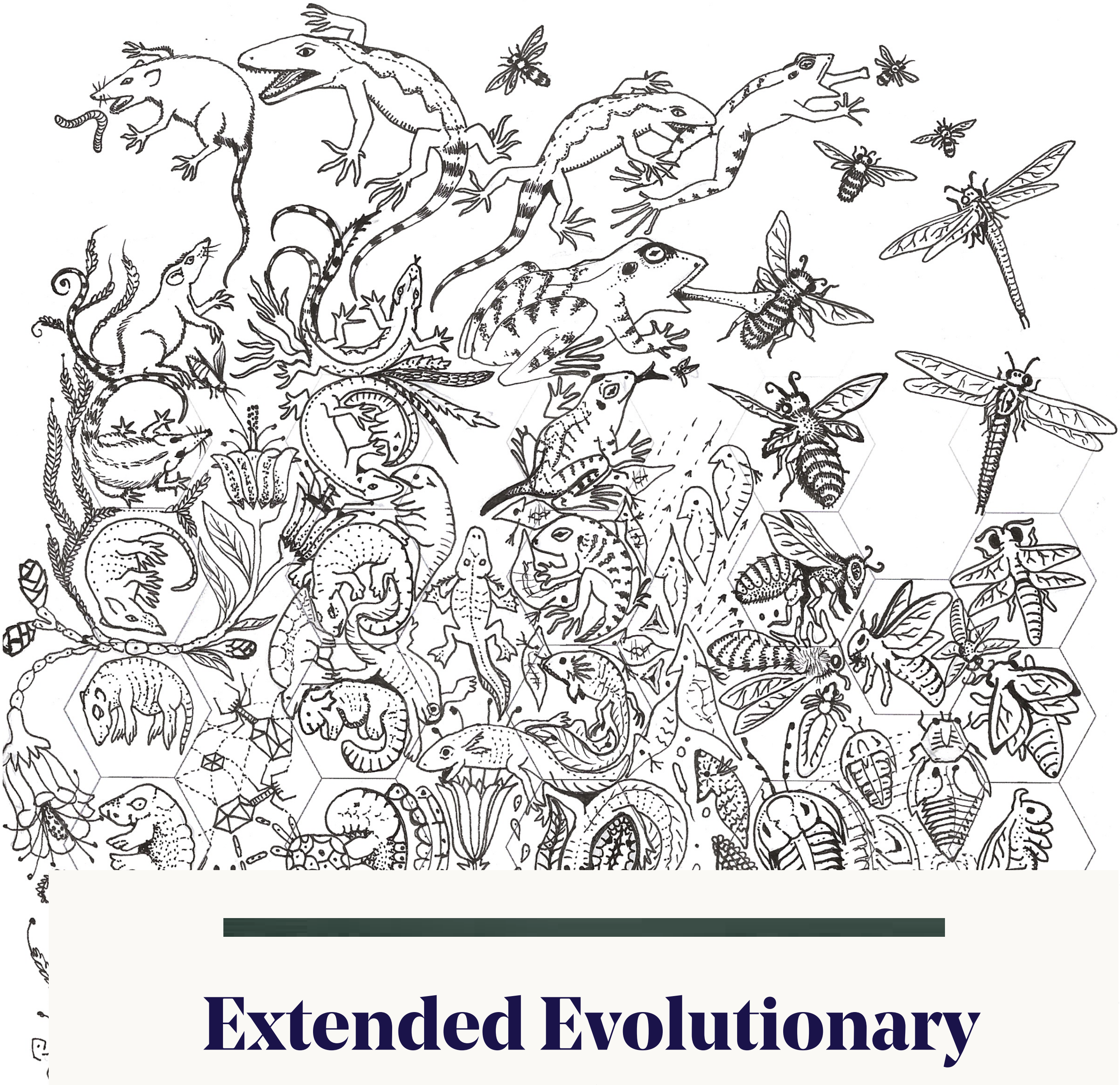

Extended Evolutionary Synthesis

A review of the latest scientific research

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Introduction

When we speak of evolution, what usually comes to mind is Charles Darwin's theory of natural selection, vividly captured by slogans such as "the survival of the fittest" or "nature red in tooth and claw." These images, however, do not fully capture the way evolution is studied today. In the past century and a half since *The Origin of Species* (Darwin 1859), evolutionary theory has itself "evolved" through a series of theoretical and methodological expansions, merges, splinters, and cuts. The biggest breakthrough occurred during the second quarter of the 20th century, when a "Modern Synthesis" redefined evolutionary theory from a "gene's-eye view," as a theory of how genetic variants evolve. By the end of the "century of the gene" (Keller 2002), the general public had adopted a new metaphor for Darwinian evolution—the idea that the complexities of life are mere vessels for "selfish genes" to make more genes (Dawkins 1976).

Now, in the first quarter of the 21st century, evolutionary thinking is expanding, reclaiming what was left out of a gene's eye view of evolution. The "extended (evolutionary) synthesis (EES)" is a family of theoretical perspectives that goes beyond a gene-centric evolution to fully embrace the complex dimensions of life. The EES includes more sources of biological innovation and adaptations, more modes of evolutionary change, more channels of inheritance, more disciplines of study, and more agency for organisms to affect their own evolution. The call for "more, more, and more" is not merely a piecemeal expansion of evolutionary theorizing. Some understand it as a deep reintegration and reorganization of the structure of evolutionary theory.

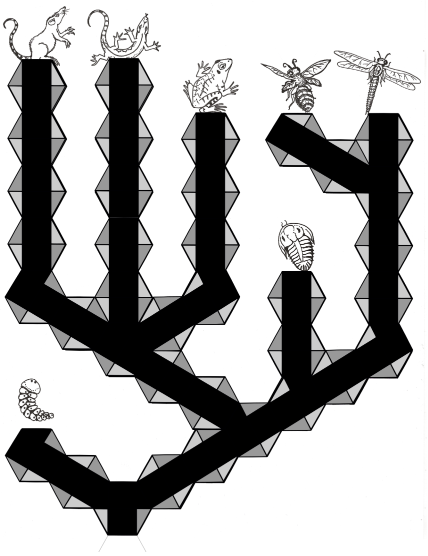
The current EES movement is supported by multiple large-scale interdisciplinary collaborations and individual projects scattered across a wide diversity of academic disciplines.

This review—intended for interested readers, reporters, researchers, and teachers—aims to serve as a road map to navigate rapidly moving terrain. To understand the EES movement, we need to ask: What happened to evolutionary biology during the 20th century and what did it leave out? Why is the EES seeking a more inclusive approach to evolutionary theorizing? And finally, what does evolutionary theory look like under EES? The review will proceed in three parts: examining the genetic turn of evolutionary theory since Darwin (Part 1); sampling multiple, independent calls for an alternative outlook (Part 2); and finally, taking a close look at the emerging structure and outcomes of an EES research program (Part 3).

The aim here is to help an onlooker grasp the contours of this ongoing movement. Miguel Brun-Usan, biologist and illustrator, and I created a range of visuals to enlighten, entertain, and inspire your understanding of the EES. We sincerely hope that you will find this review useful for your endeavors.

