirical evidence from evo-devo to the EES discussion. In fact, as Leonelli (2010) argues, studying specific study cases in biology greatly benefits from multiple disciplinary lenses. The methodology I followed in this thesis has one key innovative aspect when compared to other scholars who have also tackled the divide between SET and EES (dos Reis and Araújo 2020; Baedke, Fábregas-Tejeda, and Vergara-Silva 2020; Lewens 2019; Buskell 2020). While a historical exegesis of the construction of such frameworks is essential, I proceed differently by analyzing core concepts that are the source of disagreement among both scientists and philosophers

of science. My methodology is innovative insofar as it starts by uncovering the conceptual assumptions underlying the practice, such as, for example, by analyzing the role of concepts in structuring inquiry and identifying the aims and scope of inquiry in question.

Drawing from the general methodology of philosophy of science in practice (Ankeny et al. 2011), my claims are first and foremost grounded in empirical examples whereby the notions assessed are deployed. Chang (2012) notes that the field of history and philosophy of science has often generalized too hastily from a given set of conveniently chosen cases studies to draw its conclusions. I share a similar view about philosophical claims regarding theory-construction in biology. Following Chang's proposal (2012), I take the empirical examples discussed in this thesis to be concrete instantiations of general concepts that appear in theoretical biology. A key aspect of the methodology I adopt is in line with a requirement of philosophy of science in practice (Ankeny et al. 2011): to adopt an agnostic position with respect to metaphysical and ontological commitments underlying core causal notions and shift to how they are used in current biological practice specifically in the field of evo-devo. The methodology of this thesis can be characterized as practice-centered for at least two reasons.

(i) It starts from empirical puzzles to a reassessment of the metaphysical assumptions that are, most frequently, at the source of such divides. This avoids placing excessive focus on ontological commitments that may lead to more confusion with respect to imprecise concepts such as 'novelty' or 'compositional levels'. For example, instead of tackling the novelty debate from a definitional perspective or from the question of its semantic variation, I proceed by investigating which kind of empirical work biologists are pursuing when they seek to explain the origin of phenotypic traits.

(ii) It remains agnostic as to metaphysical assumptions in order to focus on the practical use of concepts and causal notions. As a result, the conceptual clarity it seeks to provide deliberately avoids metaphysical puzzles and focuses on scientific practice as the foundation of theoretical claims in biology. For example, my investigations of 'novelty' and 'reciprocal causation' begin by an assessment of the empirical work being done by biologists, from which I derive the philosophical implications of such notions.

Instances of this methodology can be seen in all four chapters of this thesis. For example, in my study of downward causation, I look at real cases and examples where higher levels of a system are said to cause lower-level effects of the same system by analyzing causal relations in feedback loops, the impact of environmental changes in development and evolution in ant caste determination, and the complex social relations in ant colonies. In my second chapter, I work from examples of niche construction theory to untangle theoretical, conceptual and empirical claims about reciprocal causation. In the third chapter, I move away from definitional debates about evolutionary novelties and propose a pragmatic account of novelties that describes how the notion is used in empirical examples, such as to identify and describe co-option mechanisms in evolution and their role in the emergence of phenotypic traits. And finally, in the fourth chapter, while the topic is not evo-devo, I analyze the practices of generating, reporting, and marketing direct-to-consumer genetic test results and abstract from an ethical framework for less harmful practices in genetic science.

6. Summary of chapters and key contributions

6.1. Global contribution

Competing explanations often become a locus of vivid debate in theoretical biology, especially in the criticisms that EES has encountered since its initial proposal (Futuyma 2017; Laland et al. 2014). At the heart of this thesis is the goal of untangling key conceptual issues to provide ways for the debate to move beyond the divide. While each of the thesis chapters provides independent arguments that tend towards this overarching goal, the cumulative effect of the first three chapters of this thesis is a vindication and defense of conceptual clarity of key notions in evo-devo notions. As a result, the main global contribution is to provide the tools needed for strengthening EES into a robust theoretical framework. My goal is therefore to show that moving beyond the divide is a much-needed step to make progress in theoretical biology and that philosophical inquiry can and should play a crucial role in achieving greater conceptual clarity. I achieve this goal by clarifying and setting standards of adjudication. Such standards are a result of close philosophical examination of concepts, causal assumptions and the scope of research programs. Through my practice-centered methodology and focus on the pragmatic use of concepts and causal notions, rather than on a historical exegesis, I provide the groundwork for a philosophy that is specific to evo-devo. This move is timely and important. While many biologists have approached philosophical issues from an empirical standpoint, empirical matters can also benefit from philosophical hindsight. A practice-centered philosophy of evo-devo can therefore bring forth the necessary conditions needed for core concepts of evo-devo to play a strong role in EES. An approach that starts from philosophical investigation has fewer stakes in the debate and therefore can provide a neutral and critical perspective on such matters without necessarily

implying partisanship in either side of the debate. My hope is that the conceptual clarity brought by this thesis will re-orient the debate away from unfounded claims that EES is not theoretically sound or that SET is theoretically incomplete. When moving beyond divides and bringing clarity to core concepts in evo-devo and hence in EES, I wish to focus on the fruitfulness of their respective research programs in identifying causal mechanisms responsible for phenomena such as group behaviour, the origination of novel phenotypic traits and eco-evolutionary feedback processes.

6.1.1. Chapter 1: Demystifying Downward Causation in Biology

In this chapter, I discuss the somewhat controversial notion of downward causation. Despite the ambivalence of philosophers towards the notion of downward causation, it is a widespread concept in biology, where it is frequently used in an explanatory capacity to account for certain regularities and processes. The main contribution of Chapter 1 is to provide conceptual clarity on the notion of downward causation (DC) as well as to show how it can be a useful causal notion in evo-devo. Building on interventionist theories of causation, I propose a conceptual framework that demystifies what is meant by 'downward causation' using examples from the field of ecological evolutionary developmental biology. Downward causation in biology is thought to be problematic because it relies on the assumption that entities are connected by compositional hierarchies of levels of organization. I delve into the "compositional" assumption of levels of organization and distinguish between weak and strong compositionality. I introduce examples of weak and strong compositional relations and argue that downward causation becomes unproblematic if we use features of interventionist theories of causation. This requires a shift from entity-thinking to variable-thinking. I show that an interventionist account of downward causation

successfully responds to the three central objections to downward causation in the philosophical literature and clarify the explanatory usefulness of the concept in biology by examining three empirical examples that are often labeled as instances of downward causation: (i) feedback loops; (ii) environmental effects on evolution in a case of parallel evolution; (iii) causal relations between upper and lower levels of a complex systems such as an ant colony.

6.1.2. Chapter 2: The Scope of Reciprocal Causation in the Extended Evolutionary Synthesis

The main contribution of Chapter 2 is to re-orient the debate surrounding niche construction and reciprocal causation in the EES. In this chapter I analyze the contentious notion of reciprocal causation. While reciprocal causation is said to be a main innovative aspect of EES, critics argue that there are textual and empirical grounds to say that SET has adequately captured the reciprocity between organisms and environment. Such arguments are what I call (i) the misportrayal argument, and (ii) the empirical argument. I offer a third argument to replace (i) and (ii): the scope argument. The goal of this argument is to re-direct the debate surrounding reciprocal causation clarifying the specific role of the notion within each epistemic community. I argue that a focus on the scope of reciprocal causation within epistemic communities and research programs can be fruitful to establish in what capacity reciprocal causation provides epistemic advantage to the EES. I show that different epistemic communities make use of the notion of reciprocal causation with different scopes in mind. Two dimensions of scope I analyze are time scales and the fine graininess of explanations.

6.1.3. Chapter 3: Evolutionary Novelty: A Realist Argument

The concept of evolutionary novelty has been the object of much debate and discussion. The lack of a clear-cut definition of the concept has puzzled scientists and philosopher of biology alike. Chapter 3 provides an original argument claiming that realism about novelty is necessary to account for the concept's role in EES. I draw from Brigandt and Love's account of the epistemic goal of novelty and reinvigorate the discussion surrounding novelty by proposing a stronger epistemic goal that is more coherent with the concept's pragmatic use in evo-devo. To this end, I analyze Brigandt's (2010) notion of epistemic goal and argue that there is a mismatch in how the epistemic goal of novelty is formulated by Brigandt and Love (2010; 2012) (i.e., to structure problem agendas) and epistemic optimism surrounding the concept's use in the EES. I argue that realism about novelty is necessary for the epistemic goal the concept aims at fulfilling: to identify and describe the mind-independent mechanisms that explain the origination of phenotypic traits. I analyze a candidate mechanism that partially accounts for the stronger epistemic goal of novelty I propose - gene co-option. While this stronger epistemic goal might be objected on the grounds of being too reductionist or too strongly committed to realism, I show why this goal is (i) compatible with the concept's current usage in EES; and (ii) fruitful for the debate between EES proponents and its critics moving forward.

6.1.4. Chapter 4: The Epistemic Harms of Direct-to-Consumer Genetic Tests

The research question I address in the final chapter of this thesis is not directly related to evo-devo but emerged throughout my research in epistemic questions in the philosophy of biology. Specifically, as part of a research project in data ethics, I was intrigued to delve deeper into genetic science, broadly construed. In my chapter "The epistemic harms of direct-to-consumer genetic

tests", I draw on the literature on epistemic injustices to provide an epistemic evaluation of the harms that result from the widespread marketing of direct-to-consumer genetic tests. In recent years, a growing number of private companies has started marketing genetic tests directly to consumers. Consumers submit a sample of their DNA to a private company and obtain reports about their ancestry or about variations in their genome commonly associated with risk of developing certain diseases. While genetic tests are a valuable accessory diagnostic tool when ordered by a medical practitioner, there are different implications when genetic tests are sold directly to consumers. In this chapter, I analyze three harms associated with the widespread availability of direct-to-consumer genetic tests. The first harm concerns problems of bias, accuracy, and reproducibility. I then argue that direct-to-consumer genetic tests are also a source of two epistemic harms. However, I show that even if those harms were to be mitigated, there are at least two epistemic harms that persist. First, DTC tests deprive consumers of testimonial authority, i.e., the ability to provide testimony on matters relating to their own identity. Second, the individual's epistemic agency is undermined, since in most cases consumers lack the interpretive resources and technical knowledge to resist the reduction of race and ethnicity to genetics. I propose three possible ways to mitigate these harms: focus on genetic literacy, recognize the need for increased regulatory controls, and insist on transparency and accountability for direct-to-consumer genetic testing companies. The original contribution of this chapter is precisely in identifying such harms and providing guidelines for better practices in one field genetic science, namely, recreational genomics.

1. DEMYSTIFYING DOWNWARD CAUSATION IN BIOLOGY

1.1.Introduction

Downward causation (DC) comprises a cluster of ideas that describe how upper levels of a system can influence the behavior of the system's lower levels. Downward causes are typically invoked in the literature surrounding emergence and nonreductive physicalism (Bedau 2008; Rothschild 2008; Kim 1992; Bertolaso and Buzzoni 2017). Empirical observations support the idea that there is a tension with how DC is traditionally portrayed in the philosophical literature and used in scientific practice. Philosophers tend to be ambivalent about DC and several have claimed that it is metaphysically incoherent (Hulswit 2005; Craver and Bechtel 2007). Despite such hesitancy, DC is a widespread concept frequently used in explanatory capacity to account for regularities and processes. This is the case in many disciplines that deal with complex systems composed of different levels. The underlying motivation for talking about DC is that biological entities are complex systems, composed of different levels of organization. Some changes that occur at lower levels seem to have been triggered by a change in upper-level conditions. In such cases, causation is said to be downward, and causes are described as 'top-down'. While DC (also sometimes described as top-down causes) is used rather loosely by biologists, it is frequently used in explanatory capacity to describe causal processes and complex interactions that occur between different levels of a system (a few examples include Campbell 1974; Uller and Laland 2019; Sultan 2019; Laland et al. 2013). Specific examples described as DC include a wide range of biological phenomena such as feedback loops and the impact of environmental effects on evolution (Brooks, DiFrisco, and Wimsatt 2021). Thus, the ubiquity of DC in some fields of investigation in biology seems to conflict with its incoherent portrayal in metaphysical investigations.

In this chapter, I propose a solution to the tension between DC's apparent incoherence and its widespread use in biology and philosophy of biology (Dupré 2021; Bizzarri et al. 2019; Noble 2012; Pigliucci 2019; Woodward 2010; Noble 2008; Eronen 2013; Green 2018; Boi 2017; Otsuka 2019). My proposed solution is especially relevant for understanding DC in the life sciences. While DC has already been scrutinized in many domains in the philosophy of science (Malaterre 2011; Woodward 2021b; Ellis 2016), my account defends DC's coherence specifically in the life sciences, a disciplinary area that frequently invokes DC without subjecting the concept to philosophical scrutiny. The scientific viewpoint I engage with is evolutionary developmental biology (evo-devo), a field concerned with understanding how environmental effects can shape development and evolution (Nuño de la Rosa and Müller 2021).

My argument can be outlined as follows. I show that some versions of DC rely on the assumption that upper and lower levels are related in a strong compositional relation, while other versions of the concept do not presuppose strong compositionality. In cases where compositionality is weaker, the tension between the purported incoherence of DC and its widespread use in explanatory capacity is not present. Namely, in cases of weak compositionality the most common objections against downward causation do not seem to be relevant. I show that even in the more problematic cases of strong compositionality, adopting an interventionist view of causation dissolves the apparent tension, and legitimates the use of the concept of DC in biology. This requires shifting from 'entity-thinking' to 'variable-thinking' about causes. Specifically, a downward causal relation is a difference-making relation between variables that represent properties at different levels of a biological system (examples of levels include genes, cells, tissues, organs, and so on). Hence, my analysis of DC offers two contributions. First, in disentangling DC from metaphysical assumptions about compositionality, I show how even in cases of strong

compositionality DC can still be coherent when viewed through an interventionist lens. Second, in working closely with empirical examples I expose and explain the gap between the abstract way DC is discussed by some philosophers and the practical usefulness of the concept to biological practice. While the argument presented here specifically focuses on the use of downward causation in biological explanations of interlevel causation, it is nonetheless relevant to the broader context of the EES debate. One of the claims made by EES proponents is that SET places an excessive focus on bottom-up causes running from genes to phenotype and that it is therefore gene-centric (Pigliucci and Müller 2010). Whether this is the case will not be scrutinized here. However, if bottom-up causes are said to be insufficient to explain evolutionary causation, top-down causes should be an important conceptual tool for EES proponents. Indeed, evo-devo is interested in how top-down processes (in addition to bottom-up causes) can be a part of evolutionary explanations. Therefore, showing that downward causation can be coherent in an example of special interest to evo-devo (such as top-down causation in an ant colony) makes a strong argument for the importance of downward causation *in addition* to bottom-up accounts of causation.

In Section 1.2 of this chapter, I characterize the general idea of DC and how it is discussed in the context of evolutionary biology, focusing on three common objections raised against DC. In Section 1.3, I introduce a conceptual distinction between cases of weak and strong compositionality through empirical examples. I argue that it is in cases of strong compositionality that DC poses conceptual difficulties. In Section 1.4 I introduce an interventionist response to the objections raised against DC. Finally, in Section 1.5 I highlight the usefulness of a practice-centered epistemology in the study of DC in biology. I present some concluding remarks in Section 1.6.

1.2. Downward causation and evolutionary developmental biology

Causation has been a central topic of investigation in both philosophy and biology (Baedke 2020; Campbell 1974; Mayr 1961; Uller and Laland 2019). Within biological research, causation is important to a variety of activities, including explanation, theory construction, and the analysis of the dynamics of biological systems. The concept of DC is meant to capture the general claim that upper levels of a system can cause changes in lower levels of the same system. The notion of levels is enmeshed with DC and has been the object of much discussion in philosophy of biology[1].

Although levels can be seen as a problematic way of dividing the biological world (Potochnik and McGill 2012), they have heuristic value (Brooks and Eronen 2018) and can provide a framework for analyzing DC (Eronen 2015). In his deflationary account, Eronen argues that the notion of levels is not needed for analyzing DC and that in fact, DC becomes clearer when we abandon the framework of levels. DiFrisco also proposes that levels be understood in terms of time scales or process rates. In a similar vein, Dupré (2021) shows that it is fruitful to move from a mechanistic understanding of downward causation to exploring the notion as an explanatory feature of how parts and wholes are related. In sum, several examples in the literature recommend untangling DC from descriptions according to which the world is organized into levels that are ascribed to specific entities. However, the notion of levels can be used loosely as a descriptive tool that does not presuppose any ontological commitment to an independently existing entity. This

[1] For example, Malaterre (2011) argues that the notion of DC goes hand in hand with the notion of levels, even if this may seem problematic. One reason for such ascription is that it is not clear whether levels can be ascribed to any given entity. Ascribing level-neutral variables to downward causation does not sufficiently account for the "downward" aspect of DC. For Malaterre (2011), there is a mereological component in DC since it is the whole that influences the part. Later in this chapter I deflate this claim by showing that the mereological commitment poses no problems to the coherence of DC.

will become clear throughout my argument in this chapter when suggesting the move from "entity-thinking" to "variable-thinking" to assess DC.

Hence, as a starting point, DC can be characterized as a causal relation between *x* and *y* whereby x causes y, *x* is at an 'upper' level of organization, and *y* is at a 'lower' level. Some prominent examples of putative DC offered by biologists and philosophers of biology include changes in the pigmentation of butterfly wings due to seasonal changes (Suzuki and Nijhout 2006); feedback loops, feedback inhibition, and cellular signalling pathways (Boi 2017); the behaviour of ants in colonies (Noble 2006); and natural selection as a higher-level life or death switch (Campbell 1971).

The idea of DC presents an ongoing problem to contemporary philosophy of science and its coherence has been frequently debated. Jaegwon Kim (1992) analyzes downward causes in the context of higher-order mental or volitional events that determine how lower-level physical entities will be deployed[2]. Although Kim's focus is on the realm of mental causation, the conceptual problems he identifies are worth analyzing in different contexts. Under Kim's view, if one accepts that psychological states and processes are distinct from biological and physicochemical processes (even though the former might emerge from the latter), then one is also committed to DC, namely to "the consequence that these "higher-level" mental events and processes cause lower-level physical laws to be violated" (Kim 1992, 120)[3].

[2] While the problem of epiphenomenalism is related to the metaphysics of DC, this chapter is specifically concerned with examples in which DC is used to *describe* and *explain* biological processes or mechanisms. Hence, the focus is on how biologists use the notion in explanatory capacity. A fruitful and detailed discussion of epiphenomenalism can be seen in Shapiro and Sober (2007).

[3] Micro-level phenomena that compose macro-level events lead to the emergence of certain properties that cannot solely be explained by the micro-level phenomena themselves. The relation between micro and macro levels (sometimes referred to as part-whole relation) leads to conceptual

In what follows, I introduce three main objections against DC that can be found in the literature: the vicious circularity objection (1.2.1.), the causal exclusion objection (1.2.2.), and the distinctness objection (1.2.3.).

1.2.1. Vicious circularity

A first reason why DC can seem incoherent is addressed by Kim (1999) and is known as the "vicious circularity" objection (Bedau 2008). The objection goes as follows:

> After all, higher-level properties arise out of lower-level conditions, and without the presence of the latter in suitable configurations, the former could not even be there. So how could these higher-level properties causally influence and alter the conditions from which they arise? Is it coherent to suppose that the presence of X is entirely responsible for the occurrence of Y (so Y's very existence is totally dependent on X) and yet Y somehow manages to exercise causal influence on X? (Kim 1999, 25)

According to this objection, insofar as lower levels give rise to higher levels, it is paradoxical to claim that higher levels can have causal impact on lower levels. The vicious circularity arises from the fact that if it was not for lower-level properties, higher-level properties would not exist. Due to the difficulty of establishing causal antecedence in a complex system, downward causation is seen as viciously circular and thus, metaphysically objectionable.

1.2.2. Causal exclusion

A related second objection to DC is known as the causal exclusion argument (Baumgartner 2009; Woodward 2015). The exclusion argument is mostly discussed in the context of mental

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challenges surrounding emergences, having implications for the notion of DC. I will discuss some of these implications in the following section when I assess the scope and limits of the compositionality assumption.

causation, but it provides useful insights for biological contexts. The principle of causal exclusion is the following:

> If an event *e* has a sufficient cause *c* at *t*, no event at *t* distinct from *c* can be a cause of *e* (unless this is a genuine case of causal overdetermination). (Kim 2007, 17)

Kim's exclusion argument states that if there is such a thing as DC, micro-level causes might be as good candidates as macro-level causes to explain an event. A major premise of the exclusion argument is that all physical events are caused by sufficient physical causes. In other words, due to the causal closure of the physical, no physical event would arise unless it has a sufficient cause which is itself physical. As a consequence, there is normally a more relevant micro-level cause that determines a micro-level effect, and including a macro-level cause would lead to the overdetermination of the micro-level effect. Although overdetermination is not overruled under this view, it is thought to be rare or very unlikely.

1.2.3. Distinctness

A third objection arises from asking whether there can be causal relations at all between different levels of the same, multi-level system. The distinctness requirement of causal relations, i.e., that cause and effect are distinct, establishes that if upper levels are composed of lower levels, and for X to cause Y they must be distinct, then upper levels cannot have causal powers over lower levels, because the compositional relation fails to satisfy the distinctness requirement. In a system which is a whole composed of parts, the whole is, itself, the parts put together, hence there is no distinctness between parts and whole. Craver and Bechtel (2007) have suggested a solution to the distinctness objection by stating that inter-level causes (both top-down and bottom-up) are in fact mechanistically mediated effects. They eliminate some of the obscurity surrounding DC by

arguing that the compositional relation between parts and wholes is not a causal relationship. This means that a property of the parts of a mechanism automatically belongs to the mechanism as a whole. Craver and Bechtel dissolve the notion of DC by shifting the attention to relations between compositional levels instead, proposing an account that does not rely on top-down causes.

An important point in Craver and Bechtel's account is the distinction between something constitutionally inherited (i.e., a part of the mechanism's constitution) and something that is causally transmitted. Their view proposes that in a mechanism with several levels, if a part possesses a mark, it will be possessed by the system as well, and effects are hence inherited constitutionally rather than causally transmitted. This is true of physical systems wherein a part of the system possesses a certain quantity of energy, for example, and this quantity therefore belongs constitutively to the whole system. Their strategy is to use a mechanistic account of systems to characterize DC in terms of constitutional inheritance, giving up on the attempt to analyze inter-level causes entirely. This means that characterizing a relation as mechanistically mediated does not tell us much about causes.

What all these objections have in common is what I call the compositionality assumption: that is, the assumption that the levels (upper and lower) of a system are arranged in compositional hierarchy, where upper levels are composed, or 'made of' lower levels. In the following section, I delve deeper into why the compositionality assumption can be misleading in our understanding of DC, and introduce two representative cases of weak and strong compositional relations.

1.3. Downward causation and the assumption of compositionality

In the life sciences and in the philosophy of biology, there are at least two distinct cases that appeal to DC in explanatory capacity. In both cases it is said that upper levels of a system have a

causal influence on lower levels of the system. In each case, the difference is in how strongly upper and lower levels are connected. The foregoing objections all assume one fundamental feature of DC: the fact that levels are arranged in a compositional hierarchy. However, when DC is used in biological contexts in an explanatory capacity, there are different degrees of commitment towards compositionality. While in some cases compositionality is instantiated only weakly, in other cases systems exhibit a stronger part-whole relationship. In fact, as I will argue, when DC is used in biology, compositionality does not hinder the coherence of DC.

I contend that even in cases where we do have strong compositional relations between upper and lower levels, we can still have a coherent concept of DC. The coherence of the concept, however, relies on a shift from entity-thinking to variable thinking. This means tackling causation as a relation between relevant level *properties* instead of a relation between entities[4]. In what follows I will abstract a concept of DC from concrete cases of biological explanation and examine which role compositionality plays in that concept. In the three cases I analyze (feedback loops, parallel evolution of ant castes and soldier to worker ratios in ant colonies), compositionality does not hinder the coherence of DC. In fact, even if the processes described below are often labelled as cases of DC (which typically refers to causal relations between compositional levels), I show

[4] Robert Batterman's (2001) extensive treatment of emergence and part-whole relations has already shed light into the question of compositionality. Batterman rightly points out that emergence can be thought of in situations where there are no part/whole relations. My account differs from Batterman's in two aspects. First, Batterman explicitly specifies that his example does not come from special sciences but is rather a general example (the analysis of a rainbow's emergent properties). In this analysis, I intend to focus on a special science: empirical examples from evolutionary biology. Second, Batterman also states that at best, emergent properties do not represent novel *causal* powers, but rather "the existence of new theories that play novel explanatory roles" (Batterman 2001, 115). In contrast, I propose a specific causal analysis of what is normally considered to be DC, showing that part/whole or compositional assumptions do not hinder the coherence of DC.

how, even in cases of strong compositional relations, it is still possible to have a coherent notion of DC. The first two examples fit the category of CASE 1, i.e., a weak sense of composition between upper and lower levels. The last example fits the description of CASE 2 and is the case where the objections to DC are directly applicable.

Consider the following empirical examples that illustrate cases of weak and strong compositionality, respectively:

1.3.1. CASE 1: *Weak* compositionality

In physiology, feedback inhibition is the process by which an end-product of a pathway binds to the allosteric site on an enzyme responsible for catalyzing the initial reaction in the pathway (Mason, Losos, and Singer 2010). This mechanism allows cells to regulate how much of an enzyme's product is produced. An example of a feedback loop is the glucose metabolism resulting in the production of ATP. In the glycolytic pathway, high levels of ATP allosterically inhibit the liver enzyme responsible for its breakdown. Allosteric regulation happens when an enzyme binds to the allosteric site of a complex, thus signalling that ATP production can be slowed down or stopped. Glycolysis is stimulated as the levels of end-product (ATP) falls (Berg, Tymoczko, and Stryer 2002). This is a clever mechanism of energy-saving that happens inside cells.