– Lynn

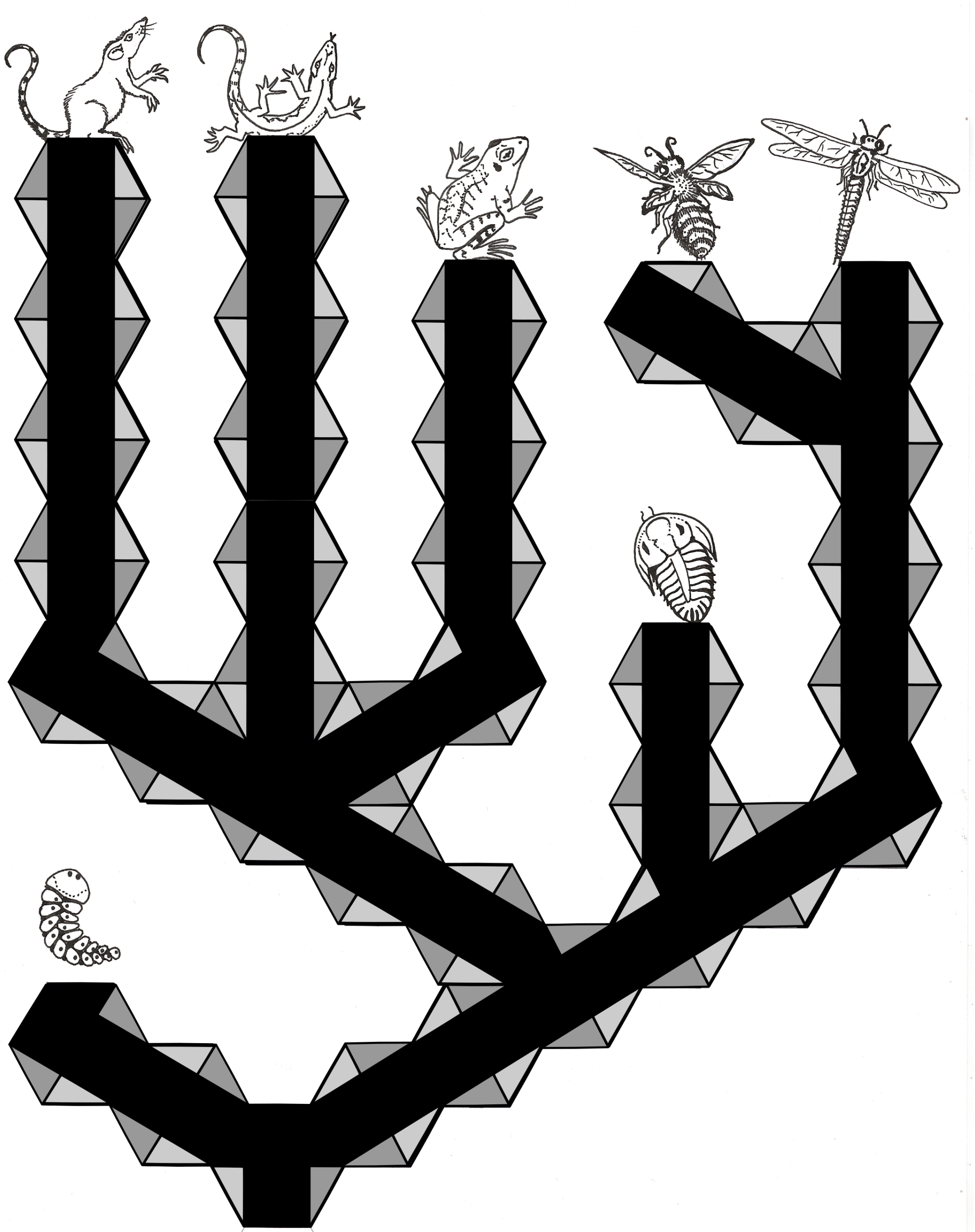
About the cover and section images



These figures are an artistic representation of different aspects of biological evolution, and a metaphor about how these aspects conform to different fields of study. The first layer, the simplest one, shows the phylogenetic relationships between a handful of living beings. This is the visible pattern of evolution, the classical focus of philogeneticists, paleontologists, and taxonomists. The second layer is concerned with the causes of that pattern: for organisms to change their phenotypes, they must change first the way they develop. Developmental stages are represented here as different embryos (this does not imply a recapitulationist, Haeckelian view). The interplay between the new variants and the omnipresent natural selection determine how phenotypes change across generations, that is, they determine the patterns seen in the first, tree-like layer. In the last layer, we show the deeper causes of development and selection that structure, in turn, the previous layer. This baroque "radiography" of evolution in action shows a great amount of intimate interactions between organisms. Such interactions are not limited to the tropic "who eats whom," but involve many informational, causal, metabolic, selective, and ecological interactions such as virus and bacteria-mediated gene transfers, co-evolution and specialization via parasitism and symbiotic partnerships, niche construction, environmental sensitivity and so on. While the drawing is not exhaustive, it captures how evolution is about "processes within processes," and how simplistic approaches to it are doomed to fail at explaining such wondrously dynamic, multilevel, and intermingled phenomenon.

— Miguel

Part I



How evolutionary theory became a gene-centric theory of evolution

Students taking their first course in evolutionary biology will often find that evolution is not what they expected. To address questions like “why do dinosaurs have feathers” or “how does this parasite come to have a life cycle through ants, birds, and cows,” they will learn that they need to look past the complex features and zoom in on where the evolutionary action actually lies: at the level of genes. Instead of studying how these traits develop and function, the students will find themselves busily calculating the relative numbers of gene variants and squinting over alignments of genetic sequences.

Evolutionary theory—as it is practiced today—is about changes in the genetic makeup of populations. It’s about random genetic mutations and their recombinations, about the long reach of genes into the selective environment, and about the faithful transmission of genetic information across generations. To explain the evolution of phenotypes is to explain the evolution of their underlying genes.

The standard curriculum of evolutionary biology is a product of nearly a century of intense focus on what the genetic world can offer to the rest of biology. The backbone of this curriculum is the Modern Synthesis, a theoretical discipline that has dominated evolutionary biology since its maturation in the mid-20th century. Instead of investigating evolutionary questions in terms of phenotypes, morphologies, embryonic structures, or ecological relations, the theories, practices, and training programs under the Modern Synthesis focus solely on the micro-evolution of genes.

However, the evolution of small genetic variants is merely one aspect of the complex evolution of life. For decades, scholars have expressed their deep frustrations over the limitations of the Modern Synthesis approach. They proposed amendments, revisions, expansions, or replacements that can enable us to return to the study of phenotypes and organisms, and how they interact with their environments. Some return to early Darwinian or even pre-Darwinian thought to revive discarded ideas. Others embrace theoretical insights from other disciplines, such as physics and complexity science.

In this section, we will take a quick tour through five major episodes of the last 150-plus years to understand how evolutionary biology became a gene-centric theory of evolution.

One aim of this short survey is to help us better understand the specific concerns that motivated an “extended evolutionary synthesis (EES),” which started to gain substantial ground in the early 2000s. A common misconception is that the EES is a full-blown refutation of Darwinian evolutionary theory. It is not. Understanding the history of evolutionary biology will show us that it has never been a single, static, or unified research field, but a dynamic constellation of concepts, assumptions, and practices. Not everyone agrees with the entire package, but no respectful scientist would reject them all.

Let us begin by thinking through what people mean by the term “Darwinism."

Darwin and Darwinism: Mid-19th century

Darwin's contribution to biology and our worldview was revolutionary (Mayr 1993; Ayala 2007). He collected compelling evidence that all life on Earth descended from a common ancestor, forming a single "Tree of Life." Darwin's **principle of common descent** (or descent with modification) states that species are not individually created but instead come into being by branching off from each other. Species are not fixed, essential categories, but populations of individuals with a variety of minute differences.

Darwin also proposed **the theory of natural selection**, where natural selection is the natural consequence of an exponentially growing population pushing up against finite, linearly growing resources. The result is a "survival of the fittest," with the supposedly "fitter" (better adapted) types surviving better and reproducing more, and able to pass down their fitter traits to the next generation(s). Gradually, evolution by natural selection results in the accumulation of small differences into complex adaptations.

We can think of the evolutionary tree as a map that represents how species are connected to each other. Evolution by natural selection is the engine that forged these connections by gradually splitting a population into new branches and pushing them further into greater differences.

Even though Darwin's main contribution to evolutionary biology was the theory of evolution by natural selection, he also accepted other modes of evolution, for instance, the principle of use and disuse often attributed to Jean-Baptiste de Lamarck (1744–1829) (i.e., traits strengthened through constant use in the parental generation are inherited by the offspring as a stronger trait, whereas traits that are not frequently used are only weakly inherited).