While it may be objected that feedback loops are not a case of DC but rather a standard case of causation, feedback loops are, in general, commonly loosely *described* in terms of DC (Ellis 2016; Boi 2017; Rothschild 2008). I will analyze the process of feedback inhibition and show that the same example can be analyzed without loss of explanatory efficacy and by assuming only weak compositionality. In George Ellis' characterization of feedback control systems, one of the reasons for considering those as a case of DC is that systems are conceptualized as wholes that act on their parts (Ellis 2016). However, when looking more closely at feedback loops such as in the

production of glucose, what triggers the setting of the metabolic pathway is not the system, but rather a specific switch triggered by the availability of the end-product of the reaction.

In cases of feedback loops, even though a feature of the external environment is described as an upper level, it is by virtue of its spacial externality in relation to lower levels. Therefore, it is only in a weaker sense that upper levels cause changes in lower levels. The upper level is the extra-cellular environment whereas the lower level would include the molecules involved in the glycolytic pathway. This example fits an instance of CASE 1, where there is a weak composition relation between upper and lower levels. Weak composition can be understood as a relation of spatial externality between features at different scales within a system (such as the extra-cellular environment and molecules in a metabolic pathway). The causal relation is said to be 'downward' because it runs from the cell environment to the cell, having an effect at the molecular level.

Another common example of DC in biology is how environmental factors can trigger genetic alterations during the development of organisms, leading to persistent evolutionary changes across time. Such a process is often described as a case of top-down causes or DC. For example, causation is said to flow "both upwards from lower levels of biological organization, such as DNA, and from higher levels downwards, such as through tissue – and environment – specific gene regulation" (Nijhout 2003). In this chapter I focus on a specific example in eco-evo-devo that fits this description of DC by describing a case of gene regulation in the prolific ant genus *Pheidole*.

Ants are highly complex social insects, and each colony is divided into different castes. *Pheidole* comprises around 1,100 species. Recently, it was shown how a parallel ant caste evolved through environmental induction (i.e., through changing environmental factors such as hormone availability at crucial stages of development), most likely caused by changing nutrient availability

(Metzl, Wheeler, and Abouheif 2018). In *Pheidole,* the queen and her workers in the colony are all female and diploid while the male caste is separate and haploid. The worker caste can be further divided into two subcastes: minor workers (performing most tasks in the nest as well as foraging) and soldiers (whose functions are nest defense and food processing) (Rajakumar et al. 2012). In some species of *Pheidole,* for example in *P. rhea* and *P. obtuspinosa,* a third female worker caste called 'supersoldiers' has a disproportionately larger head than the soldiers. The evolutionary reason for the existence of supersoldiers in some *Pheidole* species is probably linked to a selective advantage whereby supersoldiers, due to their disproportionately large heads, could block the colony entrance protecting it from ant raids (Rajakumar et al. 2012; Huang and Wheeler 2011). Rajakumar et al. (2012) demonstrated the parallel evolution of 'supersoldiers' in *P. rhea* and *P. obtuspinosa* by bringing together three types of evidence in a single study by: (1) showing that supersoldier-like anomalies can be observed in wild colonies; (2) showing that supersoldiers can be environmentally induced in the laboratory; and (3) comparing the development of soldiers and supersoldiers across twelve species.

As a study case, I focus on the experiment showing that it is possible to environmentally induce a supersoldier subcaste in a *Pheidole* species (*P. morrisi*) that did not evolve a supersoldier subcaste. The evolved supersoldier is a novel phenotype within the colony (and performs different functions in the colony than soldiers). This is a case of polymorphism, where in the same colony there are morphological differences within the same species. This novel phenotype was induced in a population of *P. morrisi* through hormone manipulation through which the hormone mediates the external environmental cue (nutrition). Both are external factors that trigger the activation of developmental switches that guide the development of a worker into a supersoldier-like individual, instead of remaining a soldier or minor worker. The homology between evolved supersoldiers and

these supersoldier-like anomalies indicates that some species of *Pheidole* evolved a novel phenotype (supersoldiers) in nature, that conferred selective advantage to the colony and hence became a part of the population. The ability to experimentally induce supersoldiers in a species that does not contain supersoldiers mimics a mechanism that was likely instantiated in nature, at a much longer time scale.

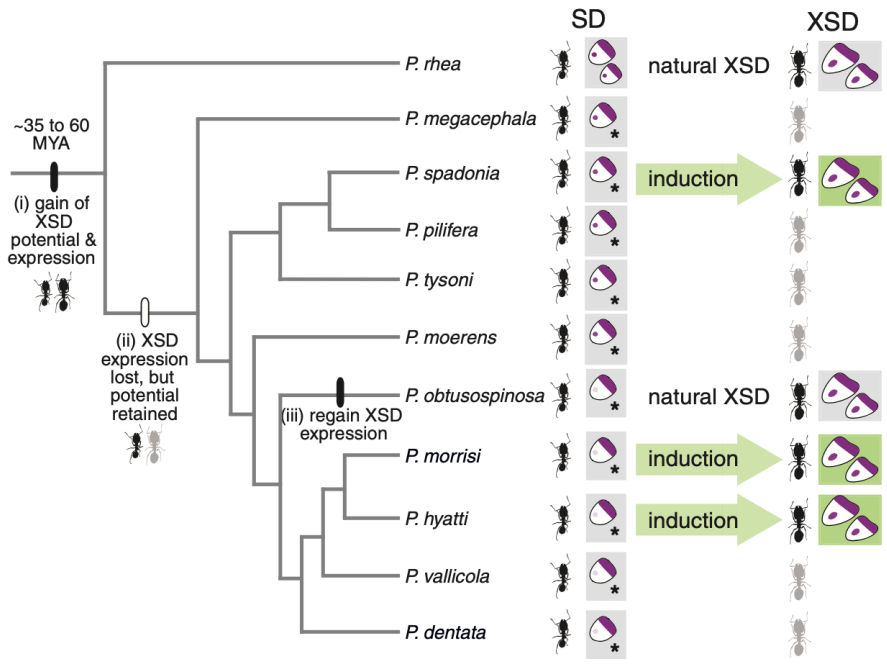

Figure 1.1. Evolutionary history of different Pheidole species showing potentials of supersoldier (XSD) development (Rajakumar et al. 2012). Reproduced by permission from *Science*.

Examples of environmental conditions triggering the expression of ancestral phenotypes are a common example used to illustrate instances of DC. This is because changes in the environment trigger a change in some micro-mechanism (cryptic developmental threshold) that leads to the expression of an alternative phenotype. It seems unproblematic to classify the general term "environment" as a higher-level instance, insofar as organisms always exist in an environment. However, this is also an example where we need not commit to the claim that the

upper level is composed of lower levels. Organisms are not a part of environments in the stronger compositional sense. The environment is simply spatially external and larger in scale. The description of how environmental factors can impact development and evolution does not fit a strong compositional account of DC but can still be understood in a weaker sense. In both examples discussed, the downward cause is a cause in the environment, which is spatially external and materially distinct from the process we seek to explain. In the following section, I discuss a positive account of DC that treats causes as difference-makers using interventionist theories of causation as a conceptual tool to frame my own account of DC.

In both examples, the process we seek to explain (feedback inhibition or the evolution of phenotypes) can be attributed to environmental factors, sometimes characterized as downward causes. This is because the environment is at an upper level in a *broad* sense (for example, an environment is at a different scale than an organism). The relation between environment and organism in these examples is that of spatial externality and scale difference, not that of composition in the strong sense. In other words, it is only in a *weak* sense that we can say an organism is a part of the environment. Several scholars have explored the attribution of levels to different scales (Baedke and Mc Manus 2018; Batterman 2001; DiFrisco 2017; Eronen 2015; Green 2018), a view I will not discuss in more detail here. The crucial point is that in some cases where DC terminology is used in biology, the upper and lower levels are related in the weak compositional sense, since the putative levels are at different scales and are spatially external to one another.

Traditional conceptions of DC rely on the view that any given complex system can be divided into levels, and, crucially, that the relation between such levels is compositional. But in some cases, we can still refer to upper and lower levels without relying on level compositionality in the strong

sense. It is in cases where we have composition in a strong sense that the objections to DC are most directly relevant. Strong compositionality occurs when an aggregate is composed of or constituted by its lower parts (as I will show in greater detail in the following sub-section). In cases of weak compositionality, e.g., where DC is used to explain environment-to-organism relations, the objections lose pertinence. In other words, at the crux of the objections to DC is the central notion of *strong* compositionality. According to the distinctness objection, for example, causation can only be instantiated by relations within each level, due to the requirement of distinctness between cause and effect. However, from the point of view of scientific practice, at least in evolutionary biology, causes and effects at different levels need not inherit the strong compositional relations that may exist among their respective levels.

1.3.2. CASE 2: *Strong* compositionality

Now consider the following example: ants are social insects living in colonies. Colonies are composed, or 'made-up' of individual ants, that engage in highly complex social relations. A colony is, by definition, an aggregate of individual ants functioning through the division of labor and social interactions, around which ants organize their life cycles. The sense in which ants compose a colony is *stronger* than the sense in which an organism is part of its environment. If a colony-level property influences individual ants, that too would be described as an instance of DC. In this example, the relation between upper and lower level is much stronger than in the case of environment and organism relations.

In *Pheidole,* as discussed above, the worker castes can be divided into two sub-castes: minor workers and soldiers. Castes can be understood as a form of morphological division of labour marked by different morphological and behavioral traits (Gregg 1942). Soldiers are significantly

larger than minor workers and exhibit disproportionately larger heads (Lillico-Ouachour et al. 2018). The existing ratio of minor workers to soldiers is known to regulate the development of larvae into soldiers or minor worker castes in an ant colony (Gregg 1942; Wheeler and Nijhout 1984; Lillico-Ouachour 2017). The developmental mechanisms of individual ants into either minor workers or soldiers have been a topic of interest for evolutionary and developmental biologists. This is mostly due to the interest in understanding which factors may regulate ant development into one sub-caste or another. Many experiments demonstrate that, in a colony, the ratio of existing soldiers plays a regulatory role on the subsequent development of larvae into soldiers. Consider the following conclusion of Gregg's 1942 experiment, which was one of the first results on the topic:

> The results indicate that the development of a given larva can be profoundly changed by the percentage composition of the adult castes in a colony. The much greater number of soldier pupae and adults appearing in a nest composed only of workers than in a soldier nest, where the conditions both biotic and physical are kept essentially constant in quality, shows that the population as such cannot be neglected in an interpretation of the origin of polymorphism. The colony behaves as a unit and automatically approaches an equilibrium by adjusting the percentages of the castes if they become shifted from the "normal" condition for the species. (Gregg 1942, 306)

Other experiments (Wheeler and Nijhout 1984; Passera 1974) have come to similar conclusions, suggesting that a colony-level property (i.e. the ratio of soldiers to workers) plays a regulatory role in the development of larvae into minor workers or soldiers. A range of hypotheses have been advanced as to why this may be the case. In a recent review (Lillico-Ouachour 2017), the main factors contributing to soldier regulation of castes were identified as: the activation of the soldier developmental program through nutrition and the availability of juvenile hormone; the inhibition of the soldier program through pheromones; and external influences such as competition and resource availability. As in any complex system, it is hard to pinpoint the exact cause for the

soldier developmental switch to be triggered, as multiple factors are involved. One factor, for example, is the mechanisms underlying rudimentary wing discs (Rajakumar et al. 2018, 20). Additionally, the literature suggests that all these factors are linked to a colony-level property: caste ratio (Gregg 1942; Wheeler and Nijhout 1984; Lillico-Ouachour 2017)). This property is responsible for maintaining colony equilibrium and leads to adjustment of the ratio through the regulation of development. The consensus is that among several other factors, the ratio plays an important role in ant caste regulation, and that it may be the cause for other intermediary causes that lead to soldier production being inhibited.

The regulation of ant castes in a colony is an example that fits our description of CASE 2, whereby upper levels of a system (colony level) are composed of lower levels (individual ants) in a *strong* sense. There are upper-level properties (the ratio of soldiers to minor workers) that depend on lower-level properties (individual ants' developmental switches at the larval stage). Both properties are putative causes of the lower-level effect (the probability of the next larvae developing into either a soldier or a minor worker). We have a situation in which upper and lower levels are made of the same "stuff". Insofar as a colony-level property influences individual ants' development, we may infer that this would fit a case of DC. This means that this example is exposed to the objections raised in section 1.2., where the assumption of compositionality in the *strong* sense poses problems to the notion of DC.

In the following section, I show how we can avoid the incoherence of DC by adopting an interventionist framework. Instead of defining cause and effect as entities or events, cause and effect are viewed as determinable properties of entities or events that may have multiple determinates. An upper-level property (such as the worker to soldier ratio) is a determinable

property that is determined by specific ratios (such as 95:5). Similarly, lower-level properties (such as the number of soldiers) are also determinables that are determined by various numbers (determinates). Variables represent determinable properties, and variable values represent those properties' determinates. There are multiple combinations of determinate lower-level properties that can realize the same determinate upper-level property. For example, suppose that an upper-level ratio is 2:1. Such ratio can be realized by multiple low-level determinate number pairs, such as <50:25>, <10:5>, and so on, as long as the ration of 2:1 remains constant. In the following section, I present an interventionist response to the objections raised against DC and highlight how shifting from entity-thinking to variable-thinking can be the first step in the direction of a coherent notion of DC.

1.4. Variable-thinking and interventionism

1.4.1. Variable-thinking and downward causation

A key step to demystifying DC and changing into a coherent concept is to shift from 'entity-thinking' to 'variable-thinking'. Part of the conceptual incoherencies of DC stem from the fact that cause and effect are seen as entities or events. An alternative view is to think of cause and effect as properties that can be represented by variables that can take more than one value. In the case of DC, I argue that what does the causal explanatory work is the relationship between variables that represent relevant properties (variable-thinking). Capturing causal relations through variables is a key feature of interventionist theories of causation, which are difference-making theories. Variables represent the causally relevant property of an object or an event. A relevant property here is the property that makes a difference towards the occurrence of an event.

Under interventionism, variables represent "properties or magnitudes that, as the name implies, are capable of taking more than one value" (Woodward 2004, 39). Furthermore, "values or variables are always possessed by or instantiated in particular individuals or units" (Ibid). Variables can be binary or assume multiple values. Therefore, when we say that "X causes Y", we are saying that a property of event E1 can be represented by a variable X (binary or not) and leads to the occurrence of a property of event E2 also representable by a variable Y (binary or not). When a change occurs at a variable X, a subsequent change will occur at variable Y, which is a necessary (though not sufficient) condition for causation. X and Y are not, in this scenario, entities, but variables that represent the relevant properties of a given entity or event. In DC, an additional feature is that X and Y are at different levels, X being at an upper level (U) and Y being an effect at a lower level (E).

The relation between properties (represented by variables) is a minimal condition to establish a causal relation. Interventionist accounts share one basic principle: causal relations can be exploited for purposes of manipulation and control – i.e. for two variables X and Y to be related as cause and effect, a necessary and sufficient condition is that it must be possible to intervene on property X such that the intervention is followed by changes in the value of Y under a range of background conditions (Woodward 2004). Woodward (2004) establishes that a causal relationship exists between two variables, X and Y, under the following condition:

> for at least some individuals there is a possible manipulation of some value of X that they possess which, given other appropriate conditions (perhaps including manipulations that fix other variables distinct from X at certain values), will change the value of Y or the probability distribution of Y for those individuals (Woodward 2004, 40).

Proper interventions can be made onto certain variables while holding other variables fixed. An intervention is defined as any ideal experimental manipulation of the value of X performed to

assess whether the value of Y will subsequently change (Woodward, 2004, 94). Note, however, that an intervention need not be a human intervention, and that any process can qualify as an intervention given it has the right causal characteristics (such as the property of being a difference-maker). In the biological examples being considered here, interventions can either be human interventions or naturally occurring ones. For example, a human intervention may be a manipulation in a laboratory setting (such as the actual manipulation of ratios within an ant colony). A naturally occurring one can also be considered as a difference-maker having the relevant causal properties (such as environmental conditions activating developmental switches in the development of larvae).

Consider the following notation applied to the examples discussed. A system can be thought of as an entity (for example, a reaction pathway or an ant colony). U is a variable representing a property of an entity at the upper level (in the colony example, U represents the caste ratio). *u* is a variable value representing a specific determinate of a caste ratio (for example, 1.405). Similarly, L represents a property at the lower level (for example, the numbers of soldiers and minor workers), and *l* represents the specific numbers (for example, 20 and 10, respectively). Values of U are multiply realizable, i.e., the same value of U may be realized by different values of L. In cases of DC, E is a lower-level effect that can take any value *e,* depending on the interventions being made on the system. One example of E is the probability that the next larvae will develop into a soldier.

1.4.2. Variable-thinking in *weak* compositional relations

Applying variable-thinking to CASE 1 seems to pose no major problems. In the case of feedback inhibition (the first example discussed as an instance of CASE 1) U is the availability of

the product; and a change in this concentration of product triggers changes in E (activation or inhibition of metabolic pathway). Because ATP is not a stable molecule, overproduction leads to energy loss. The enzyme in the first step of the pathway is allosterically regulated by ATP. If ATP binds to the allosteric site of hexokinase (the first enzyme in the glucose metabolism pathway) then ATP production stops (Berg, Tymoczko, and Stryer 2002). The ATP production feedback loop does not involve any interactions across levels that qualitatively differ from those commonly found in feedback loops in physical sciences and engineering, such as the negative feedback loop arising from the operation of a thermostat-heater system.

If we take a closer look at the ATP production process, it is hard to specify any relevant compositional relation in allosteric regulation across which a causal relation exists. The reaction happens in the enzyme-substrate complex triggered by the concentration of the product of the metabolic reaction pathway. This product is in an environment where the reaction occurs. In feedback inhibition reactions such as in the glucose metabolism, the cause is a spatially external property (the concentration of end product). The product is what binds to the enzyme's allosteric site inhibiting its functioning. The worry of vicious circularity is trivial in this example since there is no strong compositionality relation between the levels. Even though its value depends on the lower-level entities, this does not entail a vicious circularity insofar as the causal relation is captured by interventions (actual or possible) that lead to a change in the production (or not) of the end-product in the pathway.

Similarly, when considering environmental effects on the evolution of novel ant castes, an environmental factor (such as hormone or nutrient availability) can be represented by a variable. When the value of that variable changes, the effect related to that variable also changes, and is also representable by another variable (for example, the switching of a developmental threshold).

However, regardless of whether cause and effect are thought of as entities or properties, the objections simply do not apply in cases of weak compositionality. In both examples discussed, as the levels are not strongly compositionally related, circularity, exclusion, and distinctness worries vanish when levels do not stand in part-whole relations.

1.4.3. Variable-thinking in *strong* compositional relations

Under variable-thinking, I argue that the strong compositionality assumption is no longer problematic. Consider the example of a *Pheidole* colony. The upper colony level is strongly composed of its lower levels, the individual ants. There can be no distinctness between the entity "colony" and the entity "ant", which would raise suspicions concerning DC due to the non-fulfillment of the distinctness requirement. When we represent properties of the system in question by variables, such as for example an upper-level property being the ratio of soldiers to workers and a lower-level property being numbers of soldiers and workers, properties do not enter perplexing part-whole relationships, even though the entities they belong to do. The variables representing such properties can take different values, a feature that can be useful in replying to common objections raised against DC. In terms of variables and properties, U represents the ratio (upper-level property) determined by the value of a variable *u* (U being the ratio of soldiers to minor workers). L represents properties at the lower level, determined by the value of *l.* Unlike U and E, L is represented by two-valued variable (the number of soldiers and the number of minor workers). The lower-level effect E is the probability *p* that a larvae develop into a soldier or a minor worker. In the examples discussed, a downward causal relation would mean that a change in the value of U is a direct cause of change in the value of E.

To address objections more specifically, I will first introduce the notion of conditional independence to respond to the causal exclusion objection. I then introduce the condition of

independent fixability to assess the distinctness objection. Finally, I provide an account of diachronic analysis of directedness to address the vicious circularity objection. In replying to the objections, I will closely follow Woodward's recent work on downward causation (Woodward 2021b; 2021a) and show how they can be fruitful to a specific example in evo-devo.

According to the causal exclusion[5] argument, if an event *e* has a sufficient cause *c* at *t*, no event at *t* distinct from *c* can be a cause of *e* (Kim 2007, 17). Introducing conditional independence of variables is a possible solution the causal exclusion problem. Conditional independence is a condition that fixes interventions on U such that with U being fixed, the same value of E will result, regardless of the values of L. Hence, in terms of difference-making, the U-values can capture whatever makes a difference for E. Consequently, we may say that L and E are independent of each other, conditional on the value of U remaining fixed (Woodward 2020, 862).

Some additional conditions in this relation require that:

i. U are a coarse graining of L (L being of higher dimensionality than U);

ii. There is multiple realization of U by L (i.e., different combinations of L can lead to the same U).

The ratio of soldiers to minor workers (U) causes E (the probability *p* that larvae develop into either soldiers or minor workers) while simultaneously, L (the number of soldiers and minor workers in a colony) causes E. I will now argue that as L and E are conditionally independent, U

[5] Nonreductive physicalists have attempted to solve the causal exclusion problem using interventionist accounts of causation. According to Baumgartner, although interventionism is a popular candidate to solve this problem, interventionist causation still "excludes causal dependencies among supervening macro properties and effects of their supervenience basis" (Baumgartner 2009, 162). Although Baumgartner rejects interventionist causation as insufficient to solve the causal exclusion problem, I will show in section V how variable-thinking, a specific feature of interventionism, is suitable for solving the exclusion problem in empirical situations in the context of evo-devo.

and L will not overdetermine E, thus avoiding the causal exclusion problem. Condition (i) is fulfilled in virtue of the fact that U is a coarse-grained variable, meaning that there is less information in an upper-level property than in a lower-level property. The description of the colony using U (ratio) provides less information than by using L (caste population sizes). Condition (ii) is fulfilled in virtue of the fact that U is multiply realizable by L, i.e., if U is a ratio of 2:1, there are a number of possible combinations of L that could realize this ratio. Insofar as U remains constant (e.g., a ratio of 2:1), multiple interventions at L, such as doubling or halving the numbers of both soldiers and minor workers, preserve the value of U. In other words, under different interventions at L, E remains constant insofar as U remains the same, since U is a coarse-grained variable representation of the properties represented by L.

Given the fulfilment of conditions (i) and (ii), the numbers in L do not overdetermine the probability that a larva develops into either a soldier or a minor worker. In other words, no intervention on L changes E without changing U, hence, there is no risk of overdetermining E. This is because U are summary representations that are multiply realizable by different possible values of L. U and L are at different levels of description, where U captures a causal pattern that a lower-level description does not. By simply considering L, we miss the fact that there is an independence between L and E, precisely because different interventions on L can lead to the same E. It is only when we intervene on U that we see the causal pattern.

Conditional independence, however, is not a sufficient condition to respond to the distinctness objection. Recall that according to this objection, in DC, cause and effect are not sufficiently distinct. The reason is that DC is a relation whereby upper levels have causal impact on lower levels, and upper levels are, at least in some way, composed by lower levels. It follows that, for

DC to be coherent, upper and lower levels must be distinct for there to be any inter-level causal relation. A core tenet of variable thinking is that entities (or events) do not cause each other. In he switch from entity to variable-thinking, variables represent properties of entities or events that take relevant values. Changes in such values explain the difference-making relation between properties. Setting an additional condition of independent fixability of variables can be useful to ensure that the variables in DC are sufficiently distinct. Under variable-thinking, variables (and the properties they represent) do not enter into part-whole relations. However, one may still object that variables are not sufficiently distinct, insofar as they are merely representations of the same property or of two closely dependent properties. Independent fixability (IF) is a criterion that safeguards variables from this kind of problematic dependence. IF stipulates that it must be possible, at least in principle, to set each variable to any value independently of the other variable. Hence, IF allows to set apart causal from non-causal dependencies (Woodward 2015). Conditions for IF are expressed as follows:

> (IF): a set of variables V satisfies independent fixability of values if and only if for each value it is possible for a variable to take individually, it is possible (that is, "possible" in terms of their assumed definitional, logical, mathematical, mereological or supervenience relations) to set the variable to that value via an intervention, concurrently with each of the other variables in V also being set to any of its individually possible values by independent interventions (Woodward 2015).

Since DC is a relation that comprises variables at different levels such as U and L causing E (a lower-level effect), U and E are sufficiently distinct insofar as it can be shown that they are independently fixable. Let us consider U (ratios of minor workers to soldiers) and E (the probability *p* that a larvae develop into a minor worker or a soldier). The variables representing properties of U and of E can be fixed independently per the experimental possibility of independent manipulation of those variables. At the upper level, the ratio of minor workers to soldiers can be

modified, for example, by adding or subtracting minor workers of soldiers to a colony. The effect E can be independently manipulated through experimental means. For example, through nutrition or juvenile hormone stimulation a larvae can develop into either a worker or a soldier in *Pheidole* species that exhibit this polymorphism. Note that the condition of independent fixability of variables is a weaker condition than that of conditional independence. Independent fixability is a suitable solution to the distinctness objection insofar as it guarantees that changing the value at one level (U) does not imply a necessary change in E, even when E is a variable representing a lower-level effect.

In more practical terms, in Wheeler and Nijhout's (1981) classic experiment of soldier determination in *Pheidole bicarinata,* it was shown that nutritional history affects the soldier-determining sensitive period. The presence of soldiers in a colony suppresses further development of soldiers by an inhibitory pheromone acting on larval endocrine system (Wheeler and Nijhout 1984). From more recent experiments (Abouheif 2002; Rajakumar et al. 2012) we know that this polymorphism can be triggered by laboratory manipulations of the levels of nutrition and juvenile hormone, indicating that such manipulations allow for the independent fixability of variables *sensu* Woodward. IF is satisfied in these cases due to the practical possibility of manipulating U and E through different interventions. U and E are sufficiently distinct so that there can be, at least in principle, a downward causal relation between them.

The final objection to be addressed is vicious circularity. Once conditional independence and independent fixability have been clarified, it is easier to establish a condition of directedness in cyclical causal relations. According to the vicious circularity objection, if it were not for lower-level properties, upper-level properties would not exist in the first place. Therefore, it is hard to determine a cause at an upper level, given that upper levels are causally determined in the first

place by properties at lower levels. This objection is valid once the system in question is understood in the *strong* compositional sense. For example, in the ant colony example, the ratio of soldiers to minor workers (U) affects the numbers of soldiers and minor workers (L) which in turn determines the ratio (U) in an endless cycle.

As a response to this objection, I propose that we assess this example from a diachronic perspective. As suggested by Woodward (Woodward 2021a) any cyclical causal graph can be broken down into acyclical sections. What matters is directedness. For example, we may say that a property at time t_0 causes an effect at time t_1, and the effect is similarly a property. Development is, by definition, a temporal process whereby individuals change over time. When looking at the colony example, the upper-level properties U are at different temporal stages of development (even though U is causally determined by E). In terms of variables that represent properties, we have two different levels represented by properties U and E. Variable values *u* and *e* are values of properties of U and L respectively. An additional feature is that U and E are instantiated at different times.

The worry of vicious circularity arises because of the mistaken assumption that in DC, U causes the very same lower-level property L that gives rise to U. If that were the case, we would indeed have a viciously circular loop. However, this is not the case once we represent the system through variables whereby E is a lower-level effect. Upon a closer look, the lower-level property that is the effect is distinct from the lower-level realization of the upper-level U. Therefore, in the case of a property U at t_0 that causes E at t_1 to happen, the worry of vicious circularity does not apply. There is no vicious circularity insofar as t_0 and t_1 represent different developmental stages of different individuals. U at t_0 represents the upper-level property (ratio of soldiers to minor workers) and E at t_1 represents the probability of a larvae developing into either soldiers or minor

workers. There is a negative feedback loop where the ratio change causes the probability change causing a number change (and hence, ratio change) and so on.

Under this diachronic perspective, there is directedness even in the occurrence of a cycle, meaning that iteration is not problematic or viciously circular. It is possible to intervene on the system such that an intervention on U (for example, modifying the ratio of soldiers to minor workers) at t_0 leads to a change in E at t_1. Similarly, from the opposite direction an intervention in L at t_0 will lead to a change in U at t_1. Even in a cyclical relation the cycle may be iterative without necessarily being viciously circular.

1.5. A practice-centered epistemology of downward causation in biology

My argument so far has been that DC is no longer an incoherent concept once we shift from entity-thinking to variable-thinking about causation. I have drawn on interventionist theories of causation to clarify how DC can be used to explain relevant biological processes and phenomena. My argument drew on important recent work by Woodward (2021a; 2021b) on downward causation, and exclusion arguments in Baumgartner (2009) and Raatikainen (2010). At the same time, I have extended the existing account by showing that interventionist framework applies to concrete examples of DC from molecular biology, evo-devo and eco-evo-devo. This establishes the importance of interventionist accounts of causation for clarifying biological practice. Additionally, I have identified a new class of downward causation claims, those that involve weak compositionality among levels, for which the standard objections to DC do not apply. This last result holds independently of whether one adopts an interventionist account of causation. The distinction between weak and strong compositionality, however, has not yet been explored as an avenue of investigation on downward causation and this especially relevant for understanding how

the notion is used in the biological sciences. In what follows, I discuss to additional, less obvious contributions of this chapter.

The first epistemic contribution is to diffuse the tension between compositionality and DC in biology. Even if levels are a useful terminology to loosely distinguish between "upper" and "lower" levels of a system, the compositionality of levels assumption does not hinder the coherence of DC. In expressing reservations towards objections to DC, I aimed at bringing back the concept of DC and showing that it need not be considered a mysterious idea. Instead, I introduced an epistemological distinction between weak and strong compositionality that disentangles the causal question from the concept of compositional levels and applied it to examples specific to evolutionary developmental biology. My argument therefore accepts that complex systems such as organisms and biological processes can be conceptualized in terms of levels while also defending that the degree of compositionality between such levels need not be an obstacle to constructing a coherent concept of DC. Although I have mostly drawn from Woodward's interventionist accounts of causation, interventionist causation does not specifically deal with the intricacies of strong compositionality and whether compositionality considerations are generally compatible with DC. In addressing this gap, I additionally showed that adopting interventionism does not only vindicate the concept of DC in evolutionary developmental biology, but does so without the need to discard or disregard a compositional hierarchy of levels. This contributes to an epistemology of evolutionary developmental biology which crucially needs both a coherent concept of DC and to represent biological systems as compositional hierarchies.

From this analysis stems a novel approach to conceptualizing DC, which leads me to a second contribution, methodological in nature. Rather than starting from general metaphysical assumptions about causation and compositional levels of organization, I have sought philosophical

accounts of DC that fit a pragmatic analysis of the concept. Methodologically, I proceeded through a practice-centered interdisciplinary analysis bringing together the metaphysics of causation to current biological practice. It has been argued that philosophical accounts of causation are too abstract to be useful to scientists (Pigliucci 2019). In this chapter, I tried to bridge the gap between the abstractness of theories of causation and scientific practice by working from empirical examples to theoretical constructs. This practice-centered analysis of causation reveals that many cases labeled as DC involve only *weak* compositionality and are thus not problematic to begin with. There seems to be an entire class of DC cases that philosophers have neglected and that is not present in any of the objections raised against DC. The explanatory credentials of DC in general have been unjustifiably tarnished by this neglect. Hence, the second contribution I bring forward to the study of causation in biology is showing the benefits of analyzing concepts by tracing the ways practicing biologists use them. Here, the field of philosophy of science in practice (Ankeny et al. 2011; Chang 2011; 2012) has greatly shaped my approach by providing the necessary tools to apply a practice-based methodology for elucidating concepts of causation. A few examples of this practice-centered approach can be seen in the works of Dupré (2015), Dupré and Leonelli (2022), Poliseli et al. (2022), and Johnson, Russo, and Schoonenboom (2019). Working from the scientific examples to the philosophical underpinnings of DC can be a fruitful way of conceptualizing epistemological issues that are relevant to scientific practitioners. This approach can be extrapolated to understand other biological cases of DC including: the behavior of social animals in general or even complex ecological systems that involve a plethora of different causes for evolution and phenotypic change over time.

1.6. Concluding remarks

In this chapter I have advanced a solution to the most common objections to DC found in the literature. I have explained the origin of the tension between the pervasive use of DC in biological explanations and the hesitancy that some philosophers have towards its apparent incoherence. I have focused on biological examples to show how the concept of DC can be coherently applied to complex, evolving systems. I suggested we distinguish two cases of DC in biology: cases where there is a weaker compositional assumption between upper and lower levels, and cases where compositionality is a *strong* feature of such relations. I have showed that in the former, there are no major conceptual concerns raised by DC. It is in the latter, in cases compositionality in a strong sense, that conceptual problems arise. By using interventionist theories of causation such as James Woodward's, I showed how the concept of DC can be used coherently in fields such as evolutionary developmental biology. This newfound clarity is in part due to a practice-centered methodology, where I worked from examples in the scientific literature to analyze how DC can be reconceptualized coherently. My conclusion is that when scientists seek to evaluate downward cause and effect relationships, they are best understood by assessing a difference-making relation between variables that can, in principle, be manipulated and intervened upon. Philosophical and metaphysical accounts of DC need not be in tension with the way DC is used in an explanatory capacity such as in evolutionary biology. On the contrary, these two accounts overlap precisely when we shift from entity thinking to variable-thinking, a key feature of scientific practice. Such an approach could be the starting point for fruitful causal models in other complex systems such as in ecology, evolution, and to assess environmental changes and its impacts in phenotypic novelties. The manipulation of variables is a key feature of scientific practice, and the practical use of the concept of DC can be reconciled with its metaphysical analysis.

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2. THE SCOPE OF RECIPROCAL CAUSATION IN THE EXTENDED EVOLUTIONARY SYNTHESIS

2.1.Introduction

Proponents of an Extended Evolutionary Synthesis (EES) argue that reciprocity between organisms and environment is a key driver of evolutionary change (Laland et al. 2014; Müller 2017; Laland et al. 2015; Pigliucci and Müller 2019). Such reciprocity is captured by the notion of reciprocal causation: the idea that organisms can be both the causes and effects of evolution (Buskell 2019). A key example of reciprocal causation is niche construction: the process through which organisms actively engage in modifying their surrounding environment (Odling-Smee, Laland, and Feldman 2003; Laland, Odling-Smee, and Feldman 2019; Odling-Smee 2010; Aaby and Ramsey 2022). Examples of niche construction include the modification of soil conditions by earthworms (Darwin 1898), and the dam-building activities of beavers (Cooke and Zack 2008). There is evidence for niche construction across kingdoms, from bacteria, through plantae and animalia (Odling-Smee, Laland, and Feldman 2013, 51) and as such, EES proponents contend it should be considered a significant evolutionary process on par with natural selection. Reciprocal causation is considered a defining aspect of the EES (Laland et al. 2014; Müller 2017; Pigliucci and Müller 2010; Laland et al. 2015). It is therefore used to motivate the legitimacy of the EES on the grounds that there is an urgent need for reforming and expanding Standard Evolutionary Theory (SET). The innovative aspect of reciprocal causation, however, remains unclear (Dickins and Barton 2013; Buskell 2019; Svensson 2018). Broadly speaking, two arguments support the criticisms of EES skeptics towards the notion of 'reciprocal causation':

i. The misportrayal argument: claims in favour of the greater explanatory power of reciprocal causation lay on a misportrayal of SET as being excessively reliant on

unidirectional causation (Wray et al. 2014; Futuyma 2017; Welch 2017; Dickins and Barton 2013).

ii. The empirical argument: the claim that there is empirical evidence showing that reciprocal causation is a well-acknowledged mechanism in SET and that modelling reciprocal casual relations is a widespread practice in SET, such as in negative and positive frequency feedback loops, cases of co-evolution and eco-evolutionary dynamics (Svensson 2018).

While existing literature on the topic of reciprocal causation focuses on (i) and (ii), in this paper, I re-orient the debate by providing a third argument in replacement of (i) and (ii). The argument I present concerns the scope of reciprocal causation. Instead of focusing on claims about whether the notion is sufficiently accounted for by SET, I argue that the fruitfulness of reciprocal causation lies in the fact that it can be used with different explanatory scopes, within different epistemic communities. The epistemic communities in question here are EES proponents on the one hand, and EES skeptics or critics on the other (i.e., those defending that SET is sufficient and that there is no need for a new synthesis) (see Laland et al. 2014 and Wray et al. 2014 for a clear example of the arguments within each epistemic community). Two elements of scope account for how the notion of reciprocal causation is used in EES, thus setting it apart from causal claims in SET. First, there is a difference in causal time scale. While SET is concerned with the longer evolutionary time scale, EES focuses on a shorter time scale of developmental processes. Second, there is a difference in the fine graininess of explanations. While SET provides explanations focusing on natural selection as the main cause of evolution, EES explains how specific developmental or behavioral processes (such as niche construction) contribute to evolution. Because developmental processes are studied at a shorter time scale (usually that of individuals or

lineages), the explanations coming from EES are finer grained[6]. Once the scope of reciprocal causation is clarified in terms of causal time scale and fine graininess, the epistemic advantage of reciprocal causation in the EES becomes clearer and distinctively sets it apart from how the notion is used in SET. Therefore, I argue that for the debate surrounding reciprocal causation to become constructive, it should move away from the debate surrounding overarching claims about the causes of evolution towards the setting of clearer explanatory goals within the scope of each epistemic community[7]. The debate should therefore focus on the ability of each framework to support research programs that identify the *specific causal mechanisms* responsible for the salient features of evolution. Ultimately, I wish to show that thinking in terms of the scope of reciprocal causation can provide useful tools to settle the debate between the two epistemic communities in question. What is novel about reciprocal causation in the EES is not its acknowledgement, but rather, making use of reciprocal causation within explanations whose scope is different than the explanations in SET.

Philosophers of biology as well as biologists have already tackled the question of the explanatory power of EES. For example, Baedke et. al. (2020) argue that in addition to the

[6] At this point, it may be objected that SET provides fine-grained microevolutionary explanations to account for macroevolutionary processes. Similarly, it may be objected that the focus of EES on development ultimately aims at explaining the longer scale evolutionary picture. Here I contend that the degree of fine graininess is lower when the resulting explanation is at the level of a population (which are the explanations characterized under SET). Accordingly, an explanation that is at the mechanistic-individual level will be more fine-grained (such as explanations in evo-devo and, consequently, in the EES). A similiar concern may be raised with respect to time scales. With respect to the time scale of reciprocal causation in evo-devo studies, the focus is often on ontogeny focuses, which is a shorter time scale than the phylogenetic scale.

[7] The choice of the term "epistemic community" over "theoretical framework" is deliberate. The reason for this choice is that it remains unclear and controversial whether the EES represents an altogether new theory. While some of its proponents argue that it does, others insist that it is an emendation that aims at expanding SET.

likeliness (the evidential support of an explanation) and the causal power (whether an explanation comprises more causal power than another) of explanations in the EES, explanatory standards must also be considered. Indeed, explanatory standards support the evaluation of the explanatory power of EES by providing grounds to compare counterfactual situations and possible alternative answers to "what-if-things-had-been-different-questions" (Ibid, 20; Hitchcock and Woodward 2003). While their account is extremely fruitful to assess the explanatory *power* of the EES, here I focus on the specific case of the *scope* of reciprocal causation within the EES. The primary aim of this chapter is therefore to provide a framework that allows the debate between the two epistemic communities in question to move forward.

The starting point of my argument is the claim made by EES proponents that niche construction is, after natural selection, a co-directing force of evolution (Laland, Matthews, and Feldman 2016; Odling-Smee 1995). EES proponents and niche construction theorists advance a bifold account of evolutionary causes: natural selection and niche construction. Such bifold account of evolutionary causation is what justifies criticisms directed at SET as well as skepticism towards EES (Laland et al. 2014; Wray et al. 2014). The controversy can be summarized as follows. Under SET, the causes of evolution are mostly said to be unidirectional, running from environment to organisms. EES proponents, however, argue that reciprocal causation is a *better* way of understanding evolutionary causes. If, as EES proponents argue, reciprocal causation is at the core of evolutionary processes, so is niche construction, since it is a very clear example of reciprocity between organisms and environment. As a consequence of adopting this model, organisms are not just passive receivers of selective pressures, but also play a role in shaping their environments in ways that will in turn feedback to how they evolve (Müller 2017; Schwab and Moczek 2021). The recognition of the reciprocal interactions between organisms and environment entails that there

are reciprocal *causal* relations between them. The problem, however, is that the epistemic advantage of EES still remains unclear, since niche construction was already a well acknowledged process by SET (Gupta et al. 2017).

This chapter is structured as follows. In Section 2.2, I examine current criticisms addressed at reciprocal causation. In section 2.3, I show how reciprocal causation and niche construction are intertwined by analyzing empirical examples. In Section 2.4, I explain the scope argument and show the relevance of time scales and fine graininess of explanations to settle the debate surrounding the role of reciprocal causation in EES. I anticipate challenges to the argument in Section 2.5. In Section 2.6, I explain how the scope of reciprocal causation can help re-orient the debate beyond theoretical claims. Section 2.7 presents concluding remarks.

Current criticisms to the notion of reciprocal causation

Broadly construed, 'reciprocal causation' refers to the feedback interactions between organisms and their environment. In large thanks to Richard Lewontin (1985; 2000), the notion of reciprocal causation gradually made its way into evolutionary explanations. In *The triple helix: genes, organisms and environment,* Lewontin defends a view according to which there is a reciprocal relation between genes, organisms and environment, and that each of these elements "can be both causes and effects" (Lewontin 2000, 100). His portrayal of reciprocity between organisms and environment is diametrically opposed to another view that focuses on unidirectional causation, according to which:

> there is an outside force, the pre-existent environment, that dictates the "problems" organisms must solve, and inside forces of variation that generate the organisms' "solutions" to the "problems". Organisms map the autonomous external changes in the world. The external environment in such a view is the cause, the evolved morphology, physiology, and behaviour of the organism is

> the effect, and natural selection is the mechanism by which the autonomous external cause is translated into the effect. (Lewontin 2000, 100)

Recently, Laland et. al. (2013) critiqued Mayr's (1961) distinction between proximate and ultimate causes to motivate the use of reciprocal causation in evolutionary explanations. Mayr's account of causation relies on an initial distinction between two research agendas: functional biology and evolutionary biology. According to Mayr (1961), there are two kinds of causes at play in biology: ultimate and proximate causes. The functional biologist is concerned with the question of "how" something operates and functions. The evolutionary biologist is concerned with the question of "why". For Mayr, the meaning of cause is different in functional and in evolutionary biology. The functional biologist is concerned with the study of proximate causes: an immediate set of causes that act upon organisms, such as their physiological constitution. The evolutionary biologist is concerned with ultimate causes: "the causes that have a history and that have been incorporated into the system through many thousands of generations of natural selection" (Mayr 1961, 1503). To illustrate the distinction between ultimate and proximate causes, Mayr presents the case of bird migrations. In this example, the proximate causes include a bird's physiology, both internal (the link between migration and photoperiodicity is seen in the response to decrease in day length, and this is possible because of the birds' physiological response) and external (a cold air mass signaling the cold weather prompts a "physiological readiness") (Mayr 1961). The ultimate causes for bird migration include the fact that birds are insect eaters and would starve in winter (ecological causes) and the genetic constitution acquired in the course of evolutionary history (genetic causes). The proximate causes are intrinsic and extrinsic physiological causes that impact the bird's interaction with the environment more immediately, over the course of a lifetime. Mayr's account has provided some "conceptual unity for the evolutionary sciences" (Uller and Laland 2019, 3). It has also, however, been criticized as insufficient on the grounds that proximate and

ultimate causes do not take into consideration development of organisms nor the reciprocity between organisms and environment (Laland et al. 2013). Such criticism is a prelude to the debate surrounding the role of reciprocal causation in the EES, whereby reciprocal causation has gained strength as a third viable alternative to Mayr's (1961) proximate-ultimate distinction. Consider the following definitions of reciprocal causation:

> (1) Reciprocal causation captures the idea that developing organisms are not solely products, but also causes of evolution. The term 'reciprocal causation' simply means that process A is a cause of process B and, subsequently, process B is a cause of process A, with this feedback potentially repeated in causal chains. (Laland et al. 2015, 6)

> (2) Reciprocal causation is a common feature of both evolving systems (e.g. when the activities of organisms modify selective environments) and developing systems (where development proceeds through modification of internal and external environments). (Laland et al. 2015)

Since Lewontin's (1985; 2000) portrayal of reciprocal causation as dialectically opposed to unidirectional cause running from environment to organism, little has changed in the way these two accounts of causation are portrayed in the literature. Indeed, reciprocal causation has been at the centre of a divisive theoretical debate in the life sciences (Dickins and Barton 2013; Svensson 2018; Buskell 2019; Wray et al. 2014; Laland et al. 2014). The dispute is structured around the controversy of whether SET sufficiently accommodates causal relations running from organisms to environments in addition to those running from environment to organism, or whether it focuses excessively on the latter: a unidirectional account of causes running from environment to organism. This account of evolutionary causation (reciprocal *vs.* unidirectional) has ignited controversy within scholars on two grounds: (i) that such a portrayal of evolutionary causes opposes two notions that are not, in fact, contrary to each other; rather, they are complementary

(the misportrayal argument); and (ii) that there are several empirical examples showing that reciprocal causation is adequately considered under SET (the empirical argument).

2.1.1. The misportrayal argument

The misportrayal argument can be situated within the broader discussion of arguments in favour of extending SET. Once this background is clarified, the specific claims about reciprocal causation and niche construction become clearer. EES optimists argue that strong empirical evidence from evolutionary developmental biology calls for a conceptual shift in evolutionary theory (Müller 2021). This claim, which I label the extension claim, can be summarized as follows: insofar as SET has neglected several relevant evolutionary processes (such as niche construction, the emergence of novelties, and reciprocal causation), an extension of SET is needed to account for such processes, keeping up with recent empirical data coming from evo-devo. Such empirical advances therefore justify the need for conceptual change and re-evaluation of causal assumptions underlying the frameworks in question. Examples of the extension claim can be seen below under different formulations:

> **(1)** Nevertheless, our analysis suggests that the EES is more than simply an extension of 'business as usual' science: it requires conceptual change. The additional evolutionary processes that the EES highlights are more than just non- essential 'add-ons' and may be as important in shaping evolution as those recognized within the field over the past century. Consequently, the requisite changes are non-trivial. (Laland et al. 2015, 10)

> **(2)** We believe that the EES will shed new light on how evolution works. We hold that organisms are constructed in development, not simply 'programmed' to develop by genes. Living things do not evolve to fit into pre-existing environments, but co-construct and coevolve with their environments, in the process changing the structure of ecosystems. (…) SET consistently frames these phenomena in a way that undermines their significance. For instance, developmental bias is generally taken to impose 'constraints' on what selection can achieve — a hindrance that explains only

> the absence of adaptation. By contrast, the EES recognizes developmental processes as a creative element, demarcating which forms and features evolve, and hence accounting for why organisms possess the characters that they do. (Laland et al. 2014, 162-164)

A crucial element of the extension claim is to list the processes or core tenets that have been overlooked or allegedly neglected under SET. Such processes include plasticity, the origin of novelty, inclusive inheritance, constructive development, and niche construction (Laland et al. 2015; Pigliucci and Müller 2010). EES proponents claim that explaining and emphasizing such processes in their research programs provides epistemic advantage over SET. EES is therefore more comprehensive and better equipped than SET on the grounds that its scope is *different* than the scope of SET. The problem, however, is that extension claims often misportray SET. Such misportrayal has ignited controversy between theoretical biologists (for a clear example of the controversy, see Laland et al. 2014 and Wray et al. 2014). This is especially relevant in the case of reciprocal causation: a process depicted as being neglected under the standard framework and seen as a core tenet of EES.

According to EES proponents, the neglect of reciprocal causation in SET explains why niche construction was not given due attention under the standard framework. The misportrayal argument states that EES proponents misrepresent SET as not taking into consideration the reciprocity between organisms and environment. Portrayals of the limitations of SET have been heavily criticized (Gupta et al. 2017; Wray et al. 2014; Svensson 2018) on the grounds that the way in which EES portrays the limitations of SET is inaccurate and unjustified. For example, Lu and Bourrat (2018) argue that the criticism of EES proponents directed at SET is due to a semantic confusion between the evolutionary and the molecular concepts of ‘gene’. Gupta et al. (2017) argue that the claim according to which SET is narrowly gene-centric and ignores the richness and

complexity of the living world is misguided. Similarly, Charlesworth et. al. (2017) show through several examples that evolutionary biology is not "dogmatically adaptationist" (2017, 9), despite being too often portrayed as such. Lastly, Dickins and Barton (2013) show how Laland misinterprets Mayr's claims about proximate and ultimate causes. A more charitable interpretation of SET would avoid accusations of a misportrayal.

2.1.2. The empirical argument

Another argument that criticizes the EES perspective with respect to reciprocal causation is empirical. Simply put, it involves listing examples that show how SET has adequately captured feedback interactions between organisms and environments. For example, Svensson (2018) argues that negative and positive frequency dependence selection, cases of co-evolution and eco-evolutionary dynamics are good examples of reciprocal causation within SET. Specifically, the research field of eco-evolutionary dynamics (Hendry 2016) explicitly acknowledges two kinds of unidirectional effects: the effects of ecological changes on evolutionary processes and the unidirectional effects of evolutionary changes on ecological processes. Eco-evolutionary dynamics theorists plainly acknowledge that an important goal "should be to elucidate bidirectional eco-evolutionary interactions" also known as eco-evolutionary feedbacks (Pelletier, Garant, and Hendry 2009, 1584). Additionally, Gupta et. al. (2017) show, through a number of empirical examples, that niche construction has *not* been neglected in SET. An example mentioned is Fisher's (1919) conceptualization of the rest of the genome as evidence that niche construction was well-acknowledged at the core of SET. Therefore, providing strong empirical evidence that SET acknowledges reciprocal causal relations challenges the view according to which reciprocal causation is a new feature of EES.

The table below (Table 2.1) maps the debate between the two epistemic communities in question. In sum, causal claims are claims about what are the relevant causes of evolution. Under the EES perspective, reciprocal causation is the best causal model and has not adequately been addressed in SET. If this is true, and if niche construction is a key example of reciprocal causation, then niche construction plays a major role in evolution, on par with natural selection. This claim is contested by EES critics or skeptics who argue that niche construction may not be as consequential as natural selection in explaining the causes of evolution. Additionally, the debate can also be mapped by an empirical claim about the specific examples that justify the need for an extension of SET. Finally, theoretical claims are those that refer to the structure of the respective frameworks in accommodating and including niche construction in evolutionary explanations.

	EES proponents	*EES skeptics*
Causal claim	Evolution depends on two processes: natural selection and niche construction. (Feldman, Laland, and Odling-Smee 2013; Laland, Odling-Smee, and Feldman 2019)	Niche construction is not quite as consequential as their proponents suggest because ultimately, niche construction capabilities are shaped by selection and variation that conditions niche constructing activities. (Gupta et al. 2017)
Empirical claim	Reciprocal causation is key and has not been addressed by SET. There is an ongoing reciprocal causal relation between organisms and their environment.	SET research programs provides many examples of reciprocal causation and has not neglected it (Svensson 2018). Examples include negative and positive frequency dependence (Brisson 2018) and eco-evolutionary dynamics (Pelletier, Garant, and Hendry 2009; Hendry 2019; Schoener 2011).
Theoretical claim	SET does not have the adequate explanatory scope to acknowledge niche construction as an evolutionary process. An extended framework is needed (Laland et al. 2014).	SET and neo-Darwinism are sufficient to explain niche construction and there is no need for an extended theoretical framework (Wray et al. 2014)

Table 2.1. Mapping the niche construction debate into causal and empirical claims made by two epistemic communities.