Furthermore, it was not clear to Darwin how inheritance works. He considered a variety of ways organisms may have been able to "like beget like." In addition to the inheritance of factors that are transmitted without influence from the life experiences of parents, he also considered various ways parental life events can "leak" into future generations through the inheritance of acquired characteristics, also frequently associated with Lamarck. Darwin's own theory was thus partially "Lamarckian."

Nowadays, the term **Darwinism** is often associated with the following assumptions concerning the evolution of natural selection:

Gradualism is the idea that populations could generate an abundance of variations, each minutely different from each other. As mutations are small, evolution works at a slow, leisurely pace, gradually sculpting and building up traits one tiny step at a time until they accumulate into complex forms.

Some argued that for natural selection to work, the individual traits of an organism should, to a large extent, evolve relatively independently of each other. From this **atomistic** perspective, natural selection can accumulate complex forms because it can safely tinker with one part of the organism without also changing the other parts.

Finally, the late Richard Lewontin (1929–2021) noted that Darwin's theory cut **a sharp line between organisms and environments.** Many predecessors and contemporaries of Darwin did not differentiate between the influences from organism and environment in evolution—individual changes feed into and are part of evolutionary change. Darwin, however, split the world into the organismal and environmental domains, with natural selection shaping the organisms to match up with a pre-existing environment.

As Lewontin put it, natural selection is the process of organisms proposing new traits that the environment disposes. Organisms blindly throw up variations that may fail or succeed while the environment determines the winners and losers. New variants do not emerge predetermined to meet preexisting environmental challenges, but are instead randomly generated and put to the test. As a result, the direction of evolution is entirely imposed by the external environment (**externalism**) (Levins and Lewontin 1985; Godfrey-Smith 1996).

In sum, a Darwinist is mainly committed to the following theses: **evolution as a Tree of Life**, **the theory of natural selection**, **gradualism**, **atomism**, and **externalism.**

Recommended reading: Lewontin's *The Triple Helix* (2000) is a critical analysis of the ideas that development is internally determined, that evolution is externally determined, and that traits are atomistic.

Neo-Darwinism: Late 19th century into the 20th century

Darwin's theory of evolution did not receive immediate widespread support. The principle of natural selection initially failed to kindle much enthusiasm (Bowler 1983). It was eventually revived by powerful advocates in the remainder of the 19th century, though in the form of a much more restricted version of Darwinism referred to as "**neo-Darwinism,**" a term coined in the late 1880s to highlight the stark differences between the two.

One founder of neo-Darwinian thought is Alfred Russel Wallace (1823–1913). When he coined the term "Darwinism" (Wallace 1889), he excluded the possibility of Lamarckian inheritance and strengthened the role of natural selection as the *only* source of creative power, one that stands in place of the omnipotent God the Creator (Kutschera and Hossfeld 2013).

This latter idea is **pan-selectionism** or **adaptationism**. It is the position that most (if not all) traits are adaptations that meet environmental challenges, and that natural selection is the main (if not the only) cause of adaptations.

The most influential figure is August Friedrich Leopold Weismann (1834–1914), who convincingly pushed forth Darwinian thought as a pan-selectionist theory without Lamarckian inheritance (Mayr 1985). His infamous experiments on mice seemly refuted the Lamarckian idea that changes to the body can be passed on to the next generation (Weismann 1892). Weismann explains these results with his germ plasm theory, which postulates that a stable substance called "germ plasm" (in the sperms and eggs) is set aside in the parent organism early in life, sheltered from life's challenges. Only the germ line is transferred (unmodified) to the next generation, not the somatic line.

Since inheritance is supposedly only restricted to the germ line, supporters of neo-Darwinism imagined a hard conceptual and physical "barrier" between the cells that matter for evolution (the germline) and those that do not (the somatic line): **the Weismann barrier**.

In sum, neo-Darwinism is characterized by (1) the full refutation of Lamarckian inheritance, such that inherited materials cannot be changed by events in the lifetime of the parent, and (2) the full commitment to adaptationism, excluding alternative modes of evolution. Its core concept, the Weismann barrier, will soon cast a long shadow over the 20th century. Some call it the "second law" of biology (the first law being the principle of evolution by natural selection) (see, for instance, Mattick 2012; Anava et al. 2015).

The Modern Synthesis: Early to mid-20th century

Neo-Darwinism further transformed in the 1920s. The term "**Modern Synthesis**" (coined by Huxley 1942) "Synthetic Theory," or simply "the (evolutionary) synthesis" describes two major theoretical conjunctions. The first was between Mendelian genetics and neo-Darwinian evolution, which gave birth to a statistical, genetic theory of Darwinian evolution. The second was the unification of major areas of biology, especially paleontology and systematics, but also zoology, botany, and natural history, under this new, unified Darwinian theory of evolution (Huxley 1942, Mayr and Provine 1980).

The first phase was a watershed moment in evolutionary history. At the turn of the 20th century, the rediscovery of **Mendel's laws of inheritance** shed light on how discrete particles could be passed on and recombined into a predictable distribution of trait types. Traits do not blend, but are instead associated with distinct "**genotypes**" that match onto distinct "**phenotypes**." Genotypes are combinations of gene variants (genetic alleles), which in turn are segregated and recombined across generations according to Mendelian rules.

At first, Mendelian genetics was thought to be fundamentally incompatible with Darwinism. Change in the former was discrete, the latter gradual. Thanks to the ingenious feat of statisticians and mathematical biologists in the 1920s, especially the three "architects of the Modern Synthesis," R. A. Fisher (1930), J. B. S. Haldane (1932), and Sewall Wright (1932), the apparent incompatibility was finally resolved (Provine 1971; Sarkar 2008).

On the basis of their work, the main figures of the Modern Synthesis established a quantitative, empirical science of evolutionary biology with **population genetics** as the conceptual and methodological core (Mayr and Provine 1981; Craig 2010; Millstein and Skipper 2007). Population genetics is a statistical theoretical framework that formally defines evolution as changes in the genetic composition of populations (i.e., changes in the frequencies of genetic variants) (Dobzhansky 1937). The goal of population genetics is to mathematically track changes in the relative frequencies of genes as statistical features of a population, following Mendelian rules of inheritance. Only four forces could instigate evolutionary change—migration (which creates gene flow between populations), natural selection (which selectively retains or eliminates genes from the population), mutation (which introduces new variants into the

Recommended reading: To learn more about the origin of Modern Synthesis and population genetics, read Provine's masterpiece, *The Origins of Theoretical Population Genetics* (1971).

population), and random drift (which randomly fixes or removes genes from the population).

A consequence of the mathematization of evolutionary biology is that numerous simplifying assumptions need to be adopted in order to render populations tractable. Population genetics is thus, somewhat derogatorily, often referred to as "beanbag genetics" (Mayr 1963, see Rao and Nanjundiah 2011). Evolving populations are stripped down to their bare genes, like bags of beans (Figure 1). Natural selection and random drift are analogous to the process of sampling a selection of beans from one bag to another.

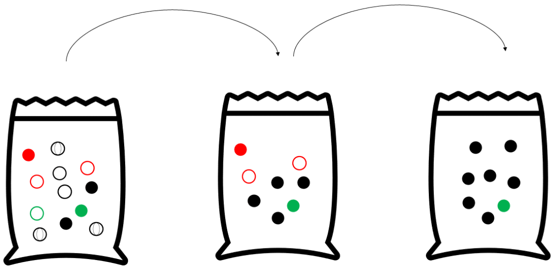


Figure 1. The beanbag analogy.

In population genetic models, genetic variants are tabulated and tracked as large numbers of independent genes with additive effects. The focus on the statistical outcomes of populations, which can be inferred autonomously from the underlying mechanisms and causes (Horan 1994; Walsh et al. 2017), makes the models flexible and highly generalizable.