2.1.3. Re-orienting the debate: the scope argument

The two arguments presented focus on showing how reciprocal causation is a well acknowledged feature of SET. There is, however, a third argument that can replace the first two arguments and contribute to settling the debate surrounding reciprocal causation. The scope argument goes beyond claims about whether reciprocal causation has or has not been acknowledged in SET. My goal is to reframe the debate about reciprocal causation by introducing a distinction between the scope of research programs making use of this notion. By bringing conceptual clarity into the scope of inquiry of the two epistemic communities in question, the scope argument shows in what capacity reciprocal causation is used in each research program and how it can be epistemically advantageous considering the different explanatory goals of the respective research programs. Ultimately, the scope argument is pluralistic: it supports that reciprocal causation can be fruitful in explanations that address longer and shorter time scales and that are finer- or coarser-grained. Such pluralistic approach is in line with how concepts and explanations in biology are currently understood (Mitchell and Dietrich 2006; Sterelny 1996; Love 2012). Specifically, I argue there appears to be a fundamental difference in the scope of inquiry that is signalled by the term 'reciprocal causation'. When EES proponents vindicate reciprocal causation, the concept is used with a different scope in comparison to how it is vindicated in SET. This overlooked difference in scope can provide a fruitful avenue to settle the debate. Namely, identifying the different scopes of EES and SET with respect to reciprocal causation brings the focus to the ability of each epistemic community to support their research programs by identifying *specific causal mechanisms* responsible for salient features of evolution. Hence, the scope argument is a candidate to replace the misportrayal and the empirical arguments discussed as it evaluates reciprocal causation in its ability to support different research programs.

This re-orientation is timely and necessary, especially if EES proponents wish to achieve a more defensible research program by clearly specifying the scope of their empirical projects and in what capacity they represent epistemic advantage over SET. Currently, the discussion of whether reciprocal causation represents a major theoretical innovation is most likely a red herring. It detracts attention from explaining *in what capacity* reciprocal causation is important to EES. The question is not whether reciprocal causation is sufficiently new to motivate the emendation project, but rather, what is the *scope* of explanations within each epistemic community when vindicating reciprocal causation. As I will argue in Section 2.4, this difference in scope can be understood in terms of: (i) time scales, and (ii) the fine graininess of explanations under each framework. Since niche construction is a common example described as a case of reciprocal causation, the next section will delve into an empirical example that will help structure the scope argument.

Niche construction and the role of reciprocal causation

Reciprocal causation and niche construction are deeply intertwined. While reciprocal causation can apply to other biological processes (such as negative and positive frequency dependence, feedback loops in molecular processes, co-evolution), in this chapter I focus on niche construction, "the process whereby organisms, through their metabolism, their activities and their choices, modify their own and/or each other's niche" (Odling-Smee, Laland, and Feldman 2003, 419). Niche building activities encompass processes of constructing a favorable environment that in turn favors survival and selection of the niche constructing species (Sultan 2015). Examples include the activity of ants, termites or the burrowing activities of earthworms who modify soil conditions, creating beneficial environments for their survival (Gupta et al. 2017) . The soil-altering activities

of earthworms, for example, were documented by Darwin in his later work *The formation of vegetable mould through the action of worms* (Darwin 1898). Earthworms belong to annelid species, which are mostly found in freshwater or marine environments. Earthworms, however, are terrestrial and are somewhat "ill-suited to the central stress that characterizes life out of water – desiccation" (Sultan 2015, 103). For this reason, earthworms have developed ways to keep the soil moist and to make water easily extractible. They engage in several activities such as tunneling through soil, compacting, and leaving a mucus coating that provides "a ready carbon source that promotes microbial activity" (Ibid). The soil-altering activities of worms results in feedback effects that shape worms' survival rates in their environments, therefore acting as a selective pressure in a loop of feedback and interaction between earthworms and the altered soil conditions.

Another example of niche construction is the activity of the North American beaver, *Castor canadensis.* Beavers make use of specific trees to construct dams that shape streams and wetlands. Such changes lead to "changed patterns of sedimentation and nutrient cycling,", altering the biological community and leading to greater species richness in the surroundings (Sultan 2015, 96). Reciprocal causation is important for niche construction because ultimately, the modified environment can in turn feedback to future generations and be the source of novel selective pressures in a reciprocal loop whereby organism and environment are both the cause and effect of evolution (Laland, Odling-Smee, and Feldman 2019). This has effects for the niche constructing species, but also for the co-occurring species in a same area. For example, in the case of beaver dams, dam density has been related to riparian characteristics selected by birds, showing that dam building activities are important for creating rich riparian conditions for bird activities (Cooke and Zack 2008). Such feedback cycles can occur at the cellular, individual or macro level, such as in evolutionary and ecological scales (Sultan 2015). In ant colonies, for example, niche construction

means that the soil is altered in ways that allow for "soil mineral availability, organic content and water-holding properties so as to facilitate the insects' regulation of temperature, humidity and gas exchange" (Sultan 2015, 38). This, in turn, creates more favorable conditions for ants to survive. Niche construction is not always a favourable process and is sometimes described as 'negative' insofar as it sometimes destroys environments. An example is human niche modification. Whether positive or negative, niche construction can be broken down into the reciprocal causal relation between organism (O) and environment (E), described as follows:

> *Niche construction* occurs whenever a population *O* changes its relativistic niche by changing a factor in *E* relative to its own features. If, by modifying a factor, *O* also modifies a natural selection pressure for itself, then subsequently the change in the niche caused by *O*'s prior niche construction may feedback to *O* either to select for a change in *O*'s features or to counteract an independent change in *E*'s factors that would otherwise have selected for a change in *O*. It may thereby either create, preserve, or destroy a synergy or matching relationship between *O*'s features and *E*'s factors. (Feldman, Laland, and Odling-Smee 2013, 43)

Niche construction therefore implies that there is a reciprocity between organisms and environments and that by virtue of this reciprocity, an additional set of evolutionary causes come into play resulting from the bidirectional interaction between E and O. Strong empirical evidence showing that niche construction is a significant cause of evolution supports the so-called niche construction *perspective,* which overlaps with claims supported by EES proponents (Sultan 2015; Laland, Odling-Smee, and Feldman 2019; Aaby and Ramsey 2022; Laland and Sterelny 2006). The niche construction perspective defends that niche construction be considered a second major *cause* of evolution, after natural selection (Laland, Matthews, and Feldman 2016).

Consider, once again, the *Castor canadensis* example explained from the two different perspectives: SET and EES. Under the standard view, the beaver's dam-building behavior is

explained as an adaptation that can be beneficial for the beavers' survival. Consequently, this survival has an impact on beaver dam-building and shapes beaver evolution. As Dawkins (2004) explains, "the *variations* in replicators have a causal link to *variations* in dams such that, over generations, replicators associated with good dams survive in the replicator pool at the expense of rival replicators associated with bad dams (…) The beaver dam is as much an adaptation as the beaver tail" (Dawkins 2004, 379, emphasis on original). Under this view, the tools of SET: variation, selection, and fitness, sufficiently explain how beavers modify their environment as a result of selective pressures. This process is ultimately random since its primary cause is random variation.

Niche construction is an example of a "standoff situation" (Baedke, Fábregas-Tejeda, and Vergara-Silva 2020) where different explanations address the same phenomenon (niche construction). In the specific case of dam-building, EES proponents and niche construction theorists disagree with the view according to which underlying variation is the main cause of dam building, since this removes any potential agency on behalf of organisms (Aaby and Desmond 2021). Critics of SET argue that the orthodox explanation for beaver dam-building is modelled in the same way as other phenotypes, i.e., in terms of fitness with regards to underlying genes. Indeed, the idea is that dam-building alleles were repeatedly selected over time and such phenotypic adaptations (or, in Dawkins' terms extended phenotypes) can be explained just like other adaptations. In response, they argue that this is an incomplete picture of all the causal forces at play. Niche construction is not a product of selection, but rather, a cause that is *on par with* selection. Indeed, the causal arrow runs not only from E → O, but also from O → E, as organisms co-evolve with their environments (Laland et al. 2015). In other words, when beavers engage in dam building activities they are not only propagating 'dam-building genes', but also transforming

their environments and therefore selection "acting on a host of beaver traits, influencing subsequent beaver evolution" (Laland and Sterelny 2006, 1752). Hence why reciprocal causation is crucial here: it is the causal account that captures the effect of an organism's modification of its environment on the organism's selection over time. The table below (Table 2.2) summarizes key aspects of niche construction under SET and under EES.

	SET framework	*EES framework*
Cause of building	Mutation / Variation	Variation *and* constructive development
Effect of dam building	Persistence of 'dam-building alleles'	Co-evolution of beavers and selective environments
Role of dam	Adaptation	Niche construction
Form of inheritance	Genetic	Genetic and epigenetic inheritance. Examples include acquired characters, by-products and accumulated outputs of multiple species. (Laland et al. 2015, 5)

Table 2.2: *Castor canadensis* dam-building analyzed from two different perspectives

Even though reciprocal causation is present in both explanations, the notion plays a different role under each framework. Focusing on whether reciprocal causation is a feature of SET is a red herring. Instead, the focus should be on the scope of reciprocal causation under each framework and its ability to support research programs. As I will show in the next section, the question is in what explanatory capacity it is used to explain phenomena such as niche construction.

2.4.The scope argument: time scales and fine graininess

So far, I have discussed two avenues of criticism directed at the role of reciprocal causation in the EES. The first was that EES critics argue there is a deliberate misportrayal of SET. The second was that skeptics also provide several empirical examples to defend that SET sufficiently accommodates reciprocal causal relations between organisms and environment. I contend that considering the scope of reciprocal causation within research programs can be a fruitful way to settle the debate surrounding reciprocal causation. While the explanatory power of the EES when compared to SET has been discussed in the literature (see Baedke, Fábregas-Tejeda, and Vergara-Silva 2020), the question of scope remains unexplored. The notion of explanatory depth (Hitchcock and Woodward 2003; Strevens 2008) can be useful here. As Hitchcock and Woodward argue some explanations can be deeper than others by virtue of their degree of generality. Accordingly, Strevens (2011) argues that explanatory relevance is a matter of causal relevance. There is often a trade-off between the degree of generality of an explanation (i.e., an explanation whose scope is wider) and explanatory depth (Ibid, 190). Here I focus on the scope of reciprocal causation within the explanations deployed by epistemic communities, and not on the overall scope of the respective theoretical frameworks (SET and EES). Specifically, I argue that there are two important aspects of the scope of reciprocal causation: time scales and fine graininess. I wish to show that scope can be useful to settle the debate surrounding reciprocal causation and argue that once the scope of explanations in EES and SET is clarified in terms of time scales and fine graininess, the innovative aspect of reciprocal causation in the EES becomes clearer and distinctively sets it apart from how the notion is used under SET. When using reciprocal causation in explanations, SET focuses on much longer time scales and more coarse-grained population-level explanations. EES, by contrast, is interested in shorter time scales and finer grained

explanations. The goal of the scope argument is, ultimately, to show that, for the debate surrounding reciprocal causation to become constructive, it should move from the debate surrounding overarching claims about the causes of evolution to clearer explanatory goals within the scope of each epistemic community. Ultimately, the debate should focus on the ability of each framework to support research programs that identify the *specific causal mechanisms* responsible for salient features of evolution. One such causal mechanism is the reciprocity between organisms and environments.

There are at least three levels at which one can talk about the scope of reciprocal causation in the EES and SET debate: the scope of a research program, the scope of reciprocal causation and the scope of explanations. The three levels are hierarchically related. The distinction is important because the scope of explanations making use of reciprocal causation depends on the scope of reciprocal causation within different research programs which in turn depends on the scope of the research programs themselves.

First, the scope of a research program can be understood in terms of a problem agenda, defined as "a "list" of interrelated questions (both empirical and conceptual) that are united by some connection to natural phenomena" (Love 2008, 877). Scope here refers to the kinds of questions that are included within each problem agenda, *versus* those that are deliberately left out. For example, in evo-devo, questions will tend to focus on identifying the causal mechanisms that explain the impact of development on evolution. Examples include: which developmental mechanisms account for the origin of novel traits? What role does developmental plasticity play in evolution? What forms of inheritance explain phenomena such as niche construction? Problem agendas help structure intellectual integration and provide structure to scientific investigation by

specifying which theoretical and empirical questions should be pursued (Neto 2020). A distinctive feature of the EES program is that it focuses on a variety of different research questions that aim at addressing phenomena at very different levels of organization (from genetic processes such as accommodation and assimilation to large-scale ecological processes). The questions are therefore heterogenous: they are both empirical and theoretical, which is another feature of a problem agenda (Brigandt and Love 2012; Love 2008). One of the sources of criticisms directed at the EES is that it does not represent a synthesis, since it groups together too many heterogenous approaches and should rather be portrayed as a more pluralistic framework (dos Reis and Araújo 2020; Craig 2010). Indeed, the wide and ambitious range of research questions EES encompasses is sometimes characterized as being too broad in scope. Second, within the scope of a research program the scope of reciprocal causation can be understood as how the notion is used within the context of a problem agenda. It refers to what kinds of causal relations can be characterized as reciprocal. For example, within SET these include negative and positive frequency dependence and cases of co-evolution (Svensson 2018). In EES, the main example is niche construction. Third, within the scope of reciprocal causation, we may also identify the scope of explanations making use of reciprocal causation, that is, the set of all phenomena that are explained in terms of reciprocal causation.

While the three levels of scope are hierarchically related, the scope argument presented here will focus on the third level: the scope of explanations making use of reciprocal causation. My working hypothesis is that there are at least (but not exclusively) two dimensions that can be helpful in delimitating the scope of explanations within a research program such as the EES, with respect to reciprocal causation: the time scales targeted in the explanations of phenomena and the fine graininess of these explanations. These two factors are related: explanations that deal with

much longer time scale will tend to be more general and coarse-grained. Alternatively, explanations that focus on shorter time scales are more fine-grained insofar as they provide a greater level of details. Minimally, there are two reasons why scope is a fruitful way of understanding the role of reciprocal causation in the EES. First, in their criticisms of SET, EES proponents are implicitly making claims about scope. Namely, what motivates the need for EES is precisely the need to pay more attention to developmental processes and how they are causally relevant to evolution (Laland et al. 2014; 2015). Indeed, evo-devo is the main discipline grounding and motivating the EES proposal (Müller 2021). However, EES proponents go much beyond development in the phenomena they seek to integrate into evolutionary explanations, and therefore the scope of their project may be seen as too broad. I assume, in accordance with Müller (2021), that evo-devo is a key discipline motivating EES (though arguably many evo-devo biologists do not support or endorse the EES program). In the case of niche construction, the EES explanations explicitly argue that there are developmental dimensions to niche construction that must be considered (Laland, Matthews, and Feldman 2016). Second, clearly delimitating the scope of a research program is an effective step in making the research questions clear and differentiating them from other research programs, thus structuring a distinct problem agenda. Indeed, evo-devo provides explanations that are different than standard population-level explanations in SET (Kaiser 2021). A clear circumscription of the scope of explanations that will be provided within a research program avoids problems such as the misportrayal argument. Welch (2017) notes, for example, that the sheer scope of evolutionary biology draws scholars to criticize standard evolutionary biology when their expertise or interests lie elsewhere. Consequently, the vaguer the scope, the more room there is for disputes based on mischaracterizations of research fields and competing explanations.

In motivating the EES, the goal of evo-devo is to provide causal-mechanistic explanations of how developmental processes shape and cause major evolutionary effects (Baedke 2020). In other words, the scope of the EES problem agenda is to explain how the developmental mechanisms of organisms bring about phenotypic changes or innovations. This has consequences for how reciprocal causation is understood within the EES epistemic community. Insofar as reciprocal causation is a core tenet of EES, the scope of this notion should be aligned with the scope of the research program. The scope of EES explanations that vindicate reciprocal causation is narrower than how SET wishes to approach such mechanisms. Indeed, under SET, these are population-level effects such as the effect of environmental factors on allele frequency and the interplay between environment and fitness. If this is correct, then EES and SET differ in the *emphasis* given on their explanations. Such difference in emphasis can be conceptualized in terms of time scales and fine graininess.

2.4.1. Time scales

The use of scale in biological explanations is not new (Potochnik and McGill 2012; Baedke and Mc Manus 2018; DiFrisco 2017; Green 2018). Scale has been presented as a viable alternative to the concept of levels of organization and as a suitable framework for describing processes in evo-devo. From the perspective of process ontology (Dupré 2012), processes are stabilized at certain time scales and therefore the temporal scale of a biological process is an important feature of its explanation. Broadly construed, scale can be defined as "the spatial or temporal extent across which observations span" (Potochnik and McGill 2012). My argument focuses specifically on time scales, whose definition I borrow from DiFrisco (2017): "the characteristic amount of time it takes for system behaviours or processes to occur." (2017, 809). Emphasis on time scale may dissolve some of the conceptual tensions surrounding the role of reciprocal causation in EES. In the range

of explanations within the scope of the EES, reciprocal causation describes processes at shorter time scales than when it is used in the framework of SET. Evo-devo theorists are interested in the role of constructive development: the view that argues that development is not genetically 'programmed', but rather that it results from feedback interactions between organisms and their environments (Müller 2021). Constructive development is a distinctive feature of EES together with reciprocal causation since the latter is the underlying causal model that describes reciprocity between organisms and environments. Therefore, the time scale within the scope of reciprocal causation in EES is developmental. Ultimately, the empirical evidence and the studies done under this research program will continue to focus on how environmental factors can modify development and vice versa. Development here is understood in the broadest sense of 'ontogeny', i.e., a description of events that occur over the course of an organism's life. Note that this is much shorter than the time period of a species' existence (which would be captured under the descriptive term 'phylogeny') (Gould 1977). In the case of niche construction, the focus is also on the developmental time scale. For example, in the *Castor canadensis* example, the target of explanation is the relevant mechanism of niche construction within that system, and how the niche constructing behaviour is passed on. This is clearly stated by proponents of the niche construction perspective. Niche construction is said to modify not only selective environments, but also developmental environments, whereby changes in the developmental environment will result in systematic changes to the phenotypic expression of inherited genes (Laland and Sterelny 2006, 1758).

Under SET, however, the target of explanation is identifying processes at a much longer time scale. Consider the example of eco-evolutionary dynamics, which is one of the empirical examples used to illustrate how SET adequately models reciprocal causation (Svensson 2018). The

phenomenon in need of explanation in this case is how ecological factors and populations interact within the evolutionary framework (Hendry 2016). This is mostly done by assessing how changes in trait frequencies impact ecological environments. Rather than focusing on the developmental time scale, studies focus on longer time scales in the magnitude of years, centuries or even thousands of years. While this may be changing more recently with the empirical observation that evo-ecological change can be seen in shorter time scales such as years and centuries (Hendry 2019), it remains that the aim of explanations in this domain of biology is to account for longer evolutionary phenomena than those primarily assessed under evo-devo. While there may be overlaps between eco-evolutionary dynamics and evo-devo, the two different research programs aim at different goals, which is reflected in the scope of the time scales under which they assess reciprocity between organisms and environment.

Reciprocal causation therefore describes causal processes at different time scales that can be distinguished and belong to the scope of different research programs. Distinguishing between two different time scales, however, still allows hierarchical distinctions between causal processes in a continuous manner (Baedke and Mc Manus, p. 41). This points to the fact that focusing on processes occurring at different rates does not necessarily mean that one explanation provides epistemic advantage over the other. Rather, insofar as two competing explanations have different scopes, they can still coexist.

Thinking about the scope of reciprocal causation in terms of time scale means that the same notion does not need to fulfill competing or excluding roles within different epistemic communities. Instead, reciprocal causation is a notion that can be equally useful through explanations whose target is processes and mechanisms at different time scales. Clarifying the scope of reciprocal causation in terms of time scales allows research programs to pursue distinct

and separate research questions within their problem agendas. Insofar as they have different targets of explanations, reciprocal causation can be used referring to different time scales to provide compatible explanations of the causes of evolution. Clarity about relevant time scales helps to avoid the tension raised by the misportrayal argument while accepting that reciprocal causation can refer to different empirical examples already taken into consideration in SET.

2.4.2. Fine graininess

Another element of scope is the difference in how fine grained the explanations of SET and EES are. One advantage of EES is precisely to provide more fine-grained explanations of how ontogeny can have causal influence in phylogeny. Indeed, evo-devo, the central discipline motivating EES, is concerned with explanations at the level of individuals or lineages, while SET is concerned with population-level explanations and how variation in phenotypic traits correlate with changes in allele frequencies in populations (Kaiser 2021). The explanations within EES are therefore more fine-grained by virtue of providing a greater level of detail concerning the mechanisms responsible for the emergence of novel phenotypic traits. Müller (2021) argues that the innovation of EES when compared to SET is showing that the properties of evolving developmental systems are as important as genetic variation in explaining phenotypic variation (2021, 1129). Genetic variation, however, is mostly measured through the frequency of traits in a population. Most of the innovative elements of EES are tied to the inclusion of developmental processes (broadly construed). These include (but are not limited to): niche modifications, epigenetic inheritance, and constructive development. Developmental explanations are finer grained than evolutionary ones insofar as they deal with shorter time scales at the level of individuals or lineages. The level of fine graininess does not necessarily imply epistemic

advantage, rather it is useful to identify the scope of explanations within research programs and the phenomena they seek to explain. For example, a key goal of eco-evolutionary dynamics is to understand the contributions of ecological changes to changes in population dynamics (coarse-grained, population-level explanation) (Pelletier, Garant, and Hendry 2009) whereas evo-devo seeks to understand how ecological changes will impact the development of individuals in ways that will cause them to interact with their surroundings differently, thereby providing an active rather than passive role to organisms (Sultan, Moczek, and Walsh 2021).

Consider, as an example the forms of inheritance under SET or under EES, in the specific case of niche construction. Under SET, the focus is genetic inheritance (that can be applied globally to the evolution of a species, measured through trait frequency). EES accepts genetic inheritance as the main form of inheritance while additionally focusing on the inheritance of organism-driven changes in their environment and how those changes are inherited in future generations. For example, under the niche construction perspective it is not sufficient to explain niche constructing behaviour in terms of 'dam-building genes'. An additional form of inheritance whose scope is within ontogeny is supported by evidence that "organisms also transmit to their offspring altered physical and selective environments, both by physical action on their biological and nonbiological environments and by habitat choice" (Laland and Sterelny 2006, 1758). This will vary depending on the niche and therefore yields less generalizable, yet more fine-grained explanations that apply to particular niches. When evaluating the explanatory power of the EES, Baedke, Fábregas-Tejeda, and Vergara-Silva (2020) argue that explanations in EES are less idealized than those in SET by virtue of the fact that they identify a range of causes (under the framework presented here, this claim is compatible with the fine-graininess of explanations in EES). The presence of many causes means that, when compared to SET, causal factors in EES explanations individually play a smaller

causal role. My argument is compatible with their views about the EES, with the main difference that I introduce two dimensions of scope to support my claims. Table 2.3 below summarizes the differences in scale and fine graininess of explanations under both SET and EES.

Scope	*SET*	*EES*
Time scale of change	▪ Change in allele frequencies, longer-term ▪ Phylogeny	▪ Organism-driven change, shorter term ▪ Ontogeny
Fine graininess	▪ Global, general, coarse-grained explanations ▪ Selective environments ▪ Population-level	▪ Local, specific, fine-grained explanations ▪ Developmental environments ▪ Individuals or lineages

Table 2.3: The scope of reciprocal causation

2.5. Challenges to the scope argument

Time scales and fine graininess are two among other potentially relevant elements to analyze the scope of a research program. For example, spatial scale might also be a good candidate to refine the scope, as well as the type of causal explanation involved. Introducing time scales and fine graininess of explanations can nonetheless raise concerns. Here I discuss two concerns that may be raised against the scope argument.

First, I will consider a general objection against the use of time scales to describe processes occurring at different rates. Indeed, time scales may introduce a distinction that is just as problematic as that of 'levels of organization'. Recall that the 'levels' problem refers to the idea that the biological world is too messy to be organized into compositional levels (Brooks 2021;

Potochnik and McGill 2012). Like hierarchical levels, time scales, are continuous and it is perhaps too unnatural and unrealistic to attribute specific time scales to different research programs. Furthermore, it may be too simplistic to attribute a specific time scale to explanations in evo-devo and, more generally in EES. This is because there is a complex interplay between processes at different time scales occurring simultaneously. For example, as Baedke (2021) argues, phenomena such as morphogenesis and adaptation occur at very different time scales and are nonetheless related. Indeed, the goal of evo-devo is to show how development and evolution are integrated, and therefore the goal is to arrive at comprehensive explanations at both shorter and longer time scales. If this is the case, the scope of the research program goes much beyond ontogeny and the scope argument would not be appropriate to the explanatory targets in question.

While this may be the case, there are methodological reasons to support the scope argument with respect to time scales. Specifically, with respect to reciprocal causation, the role it plays in EES is specific and fine grained enough to account for individuals or lineages. Take for example niche construction. The reciprocal causal feedback is between an organism and environment, as well as in some cases such as *Castor canadensis* the surrounding species affected by dam-building activities. In the case of niche construction, the scope is, indeed, a shorter time scale. The implicit goal seems to be how focus on this scale allows to introduce niche construction as a *cause* of longer-term evolutionary processes. In EES, explanations of long-term phenomena are derived by extension from explanations of short-term phenomena. Alternatively, under SET, the scope of enquiry is the study of niche construction as an adaptation, which by the nature of the concept of adaptation already involves a much longer time scale. Reciprocal causation is therefore, under SET, part of a much longer time scale than that of EES. Even if the overarching goal of EES may be to arrive at explanations that target the same scope as SET in terms of time scales, currently the

research program specifically emphasises causal-mechanistic explanations of developmental processes and their interplay in niche constructing activities.