In the second phase of the synthesis, proponents of the Modern Synthesis pushed to unify biology around a genetic, statistical model of evolution (e.g., Huxley 1942, Mayr 1942, Simpson 1944, Rensch 1947, Stebbins 1950). For instance, a seminal 1947 Princeton conference integrated genetics, paleontology, and systematics (Jepsen et al. 1949). As a result, a **gene-based definition of species** became widely adopted, i.e., in terms of the reproductive isolation of gene flow between populations (Mayr 1942, 1949). Consequently, macroevolution (the evolution of higher taxa) was treated as the accumulation of differences following speciation at the micro-level. Macroevolution is thus the extrapolation of microevolution, the genetic evolution of populations ("**extrapolationism**") (Mayr 1942).

Proponents of Modern Synthesis continued to uphold the pan-selectionist view that natural selection is the only force that can create complex adaptations from the raw ingredients of small, random variations (Stoltzfus 2017). As Muller (1949) concluded in the proceedings of the Princeton conference, evolutionary theory, *"…based on the natural selection of, mainly, minute variations, taken out of a great store of hereditary variations in numerous directions… now it constitutes a really vigorous 'neo-Darwinism'."* (p. 422).

In sum, the Modern Synthesis established a unified quantitative evolutionary biology centered on a statistical population genetics and neo-Darwinian, pan-selectionist thought.

Advanced reading: Smocovitis's (2020) Oxford Bibliographies entry on the Modern Synthesis is an excellent reference guide.

Advanced reading: Any characterization of the Modern Synthesis can only be partial (Love 2017). Even the founding figures disagreed with each other. Smocovitis's *Unifying Biology* (1996) reconstructs the diversity of views under the Modern Synthesis. For a recent reflection, see the special issue *Revisiting the Modern Synthesis* (Huneman 2019).

Expansion of evolutionary genetics in the molecular era: Mid-20th century

A “**molecular revolution**” ushered in a new era. Following the establishment of DNA as the carrier of biological specificity (that is, changes in DNA determine specific biological differences) in the 1940s and the discovery of the double-helix structure of DNA molecules in the 1950s, the “century of the gene” swept through all areas of biology (Keller 2002). The dominant metaphor is that genes are the “blueprints” and “programs” of life.

Recommended reading: Learn more about the molecular turn in biology with Evelyn Fox Keller’s (2002) book, *The Century of the Gene*.

Instead of working with abstract, statistical entities, the Modern Synthesis now had a material, physical basis of genes (Waters 1994). Population genetics incorporated the molecular toolkit and continued to serve as the foundation of a more expansive **evolutionary genetics**.

A gene-centric theory of evolution was further pinned in place by the conceptual pegs of **inclusive fitness theory** and **Mayr’s influential distinctions**, its contours sharpened by the **decontextualization practices** of molecular biology.

From the gene’s-eye view, evolutionary questions such as the origin and maintenance of group selection, altruism, and cooperation become problematized as evolutionary conundrums. **Kin selection theory** and **inclusive fitness theory** were developed to explain why individuals would sacrifice their own reproductive gain to promote that of others—because it indirectly promotes their own genetic lineage as well (Hamilton 1964). Group selection was recast in terms of individual selection (Williams 1966).

Ernst Mayr famously distinguished between two types of explanations in biology—**proximate versus ultimate causes** (Mayr 1961). When confronted with a biological phenomenon, say, the metamorphosis of butterflies, “proximate causes” explain how it works (e.g., how does a larva transform into a winged adult?) whereas “ultimate causes” focus on why something is the way it is (e.g., why do butterflies go through metamorphosis?). The former is the realm of developmental biology, physiology, and cognitive and behavior studies whereas the latter falls under evolutionary biology. As proximate questions about how a thing works are not sufficient to tell us why they work the way they do, the proximate sciences were thus seen as inconsequential to evolutionary biology.

He also coined the distinction between **soft versus hard inheritance** (see Mayr 1982). The former refers to Lamarckian inheritance and the effects of the environment on inheritance. These were excluded from contemporary evolution. The latter, on the other hand, is the inheritance of genes sequestered away behind the Weismann barrier.

The molecular focus further entrenched the importance of the Weismann barrier. Crucially, the focus on molecular biology changed how model organisms were selected and raised. To study genes and their products within organisms, model organisms were chosen and cultivated for their ability to fully develop within the laboratory in **decontextualized, controlled conditions**. So that they could be studied without the influence of the environment, they were especially selected for a particular characteristic: the early separation of the germline from the somatic line (Gilbert 2003b; Minelli and Baedke 2014). Studying organisms outside of the context of their natural environment allowed the researcher to study genetic influences using standardized protocols from any laboratory in the world.

Dealing with dissent and discontent: Late 20th century

As empirical evidence for natural selection "in the wild" grew (see Endler 1986, Kingsolver et al. 2001), discontent simmered under the shadows of the Modern Synthesis. Several types of findings, in particular, generated significant debates over the dominance of neo-Darwinism and the Modern Synthesis. These dissents, however, were either assimilated into the mainstream theory, dismissed, or ignored.

In the 1960s, Motoo Kimura's (1924–1994) proposed **the neutral theory of molecular evolution**, arguing that not only is there an abundance of genetic diversity in populations, but that they are largely "neutral," i.e., they do not show up as selectable traits (Kimura 1968, 1983, 1991; Ohta 1973).

Neutral theory was seen as "non-Darwinian" because it rejected the pan-selectionist, adaptationist assumption that evolutionary change and genetic diversity are predominately driven by natural selection (King and Jukes 1969; Gould 1982). Instead, neutral theory holds that molecular evolution is mostly the random fixation of neutral mutations. Advantageous mutations are rare.

Even though the original architects of the Modern Synthesis (e.g., Fisher) dismissed the importance of chance and random genetic drift in evolution, the research program eventually assimilated the neutral theory as providing the baseline "null model" for evolutionary genetics, one that can be used to detect the presence of natural selection (Veuille 2019). Neutral theory became a foundational pillar of evolutionary genetics (see Kern and Hahn (2018) and Jensen et al. (2019) for renewed debates on the occasion of the neutral theory's 50th anniversary).

Another influential debate comes from the "paleobiological revolution" that coalesced around **the theory of punctuated equilibrium** (see Gayon 1990; Sepkoski 2012).

According to gradualism, evolution is slow and continuous. Gaps in the fossil record thus merely reflect incomplete records. The alternative theory offers a different interpretation: perhaps the intermediate forms never existed. This is because evolution might instead move in short, drastic spurts after long periods of stasis (Grene 1958a, b; Eldredge and Gould 1972; Gould 1977; Gould and Eldredge 1977). Stephen J. Gould (1941–2002) and Nile Eldredge (1943–), for instance, argued for a new "hierarchical" theory of evolution, rejecting core neo-Darwinian and Modern Synthesis assumptions such as extrapolationis, pan-selectionism, and gradualism (Gould 1980; Eldredge 1985).

In response, Modern Synthesis defenders argued that punctuated equilibrium is equivalent to theories they've already proposed (see Mayr 1982). At the very least, they countered that the phenomena can be adequately explained by the Modern Synthesis (see Futuyma 2015).

The third critique emerged from organismal biology, especially developmental biology. Against the supremacy of natural selection, **non-adaptive hypotheses** were proposed to explain the emergence of dramatically novel forms from bio-physical forces and developmental processes that can constrain or facilitate new phenotypes (Gould 1980; Gould and Lewontin 1979).

C. H. Waddington (1905—1975) proposed a rich theory of **evolutionary systems** that recenters the role of the organism in evolutionary biology (Waddington 1959a, 1959b). However, despite his many efforts, including the organization of multi-year conferences in the 1960s to try to break through the Weismann barrier, his work was largely ignored by the mainstream (though eventually, his concerns lay important groundwork for the extended synthesis movement) (Peterson 2011). In Part II, we will survey current challenges against the Modern Synthesis and neo-Darwinism that come from organismal biology.

Recommended reading: In *this mini-series*, Peterson writes about Waddington's efforts to bring the organism into evolutionary theorizing.

In the 1990s, biological structuralism rose against neo-Darwinism to embrace internalist, structural explanations over the externalist, functional focus of selectionism (Goodwin 1990). It was refuted as it radically rejects the power of natural selection (Baedke 2021).