Another challenge raised against the scope argument is that the scope of reciprocal causation in EES is still not sufficiently distinct from that of SET to justify the need for an emendation or a radical "conceptual change", as EES proponents suggest. According to this objection it would be a mistake to say that the explanations using reciprocal causation in the EES are more fine-grained because the focus on genes under SET provides even more fine-grained explanations at the micro-level. For example, if reciprocal causation is considered within the field of eco-evolutionary dynamics, it is mostly done so with the aim of unravelling how genetic changes and ecological changes co-vary. Most lower-level changes are assessed at the genetic level, whereby small-to-modest-effect genes are the key factors underlying the dynamics between organisms and environment (Hendry 2013). Explanations whose target is to assess how genetic variation cause ecological changes are therefore also fine-grained and perhaps even more so than those in EES.

In response to this challenge, I emphasize that the scope argument is specific to reciprocal causation. Even if areas of study that acknowledge reciprocal causation under the standard framework (such as eco-evolutionary dynamics) are assessing genetic variation, the scope of such change is still measured at the population-level, rather than at the individual level. Generalizations are made from the population of one focal species to another, and the scope is therefore less fine-grained because the resulting explanations are at the level of populations. Evo-devo, on the contrary, also focuses on some genetic mechanisms (such as gene co-option) to explain mechanisms such as morphogenesis. The goal is therefore to understand how environments shape development and how development of organisms responds accordingly.

2.6. Reciprocal causation, revisited

So far, I have shown how focus on overarching claims about the causes of evolution has led to stagnation and has prevented the debate surrounding reciprocal causation from moving forward. I have suggested instead that we re-orient the discussion in terms of the *scope* of reciprocal causation under different research programs. This involved a description of different time scales and the fine graininess of explanations under EES and SET. From the perspective of SET, depicting niche construction as a consequence of natural selection and sometimes as superfluous does not provide SET any epistemic *advantage*. Alternatively, when EES proponents argue that there is an explanatory advantage to thinking of niche construction within the framework of reciprocal causation, the epistemic advantage of EES also remains unclear and becomes the target of criticisms (Dawkins 2004; Wray et al. 2014; Gupta et al. 2017) .

The scope argument supports the view that for the debate between EES and SET to become constructive, what matters is their ability to support research programs that identify the specific causal mechanisms responsible for the salient features of evolution. Reciprocal causation is a core tenet of EES and therefore should be scrutinized from the perspective of the scope of different research programs for the debate to flourish. It has become clear that SET and EES identify reciprocal causation in their research programs. The difference is rather in the scope of reciprocal causation within each epistemic community. This view is compatible with what Buskell (2019) labels as the "empirical aptness" of reciprocal causation. In other words, reciprocal causation is useful when it is used to structure and guide inquiry across a community of researchers. As a result, reciprocal causation plays different roles under each program by virtue of its scope when used in explanatory capacity. It is a matter of the emphasis of different research programs and their respective problem agendas. Reciprocal causation is therefore a red herring, i.e., it is a distraction

that shifts the debate from the usefulness of this notion to fruitless theoretical disputes. What is novel about reciprocal causation in the EES is not its acknowledgement, but rather making use of reciprocal causation within explanations whose scope is different than the explanations available in SET.

Therefore, for the epistemic advantage of EES vindicated by its proponents to become clearer and motivate the need for an emendation of SET, EES would benefit from greater specificity about the scope of reciprocal causation within its research program. When the debate is re-directed according to the scope of reciprocal causation, it becomes clearer that natural selection and niche construction are distinct processes that are not on explanatory par. While the misportrayal argument is valid, it does not provide insights into the role of reciprocal causation in explanations within different research programs. Similarly, while the empirical argument is fruitful in establishing the ubiquity of reciprocal causation in SET, it does not specify how reciprocal causation supports the explanatory targets of the research programs in question.

I have suggested instead that when analyzing the scope of reciprocal causation within research programs, the epistemic advantage of this notion becomes clearer to achieve different explanatory goals that differ in their scope. It follows that the epistemic advantage of EES is not related to *which* processes it describes, but rather to the scope of the explanations used to describe such processes. It is in the ability to foster empirical research at shorter time scales and a higher level of fine graininess that the EES research program is epistemically advantageous and novel. Additionally, focusing on different scopes allows both views to coexist insofar as their explanations differ in scope. As Mitchell and Dietrich (2006) argue, there are many examples in biology where similar phenomena have different explanations and an isolationist stance with regards to each research program would be a mistake. I agree with this view and add that

understanding the difference in emphasis or scope of research programs can be a fruitful step for a better integration between research fields. Reciprocal causation can be a red herring motivating further isolationism among scientists. The case of niche construction, which represents a clear case of reciprocal causation, can be understood from different perspectives that coexist. This is because SET and EES are not equally important for explaining the course of evolution since their research programs emphasize on different timescales and provide explanations that are finer or coarser grained. Another fruitful avenue of research would be to assess other examples of reciprocal causation that are not restricted to the specific case of niche construction.

In sum, the scope argument allows to re-orient the debate in more fruitful ways, namely, it sets the stage for EES proponents to position themselves in an epistemically advantageous position to defend their claims. Indeed, clarity and scope specificity may lead to a more defensible formulation of EES. Despite the inclusion of very different processes under the core tenets of EES, one aspect of the scope of the research program is very clear: the focus on evo-devo as the main theoretical and empirical basis for arguing that an extension is necessary. For example, the emphasis of EES on niche construction is important even if the causal claims it makes are no different in substance than the ones made in SET. The debate surrounding reciprocal causation and niche construction should no longer be centered about whether these phenomena are neglected in SET, but rather, what is their scope and how does that scope contribute to achieving the epistemic goals of each research program.

2.7. Concluding remarks

Reciprocal causation is a contentious topic and has been the object of much philosophical and scientific discussion. Philosophical contributions can contribute to re-orienting the debate

surrounding the role of reciprocal causation in the EES and whether reciprocal causation is responsible for the epistemic advantage of EES vindicated by its proponents. While most of the debate focuses on overarching claims about the causes of evolution, in this chapter I have shown a viable alternative to re-orient the debate: the scope argument. While niche construction is acknowledged under both theoretical frameworks, little, if anything, is said about the scope of reciprocal causation under each framework. Focusing on the explanatory scope of reciprocal causation is timely and important for the debate to move forward. Despite empirical challenges, there is hope that it is increasingly possible to model reciprocal causal processes. Here, I have argued that time scales and fine graininess of explanations can be a useful perspective to move beyond the debate around overarching claims about the causes of evolution. Analyzing an example such as that of *Castor canadensis* dam-building from different angles can provide fruitful insights as to the scope of explanations that make use of the term 'reciprocal causation'.

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3. EVOLUTIONARY NOVELTIES: A REALIST ARGUMENT

3.1.Introduction

The concept of an evolutionary novelty has been the object of much discussion in the history of evolutionary biology (Brigandt and Love 2010; 2012; Mayr 1960; Moczek 2011; Müller and Newman 2005; Müller and Wagner 1991; Oakley 2017; Peterson and Müller 2013; 2016; Pigliucci 2008; Wagner 2015). Disagreements surrounding the concept stem from the lack of a clear-cut definition about what, exactly, counts as a novel trait. A key difficulty is to establish the boundary between quantitative change in traits (such as evolution in the size of an insect's wing appendix) and qualitative change in traits (such as the evolution of insect wings as distinctively novel morphological features) (Müller and Newman 2005). While some conceptualize evolutionary novelty as a kind of qualitatively distinct phenomenon deserving its own explanatory framework, others contend that novelty is not a special phenomenon and that it can be explained by current evolutionary principles as laid out by Standard Evolutionary Synthesis (SET) (for example, gradual quantitative change) (Futuyma 2017; dos Reis and Araújo 2020). Recent empirical evidence from evolutionary developmental biology (evo-devo) has motivated a proposal to extend SET into a framework that also incorporates developmental mechanisms and processes in evolutionary explanations (Müller 2021b). Consequently, proponents of an Extended Evolutionary Synthesis (EES) claim that 'evolutionary novelty' deserves its own explanatory framework since it requires different explanations than the concept of 'adaptation', explained in SET (Müller 2021a). While novelty and adaptation are related concepts, they have different goals in theoretical biology. On the one hand, 'adaptation' refers to features that were selected due to underlying variation and environmental pressures (Lewens 2007; Charlesworth, Barton, and Charlesworth

2017). On the other, novelty refers to the emergence or origination of functional or morphological features (Moczek 2011; Müller 2021a). Explaining the evolutionary origin of novelty is a core goal of the EES. Additionally, EES proponents are broadly aligned in their claims that novelty deserves a distinct set of explanations from those available in SET.

Philosophers of biology have also taken an interest in the conceptual imprecision of novelty (Brigandt and Love 2012; Neto 2020). The diversity of definitions of novelty can be perplexing. In its most general form, the definition of an evolutionary novelty points to some qualitative morphological feature that originates in the evolutionary history of a species (Müller and Wagner 1991; Mayr 1960; Peterson and Müller 2013; Pigliucci 2008). While there are disagreements as to what novelties are, this does not mean that the concept's vagueness makes it useless for theorizing in biology. In this chapter, I draw on Brigandt's notion of a concept's *epistemic goal* to defend a realist stance about novelty.

Brigandt and Love have suggested that the epistemic goal of the concept of novelty is to "structure a problem space and set research agendas" (Brigandt and Love 2010; 2012). A research or problem agenda is a set of several related problems and their connections (Love 2008). Usually, the research questions within a problem space are answered by a plethora of disciplines. In the case of novelty, the research questions come from developmental biology, paleontology, systematics, epigenetics, and comparative development (Ibid). For example, the novelty problem agenda seeks to address heterogenous questions such as: "what regulatory genes control appendage formation?", "what is the phylogenetic juncture for understanding jaw origins?", "how is variation generated?", to cite a few examples (Brigandt and Love 2012). A problem agenda also sets criteria for evaluating the adequacy of potential solutions and for integrating different sources of evidence in support of such solutions. In the case of evolutionary novelty, the overarching problem is an

explanatory one. Namely, the problem is *how to explain the evolutionary origin of novelty.* Brigandt and Love (2010; 2012) suggest that the lack of a clear-cut definition of evolutionary novelty does not mean the concept is meaningless or futile in scientific practice. On the contrary, its utility stems from the diversity of interpretations and definitions of the concept of novelty. Hence, for Brigandt and Love (2010; 2012), the epistemic goal of novelty is precisely to structure a problem agenda and to provide criteria of explanatory adequacy.

While this interpretation clarifies the role of the concept of novelty in evo-devo, Brigandt and Love are not committed to the term 'novelty' ever achieving a stable status. The concept's unproblematic instability for Brigandt and Love (2010; 2012) contrasts with how biologists defending EES use the concept of novelty. This is especially important for evo-devo and the EES debate, since a central goal of evo-devo is to explain the origin of phenotypic novelty (Müller 2010a). I argue that in following how biologists see the role of the concept for an emendation of SET, a commitment to realism about novelties is necessary for the concept to motivate the claims made by EES proponents. Realism about the origination of novelty entails that 'novelty' refers to a definite and mind-independent set of mechanisms. A terminological clarification is key here. There are at least two ways in which 'novelty' may be understood. The first is that 'novelty' describes a given phenotypic trait (for example, a turtle's hard shell). The second is that 'novelty' describes a subset of origination processes (for example, the biological processes and mechanisms that led to the formation of hard shells in turtles). In the realist argument presented in this chapter I am interested in the second sense of novelty. Namely, 'realism about novelties' is shorthand for realism about the mechanisms that bring about the origination of phenotypic characters.

A realist commitment about evolutionary novelty entails that the concept has a stronger epistemic goal than the one proposed by Brigandt and Love. Namely, the epistemic goal of novelty

I reformulate is *to discover the mind-independent mechanisms that explain the origination of phenotypic characters*[8]. If one subscribes to realism about novelties (which biologists using the concept often seem to), then the concept plays a stronger goal than the one identified by Brigandt and Love (2010; 2012). As I will argue, the concept's epistemic goal is to arrive at true claims about the mechanisms that bring about the phenomenon of origination of phenotypic characters. This chapter contributes to the novelty discussion in two ways. First, by advancing a realist thesis about evolutionary novelty, this chapter aims at providing conceptual clarity surrounding the concept's role and use within the EES framework. Second, it provides ways for the debate surrounding EES to move forward by outlining the necessary conditions that need to be met for the concept of novelty to achieve its epistemic goal within contemporary evo-devo and in the context of the EES.

This chapter is structured as follows. In Section 3.2, I provide a historical background of the novelty discussion and explain what epistemic optimism about novelty means in the context of EES. In Section 3.3, I delve into the notion of a problem agenda and argue that Brigandt and Love's (2010, 2012) suggested epistemic goal for the concept of novelty does not match the concept's use. In Section 3.4, I present an argument defending realism about novelty. In Section 3.5, I discuss co-option mechanisms as an empirical example that supports my claims. In Section 3.6, I respond to potential challenges to the realist argument and present concluding remarks in Section 3.7.

[8] In this context, character here refers to any trait or feature that is observable. The choice of the term "phenotypic trait" is compatible with characterizations of novelty in the literature (for example, see Müller 2021a).

3.2.Background

3.2.1. Historical overview

'Evolutionary novelties' refers to a range of innovations, such as novel functions (flight or vision), novel body parts (appearance of new limbs), transformations of pre-existing body parts (the transformation of fins into limbs), and even behavioural novelties (the behaviour of birds opening bottles of milk) (Reader and Laland 2003; Pigliucci 2008). Morphological novelties, specifically, refer to the appearance of novel body parts, considering that they represent a qualitative difference from the inferred ancestor of the groups being compared. Examples include the appearance of turtle shells, feathers, or the emergence of new structural elements to metazoan body plans (Müller 2010; Peterson and Müller 2013; Hirasawa, Nagashima, and Kuratani 2013). The concept of novelty is often associated with that of qualitative change. What counts as qualitative change, however, is problematic and the topic of disagreements.

Ernst Mayr was one of the first to propose a formal definition of evolutionary novelties in 1960, and a pioneer in setting the problem of novelties apart from the notion of evolutionary change through variation and selection (Mayr 1960). Empirical findings have changed the course of biology since then, but an intuition that the evolutionary process allows for the appearance of radically new features was already present in Mayr's time. Mayr (1960, 351) proposes that what counts as an evolutionary novelty is "any newly arisen character, structural or otherwise, that differs more than quantitatively from the character that gave rise to it". Mayr (1960, 351) carefully points out that, in his view, changes such as size or pigmentation, do not qualify as an evolutionary novelty, but would rather count as quantitative variation. Hence, a 'novelty' tentatively refers to changes that would "permit an organ to perform a new function" (Ibid). The focus of Mayr's account is on which quantitative change could lead to major functional shifts that constitute

significant novelty. While Mayr is interested in the transition from quantitative to qualitative change, under his account qualitative change in function originates in small quantitative change. Mayr's endeavour was very much in line with the commitments of SET, in that small and gradual quantitative changes sufficiently account for qualitative innovations in function.

Müller and Wagner (1991) later provided a definition limited to morphological evolutionary novelties. Their definition is also based on heterogeneity and qualitative change: "A morphological novelty is a structure that is neither homologous to any structure in the ancestral species nor serially homonomous to any part of the same organism" (Müller and Wagner, 1991, 243). Homology is classically defined as any similarity in structure between organisms that can be explained by descent from the most immediate common ancestor. Like 'novelty', 'homology' is a highly debated term in evolutionary biology. 'Homonymy' refers here to the existence of other similar structures to the one in question in the same organism (for example, fingers or teeth could be considered homonomous to each other). Müller and Wagner (1991) differentiate between functional novelties (which arise from the possibility of an organ exercising a double function) and morphological novelties, highlighting the circularity of the evolution of function: "New structures arise from new functions, and new functions from new structures" (Muller and Wagner, 1991, 231). A functional definition (i.e., one that considers change in function of an organ as a novelty) has the disadvantage of being nearly all-inclusive. With the concept of homology incorporated into a definition of novelties, Müller and Wagner's (1990) definition is restrictive insofar as it requires a physical, qualitatively distinct element to exist for something to be considered a morphological novelty.

Müller and Wagner (1991) propose that the least theory-laden account of novelties "consists simply of the statement that all traits characteristic of a supraspecific taxon were a novelty at some

point in the evolution of that group" (Muller and Wagner, 1991, 236). Because of the polysemic nature of the concept of novelty, one strategy has been to create a typology of different *kinds* of novelties. For example, some consider the origin of multicellularity a novelty, often called Type I novelty, which refers to "primary multicellular assemblages" (Peterson and Müller 2013, 347). Others argue that only new morphological features count as novelties, insofar as those were not present in the ancestor stage of a species. These are often referred to as Type II novelties (Müller 2010). Type III novelties are usually defined as a "major change of an existing body plan character" (Müller 2010, 310). Examples include the narwhal tusk or the beetle horn. A Type III novelty can be fixed in populations and is said to be adaptive. 'Novelty' and 'adaptation' are closely related terms and are often conflated. The difference mostly lies in the fact that adaptations were initially a novelty that became fixed in a taxonomic group. The explanations for novelties and adaptations, however, differ in scope. While an adaptation can be explained in terms of frequencies of a trait in a population over time, novelties account for the mechanisms that explain the origination of new traits. In cases where changes in existing body plans can be considered 'novelties', there has been a tendency to explain novelties as 'adaptive'.

Müller and Wagner (1991) have rightly pointed out that the developmental origin of novelties is often lost in discussions focusing on quantitative change. It remains unclear, however, how some types of novelty differ from adaptations in the many typologies proposed. Consider, as an example, two different definitions of a Type III novelty. According to Müller's classification, a Type III novelty refers to "major variations of an existing body plan element through progressive individualization, with a new quality or functional capacity" (Müller 2021a, 73). Under Wagner's most recent account, a Type II novelty has roughly the same meaning as Müller's Type III novelty and is defined as characters already present in the ancestor species with some variational

characteristics (Wagner 2014). A more recent summary of such definitional variation was summarized by Müller (2021) under the following typology:

Former classification (Muller and Wagner 1991; Peterson and Müller 2013; Wagner 2014)	***Revised classification***	***Examples***
Type I	**Constituting novelty** Definition: "The different kinds of spherical and/or hollow, layered, elongated, or segmented shapes of first multicellular body assemblages" (Müller 2021a, 73)	The origin of multicellularity
Type II	**Discretizing novelty** Definition: "New characters added to existing body plans" (Müller 2021a, 73)	Skeletal elements, insect wing hearts, the firefly lantern.
Type III	**Individualizing novelty** Definition: "Uniquely specialized characters that developed from elements of existing body plans" (Müller 2021a, 73)	Beak shapes in Darwin finches, the narwhal tusk, nasal appendages in star-nosed moles.

Table 3.1: Former and revised typology of novelties based on Müller (2021)

Different concepts of novelties are also problematic due to the fuzziness of the concept's boundaries. As a result, some phenomena may be classified as a novelty under one definition, but not under another. Consider for example a definition that requires non-homology (that is, the absence of a morphological feature in a species' ancestral lineages). Under such a definition, a Type III novelty cannot be considered a novelty, since the presence of a modified body-plan is

recorded in ancestors, guaranteeing at least some degree of qualitative similarity between both stages. For example, the narwhal's tusk gradually evolved over long periods of time, and it is unclear whether it should be considered a novel feature in that it evolved from a pre-existing feature (a tooth that punctured the head). Therefore, the tusk is not *significantly* novel, and it would be problematic to consider it as such under a definition that requires non-homology.

Yet another problem related to evolutionary novelties is that there is phylogenetic evidence for the appearance of novel features, through the study of fossil records. For example, the appearance of turtle shells from the fusion of modified ribs (Hirasawa, Nagashima, and Kuratani 2013). The appearance of shells represents a leap, from the point of view of fossil evidence, from the turtle's soft-shelled ancestors (Cebra-Thomas et al. 2005). While hard turtle shells became a fixed characteristic in turtles indicating that they do provide selective advantage, the concept of adaptation is not sufficient to account for how they emerged in the first place. Rather, the variation-selection dyad can explain the modification of some existing feature, but not the mechanisms responsible for the phenomenon of origination. This is not to claim that novelties appear through an evolutionary discontinuous process, but rather, that there are specific evolutionary mechanisms (such as, for example, co-option mechanisms) that can explain how novelties emerge in the first place and are subsequently selected. This distinction motivates separate explanatory frameworks for novelties and adaptations.

While the theoretical discussion surrounding novelty focuses on definitional and typological questions, these matters rarely come into play when the concept is used in empirical practice. Scientists frequently refer to novelty more broadly using terms such as "phenotypic novelty" or "phenotypic innovation", especially when they seek to identify the underlying mechanisms that explain the evolutionary origin of novelties. For example, gene co-option describes the fact that

ancestral gene regulatory networks are deployed for a different function than an already existing one (Abouheif 2013; Chipman 2010; Olson and Nedelcu 2016; True and Carroll 2002). Gene co-option is often considered to be a kind of mechanisms that can provide an explanation of some kinds of novelties, such as eyespots of butterflies (Murugesan et al. 2022). This pragmatic use of novelty as referring to specific developmental mechanisms that bring about the phenomenon of origination can be observed in other sub-disciplines such as plant biology and entomology (Kapheim 2016; Bush et al. 2017; Liu and Moschou 2018; Müller 2021a; Wright 2017). Hence, instead of classifying traits as novel (and if so, which kind of novelty they are), the focus is in identifying which underlying processes and mechanisms can account for the phenomenon of origination of phenotypic characters over the course of evolutionary history.

3.2.2. Evo-devo, epistemic optimism, and the role of novelty in the EES

This pragmatic use of novelty is compatible with the role the concept plays in differentiating the EES and the SET agendas. In EES, novelty is considered a core concept in need of its own set of explanations (Pigliucci and Müller 2019; Müller 2021b). One of the central contributions of evo-devo to EES is precisely that of aiming to explain the origins of phenotypic novelty (Müller 2017; 2021b), which according to its proponents is not sufficiently explained by the interplay between genetic variation and selection posited by SET. EES proponents point to the insufficiency of SET's framework for explaining the origination of novelties based on the claim that SET has a track record of overlooking developmental processes (Laland et al. 2015; Laland et al. 2014). Under the EES perspective, giving due emphasis on developmental mechanisms is a necessary condition to a well-rounded explanation of the origin of novelty. Hence, by focusing on the interplay between development and evolution, EES' problem agenda is a *better* candidate to

provide explanatory breadth required to account for such processes because it can incorporate empirical findings of evo-devo. This is because one of the goals of EES is precisely that of integrating developmental processes into evolutionary explanations (Müller 2021b; 2017; Love and Lugar 2013). Indeed, one of the main criticisms directed at SET is that merging Mendelian inheritance and Darwinism into a common framework led to excessive gene-centrism and excessive focus on population genetics. Consequently, other important evolutionary processes were neglected, such as the evolutionary origin of complex phenotypic organizations (Müller 2021b; 2017). Instead, EES proponents such as Laland and Müller argue that processes such as the origin of novelties, developmental plasticity, niche construction and inclusive inheritance must be core tenets of a suitable explanatory framework that incorporates recent empirical findings in biological research. Under this view, while SET can successfully account for the *modification* of traits under the concept of adaptation, its explanatory breadth is insufficient to account for the *origination* of novel traits under the notion of novelty. Namely, integrating developmental explanations into evolutionary ones yields a *better* (as in more explanatory and predictive) picture of evolution, according to EES proponents.

EES is, to a certain extent, motivated by epistemic optimism[9] about its explanatory breadth. Proponents of an emendation of SET provide clear descriptions of its core concepts and outline which assumptions would benefit from such epistemic optimism (Baedke, Fábregas-Tejeda, and

[9] Psillos (2006) uses the term *epistemic optimism* to describe an epistemological thesis of scientific realism according to which science delivers both theoretical and observational truths about the world. In this context, I use *epistemic optimism* as a special case of Psillos' use. Here, *epistemic optimism* describes the stance according to which knowledge about developmental mechanisms that explain the phenomenon of origination of phenotypic characters yields *better* explanations of novelty. Such epistemic optimism can be seen in claims made to justify the need and pertinence of EES (for examples see Müller 2017; Laland et al. 2014).

Vergara-Silva 2020). For example, Laland et. al (2015) list the explanatory content of EES as encompassing constructive development and reciprocal causation, seeking to "include processes that generate *novel variation*, *bias selection* and *contribute to inheritance*" (emphasis in the original, Laland et al. 2015, 7). The epistemic optimism of EES proponents can therefore be summarized under the following claim: if due attention is given to traditionally neglected concepts in SET, then an extension is in fact, justified. Such extension should be put in place as an amendment that ought to be taken seriously as a prosperous research program that will eventually come to be integrated within SET. Underlying such epistemic optimism is a realist claim: the success of EES is about its ability to deliver true claims about the mechanisms that drive evolution, but that fall outside of the purview of SET. This chapter focuses on one dimension of such integration: the concept of evolutionary novelty.

There are good reasons to adopt such epistemic optimism about evolutionary novelty considering recent empirical developments[10]. Buskell (2019) also diagnoses EES proponents as optimists insofar as they "see new tools, models, and concepts as expanding the core of evolutionary theory through methodological and conceptual revision" (Buskell 2019, 268). In fact, it is crucial to examine biologists' commitment to novelty when they adopt such optimistic viewpoint. For example, research on gene co-option and stress-induced innovation shows that there are specific mechanisms responsible for functional changes that lead to innovations (Murugesan et al. 2022; Love and Wagner 2022; Chipman 2010; Badyaev 2005). Identifying such

[10] Other key contributions in evo-devo also support epistemic optimism about EES. Examples include constructive development (Müller 2017), epigenetic inheritance (Hemminger 2021), reciprocal causation (Buskell 2019; Schwab, Casasa, and Moczek 2019), developmental bias (Brigandt 2020; Parsons et al. 2019) and evolvability (Sterelny 2007). While a comprehensive account of the legitimacy of EES should discuss these notions at length, this chapter focuses exclusively on the problem of the evolutionary origin of novelty.

mechanisms is a necessary condition for the strengthening of the concept of novelty and transcends the definitional disputes. The idea is that, in retrospect, once the right mechanisms are discovered, it will become clear what the term 'novelty' had been referring to, clarifying what it seeks to explain. Hence, when the concept of novelty is used, there is optimism that uncovering a set of specific mechanisms will *successfully* account for the evolutionary origin of phenotypic characters. In fact, there would be no motivation to study the phenomenon of novelty separately from adaptations if biologists were not optimistic that some mechanisms will be uncovered.

The centrality of evo-devo to explanations of the origins of novelty supports, through empirical results, the claim that novelty deserves its own set of explanations that integrate evolution and development into a coherent framework. The concept of novelty is important to the EES since adequate explanations of novelty seek to integrate evolution and development[11]. Therefore, novelty is a notion that exemplifies epistemic optimism about EES insofar as explaining novelty is one of the goals that sets EES and SET apart. Take for example, another core mechanism that helps account for novelty: developmental plasticity. According to Laland et. al. (2015), a traditional interpretation of developmental plasticity explains phenotypic variation in terms of adaptation to variable environments whereby plasticity is a "genetically specified feature of individuals (i.e., a reaction norm) that can evolve under selection and drift" (Laland et al. 2015, 5). Alternatively, the EES contends that the view according to which the evolution of phenotypic plasticity is modulated by genetic variation cannot account for the origins of phenotypic novelty. In this context, phenotypic plasticity can be defined as "the ability of individual genotypes to

[11] It is important to note that while SET is a theory, EES does not claim to be a new theory that should replace SET. Rather, EES is an amendment that can be deployed alongside the tenets of SET to stimulate different research programs in evolutionary biology.

produce different phenotypes when exposed to different environmental conditions" (Pigliucci, Murren, and Schlichting 2006, 2363). Even before the EES discussion began, the work of West-Eberhard (2003) already developed a similar view with a rigorous study of phenotypic plasticity. Rather, the EES interpretation is interested in understanding "how plasticity contributes to the origin of functional variation" as well as how plasticity can "limit or enhance evolvability, and initiate evolutionary responses" (Laland et al. 2015, 5). Under EES, therefore, plasticity is a key mechanism that, if understood correctly and sufficiently, can partially or fully explain the evolution of phenotypic novelty across taxa. In the following section, I delve deeper into how the epistemic goal of novelty is described in the literature. This exposition is a key step toward showing that there is a mismatch between how novelty is conceptualized in the philosophical literature and how it is used in biological practice. Clarifying this mismatch is also important to show in what ways the current use of the concept in biology presupposes realism about novelties.

3.3. Problem agendas and the epistemic goal of the concept of novelty

Despite the polysemic nature of the concept of novelty, Brigandt's notion of an epistemic goal (2010; 2012) provides a fruitful framework that simultaneously captures the concept's slippery nature and defends some degree of stability: namely the fact that even though the meaning and inferential role of a concept might change over time, its epistemic goal remains stable. This stable epistemic goal explains how a concept can rationally vary over time. In this section I outline Brigandt's (2012) account of rational conceptual variation and summarize Brigandt and Love's (2010; 2012) account of the epistemic goal of the concept of novelty. I also explain why the epistemic goal they identify is too weak for how the concept is meant to be used in EES.

3.3.1. The epistemic goal of a variational concept

While novelty can take disparate meanings under different definitions of the concept, it nonetheless captures a common goal of explaining the emergence or the appearance of something *significantly* novel in the history of life. In other words, despite confusion and lack of agreement over a unified definition of novelty, scientists keep using the term in a pragmatic way and seem to converge on its general goal. Brigandt's account of variational concepts in biology provides an explanation of why this might be the case. Brigandt (2010; 2012) shows that while reference (what the concept refers to, such as underlying processes, material entities or physical properties) and inferential role (the way in which the term is used, including a concept's definition which may or may not change over time) are vital components of a scientific concept, they are not sufficient to explain a concept's role within a scientific community. A third vital component is "the epistemic goal pursued by the concept's use" (Brigandt 2012). Concepts whose reference and inferential roles change over time maintain a stable usage because they converge on an overarching goal. Hence, the notion of an epistemic goal is introduced to provide a rational explanation for the variation of concepts in biology. In other words, Brigandt's framework allows for conceptual change while still showing how, despite differences in meaning and reference, a concept is used in similar ways by biologists. Such cohesion accounts for the rational change of a concept's meaning and is ensured by the stability of a concept's epistemic goal over time.

Consider the example discussed by Brigandt (2010, 2012): the shift from the classical concept of gene to the concept of gene in molecular biology. While the concept's inferential role and meaning have changed over time, its epistemic goal explains the concept's stability. The classical gene concept aimed at predicting patterns of inheritance. With the successes of molecular biology, the molecular gene concept aimed at explaining how genes bring about their molecular

products. In both cases, while the meaning of the concept of gene changed as well as its inferential role, a common epistemic goal guaranteed the stability of the concept, namely, the general goal of explaining how DNA codes for different molecular substances (such as RNA and polypeptides) (Brigandt 2010b). The epistemic goal of the concept of gene captures the two intermediate goals of the classical and the molecular gene concept respectively, accounting for rational variation in the concept's meaning and inferential role.

Similarly, when establishing a stable epistemic goal for the concept of novelty, the concept's definitional variation need not impede scientific progress and paralyze enquiry. The lack of agreement and the under-specified meaning of novelty is no reason to stop using the concept (Brigandt and Love 2012). On the contrary, despite this lack of agreement on a unified definition, one reason for its widespread use is to distinguish explanations of adaptive traits from those of novelties. For example, when scientists refer to a phenomenon as a 'novelty', they often use this term in a general sense, rather than specifying which definition of novelty they take to be the best. While the concept's reference and inferential role may change over time and across different research areas, the concept's epistemic goal has remained stable. This is likely because despite disagreements over what does or does not count as a novelty, there is a general underlying intuition that in some cases, it is better to use the term 'novelty' than 'adaptation' depending on the kind of underlying mechanisms needed to explain the phenomenon in question.

3.3.2. The novelty problem agenda:

Brigandt and Love (2012) suggest the epistemic goal of the concept of novelty is to structure problem agendas and set problem spaces. A problem agenda can be defined as "a "list" of interrelated questions (both empirical and conceptual) that are united by some connection to natural phenomena" (Love 2008, 877). A problem agenda therefore consists of a set of intertwined

problems and the relations among them. Crucial to a problem agenda are also criteria of explanatory adequacy that provide structure and account for the kinds of explanations and the standards they need to meet in order to answer the research questions being posed. Criteria of explanatory adequacy are tools for assessing how different sources of evidence can be integrated in support of potential solutions to the problems within a given agenda.

In the case of evolutionary novelties, the overarching problem is an explanatory one, namely: how to explain the evolutionary origin of novelty (Brigandt 2012, 81). In the explanation of novelty, Brigandt (2012) outlines two steps that need to be met for an adequate explanation of the evolutionary origin of novelty. First, an account of novelty should lay out and explain the structural changes that lead up to a novelty and how a novelty is qualitatively different from the previous structures. Second, a causal-mechanistic account is needed to explain morphological transformations (Brigandt 2012, 81).

Consequently, explaining the origin of novelty is a complex problem composed of a set of interrelated questions. The complexity of the problem means that biologists need to construct a problem agenda that requires integrating different research fields and disciplines (paleontology, developmental biology, morphology and so on) with different kinds of empirical data to tackle the multiple research questions. Three dimensions of a problem agenda are crucial: history, heterogeneity, and hierarchy. First, there is a historical controversy: on the one hand, 20th century neo-Darwinian thought claims that population genetics is explanatorily sufficient to account for the origination of novelties. On the other, 21st century evo-devo claims that any framework aiming to explain the phenomenon of origination of novelties must include specific developmental processes. A second characteristic of a problem agenda is the heterogeneity of questions, ranging from empirical questions (e.g., pinpointing what regulatory genes control the formation of a novel

morphological feature); theoretical questions (e.g., how to adequately represent developmental processes through mathematical models); pattern questions (e.g., what common features explain the origination of novelties in each case) and process questions (e.g., how do specific processes contribute to difference in shape or body parts). The third aspect of a problem agenda is hierarchy. Hierarchy refers to the way in which different components of a problem agenda stand in systematic relations, which questions to pursue first and the degree of abstraction and generalization of explanations within the hierarchy (Brigandt and Love 2012, 424).

Insofar as the epistemic goal of novelty is to structure a problem agenda whose aim is to explain the evolutionary origin of novelty, Brigandt and Love (2012) argue that there are other criteria that are particular to this specific problem agenda, namely:

(i) To address both morphology (form) and function.

(ii) To be sufficiently abstract and general.

(iii) To exhibit sufficient complexity and balance.

In sum, under Brigandt and Love's account, the epistemic goal of novelty is to structure problem agendas according to a set of criteria of explanatory adequacy. This broad epistemic goal ensures the stability of problem agendas despite conceptual or theory change.

3.3.3. The limits of a broad epistemic goal

Under Brigandt's account of conceptual variation, the stability of the term 'novelty' is due to the stability of its epistemic goal which is to establish criteria of explanatory adequacy by setting research agendas and structuring problem spaces. Because the epistemic goal of the concept of novelty has remained stable over time, changes in definitions and inferential role of the concept can be rationally explained. The problem, however, is that Brigandt and Love's account does not commit to the term 'novelty' obtaining a stable status. This is because the epistemic goal of setting

problem agendas remains compatible with the term 'novelty' changing meaning, reference, and inferential role *indefinitely* as the theories and the models change. In fact, they take this change to be rationally justified as long as the epistemic goal remains stable. As Brigandt argues:

> given a concept's stable epistemic goal, a change in its inferential role (e.g., a change in a term's definition) is rational provided that the revised inferential role (the inferences and explanations supported by the revised concept) meets the epistemic goal (the inferences and explanations aimed at) to a higher degree than the previous inferential role. A change in reference is likewise epistemically warranted if it results from a rational change in inferential role" (Brigandt 2010 37).

In the case of novelty, however, the concept's epistemic goal of structuring problem agendas only partially accounts for the role the concept is meant to play in EES. Namely, in EES the concept of novelty plays a much stronger and stable role: biologists using the concept aim at identifying the definite set of mechanisms that account for the origin of phenotypic characters (including new traits, functions, or morphological features). This goal is specific insofar as it encompasses a definite set of mechanisms. I argue that it is by virtue of this specificity that it is possible to employ the concept differently in SET and EES, thus motivating and legitimizing calls for an emendation of SET. The stronger epistemic goal of novelty can therefore be reformulated as a commitment *to discover the mind-independent mechanisms that explain the origination of phenotypic characters*. This stronger epistemic goal presupposes realism about novelty, i.e., that there *is* a definite set of mind-independent mechanisms that give rise to novelties. Realism about novelty is, as I contend, is a necessary condition to account for the concept's pragmatic use in the life sciences. Realism about novelties entails that the term 'evolutionary novelty' will eventually come to refer to the phenotypic changes that the relevant set of definite mechanisms bring about. Empirically, current work on gene co-option (discussed in Section 3.5) provides evidence that biologists are starting to converge on a partial set of the correct mechanisms that explain the

evolutionary origin of novelty. Theoretically, a more specific epistemic goal that focuses on identifying a set of mechanisms is compatible with the kind of mechanistic explanations evo-devo provides (Baedke 2020). Since evo-devo is a core discipline motivating EES, there are good reasons to strengthen the epistemic goal of novelty.

Brigandt's framework (2010) can be useful in several cases of imprecise concepts in biology. In fact, the stronger epistemic goal I propose is still compatible with that of structuring research agendas. For many biological concepts such as lineage, adaptation and species, imprecision has been seen as positive on the grounds that it facilitates integration in science and sets a problem agenda common to different fields of inquiry (Neto 2020). My argument does not take issue with this specific claim about conceptual imprecision. Imprecision is helpful in the case of novelty research as a temporary stage, since when the concept is used by biologists the goal is to reach referential stability. Rather, I am interested in showing why the epistemic goal of novelty is too broad to account for how the concept is used *in practice*. Moreover, there are good reasons to believe that there is a gap between epistemic optimism about novelty in EES and how the concept's epistemic goal is described by Brigandt and Love. If this is true, there are also good reasons to believe that a stronger epistemic goal for novelty is already in place. This goal is therefore conditional upon realism about novelty: i.e., the view according to which the term 'novelty' refers to the phenotypic changes brought about by a relevant set of definite mechanisms.

3.4. A realist argument supporting the stability of novelty: the case for a stronger epistemic goal

3.4.1. Realism about novelty

So far, I have shown that the epistemic goal of novelty proposed by Brigandt and Love only partially accounts for the role of the concept in the EES. I have argued that a stronger epistemic goal for the concept might already be in place, namely, to identify the relevant set of definite mechanisms that account for the origin of phenotypic characters. This claim is reliant upon a realist commitment with regards to novelty, i.e., that the goal of the concept of novelty is, ultimately, to focus a research agenda on identifying a set of mind-independent mechanisms that sufficiently explain the origin of phenotypic characters. Additionally, when scientists make use of the concept they do so with a specific target of explanation in mind and wish to provide true claims about an existing phenomenon. While Brigandt (2012, 80) notes that the primary function of novelty is to "point to a phenomenon in need of explanation", the phenomena themselves that need to be explained are not specified (even though the criteria of explanatory adequacy are laid out). As I will argue in this section, a commitment to realism about novelties is necessary for the concept of novelty to support epistemic optimism surrounding the concept's role in EES. The concept of novelty does *more* than establish a problem agenda. In fact, the concept of novelty as it is used in practice has the epistemic goal of finding out the *true nature* of mechanisms that give rise to novelties. An assumption that such mechanisms exist and that there is a definite set of them is therefore essential, even if this definite set has not yet been uncovered. So, what, exactly, would realism about novelty imply?

Broadly speaking, scientific realism is a view committed to two claims (Psillos 1999; Egg 2017):

1. That our best scientific theories are true.
2. That the entities that are the object of study of such theories are real, that they exist.

Realism implies that the phenomena that theories track and seek to explain are real, even if the theories that describe such phenomena change over time and are replaced by better explanations. While scholarship on scientific realism mainly focuses on well-established physical theories that can be analyzed in retrospect, my argument is prospective: it highlights conditions that are necessary for the concept of novelty to play the central role it is meant to play in EES. Furthermore, the realist commitment I advance is a commitment to the phenomenon of novelty, and not to a body of theories.

Psillos (2006) describes three theses to which the realist is committed. First, there is a metaphysical thesis according to which the world has a definite and mind-independent structure (2006, 688). Second, the semantic thesis is that theories should be taken at face value, since they provide true descriptions of the observable and the unobservable. Namely, the theoretical terms used in theories have factual reference (Ibid). Third, the epistemological thesis is that our best available theories are well confirmed and approximately true of the world. Consequently, the entities that are posited by our best theories are very similar to those entities that exist in the world (Ibid). While scientific realism has been debated intensely, I will not attempt a defence of realism in general here and focus on the specific case of realism about 'novelty'.

Realism about evolutionary novelty broadly means a commitment to realism about the mind-independent mechanisms or set of mechanisms that explain how novel features emerge in evolution. For example, novel forms of butterfly eye-wing spots (Murugesan et al. 2022) or the evolution of multicellularity in green algae (Olson and Nedelcu 2016) can be explained in terms of the underlying mechanism of gene co-option. Following Psillos' (2006) description of realist commitments, realism about novelties implies a commitment to three theses:

i. Metaphysical realism about evolutionary novelty: there exists a definite and relatively specific set of mind-independent mechanisms that sufficiently explain the evolutionary origin of novelty.

ii. Semantic realism about evolutionary novelty: the term 'novelty' refers to the resulting phenomenon of such mind-independent mechanisms.

iii. Epistemological realism about novelty: the goal of research into the evolutionary origin of novelty is to provide *true descriptions* of the relevant mechanisms. Successful research in evolutionary biology provides reasonable grounds for hope that such true descriptions will be found.

Note that with regards to (iii), even if the concept has not yet been stabilized, the aim is to stabilize it by identifying a relevant set of mechanisms. While gene co-option is not the only mechanism, it is an example that points to the kind of research being done with the goal of explaining the evolutionary origin of novelty. Being committed to (i), (ii) and (iii) provides the necessary conditions for the concept of novelty to play the strong role it plays in EES.

3.4.2. Why realism about novelty is relevant for greater conceptual clarity of core EES tenets

Recall that evo-devo is the central discipline from which empirical evidence directly supports the claims calling for the need of EES (Müller 2021). A central goal of evo-devo is precisely to explain the emergence of phenotypic novelty (Müller 2021a). Namely, EES proponents argue that there is empirical evidence supporting the fact that there are mechanisms responsible for the origination of novel traits. There are at least two reasons why realism about evolutionary novelty is necessary for the concept to warrant the epistemic optimism of EES proponents.

First, realism about evolutionary novelty is necessary for researchers in fields adjacent to evo-devo if there is any hope of delimiting the concept and thence, distinguishing the EES research program from SET. Clearly establishing which sets of mechanisms should be studied and understood to explain novelty is necessary to set research agendas apart and set the appropriate criteria of explanatory adequacy. For example, the study of trait variations in population genetics is the foundation of the study of adaptation. Such studies are within the scope of SET. However, in evo-devo, it is the study of a given set of developmental mechanisms that is meant to provide for the explanation of the evolutionary origin of novelty. As will be shown in the following section, gene co-option is an example of such mechanisms (Love and Wagner 2022).

Second, realism about novelty is necessary for EES to claim any epistemic advantage over SET, where the epistemic advantage is to explain different phenomena that were not sufficiently considered or incorporated into evolutionary explanations under SET. For example, while SET successfully explains the modification of existing traits through the concept of 'adaptation', it might not give due attention to how these traits originate in the first place, which motivates the use of the term 'novelty'. If there are no specific mechanisms to be identified as part of the novelty problem, then EES would provide no real epistemic advantage over SET, or at least this advantage would not be clear enough to move beyond the current state of the debate. This criticism that EES entails no real extension or expansion has been put forth in the literature. Recall that one argument by EES skeptics is that adaptive variation sufficiently accounts for the emergence of novel traits (Charlesworth, Barton, and Charlesworth 2017). Another argument is that EES does not entail an extension nor a synthesis when compared to SET (dos Reis and Araújo 2020).

There are at least two ways in which realism contributes to the ability of EES to address these objections.

(i) Realism about novelty allows the debate to move beyond definitional questions. A realist commitment to the phenomenon of novelty means that definitional questions can be abandoned. Conceptual analysis is unlikely to yield consensus on the question of novelty. Rather, empirical work specifically dedicated to identifying the mechanisms responsible for the origination of phenotypic characters is more likely to show that novelty deserves its own set of explanations.

(ii) Realism about novelties clarifies the mistaken conflation of 'adaptation' and 'evolutionary novelties'. If indeed such mechanisms are discoverable (which empirical work on co-option shows they are, as I will discuss in Section 3.5), then it becomes clear that *different* mechanisms explain novelties and adaptations. Even if adaptations and novelty are related and novelties eventually become adaptations, biologists seek and investigate different mechanisms, through different methods, to explain the two notions.

3.5.Co-option mechanisms

So far, I have argued that the epistemic goal of novelty requires a commitment to a set of definite mind-independent mechanisms that provide suitable explanations for the origin of phenotypic characters. One of the motivations for advancing a stronger epistemic goal for novelty is that a shift can be observed in how biologists use the concept in current empirical and theoretical research. This is a descriptive claim: because in practice novelty has been used with the clear aim of identifying the relevant mechanisms, then a stronger epistemic goal for the concept might already be currently in use. There are several candidate mechanisms that can explain the origin of such characters. At the genetic level, good candidates include gene duplication and changes in gene regulation (Wray 2003). At the cell or tissue level, the process of cell differentiation could

also be a candidate (Leys and Hejnol 2021; Wagner, Erkenbrack, and Love 2019; Arendt et al. 2016). Even though all the relevant mechanisms might not have been identified yet, research seeking to understand the evolutionary origin of novelty does so with the hope that one day, they will. Recall that the argument I advance is prospective (unlike many realist arguments about past or current physical theories). Hence, even though all mechanisms have not yet been identified, there are current empirical examples that already point towards mechanisms that partially explain the evolutionary origin of novelty. In this section I discuss one example of such mind-independent mechanisms that feature in the epistemic goal of evolutionary novelty: gene co-option. I aim to show that gene co-option gives empirical grounds for epistemic optimism about EES. Research on co-option, for example, not only aims at uncovering *how* such mechanisms are deployed, but also how they *explain* the origination of novel traits.

3.5.1. Co-option and the origin of multicellularity

Consider, for example, what Müller and Wagner would call a Type I novelty, referring to the origins of multicellularity. A very strong candidate mechanism that explains this type of innovation is the co-option of existing genes for new functions (Olson and Nedelcu 2016; Grosberg and Strathmann 2007). Broadly, the term 'co-option' refers to mechanisms of deployment of existing ancestral genes for a novel, unexpected function. By changing their patterns of regulation as a response to environmental stressors, genes can be co-opted to generate novel developmental or morphological features (True and Carroll 2002). For example, co-option is central to the evolution of genes responsible for the differentiation of somatic cells in multicellular lineages (König and Nedelcu 2020). Moreover, multicellularity evolved independently at least twenty-five times in both prokaryotes and eukaryotes, which suggests that multicellularity "is a common

adaptation in response to various ecological pressures such as predation, nutrient limitation, or changing environments" (Olson and Nedelcu 2016). Explanations for the origin of multicellularity make use of the notion of adaptation in a different explanatory capacity than the concept of novelty. Adaptation is a key concept to explain how multicellularity became a constant evolving feature in eukaryotes and prokaryotes but is not sufficient to explain how this happened in the first place. Labelling the origin of multicellularity as a novelty, as Brigandt and Love argue, sets apart a problem agenda of its own, interested in a different kind of problem than the adaptation agenda. In practice, novelty does more than structuring a problem agenda: it is used with the aim of providing a description of the mind-independent mechanisms (co-option being an example of one such mechanisms) that explain the evolutionary origin of a novel trait (in this case, multicellularity).

3.5.2. Co-option and phenotypic plasticity

Another example where co-option mechanisms are used to explain the emergence of a novelty is in research on phenotypic plasticity, defined as: "a property of individual genotypes to produce different phenotypes when exposed to different environmental conditions" (Pigliucci, Murren, and Schlichting 2006, 2363). Butterfly eyespots are highly plastic, meaning that under different temperatures, they may exhibit more or less conspicuous shapes. The diversity of butterfly wing eyespots is a case of plasticity that has fascinated biologists for a long time. Eyespots in butterfly wings are ecologically significant in that they help avoid predators and are a form of mate-signalling (Beldade and Monteiro 2021). For example, Brakefield et al. (1996) have shown that the *Distallis* gene was likely co-opted to be involved in the formation of butterfly eyespots. Moreover, wing-patterning genes are associated with plasticity whereby genes were co-opted to

regulate the seasonal phenotypic plasticity of the wing (van der Burg et al. 2020). Eyespot patterns are also referred to as a novelty since they emerge from the same underlying ancient gene network through co-option mechanisms. The link between co-option and plasticity is important because plasticity is one of the central notions of EES. Hence, identifying and studying the exact mechanism responsible for some cases of plasticity provides empirical evidence that the epistemic optimism of EES is warranted.

3.5.3. Co-option and the origin of a novel function from an existing trait: the case of stress-induction

Models of stress-induced evolution emphasize the possibility of a creative role for stress in evolution (Love and Wagner 2022). Under this view, stress-response mechanisms are co-opted and permanently stabilized "to control the development of novel features" (Ibid, 2). Stress-induced models that assess co-option mechanisms are concerned with the specific mechanisms responsible for the origination of novel traits. In such explanations, co-option mechanisms are suitable candidates to explain *how* novel features emerge. Whether such features will be selected for and become adaptations requires a different explanatory target that seeks to account for modification, instead of origination of traits or functions. The concept of adaptation is, in the former case, the best candidate to account for processes of modification and inheritance of an existing trait. It does not, however, explain the mechanisms responsible for its origination.

Consider, as an example, the evolution of the eye. Often described as a novelty, the evolution of the eye has long puzzled evolutionary biologists. The most common explanation for the evolution of the eye is through the action of natural selection on morphology. This kind of explanation, however, appears to be incomplete insofar as it leaves important features of the eye

unexplained (Swafford and Oakley 2019). Light-induced stress is therefore an additional critical driver of eye evolution (Ibid). Stress reactions are likely to account for how the lens crystallins in animal eyes evolved, a well-studied case of co-option (True and Carroll 2002). Crystallins (soluble proteins) in the lens function to refract light, contributing to the formation of a focused image on the retina. As a stress response, it is likely that "there was an ancient event in which one of these proteins was co-opted into a refractive role in the lens in the common ancestor of vertebrates" (True and Carroll 2002, 58).

The concept of novelty appears to be appropriate to account for the evolution of the eye, i.e., when the goal is to explain how co-option mechanisms are a key mechanism accounting for the phenomenon of origination. Hence, once the target of explanation is specified, it becomes clearer that the concept of novelty fulfills a different role than the concept of adaptation, thus justifying its use in the literature as a concept that aims at explaining mechanisms that are of a different nature than those explained by the notion of adaptation.

3.6.Challenges to the realist argument

While research on gene co-option seems like a promising example of the relevant mechanisms that explain the evolutionary origin of novelty, there is a risk that singling out specific mechanisms, especially genetic ones, implies a commitment to a reductionist view of novelty under which a set of complex processes and interactions would, at least in principle, be *reducible to* a specific set of definite mechanisms, mostly genetic. In fact, one may argue that a realist argument about novelty would undermine the pluralistic nature of the concept. Under this objection, narrowing the epistemic goal would not be compatible with the interdisciplinary integration that characterizes evo-devo, whose strength is to draw from different fields such as development, evolution,

paleontology, molecular and systematics biology (Buskell 2020). Such an objection would be compatible with the epistemic goal advanced by Brigandt and Love (2010; 2012) and consistent with defenses of biological pluralism (Mitchell 2003; Neto 2020; Brigandt 2013; 2010a; Mitchell and Dietrich 2006; Dupré 2018).