Despite these challenges, evolutionary genetics prevailed. Meanwhile, the general public embraced gene-centric evolution. Richard Dawkins (1941—) famously articulated the gene's-eye view with **the selfish gene metaphor** (Dawkins 1976), a replicator model of evolution. The metaphor takes genes as the fundamental and only unit of evolution. Individuals and phenotypes are merely the means, the vessels, for genes to self-replicate and make more genes.

Recommended reading: Ågren offers an in-depth appraisal of the selfish gene theory in *The Gene's Eye View of Evolution* (2021). Listen to a podcast interview with the author *here*.

Evolutionary biology into the 21st century: Standard evolutionary theory

Following a common practice from the EES side of the debate, I will use the phrase "**standard evolutionary theory**" to refer to the theory of evolution practiced today.

Proponents of the EES examined the content of classic textbooks on evolutionary biology and found that teaching practices and research routines are still built around the concept of evolution defined and modeled in population genetics. One of the most popular textbooks is *Evolution* by Futuyma and Kirkpatrick (2017), now in its fourth edition. Table 1 is a summary of how it characterizes the core principles of current evolutionary biology. From these principles, it is clear that evolution is still defined as changes in the frequencies of genetic variants. We can also find the core Darwinian, neo-Darwinism, and Modern Synthesis commitments.

As a research program practiced and taught in the academy, today's evolutionary theory is a gene-centric theory of evolution. Main figures in evolutionary genetics insist that evolution defined this way is the *"only credible process underlying the*

Table 1. Principles of evolution (adapted from Futuyma and Kirkpatrick 2017, Box1A)

1. Phenotypes are distinct from genotypes.
2. There is no inheritance of acquired characteristics.
3. Hereditary variations for continuous and discrete traits are both based on genes.
4. Mutations do not arise in response to need, but by random mutation.
5. Evolution is change of a population, not of an individual.
6. Changes in allele frequencies may be random (genetic drift) or nonrandom (natural selection).
7. Adaptations are traits shaped by natural selection, which accounts for both small and greater differences between species.
8. Natural selection can alter populations when there are new combinations of genes.
9. Populations usually have a considerable amount of standing variation that can allow them to respond quickly to changing environmental conditions.
10. Species differences evolve in small steps based on an accumulation of genes over multiple generations.
11. Species are defined as separately evolving "gene pools" with no gene flow between them. They consist of interbreeding (or potentially interbreeding) individuals that do not exchange genes with other groups.
12. Speciation usually occurs through geographic isolation.
13. The evolution of higher taxa (macroevolution) arose from the accumulation of small differences rather than the sudden appearance of drastic new mutations.
14. All organisms evolved from a common ancestor, branching out from a great Tree of Life.

Recommended reading: Bonduriansky and Day (2018) explain the historical fixation on genetic evolution in *Extended Heredity: A New Understanding of Inheritance and Evolution.*

evolution of adaptive organismal traits" (Charlesworth et al. 2017, p. 10).

First, genes are the fundamental currency in the key processes of evolution: they are the origin of variations, the only elements that can be inherited, and the main targets of natural selection.

Second, phenotypic evolution only occurs when it can be accounted for by genetic evolution. In the era of increasingly cheap high-throughput sequencing, phylogenetic analysis moved from a largely morphological comparative biology to the evolutionary comparison of genetic sequences.

The molecular-centered toolkit is a fundamental component of evolutionary analyses, both in the field and in the wet and dry lab. The utility of molecular biology, alone, does not fully define what it is for evolutionary biology to be gene-centric (see, for instance, Gilbert 2000a's analysis that molecular biology could have been compatible with Waddington's approach). It is molecular biology coupled with the statistical models of population and quantitative genetics and the exclusion of non-genetic influences that establish genetic evolution as evolution.

A consequence of focusing on evolutionary genetics is that the study of evolution becomes centered on traits that have a strong correlation (i.e., a linear, direct mapping between genotypes and phenotypes) between genetic variation and phenotypic variation. The evolution of organismal structures and phenotypic complexity remains unaddressed, only implied by the evolution of genes.

Putting it all together:
The structure of standard evolutionary theory

Philosophers and historians of science have long observed that the practitioners of an established science will, implicitly or explicitly, repeatedly try to hone and fit the theorems, assumptions, practices, and findings into a coherent and elegant science (Kuhn 1962; Lakatos 1976; Ankeny and Leonelli 2016).

We can metaphorically visualize the commitments of scientific framework as polygonal pieces of a tangram (Figure 2). A tangram is a popular puzzle game consisting of geometrical pieces that can be put together to form different shapes. The goal of the game is to fit the pieces together to form a target shape, for instance, a square like the one below. In a tangram, different shapes need to be puzzled out to fit together to form a perfect square. When a new study is conducted and new phenomena are uncovered, the first reaction is to try to reframe and categorize it in terms of the fitted shapes, so that they, too, can neatly fit into the whole. Those that cannot are set aside as anomalies, exceptions, or mistakes.

What are the tangram pieces that make up standard evolutionary theory?

Figure 2. A tangram and its pieces.

Denis Walsh argued that standard evolutionary theory has become **a fractionated theory**, where key processes of evolution are treated as quasi-autonomous from each other (Walsh 2015; Huneman and Walsh 2017a). This fractionation manifests itself in several areas (Figure 3).

First, the process of evolution is idealized as a linear procedure proceeding from the generation of variation, the development of these variants into phenotypic variations, and the subjections of these variations to natural selection. The components of Darwinian evolution—variation, inheritance, selection are treated as independent from each other (Denis 2015; Watson and Thies 2019; Uller and Helanterä 2019; Uller et al. 2019).

Variation is regarded as the product of blind, random mechanisms. They are not created in anticipation of selective environments. Nor are they the outcomes of transmission mechanisms. Selection then acts on these variants independent of whether and how they will be inherited. The mechanisms of inheritance operate independently of selection and variation, determined merely by the productive and transmission process. The common thread connecting all three processes: genes as the fundamental currency of evolution.

Phenotypes and developmental processes are background elements in this picture of evolution. They are the "long reach of the genes" (Dawkins 1999), the vehicles that manifest genetic differences to the forces of natural selection. Even though phenotypes are the "interactors" between organisms and environments that are selected and inherited across generations, it is the underlying genetic "replicators" that are the true subjects of evolution (Hull 1980).

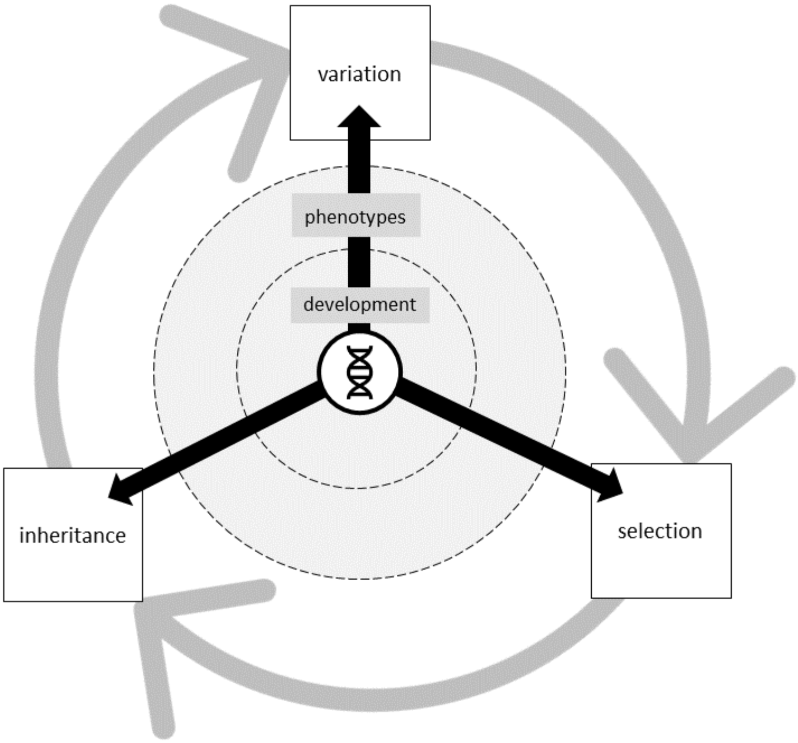


Figure 3. The fractionations of standard evolutionary theory

Biological processes are also divided into internal–external dichotomies (Figure 4). Compared to that of the external environment, organisms and their internal processes are seen as playing distinct roles in evolution, Genotypes are the underlying genetic factors that map onto phenotypes, which are the outward-facing traits visible to natural selection. Development, physiology, behavior, cognition, etc., are proximate causes thought to be irrelevant to evolution, which is instead ultimately explained by the selective environment (ultimate causes). The only internal processes that are relevant for evolution are the processes of variation and inheritance, whereas external forces determine the outcome of natural selection.