While co-option is the main example singled out in this chapter, there are other mechanisms that may account and explain the evolutionary origin of novelty that involve more complex and reciprocal interactions between developmental systems and environmental factors. Indeed, such mechanisms are not limited to the genetic level. A commitment to realism about novelty does not entail a commitment to genetic reductionism or some version of monism. First, the mechanisms one is committed to are not exclusively genetic ones. For example, Newman (2022) argues that dynamical patterning modules involve the complex associations of gene products and the physical effects they can mobilize in the context of cell aggregates, being another candidate mechanism for novelty. The definitions of novelty outlined in Section 3.2 also point towards the different levels at which mechanisms are identified to explain the evolutionary origin of phenotypic traits. For example, Müller and Wagner's (1991) definition focuses on the morphological level, while Peterson and Müller's (2013) typology includes definitions at the cellular level. Second, identifying the relevant set of mechanisms can be constructive for other disciplines that also address the evolutionary origin of novelty. Other disciplines such as paleontology, phylogeny and morphology that also constitute the novelty problem agenda also rely on realism about mechanisms as much as evo-devo does. In fact, the best hope of integrative pluralism for such disciplines into a cohesive explanation of novelty is if there is some set of definite mechanisms upon which different explanations aim to converge. The realist commitment implies that there is an explanatory

connection between the concept of novelty and the real and existing mechanisms that explain novel traits.

Another challenge that could be raised against realism about novelty is the "pessimistic induction" challenge (Psillos 1996; Laudan 1984). According to this cluster of arguments, there are historical examples where specific mind-independent mechanisms were thought to be the best candidate explanation for a given phenomenon, and they were proven to be wrong. Consider Hesse's (1976) 'no privilege' principle, i.e., the principle stating that current theories are no less immune to radical change than past theories. In biology, one example is the different explanations of heredity over time. Consider, for example, the mechanisms that explain adaptation under Lamarckism that were thereafter replaced by Darwin's explanation of descent with modification. Lamarck's transformism (1809) via inheritance of acquired characters, for example, was thought to explain how organisms adapted to their environments over the course of their lives from a comparative study of invertebrates. Only later was this claim refuted acknowledging genetic inheritance as the principal form of inheritance (Sloan 2019). With new empirical evidence, Lamarckism was replaced by Darwinian inheritance. Transformism was no longer taken to be a *true* description since it did not correspond to existing, mind-independent mechanisms even though they were thought to exist at some point. According to this line of argument, even though mechanisms such as gene co-option are shown to be relevant to novelty, it might not still be the principal mechanism and other mechanisms might be better candidates instead.

It is common that assumptions and models change over time and are replaced by new ones. However, even when their assumptions and models change, biologists still work under the hope that there is a stable reference to their central terms. When investigating a phenomenon such as 'evolutionary novelty' in the EES context, biologists are, in practice, working under the

assumption that there is a set of mechanisms that explain the phenomenon in question. In fact, they *should* be working under such assumption if they wish to convincingly differentiate from SET. In other words, the concept of novelty as it is used in evo-devo presupposes a hope that stable mechanisms will be found. While a commitment to the mechanisms' existence *per se* is not needed, the realist argument still holds with a commitment to the hope that these mechanisms will be uncovered. This is aligned with the role of the concept of novelty plays in structuring inquiry and setting explanatory targets in EES. Whether this hope may or may not be fulfilled does not alter the fact that there is still a legitimate and concrete goal in using the concept of novelty. The goal being to uncover the mechanisms that give rise to phenotypic characters. Whether or not mechanisms such as co-option will no longer be the principal mechanism or even come to be replaced or by other suitable mechanisms to explain the origination of phenotypic characters does not hinder the realist commitment discussed here and is something that only future empirical research will define.

3.7. Concluding remarks

In this chapter, I have drawn on Brigandt's notion of a concept's epistemic goal to argue for realism about the phenomenon of novelty. I have explained why the epistemic goal proposed by Brigandt and Love (2010; 2012) may be too broad to account for the concept's usage in EES. I have proposed a stronger epistemic goal for the concept of novelty that is committed to realism about novelty. Namely, the stronger epistemic goal I propose for novelty is to discover the mind-independent mechanisms that explain the origination of phenotypic characters. I have shown why, in light of the concept's role in EES, a stronger epistemic goal is fruitful for the debate surrounding SET and EES to move forward. While scientific realism is a commonly discussed view in the

literature in philosophy of science, applying realist arguments to the case of evolutionary novelty is a unique argument that has not yet been put forth in the relevant literature.

Here I based my argument on how the concept of novelty is being used by biologists in practice, especially considering the role of novelty in motivating the need for an emendation of SET. Namely, biologists do not seek to classify different types of novelties, but rather, when using the concept, they are referring to mechanisms that bring about the origination of phenotypic traits. One example of a mechanism that partially explains the evolutionary origin of novelty is gene co-option. My account is still compatible with Brigandt and Love's treatment of the question, although it provides additional specifications (through a realist commitment) that ensures greater stability for the concept of novelty. This commitment is compatible with the centrality of the concept of novelty in the EES. More specifically, I aimed to show that strengthening the epistemic goal of novelty can be a valuable tool for the debate between EES critics and its proponents to move forward, insofar as it supports the epistemic optimism surrounding EES and helps demarcate different sets of explanations.

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4. THE EPISTEMIC HARMS OF DIRECT-TO-CONSUMER GENETIC TESTS

4.1.Introduction

Sigrid E. Johnson, an adopted half-Black, half-Italian woman, took a DNA ancestry test when she was 62; to her surprise, the results showed that she only had around 2.978% African ancestry (Padawer 2018). Johnson had been confident she was Black, had identified as a Black person and was a member of African American communities that also saw her as being Black; following these results, she recalls being deeply unsettled, and questioning her identity. Who was she? She had never imagined that she might not be Black[12]. A second test taken three years later revealed a much higher percentage of African ancestry, with around 10 percent DNA from Benin/Togo, 9 percent from Mali, and 8 percent from Ivory Coast/Ghana. Overnight, Johnson's results were different because the company that did the test changed its algorithm. Discrepant results are a frequent experience in direct-to-consumer (DTC) genetic testing, but one may ask: how can results be so variable, since Johnson's underlying DNA is the same since birth? Consumers seeking health data have experienced similar frustration at the variation in their results and risk factors shown in tests (Peikoff 2013). For example, consumers have reported being classified as "below risk" and at "increased risk" for the same conditions by different testing companies (Kutz 2010).

In this chapter, I show that there are two types of harms related to the mass-marketing and consumption of DTC genetic tests. First, there are general harms that can, in principle, be mitigated by appropriately tackling problems of bias, reproducibility, and accuracy. However, even once

[12] A direct quote from Johnson is included in the original story: "Two percent African?! I thought, Well, who am I then? I knew that at my age, I shouldn't really care what people think, but I was embarrassed to show it to anyone besides my son and my cousin, who's like a sister to me. I was afraid people would think I was a fraud. I was so disappointed, and in my heart of hearts, I didn't believe it, because how could I not be black? I'd lived black. I was black." (Ibid)

these problems are dealt with, a second kind of harm persists that is epistemic in nature. Grounding my argument in the notion of epistemic trust between laypersons and experts (Baier 1994; Grasswick 2018; Hardwig 1991; Hawley 2017; Grasswick 2010), I argue that there are two epistemic harms consumers may face when taking DTC genetic tests. In the first case, these tests deprive them of their testimonial authority on matters relating to their own identity; in other words, consumers' testimony about their identity is undermined. Second, such tests also undermine epistemic agency, since in most cases consumers lack the interpretive resources and technical knowledge to resist the reduction of race and ethnicity to genetics.

This chapter is structured as follows: In Section 4.2, I discuss some background on the emergence of DTC genetic tests. In Section 4.3, I discuss problems of bias, accuracy, and reproducibility. In Section 4.4, I argue that such problems result in general harms to consumers, and I discuss each harm separately. In Section 4.5, I argue that even if it is, at least in principle, possible to mitigate these general harms, there is a more concealed type of harm that is epistemic in nature. I explain why trust is paramount to epistemically just relations. In Section 4.6, I discuss in more detail two kinds of epistemic harm. In Section 4.7, I outline some harm mitigation strategies, and I present my concluding remarks in section 8.

4.2.Background

In 2003, the Human Genome Project achieved the first complete draft of the full human genome. This turning point in the history of biology was the dawn of a new era for genetic data and information. While genetic analysis is often a joint scientific endeavour between scientists, academia, and research institutions, private companies were quick to create ways of commodifying genetic information. This was largely due to progress in other areas such as machine learning and the rapid growth of data-intensive science. A key factor in establishing the credibility of data-

driven science is to determine whether patterns in data are meaningful, rather than assumed or spurious correlations (Leonelli 2020). This general criterion should be taken into consideration in any scientific endeavour that makes use of big data and data processing techniques. As sequencing technologies rely on vast amounts of data, and are aimed at finding meaningful patterns, they should be subject to significant levels of scrutiny and critical evaluation.

Mass marketing of genetic products was motivated by the promise that gene-disease associations and Genome Wide Association Studies (GWAS) could accurately construct an individual's risk profile for developing certain diseases based on their genetic constitution. Genotyping technologies usually share a common underlying principle: to extrapolate individual genome information by comparison to a reference database. Once DNA is extracted from human samples (such as saliva), repeated measurements of short sections of DNA are taken and compared against a database that represents a reference genome (Dudley and Karczewski 2013). The goal is to detect SNPs (Single Nucleotide Polymorphisms) and to establish a comparison with the reference database. Thenceforth, it is possible to compare variation in the sample genome against information from that database, thus allowing inferences to be made. The resulting percentages indicate the likelihood of genetic variations that are frequently correlated with the onset of a particular disease. This technique can be used to obtain information on two domains. On the one hand, it is possible to check for genes that are normally correlated with a higher chance of developing a certain disease, a risk that is normally assessed through health reports. While there was initial controversy about the delivery of health reports when they were first being marketed, the FDA has recently authorized 23andMe to sell them. For example, the 23andMe PGS Genetic Health Risk Test (DEN160026) includes reports that identify genetic markers for late onset Alzheimer's and Parkinson's diseases, among several others (for a full list of tests, see Food and

Drug Administration 2021). On the other hand, a different category of tests is designed to determine an individual's ancestry by matching their genome to a database and seeing which portions of the variations overlap with a percentage of a population from a given geographical location. Since ancestry tests do not provide any health-related information, they are currently not regulated in the U.S. This is likely because they are not perceived as having the same impact as misdiagnosing someone with an increased risk of developing a particular disease. However, the assumption that ancestry tests are innocuous is misguided, as I will show throughout this chapter by outlining the epistemic harms that may emerge from them.

Matching a person's genome to a given ancestral profile involves complex statistical and computational methods, such as PCA (Principal Component Analysis). PCA first involves the reduction of high-dimensionality to lower-dimensionality datasets. Since any two humans share as much as 99% of their genome, theoretically, most relevant mutations are in the section where they differ. In other words, there is no need to analyze all 3 billion base pair combinations, which would be an unfeasible task that would render genetic products significantly more expensive. Because companies do not analyze all 3 billion base pair combinations, they are able to market an affordable product, with a cost that ranges, in most cases, from $90 to $150. Full genome reports would likely cost around $3000, which would make them much harder to market.

Historically, the first wave of DTC genetic tests marketed to the public were focused on nutrition and health reports. Later on, ancestry tests became an increasingly popular and lucrative product (Hogarth and Saukko 2017). In 2013, health reports provided by 23andMe were banned by the Food and Drug Administration (FDA) in the United States due to several controversies (for examples see Curnutte 2017; Green and Farahany 2014; Pollack 2013). More recently, however, some companies, including 23andMe, as mentioned, have received FDA clearance to

commercialize health reports that identify genetic variants commonly associated with an increased risk of developing disease. By 2019, more than 26 million consumers had provided samples of their DNA to seek information about their genome (Regalado 2019). While most consumers wish to satisfy their own curiosity about ancestry and heritage, some also actively seek to modify their lifestyles through the information provided in purchased health and nutritional reports.

While personal genomic information has become widely accessible (with many testing kits being sold for less than US$100), consumers often lack the necessary material resources to process and extract information from their own data. Such resources include the relevant sequencing technologies needed to determine sequences of nucleotides. This task is delegated to companies who specialize in providing this service and analyzing consumer genetic data by comparing it with existing databases. Because consumers therefore *depend* on providers to process their personal genetic information, they are often in a position of vulnerability with regards to this information. This raises the prospect of at least three types of harms, as I address here[13]. First, DTC genetic tests have problems of accuracy, bias, and reproducibility, leading to general harms that include misinformation regarding the nature of the results obtained, and false expectations on the part of consumers due to deceitful marketing of what such products can deliver. In addition, there is a

[13] While this chapter focuses on the general and epistemic harms of DTC genetic tests, a fourth type of harm includes privacy issues. Those should be discussed separately as they are beyond the scope of this chapter. DNA is shared among family members and alarming results can lead to issues of disclosure. One example is whether a person has the moral obligation to communicate increased disease risk to a family member who shares genetic information (Gostin and Hodge 2021; Fisher and Harrington McCarthy 2013; Hogarth, Javitt, and Melzer 2008). Also related to the problem of privacy is the fact that a few private companies have in their hands a significant amount of genetic data that is valuable and could potentially be sold to insurance companies. Although there is increasing regulation being drafted and implemented (such as, for example, the Genetic Non-Discrimination Act in Canadian regulation), this still raises concerns as to the ownership and value of such genetic data.

more concealed type of harm that is epistemic in nature. I will discuss each of these three separately in the following sections.

4.3.Accuracy and reproducibility of DTC genetic tests

In 2006, the United States Government Accountability Office produced a report indicating that there were serious problems of accuracy and reproducibility in DTC genetic tests. The report concluded that many companies made 'medically unproven predictions' (Kutz 2010). Using undercover consumers, the GAO obtained different results from a number of companies for the same samples. For example, identical DNA submitted to different companies yielded different risk profiles; in addition, many of the risk predictions contrasted with consumers' actual illnesses and family histories. Following this report, measures were implemented to regulate companies who were providing health data. For consumers seeking to uncover their ancestry, however, there was no specific product regulation, and the same problems of accuracy (as shown in the case of Sigrid E. Johnson) persisted. In this section, I will outline some of the reasons why results can be so misleading. In my analysis I distinguish between problems of Eurocentric bias, accuracy, and reproducibility of DTC genetic tests.

4.3.1. Eurocentric bias in datasets

One significant problem is the lower accuracy of results for admixed samples. Principal Component Analysis (PCA) methods identify the main axes of genetic differentiation between individuals (Dudley and Karczewski 2013; Ringnér 2008), and are often used in combination with Genome Wide Association Studies (GWAS) to assess ancestry patterns. GWAS are a key source of information for insights into the genetic origins of the predisposition to some diseases, and are typically used as reference databases against which to compare risk across populations. PCA methods offer one way to analyze relevant trends and summarize the high-dimensionality data

obtained in GWAS. One reason why PCA has been shown to be less accurate for admixed DNA results is that reference databases, and the vast majority of GWAS, use population samples that are predominantly European (Martin et al. 2017). This bias is likely to extend into the reference populations being used by DTC genetic testing companies. For example, as of now, the reference population in 23andMe is composed of around 14,000 people with known ancestry, sub-divided into roughly 45 geographical locations corresponding to a given ancestry. Within this population, data sets for European samples typically have more data than other subsets. While companies like 23andMe acknowledge this bias[14] and have made moves towards rectifying it by including more diverse databases, DTC tests on the whole are still heavily marketed as being equally accurate and precise across ethnicities. For example, in 2001, the company Sciona stated in its website that 'your genes govern how your metabolic pathways digest and dispose of nutrients and toxins within your body,' in order to sell personalized nutritional advice (this material is available thanks to Saukko's [2017] comprehensive research and thorough analysis of metaphors used in direct-to-consumer tests).

Ancestry test results and disease reports for individuals of admixed DNA are prone to sampling bias due to the lack of diversity in reference databases. When interpreting results that represent admixed populations (e.g., for someone with both African and European ancestry, or a Mexican-American individual) PCA analysis encounters an extra level of intricacy, due to the fact that admixed samples have DNA coming from different geographical locations (Kidd et al. 2012; Kim et al. 2018). Sampling bias occurs when the population chosen as a reference is not

[14] An example can be seen at the bottom of this page from the company's website: https://www.23andme.com/en-ca/ancestry-composition-guide/#:~:text=Your%20Ancestry%20Composition%20report%20shows,14%2C000%20people%20with%20known%20ancestry.

representative of one or more individuals about whom one wishes to make inferences. For example, inferences being made from the sequenced genome of an individual with African ancestry will be less accurate if compared against a database containing sequenced genomes from individuals of European descent. The lack of diversity in most databases, therefore, leads to systematically less accurate results for individuals with admixed DNA. For example, Kim et al.'s (2018) study shows that most disease-associated loci were discovered in non-African populations and therefore 'alleles segregate at intermediate frequencies in non-African populations but are found at extremely low or high frequencies in Africa' (Kim et al. 2018). Contrary to null expectations, GWAS using African cohorts show that risk allele frequencies are similar across the five continental populations. While there continue to be many successful initiatives to diversify databases in this field, it remains unclear whether DTC testing companies consider database diversity for their predictions (Kim et al. 2018).

Consider, for example, reported ascertainment bias in Polygenic Risk Scores (PRS) predictions, a type of score used to predict the genetic liability of certain human traits (De La Vega and Bustamante 2018). A central finding in this study was that flaws in the construction of Polygenic Risk Scores can affect how they perform in real-world populations; one major pitfall being that they suffer from the same ascertainment bias as most genetic research. In genetic science, ascertainment can be defined as a 'systematic deviation of population genetic statistics from theoretical expectations' (Lachance and Tishkoff 2013). Due to the lack of database diversity, it has been shown that risk estimates are more accurate for populations who are most like the samples they are being compared against. In most cases, because databases are primarily composed of individuals from WEIRD societies (Westernized, educated, industrialized, rich, and democratic) (Henrich, Heine, and Norenzayan 2010), thereby excluding ethnicities who do not belong to this

category, they are not representative samples of overall populations. Consequently, while there might be high prediction accuracy for European populations, such predictive accuracy decreases significantly when considering, for example, Hispanic/Latino individuals and African Americans (Henrich, Heine, and Norenzayan 2010; M. S. Kim et al. 2018). This can be seen in the different *p*-values that show higher risk allele frequencies than European samples. The study showed that some analytical findings on individual SNPs are at odds with clinical data available for the African American population. Such a discrepancy may indicate that genetic risks are currently being misestimated for individuals with African ancestry (M. S. Kim et al. 2018). In sum, when the reference genome is itself a biased sample; as in this case, overrepresenting European ancestry, questions of predictive accuracy arise when considering results for non-European individuals.

4.3.2. Accuracy and reproducibility

Reproducibility has often been characterized as an epistemic value in science, alongside other values such as predictive accuracy and the internal consistency of a theory (Douglas 2009). The reliability of any measurement depends on the capacity to obtain reproducible and consistent results when the procedure is repeated under the same conditions (Hand 2005). While there are cases where the attribute being measured may change over time (for example, behaviour or well-being), in the case of DNA information, the underlying attribute—that is, the sequence of base pairs in a DNA sample—remains the same. Hence, we *expect* information provided about our DNA to be reliable because the underlying attribute remains the same over time. Despite this, the widespread availability of DTC genetic tests has exposed problems with the reproducibility of results. On the one hand, different companies may use different techniques for measuring the same sample (a person's DNA). On the other, data processing methods may be updated over time, and because the information provided is usually a prediction or an estimate, consumers might find

changes in their reports overnight. While accuracy and lack of reproducibility can affect any consumer of DTC genetic tests, there seem to be systematic biases against consumers who have admixed DNA.

Consider, once again, the USA's Government Accountability Office report (GAO), produced in 2010, in which undercover consumers sent DNA samples to different companies with surprisingly inconsistent results. This report clearly indicated that different companies deliver different results for the same samples (Kutz 2010). Although the underlying DNA is the same, it can be interpreted in significantly different ways, leading to contradictory risk factor profiles. Take, for example, the following case: a 63-year-old male received risk predictions from different testing companies for atrial fibrillation, ranging from average to below average (Kutz 2010). In other cases, risk predictions were shown to conflict with already diagnosed conditions. For example, in the GAO's report, four out of five consumers reported obtaining different results than their actual conditions, and only one testing company asked for the consumer's medical history. Since 2010, sequencing technologies have greatly improved, and we can see efforts to diversify databases (such as the Global Genetics Project or the African Genetics Project).

4.4.An account of general harms

When considering the reproducibility problems of DTC genetic tests within and across companies, one significant harm is that in many cases companies seem to be violating a contractual obligation to deliver meaningful information. Most consumers seeking information about their ancestry hope to gain knowledge about their family background and geographical genetic heritage. Genetic information can help shape a person's narrative about herself, and can affect her identity and sense of belonging (Appiah 1998; DeGrazia 2005). As shown in Johnson's case, misleading

information and discrepant results across companies can be psychologically distressing and significantly alter one's sense of belonging. Consumers *trust*[15] providers, who hold a position of epistemic privilege, to deliver meaningful information, and may change their narratives about themselves based on that information.

A second harm results from the fact that providers often downplay the probabilistic nature of data and instead use deterministic language to market their DTC tests. In the case of BRCA1 and BRCA2 tests for mutations associated with breast cancer, it is important to note that approximately 85% of patients with breast cancer have no family history (Brewer et al. 2017); hence, BRCA1 and BRCA2 mutations are not identified in such cases. Only about 15% of cases of breast cancer are associated with BRCA mutations. However, consumers taking BRCA tests and getting a negative result may be led to believe incorrectly that they are not at risk for breast cancer. In other words, in most cases where breast cancer is not hereditary, its causes are largely unknown. Hence, taking a mutation test for breast cancer is only relevant when there is family history. The sale of BRCA1 and BRCA2 tests, however, is not limited to customers who have a family history, which allows for the heightened demand for genetic tests for which there is no explicit medical reason (Williams-Jones and Burgess 2004). For example, the FDA has recently authorized the sale of DTC tests that report mutations in BRCA genes (FDA 2020). Despite disclaimers stating that the raw data might not be accurate or suitable for medical use, patients seeking DTC genetic tests may be ill-informed as to how to interpret such tests, and under which circumstances they are in fact useful (this problem applies especially to health and nutritional reports) (Tandy-Connor et al. 2018). Unnecessary use of DTC genetic tests can end up creating

[15] While trust is an extensive philosophical topic, the main accounts of trusts I build from in this article are proposed in Grasswick (2010) and Hardwig (1991).

more demand for superfluous health check-ups, and increased pressure on health resources that could be redirected to patients with more legitimate healthcare needs.

A third harm relates to unnecessary (and potentially negative) changes in lifestyles that can be prompted by certain test results. For example, a person who discovers from their test results that they have an increased risk of coronary disease is likely to change their lifestyle in a positive way, making healthier choices. It might be argued that, in this case, such changes are desirable even if the person is not at a high risk. The problem, however, is when false negative results are obtained. Consider the example of a hypothetical consumer, X, who has been told that her risk of developing heart disease is 'below average.' This person might make poor diet and lifestyle choices based on such results, which are only probabilistic. This kind of error becomes even more problematic when one considers that consumers have reported obtaining different results from different testing companies. Similarly, false positives have also been identified in DTC genetic test results (Tandy-Connor et al. 2018), and can have negative effects on the consumer. A person who is misdiagnosed as having an increased risk for a disease when, in fact, the risk is average or below average, may experience unnecessary distress and anxiety. Another potential consequence is that consumers will seek additional health services, leading to increased demand for publicly funded services such as genetic counselling. This could place unnecessary strain on healthcare systems by requiring medical personnel to devote more time than they can afford to interpreting results and advising on lifestyle decisions (Williams-Jones and Burgess 2004). While personalized health services can, in some cases, significantly cut health costs by using more targeted and effective treatments, the Canadian Medical Association warns that increased demand for DTC genetic tests can negate any such savings by causing a concomitant increase in demand for physician

consultations and the resultant follow-up and medical investigation (Canadian Medical Association 2017).

Problems of accuracy and bias in reference databases may also exacerbate health disparities across groups. I have mentioned that the predominance of European DNA in these databases leads to less accurate results for consumers whose DNA is from mixed origins (such as African Americans or Mexican-American individuals). Because there is a significant overlap between racialization and marginalization, systematic errors affecting individuals who do not have exclusively European ancestry can perpetuate health disparities for marginalized groups. Despite disclaimers being offered regarding the accuracy of information, tests continue to be marketed as delivering meaningful results, and the interpretation of these results can still lead to changes in lifestyle and identity.

4.5.Epistemic trust as the foundation of epistemically just relations

So far, I have shown that bias, accuracy, and reproducibility problems in DTC genetic tests yield misleading results that can also be ethically problematic. One may argue that once such problems are solved, then the general harms will be greatly reduced, and may not even constitute a problem in the future. For example, 23andMe has publicly stated that Eurocentric bias means that results are more accurate for individuals of European ancestry, and that this is due to a lack of diversity in many reference databases. As part of its mitigation strategy, the company has highlighted initiatives such as the Global Genetics Project and the African Genetics Project. Another objection could highlight that overall, testing and validation yield very high precision (i.e., whether the piece of DNA predicted by the system as belonging to a given population *actually* comes from the given population) and recall percentages (i.e., of the fragments of DNA from a

given population, how often the system can predict that they *are* from the given population) (23andMe 2022). In principle, insofar as companies strive to improve these percentages, there might not be any real underlying harm being done to consumers.