To conclude, under standard evolutionary theory, new findings and studies are categorized into these fractionated components that are pieced together into the following tangram (Figure 5).

Each scientific framework has its own theories, practices, and routines (Ankeny and Leonelli 2016). For standard evolutionary theory, the narrow focus on genetic evolution allowed for a high-resolution and precise analysis of concrete concepts and materials that could be measured, analyzed, modeled, manipulated, and passed down in the form of statistical models, molecular techniques, and standardized laboratory practices and model organisms that are decontextualized from the environment. Genetic evolutionary models demonstrated high predictive power for short-term evolutionary outcomes.

It is crucial to remember that standard evolutionary theory is also a reaction to the biology of its time (Depew and Weber 2013; Futuyma 2015). It refuted theories that attributed the source of evolution to the internal power of organisms, some of which lacked empirical support and drew on questionable principles.

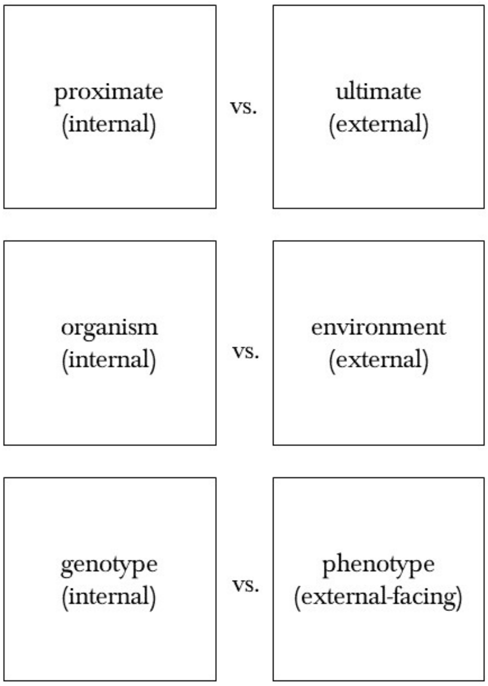


Figure 4. Internal-external dichotomies of standard evolutionary theory

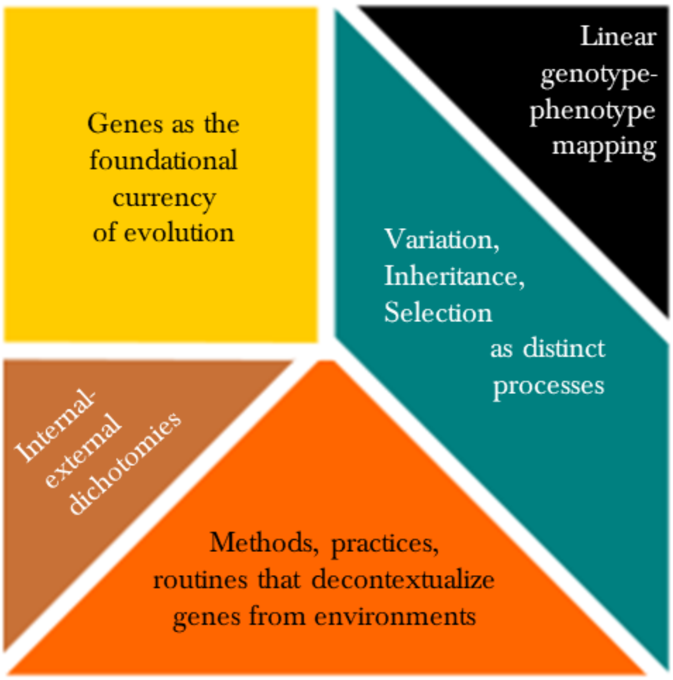


Figure 5. The tangram pieces that constitute standard evolutionary theory, fitted together into a coherent framework.

Where the theory applies (in the molecular and genetic domain), it works well. Yet relying on standard evolutionary theory as the only framework of evolution comes with a cost.

The explanatory and predictive power of genetic evolution rests on models, methods, and protocols applied to idealized mathematical scenarios and specialized model organisms (Baedke et al. 2020). To track the dynamics of genetic evolution, theoreticians need to make simplifying assumptions that idealize away the environments around genes, but by doing so, they screen off factors that can be evolutionarily relevant. For instance, back to the beanbag analogy, by ignoring the ways beans might chip and dent as they bump into each other, we're ignoring an important way beans change through time. The benefit of abstracting away from actual biology is the ability to rigorous model and predict evolutionary change must be weighed with the risk of erroneously omitting important factors.

Powerful molecular tools allow us to precisely access the molecular world of genes and proteins, yet they offer us mere shadowy glimpses of the evolutionary influence of cells, tissues, organisms, social relations, and environments.

Standardized model organisms are bred, raised, and processed in decontextualized, standardized artificial environments to cut out "noise," but by doing so, we also throw out the actual signals.

Furthermore, these practices also derive broad stroke, generalized ideas about evolution from a very narrow subset of biology: eukaryotic, bisexual macroorganisms (see Kutschera and Niklas 2004; O'Malley 2014).

While a genetic approach may be thought of as a heuristic map that can temporarily help research and teach evolutionary theory, unfortunately, the "maps have become the world" (Winther 2020). The very nature of evolution is defined in terms of genetic evolution. Even though genes are exposed to "the eye of natural selection" they only exist in organisms in their environments. The cellular, physiological, developmental processes through which organismal change is achieved are assumed to be irrelevant, transparent conduits, mere "middlemen" that do not make a difference, that connect genes to natural selection. At most, organisms and environments are either seen as a background condition of evolution or mere products of evolution.

According to proponents of alternative approaches, the gene-centricism of evolutionary theory has left out, excluded, distorted, and marginalized important principles and areas of study in evolutionary biology. There is a need to return to the evolution of phenotype, with genetic evolution offering one aspect of phenotypic evolution.

As we will see, the main challenges against standard evolutionary theory come from areas of biology that studied how organisms develop, operate, behave, and interact with others and their environments. The organism and its phenotypes are missing from the tangram of standard evolutionary theory.

Disciplines that focus on organismal processes and interactions bring attention to phenomena excluded from a genetic evolutionary theory and break the various dichotomies that define standard evolutionary theory.

Part II

Challenges from organismal biology: Six selected cases

Standard evolutionary theory assumes that **the ways organisms develop, function, behave, and interact** (aka the "proximate" sciences) are evolutionarily relevant in only one specific way: they are the phenotypic outcomes of genetic variants that expose the latter to natural selection.

However, researchers in the fields of developmental biology, physiology, biophysics, the behavioral sciences, as well as the biology of social and cultural phenomena, etc., have found that the proximate sciences could have a significant impact on evolution in significant ways.

In this section, we examine a range of illustrative examples that challenge the "tangram" of standard evolutionary theory from an organismal perspective. The selection is not meant to be exhaustive. Many of these examples were independently developed from different research disciplines. We will seek to cover their beginnings and current research, but can only be selective. It should become clear that despite their independent origins, there is significant overlap between these phenomena. The commonalities undergird the multidisciplinary collaborations for an extended evolutionary synthesis (EES).

Table of Contents (click to jump to section)

At the end of each section, a table will summarize the main theories, concepts, and examples.
In text, examples will be highlighted by a purple box.

Theories	Concepts	Examples

How development drives evolution

During the development of multicellular organisms, a single cell divides and proliferates into an aggregate of cells, which then acts as a coherent entity. It then undergoes reshaping into the specialized tissues of a developing embryo. A common misunderstanding of this process treats development as a mere readout of an evolving "genetic blueprint." Development—a proximate cause—is thus seen as irrelevant to evolution. Indeed, the fields of embryology and developmental biology were not included in the construction of the Modern Synthesis and were left out of evolutionary biology (Gilbert et al. 1996).

The field of **evolutionary developmental biology** ("**evo-devo**") is one of the major contributors to a new theoretical framework of evolutionary biology (for instance, Amundson 2005; Müller 2007, 2020; Carroll 2008; Moczek 2012). Under evo-devo, evolution is not treated as heritable changes in gene frequencies, but as the evolution of the *phenotype* through heritable changes in *development*.

Increasingly, evo-devo studies can be divided into two sets of questions (Figure 6): "traditional" evo-devo asks how development evolves. A "**devo-evo**" (**developmental evolutionary biology, or developmental evolution**) branch of evo-devo, on the other hand, examines the direct impact of developmental processes on the strength, rate, direction, and dynamics of evolution (Gilbert 2003a; Müller 2007; Moczek 2012). Devo-evo studies flip our understanding of the relationship between development and evolution. Instead of thinking of developing organisms as a passive putty molded and

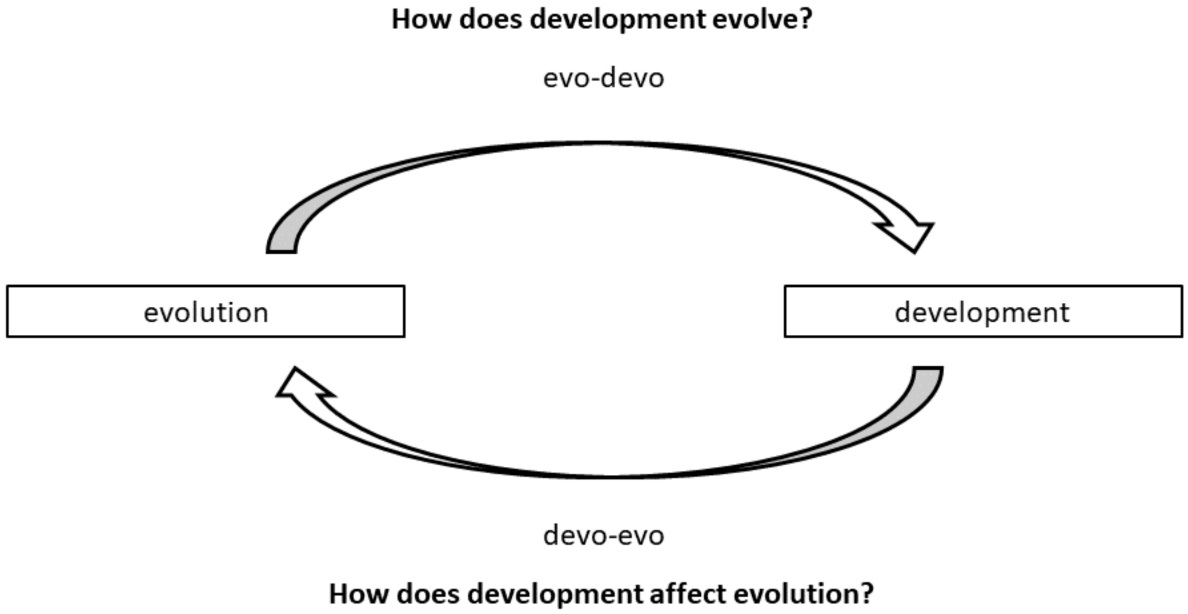


Figure 6. The relationship between evo-devo and devo-evo.

sculpted by natural selection, development is instead found to be a complex and dynamic process actively guiding phenotypic evolution.

example

Consider the problem of "hot spots" of evolutionary innovation and diversity in regions that are normally conserved across species. Beetles exhibit a fantastic array of big, small, and oddly shaped horns on the top of their heads (i.e., thoracic horns at the first thoracic segment). These thoracic horns are novel traits in evolution, while the head itself is deeply conserved across species.

Armin Moczek and his team found that the horns, as true novel traits, did not evolve from the appearance of new genes alone. Instead, these evolutionary innovations also re-purposed the developmental circuits of other structures (Hu et al. 2019a, b; Linz and Moczek 2020). One of these is the so-called "pupal horns" of beetle pupae that help them break through head capsule cuticles. A surprising finding is that evolutionary pathways used for the development of wings were also co-opted for the development of adult horns!

One take-home message from these studies is that we need to reexamine the orthodox idea that there are such things as "gene-for X" (e.g., "genes for wings" or "genes for horns"). As the genetic networks of early developmental processes were used in later or other contexts, basic developmental packages could become involved in multiple phenotypes and their evolution. New traits are not always caused by the appearance of new genes.

A more general lesson is that developmental processes can influence which phenotypes can actually appear, how they appear, how likely, and how frequently (Uller et al. 2018). Many argue that development can thus "bias" the direction of evolution. Minimally, when certain traits cannot develop, they cannot evolve. Developmental processes can further dictate how organisms evolve as well. The study of "**developmental bias**" is a core component of evo-devo/devo-evo studies (Alberch 1980; Maynard-Smith et al. 1985).

Advanced reading: A special issue in *Evolution and Development* about developmental bias, edited by Moczek (2020). See especially the introductory article "Biases in the study of developmental bias."

To visualize developmental bias, we can make use of what is known as a "**morphospace**" or phenotypic space. Let us image evolution as carving out a path in a multidimensional space of physically possible traits. Each axis in the morphospace represents variations on a phenotype. Each dot stands for a possible

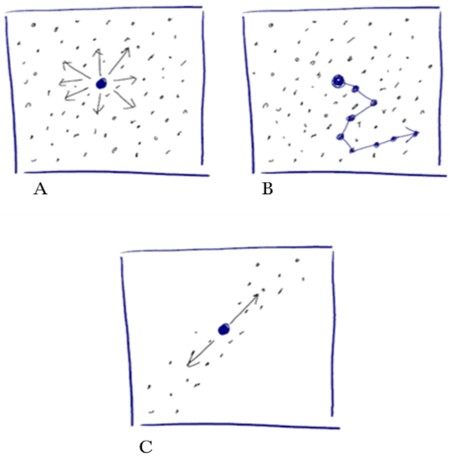


Figure 7. Two-dimensional morphospaces. The X and Y axes each represent traits varying on a dimension (e.g., length, width).

organism with a combination of traits. Standard evolutionary theory tells us that genetic mutations are small and abundant as well as randomly generated. This will generate a densely covered, evenly populated morphospace (Figure 7A). Natural selection can connect the dots to draw out any path within this space (Figure 7B).

The study of developmental bias has revealed that natural selection is not the only game in town. The process of development—how organisms change throughout their life cycles—can have a major impact on the direction, rate, and magnitude of evolution. In some cases, developmental features can prevent certain types of traits from developing, even if there is an abundance of small genetic mutations. In other cases, there is a "**canalization**" of phenotypes, that is, even as genetic mutations accumulate, there is no new phenotypic expression as phenotypes are stabilized by multiple physiological and developmental processes. Using the two-dimensional morphospace as a metaphor, we can see that the morphospace is not fully filled (Figure 7C). Evolution can only push in a few directions because there are "developmental constraints" against the other possibilities (Gerber 2014).

Yet the impact of developmental architecture on evolution is not merely "negative" (in that it restricts evolutionary possibilities). From the perspective of standard evolutionary theory, natural selection can still act as it pleases as long as the available phenotypes are still the result of an abundance of small, genetic mutations that map onto phenotypic variation.