Against this objection, however, I suggest that there is a more concealed type of harm embedded in these tests, epistemic in nature, which stems from the asymmetrical knowledge dynamics between consumers and providers. As part of my argument, I show that even if problems of bias, accuracy, and reproducibility were eliminated, some important epistemic harms would still need to be rectified. If it is true, as I assume, that consumers of DTC genetic tests seek knowledge about their own genetic composition, it then follows that, as knowledge seekers, they are epistemic agents. Hence, the harms I discuss are epistemic because they challenge the status of the consumer as a knower and undermine their capacities as an epistemic agent. In this section, I explain how relations of trust are established between laypersons and experts.

Within the literature on epistemic injustices, a term coined by Miranda Fricker (2007), relations of trust between experts and laypersons have been extensively discussed (Baier 1994; Grasswick 2010; Hardwig 1991; Hawley 2017; Hendriks, Kienhues, and Bromme 2016; Leefmann and Lesle 2020; McCraw 2015; Wilholt 2013). According to Fricker, a hermeneutical epistemic injustice occurs when 'a gap in collective interpretative resources puts someone at an unfair disadvantage' (Fricker 2007, 1). Fricker offers an example of sexual harassment to clarify what is meant by such a gap. A woman who was a victim of sexual harassment was not able to identify this abuse because she was unaware of the concept of 'harassment' itself, and of the fact that it could refer to sexual advances. Consequently, she was unable to name her experience, and incurred a series of harms (such as wanting to change jobs and not being able to state a reason, hence being denied unemployment benefits). Additionally, the harasser was himself in a similar position of

cognitive ignorance, the difference being that this position suited his immediate purpose, which was to leave his conduct unchallenged (Fricker 2007). Note that when a hermeneutical injustice occurs, both parties are in a position of relative ignorance, with the difference being that one party is favoured by this position and the other is directly disadvantaged, creating an asymmetrical ignorance. Fricker's argument builds from the idea that underlying knowledge relations are also power relations, an argument previously made and developed by Michel Foucault (1980).

Fricker's theory of epistemic injustice is a valuable tool to apply to asymmetric knowledge relations, of which one example exists between scientific and lay communities. While much emphasis has been given to both testimonial and hermeneutical injustices, an important epistemic harm also stems from how knowers place their trust in knowledge providers, a relation known as epistemic trust. Grasswick (2018) distinguishes between responsibly and irresponsibly placed trust. In an ideal scenario, there would always be a balance between the degree of trust an agent places in a source and the trustworthiness of that source. However, in some cases, one irresponsibly places trust in a source while ignoring its trustworthiness (or lack thereof). These are cases where, despite there not being good reasons to trust the source, the agent still does so, generally due to a lack of means of assessing its trustworthiness. This is what Grasswick calls 'irresponsibly placed trust,' and it occurs when a person is not capable of identifying or properly considering the reasons why they should not trust a source. What is important for our purposes is that irresponsibly placed trust can be epistemically harmful to the person placing that trust (the epistemic agent).

Epistemic trust is an essential foundation of scientific knowledge-sharing practices (McCraw 2015; Grasswick 2017; Hardwig 1991; McCraw 2015) and is therefore key to relations between scientific and lay communities. I assume that most consumers of DTC tests are laypersons; i.e., consumers without a high degree of expertise in genetics who are seeking to satisfy

their curiosity about their own genome. For trust to be possible, a layperson (L) trusts the information provided by an expert (E) because E is believed to be trustworthy and to provide meaningful information. When consumers receive test results, they are in a position of relative ignorance when it comes to the knowledge possessed by E. A successful personal trust relation must fulfill two basic conditions: competence and sincerity (Hardwig 1991; Grasswick 2018). Competence means that the knowledge holder has the necessary skills to produce knowledge in a specific domain. Sincerity means that the one who is trusted will accurately convey results to the one placing trust, and sincerely express their knowledge in a truthful way. While accounts of institutional trust are often modeled on accounts of personal trust, Grasswick (2018) emphasizes that trust in institutions also depends on the 'trustworthiness of the specific practices of the institution' (p. 77). Grasswick (2018) therefore suggests that we expand the criteria of competence and sincerity in personal relations by adding some specifications that apply to trust in institutions and groups of experts. First, the competence condition must be reframed as the condition of competently conveying significant knowledge. This means that, in the case of science, for example, we trust scientists to be engaging in 'epistemically valuable work' (p. 78). The sincerity condition is only sufficient when accompanied by a 'care' clause, which Grasswick names 'the sincerity/care condition.' In other words, sincerity captures a minimal condition of care. Knowledge holders must care for laypersons if they are to sincerely convey the knowledge in question. For example, a doctor must care for her patient in order to sincerely convey a difficult diagnosis, and not because she feels pressured to provide a conclusive diagnosis.

In some cases, there are valid reasons for a group, especially minorities or disadvantaged groups, to withhold trust on a group basis. Often such reasons are grounded in historic relations between laypersons and institutions or experts. By contrast, in other cases, individuals place their

trust irresponsibly in experts due to a position of relative epistemic ignorance; that is, because they lack the information or knowledge needed to assess trustworthiness. A famous historical example can be seen in the tobacco industry, which, in its efforts to associate smoking with health benefits, used members of the medical community to endorse its products (Oreskes and Conway 2010). Because consumers lacked the interpretive resources to understand the dangers to their health posed by smoking, they misplaced their trust in tobacco company providers, who labeled themselves as scientific experts.

In the tobacco industry example, the connection between trust and vulnerability is relatively clear (Baier 1994). When an individual places trust in experts, they are entering into an inherently asymmetric relationship. Since laypersons rely on these experts to deliver accurate and meaningful information, they are in a vulnerable position, where they take information on faith. Take, for example, a doctor who gives a patient information about their health, or a scientist who shares some ground-breaking discovery with the public. In both cases, an expert is in a position of specialized knowledge; this would appear to justify placing one's trust in them, but laypersons may not have all the resources to assess the validity of expert claims. For example, in the case of the scientist, it is generally accepted that although a scientist's job is not to uncover *the truth* they are committed to making *true claims* about the functioning of the world. Similarly, a doctor is responsible for giving patients truthful information about their underlying condition, and appropriate treatment alternatives that match the true state of a patient's health.

4.6.An account of the epistemic harms

In the previous section I have shown that trust is fundamental to asymmetrical epistemic and power relations between laypersons and experts. I will now show that in relations between

consumers and DTC genetic testing services, the conditions for trust are not adequately fulfilled. Competence to deliver meaningful information, and sincerity in delivering this information because of care for another, are necessary and sufficient conditions for successful trust relations between laypersons and expert communities. In the case of DTC genetic tests, these two conditions are not met, which results in two kinds of epistemic harm to consumers: deprivation of testimonial authority, and hermeneutical injustice through the use of reductionist rhetoric. Before delving into each type of harm, I will explain why the conditions for epistemic trust are not satisfactorily fulfilled.

First, the sincerity condition is only partially fulfilled, insofar as there are significant problems of bias, accuracy, and reproducibility in data processing techniques in recreational genomics. While experts have the knowledge to process and deliver the information, in many cases company representatives do not competently address many of the limitations of such inferential techniques. An example of this lack of care can be seen in Sigrid E. Johnson's case, mentioned earlier. Distressed by her own results, Johnson was unable to obtain satisfactory explanations from the test providers themselves. The depth of information made available by providers varies greatly; while some are relatively transparent about the limitations of the results they provide, others provide little to no information on the matter.

Second, when considering the care condition, even when test providers wish to deliver results with sincerity, it is not easy to maintain that they do so out of care for consumers. Amongst their goals is the wish to sell as many tests as possible, as well as to build a valuable genetic database that could potentially lead to further financial gains. Therefore, such companies are not beholden to their customers, but rather to their shareholders, which puts the interests of customers and shareholders in conflict. Consider the following example of personal trust: Suppose a

physician suspects that a patient might have a higher risk for developing disease X, normally associated with a population of ethnicity Q. If the physician asks her patient to take a genetic test to find out whether they have a common ancestry Q, it is because the physician would like to *care* better for the patient by delivering meaningful information. If the physician requests a genetic ancestry test, it is safe to assume that she will deliver the results to the patient in a sincere way, by virtue of the care that she has for her patient. In the case of mass-marketed genetic tests, consumers rely on the sincerity of the testing company, without the care component which secures justified trust in knowledge holders. (Hence, the consumer may be unwittingly irresponsible in placing trust in the knowledge provider.) It is within reason to question whether the care relation is fulfilled to a degree that would match the epistemic trust relation between a physician and her patient.

Third, given the current technical and financial limitations of DTC genetic testing services, it is an overreach to claim that they could (at least in principle) deliver the sort of ancestry information they claim. Even if the accuracy of such tests were to improve, it remains questionable that they would deliver meaningful information about a person's ancestry. While DTC genetic tests can be highly useful to find living relatives, it is not clear how they can contribute to information about ancestry and ethnicity, which are complex constructs that cannot be reduced to genetic information (even if such information were meaningful).

4.6.1. Epistemic harm 1: consumers of DTC genetic tests are deprived of their testimonial authority on matters relating to their own identity.

Most consumers seeking to purchase a genetic test wish to get insights about their ethnicity, background and/or health risk profiles. In the case of ancestry tests, many seek to understand their own identity better by looking for answers to questions such as: Who am I? Where did my ancestors come from? What genetic background makes me the person I am today? These questions

represent a common yearning to make sense of one's place in the world, but the determinants of identity go far beyond genetic composition. Nordgren and Juengst analyze the rhetoric used by DTC genetic testing companies, as well as consumer testimonials that obtaining knowledge about their ancestors has been valuable and empowering and is linked to their understanding of themselves (Nordgren and Juengst 2009). While race and ethnicity are important constituents of one's identity (Appiah 1998; Mills 2015a), they are not its sole constituting factors. Consider, once again, the very low percentage of African ancestry indicated by Johnson's first test results. Ancestry percentages are not proportional indicatives of belonging to a given racial category. Johnson's appearance as Black and her identification with the Black community were integral to her identity, regardless of the percentage of African ancestry indicated in the first test taken. Furthermore, Johnson has the epistemic authority to say that she is Black; the percentages she received undermined that authority by falsely marketing the idea that the relation between ancestry and identity can be precisely expressed through a percentage value. One of the problems with Johnson's ancestry result tests is that they seemed to indicate that in some way, she is 'less' Black than she believes and self-identifies. In other words, the test results she received claim (through all kinds of rhetorical techniques and deceitful marketing) to have epistemic authority to deliver meaningful information that can determine a person's ancestry and supersede their experience. This can have harmful consequences, because it can suddenly shape how someone thinks of themselves in ways that are contradictory to their existing and deep-rooted self-perceptions. For example, someone might always have thought herself to be X, but test results coming from a source with some authority say she is Y, thus compromising her trust in her own judgements about herself.

Widespread marketing of DTC genetic tests usually upsells the idea that there is a straightforward relation between ancestry, race, and identity, by using rhetoric that supports this

equation. For example, in a 2016 television commercial, 23andMe markets its tests with the use of consumer testimonials from individuals seeking to understand 'who they are' (23andMe 2016). There are important arguments in the philosophy of race that elaborate on the complex relationships between race, ethnicity, and identity. Charles Mills (2015), for example, argues that the metaphysical depth of racial categories is partly due to the fact that race can go much beyond ancestry. More specifically, when we attribute racial categories primarily to an ancestral criterion, there is a failure to capture the metaphysical dimension of race. (An ancestral criterion can be understood as the classification of an individual into a group based on ancestry.) Mills states that 'People focus on ancestry because in this world ancestry and the other attributes usually go together, but separating them shows that ancestry is not really the important thing. What is important is the intersubjective/subjective criterion of what ancestry is *thought* to be' (Mills 2015, 59). Any constructionist view of race would therefore object to the claim that ancestry and identity are linked in a straightforward way, an idea heavily marketed by test providers. This leads to the second epistemic harm, discussed below.

4.6.2. Epistemic harm 2: reductionist rhetoric that reduces ethnicity and race to DNA is a hermeneutical injustice

Hermeneutical injustices occur when a person or group cannot make full sense of their own experience, due to a lack of understanding or interpretive resources (Fricker 2007). An important assumption of my argument is that most consumers of genetic tests are not specialists in genetics and therefore do not have the necessary resources to analyze the limitations of such tests in depth. DTC genetic testing companies seem to take advantage of this shortfall when they oversimplify the relationship between ethnicity and DNA. In other words, the suggestion that race and ethnicity are reducible to ancestry is a kind of hermeneutical injustice, because consumers do not readily

have the technical knowledge or the interpretive resources to resist such reduction. Hence, when they purchase a genetic test, they do so because they trust test providers to deliver a specific kind of report that will supposedly provide meaningful information about their ancestry. Consumers are often lured in by essentialist rhetoric that promises answers to complex questions regarding identity. While many family members have been reunited thanks to DNA tests, in other cases meaningless results can prove to be distressing to consumers. One extreme example of the reduction of race and ethnicity to DNA can be seen in the case of white supremacists rushing to take DNA tests to prove the purity of their ancestry (ironically, many have been disappointed to find that they have ancestry from many geographical regions, even if in low percentages) (Murphy 2019). This epistemic ignorance regarding the scope of test results can be harmful in the long run: when consumers take test results at face value, they are susceptible to an essentialist and reductionist discourse concerning race and ethnicity.

A potential objection to my claims about the epistemic harms emerging from the widespread commoditization of DTC genetic tests might be that once accuracy and reproducibility problems are adequately tackled, and efforts made to diversify databases, then the epistemic harms would go away. However, even if DTC genetic tests were extremely accurate, the salient point is that what they actually deliver is a completely different kind of information from what they lead consumers to expect. While consumers seek knowledge about themselves as epistemic agents, they do not necessarily obtain this specific kind of information when submitting their own DNA samples.

4.7.Harm mitigation strategies

While problems related to accuracy and reproducibility can lead to epistemic harms from the marketing of DTC tests, there are valuable tools both at the individual and policy level that can help mitigate those harms. At the personal level, a focus on genetic literacy may provide much needed interpretive resources to analyze and interpret results. At the policy level, successful cases of regulation (such as the FDA's regulation of 23andMe's Personal Genome Service) could point to the equally important need for regulation of both ancestry and health-related tests.

4.7.1. Genetic literacy

McCraw (2015) considers that a fundamental condition for justified trust is the quality of communication. To reduce the epistemic gap between consumers and providers, DTC companies should establish more direct communication about *how the science works.* For example, one crucial insight that could be shared is the probabilistic nature of genetic data. In the 2010 GAO report, consumers who sought interpretation or information about their results encountered insufficient support from the very genetic counsellors whose role should be to provide the above (MacDonald 2002; Hawkins and Ho 2012). Furthermore, in Johnson's case it was reported that when contacting the test provider, different company representatives had different answers as to the degree of confidence she should have in her results, and there was no accountability for these discrepancies. This lack of transparency and accountability, as well as poor communication, is especially misleading and confusing to consumers who place excessive trust in results. A similar point has been proposed by Grasswick (2010) when arguing for methods to increase the trust of marginalized communities in science. In Grasswick's example, however, there is a lack of trust, whereas in the examples of DTC genetic tests, we seem to be facing excessive trust in the information delivered by a genetic product, simply by virtue of the fact that such information is

'scientific.' Much can be learned from the idea of 'cooperative epistemologies,' which would involve laypersons in the scientific process and set expectations more clearly. For example, Hookway (2010) suggests that many participatory activities, such as discussion, deliberation, and a safe space to ask questions, are crucial to successful epistemic trust relations. These groups should also feature genetic counsellors and specialists who have no third-party interest in the company, in order to foster a neutral environment for questions and information sharing.

Genetic literacy in prevention science can be defined as 'the degree to which appropriate prospective participants are familiar with and can apply information about the use of genetic data to make appropriate research participation decisions' (Fisher and Harrington McCarthy 2013, 314). While genetic literacy is a prerequisite for study participants, it is not required for the consumption of DTC genetic tests. For example, a lengthy exam in which participants must score 100% is required before they are able to participate in the Personal Genome Project (Curnutte 2017). The promotion and assessment of genetic literacy could also be incorporated into the process of selling and consuming genetic information without a clinician's mediation, so that consumers are less likely to suffer debilitating consequences as the result of DTC genetic tests.

4.7.2. Increased regulatory controls

When disruptive technologies and the resulting products first become available, existing regulatory frameworks are usually inadequate (Curnutte 2017). This has certainly been the case for DTC genetic tests. In the United States, for example, it was roughly a decade after 23andMe first marketed its products that regulation started to enable health reports to be issued by a non-medical provider. In the United States, the FDA has come to an agreement as to which health-related tests can be sold, based on empirical data about accuracy and validity, but in many countries such regulation does not yet exist. In Canada, for example, both ancestry and health-related DTC

tests can be directly bought and sold by and to the public. In 2017 the Canadian Medical Association (CMA) issued a policy report (CMA Report PD17-05) warning about the very low predictability of such tests (Canadian Medical Association 2017). Furthermore, the CMA highlights that some physicians lack the appropriate resources to interpret or to provide reassurance about test results with their patients. Since 2017, when the prohibition of genetic discrimination came to the fore, the landscape for genetic regulation has changed; however, there is still no consumer protection against misleading or inaccurate results. With DTC genetic tests available in the Canadian market for some years, and given their potential effects on consumers, this shortcoming is significant.

4.7.3. Transparency and sincerity in accuracy disclaimers of test results for different ethnic groups

Transparency standards are not homogenous across test providers. While some companies, such as 23andMe, provide extensive information about test validity, others provide little to no information to anyone interested in purchasing an ancestry test. In many cases, information about precision and recall, the methodology of tests, or diversity in the databases being used is simply not made available in a clear and transparent way. This is another standard that could be homogenized across test providers and would benefit from regulatory control. For example, if the levels of result precision for each ethnicity were made explicit, that would be a very easy first step towards more successful relations of epistemic trust. Consequently, consumers could make more informed decisions based on the available information. Other tools that could easily be implemented would be a brief comparison between more and less precise reports, and a step-by-step explanation of how to interpret results; for example, that ancestry tests can be very useful in finding relatives, but may not deliver meaningful information about race and ethnicity. This kind

of information should be made available before consumers purchase products, so that they can exercise their epistemic agency before the transaction takes place.

4.8.Conclusion

In this chapter, I have discussed general and epistemic harms that can emerge from the widespread sale of recreational genetic products, such as direct-to-consumer genetic tests. First, I have discussed how problems of bias, accuracy, and reproducibility are not adequately addressed, and result in general harms to individuals receiving test results. I have explained the harms that result from the risk of both false positive and false negative results, and have provided evidence for a low-level of reproducibility of DTC genetic tests by analyzing cases where consumers obtain different risk profiles from different providers, even though their DNA remains the same throughout their lives. I have subsequently argued that even if there are good reasons to think that problems of bias, accuracy, and reproducibility are being confronted, there is a more concealed type of epistemic harm that has yet to be addressed. I have situated my argument in a framework of epistemic trust between experts and laypersons, and outlined two conditions for justified trust: competence and sincerity/care, which have been extensively analyzed by Grasswick (2018). I have discussed two epistemic harms that arise from the widespread use of DTC genetic tests. First, I have shown that consumers are deprived of their testimonial authority on matters related to their own identity. Second, I have shown that reductionist rhetoric is a type of hermeneutical injustice, because consumers often lack the interpretive resources necessary to resist the reduction of race and ancestry to DNA. From an epistemic perspective, I have proposed two main solutions to address the moral harms that result from the widespread marketing of DTC genetic tests. On the one hand, genetic literacy can be a key to reduce epistemic asymmetries between providers and

consumers. On the other, better regulation of the use of DTC genetic tests for both health reports and ancestry tracing should be made a policy priority, to avoid the unnecessary use of health resources and the perpetuation of health disparities. While DTC genetic tests are marketed as recreational products, they clearly have serious implications both at the policy level and at the consumer level.

Analysis of the epistemological underpinnings of consumer-provider relations can be a fruitful approach to understanding the moral and epistemic harms that can result from the commodification of genetic data. While epistemic trust asymmetries can be problematic and put consumers in a vulnerable position, scrutinizing such asymmetries from a philosophical standpoint brings conceptual clarity to the recognition of underlying harms and wrongs that can ensue from interactions between experts and laypersons.

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CONCLUSION

By way of concluding, I will evaluate some outcomes of this work, the philosophical contribution it brings to the field, as well as some perspectives for future research problems. The result of this thesis is a collection of chapters that zoom in on different puzzles that have emerged over the history of evo-devo. While philosophical interest in such notions often comes from a historical and exegetic perspective, I based my arguments on a practice-centered approach aiming to provide conceptual clarity to contentious notions that appear in the debate surrounding the EES between its proponents and critics. My goal was to provide conceptual foundations that enable the debate to move forward in fruitful ways. As a result, this thesis presents a collection of chapters that untangle causal, conceptual, and epistemic problems in evolutionary developmental biology through the lens of philosophy.

With this overarching goal in mind, I explored three crucial topics to establish the conceptual foundations of evolutionary developmental biology. Globally, I provided the tools needed for strengthening EES into a robust theoretical framework. Through my analysis of several core notions in evo-devo, I have shown that moving beyond the divide between the EES' critics and its proponents is a much-needed step to make progress in theoretical biology. I have done so by proposing criteria of adjudication on questions at the heart of the EES. In the case of downward causation, the criterion I propose is whether in evo-devo the dependencies among causal variables at different levels satisfy the criteria of conditional independence and independent fixability. In the case of reciprocal causation, the criterion I proposed was whether the reciprocity of causes on a fine-grained, shorter time scale explains evolutionary processes that the reciprocity of causes on a more coarse-grained, longer time scale does not. For novelties, I have defended that an important

criterion of adjudication of EES claims is whether a distinct set of mechanisms is identified that explains the origination of phenotypes.

Philosophical inquiry can and should play a crucial role that contributes to greater conceptual clarity. The best way to do so is, however, not through a strictly metaphysical and theoretical approach, but rather through a practical one that works closely with empirical examples. A secondary contribution of this thesis also emerged from this practice-centered approach and was to propose an argument based on the notion of epistemic harms. My goal was to better understand the social implications of commercializing technological advances in genetics.

First, I delved into the notion of downward causation to show why and how it can be a coherent notion in biology. I have tried to move away from the traditional metaphysical objections against downward causation (Kim 1992; Bedau 2008; Baumgartner 2009) to show how the notion can be useful in scientific practice. Ant colonies and the relations between higher and lower levels of a colony were my choice of example to apply interventionist theories of causation to an empirical case of downward causation (Rajakumar et al. 2012; Gregg 1942; Wheeler and Nijhout 1984). My hope is that a similar conceptual analysis can be useful for understanding other complex systems. For example, future avenues of research that could stem from my work on downward causation could apply my framework to other levels of biological organization such as: a better understanding of epigenetics (at the genetic level) (Müller 2010; Ashe, Colot, and Oldroyd 2021; Baedke 2018), an account of the top-down relations of tumor environments and cancer cells (at the cellular level) (Xu, Boudreau, and Bissell 2009; Malaterre 2011), social relations between organisms across taxa, and ecological processes that are said to be top-down such as the environmental effect on developmental processes that in turn play a role in evolutionary outcomes.

Second, I delved into another causal notion that has ignited controversy: reciprocal causation (Dickins and Barton 2013; Laland et al. 2013; Buskell 2019; Svensson 2018). I moved away from the debate centered on theoretical claims about reciprocal causation to show that the difference in scope between SET and EES is a better way to establish the notion's fruitfulness in the context of EES. One point I would like to develop further stemming from this work would be a comparative analysis of reciprocal causation in models of eco-evolutionary dynamics (Hendry 2016), evo-devo (Schwab and Moczek 2021) and eco-evo-devo (Sultan 2017a). Reciprocal causation is a foundational notion of the EES research program and understanding the variation of this notion in different research fields through specific models that describe reciprocity would be fruitful to further clarify the notion of reciprocal causation. In the same vein as my interventionist hypothesis on downward causation, an interventionist account of reciprocal causation could also explored in future inquiry (Woodward 2004). In sum, the two first chapters of this thesis bring together insights from the metaphysics of causation and biology, by bridging the gap between abstract theorizing about causation and the usefulness of the notion in biological practice. Philosophically, through my examination of causation (downward and reciprocal) I hope to have shown that the metaphysics of causation need not stay purely abstract, but rather, can be helpful to understand how causal notions are deployed in evo-devo.

Third, I delved into the source of the debate surrounding the concept of novelty (Brigandt and Love 2012). From a philosophical perspective, the concept of novelty's epistemic goal so far was identified as that of setting research agendas (Brigandt 2010b; Brigandt and Love 2010; Love 2008). In analyzing how the concept is used in practices as well as the role it plays in the EES research program, I argue that there is a stronger epistemic goal already in place for the concept. The framework I develop is based on a realist argument (Eronen 2019; Psillos 2018; 1996; 1999).

Namely, I show why a realist commitment to novelty is necessary for the concept to play such a strong role in framing research programs. In future, I would like to delve deeper into the role of scientific realism in structuring disciplinary fields around other concepts. This argument is relevant for evo-devo because a core feature of the discipline is identifying relevant mechanisms and providing mechanistic explanations of evolutionary phenomena. Another avenue of research would be, more generally, to defend a realist position about biological mechanisms in general, which could also provide conceptual clarity to other ambiguous concepts in biology.

And finally, a secondary aim of this thesis was to analyze practical implications of current practices in biology and, more specifically, in genetic science. Specifically, I aimed at advancing an ethical framework that accounts for the epistemic harms resulting from the widespread marketing and consumption of direct-to-consumer genetic tests (Food and Drug Administration 2021; Hogarth and Saukko 2017; Udesky 2010). This practical turn in the fourth chapter of this thesis could also lead to other avenues of research that deal with genetic science broadly construed. Specifically, in this paper several notions that could benefit from philosophical scrutiny emerged, such as the scope of polygenic risk scores and the concept of 'admixed' DNA. In future, this is an avenue of research I would like to pursue at the intersection of philosophy of biology and data ethics. In this case too, the methodology of philosophy of science in practice would be a valuable tool.

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