A key characteristic of developmental bias is that changes to developmental processes can also create novel variants in response to genetic or environmental perturbations. Developmental processes are complex dynamics that involve multilevel interactions, from the genetic level to the tissue and organismal level. These dynamics also include inputs from the environment.

Changes at any of these levels, not just genetic mutations, can trigger coordinated responses across multiple levels, thus generating novel phenotypes. This type of phenomenon is sometimes called "**facilitated variation**" (Kirschner and Gerhart 2006; Gerhart and Kirschner 2007) or "**emergent variation**" (Badyaev 2011).

Understanding bias as not just the constraining (developmental constraint) but also the constructive effects (facilitated variation) of development on evolution allows us to think about the complex ways development can reciprocally interact with natural selection (Félix 2012; Uller et al. 2018; Salazar-Ciudad 2021). Against gradualism, the reality may be that while simple traits may evolve through gradual accumulation of small variants, complex traits will tend to evolve through quick leaps ("punctuation") (Salazar-Ciudad and Jernvall 2005).

example

Biological structures with **serial repeated characters** such as the teeth, fingers, insect segments, or pigmented patterns are classic model systems for the study of developmental constraints. These repeated units look alike because they share similar or the same developmental "modules." They are thus excellent systems to examine how tightly integrated these developmental modules are ("**modularity**"), which can constrain possibilities in a morphospace. The properties of these modules can determine how easy or difficult it is to evolve new variations ("**evolvability**").

For instance, analyzing the global genetic database of Maine Coon cats, which have a tendency toward polydactyly (the possession of extra digits), Lange et al. (2014) found that these extra digits are not generated randomly. Physico-developmental processes result in strong tendencies to develop repeats on only specific digits.

Another example of developmental constraint is the eyespots of butterfly wings, which are often repeated along each wing and on both sides. They look stunningly like the eyes of snakes or owls, confusing predators. In the wild, the two main eyespots of African Mycalesina butterflies naturally vary in their size as well as the relative colors of their concentric rings (some have thicker black bands than others).

Patrícia Beldade, Paul Brakefield, and others have examined how far they can push the independent evolution of the two eyespots by artificially selecting for different eyespot colors and size (Brakefield et al. 1996; Beldade et al. 2002). Standard evolutionary theory would predict that we could push the populations to evolve in any direction (that is, any combination of eyespot size and color) as there already are natural variations of these traits in the population to select from.

Yet after evolving the species *Bicyclus anynana* for multiple generations, they found that only the size of these eyespots fit this prediction. It is relatively easy to evolve the sizes of each eyespot independently (they could easily evolve butterflies with one big and one small eyespot). However, it is not quite possible to do so with the colors (they couldn't easily evolve one eyespot with a big black band while the other has a thinner black ring) (Allen et al. 2008). The difference between size and color is explained by their respective developmental structures, which shows that preexisting genetic variation is not enough for selection to create new types. The developmental constraints must allow it.

Interestingly, in one species, artificial selection can freely evolve butterflies with eyespots that vary in color composition (Brattström et al. 2020). The appearance of these new types enabled a burst in diversity of new eyespot morphologies in that lineage. This shows that when evolution breaks through developmental constraints, the previously impossible variations are now available for selection.

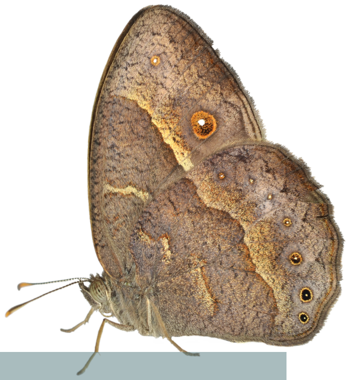


Table 2.

Theories	evo-devo devo-evo
Concepts	developmental bias morphospace developmental constraint evolutionary innovation emergent variation facilitated variation modularity evolvability canalization
Examples	serial repeated characters (digits, eyespots on wings) innovations in beetle horn evolution

Why physics matters for evolution

The gene-centric focus of standard evolutionary theory can easily distract us from the effects of physics on the developing organism.

example

A striking example is the role of gravity in chick development (Kochav and Eyal-Giladi 1971). Eggs rotate and spin at a regular speed as they pass through the hen's reproductive tract. While rotating, the lighter elements remain at the top end of the yolk thanks to the presence of gravity. This region is important—it marks the back end of the future chick. Gravity and its effects on egg development are clearly not part of the genetic program but are essential for the shaping of the embryo.

Two crucial facts about the developmental process are commonly ignored under the genocentric framework: (1) that it is the physical properties of cells that determine how they move, stick together, stop, or separate from each other and (2) that the genes and proteins of a developing embryo often act by harnessing the resultant mechanical forces and fluid flow in the specification of organismal form. In the molecular era of the 20th century, these physical and mechanical aspects of development have been sidelined in favor of explanations focused exclusively on molecular signaling pathways and genetic circuits.

Stuart Newman has long championed that biology should take seriously the importance physical factors such as adhesion, surface tension, viscosity, phase separation, gravitational effects, etc., that determine organismal form (Newman and Frisch 1979; Newman and Comper 1990; Newman 1994). As these physical properties are also characteristic of some kinds of nonliving matter, they are **"generic" physical mechanisms** that inherently generate shapes and forms, for instance, the formation of cavities, layers, segments, tubes, and appendages. The origin of complex multicellular form appeared before the evolution of complex genetic programs. It was physical processes, with early genes enabling cells to access the generic physical mechanisms, that made multicellularity possible.

example

An example is cell adhesion. Cells stick together in multicellular organisms through adhesive proteins on their surfaces. In animals, cadherins typically perform this role. Even though these proteins are the products of genes, they don't acquire their function—stickiness—without the right environment. Cadherins depend on calcium for their function; they are not sticky in the absence of this ion. A sudden shift in environmental calcium can thus transform single cells into multicellular masses, a major morphological transition based in biophysics. Other examples include surface tensions and electrophysiology (Foty et al. 1996; Brodsky and Levin 2018).

The major body forms we see today were created early in the evolutionary history of animal life (Newman 2016). From the physico-genetic, **"biogeneric" perspective**, the new forms did not evolve through the long accumulation of small genetic mutations. Instead, the major morphological motifs or features can be explained as the natural result of their unique physical properties and mechanisms (Newman 2002; Newman et al. 2006).

Recommended reading: *Physical mechanisms of development and evolution: An interview with Stuart Newman.*

example

For instance, separation between cell groups arises when there are differential adhesions of cells. Cavities and lumens form when there is asymmetric distribution of adhesion molecules on cell surfaces. Patterns that can shape future tissues come from sedimentation by gravity, or the diffusion of morphogens and their interaction with the cells' gene expression. An ancient multicellular animal might have been able to easily shift between these different forms depending on the balance of these factors. As evolution proceeds, however some morphologies could become locked into a stable state when selection favors genetic changes that further stabilize these states.

example

When considering convergent traits between species, rather than attributing their similarities to similar sources of natural selection, it is also important to consider whether their traits arise from shared generic physical mechanisms. In their latest paper, Arias et al. (2020) argue that the similar developmental trajectories of myxobacteria and dictyostelids are more due to shared generic physical processes and similar agent-type behaviors.

Standard evolutionary theory assumes that new, complex, and adaptive forms evolve only through the accumulation by natural selection of random, small changes in genes. By studying the roles of physical effects in morphogenesis, physico-genetic arguments show that phyletic transformations can be based on transitions in bio-physico-chemical properties and mechanisms inherent to the developing animals (Newman 2019). The genetic underpinnings of these transformations can be novel toolkit genes that endow the developing tissues with new inherent morphogenetic propensities (**the principle of inherency**). But they could also be existing genes for which environmental effects elicit new physical properties, with the morphological outcomes reinforced by subsequent evolution of stabilizing genetic interactions. These studies show that we need to refocus on the physical mechanisms and properties that matter, not just genetic information.

Recommended lecture: *Inherency and Agency in the Evolution of Development* by Stuart Newman.

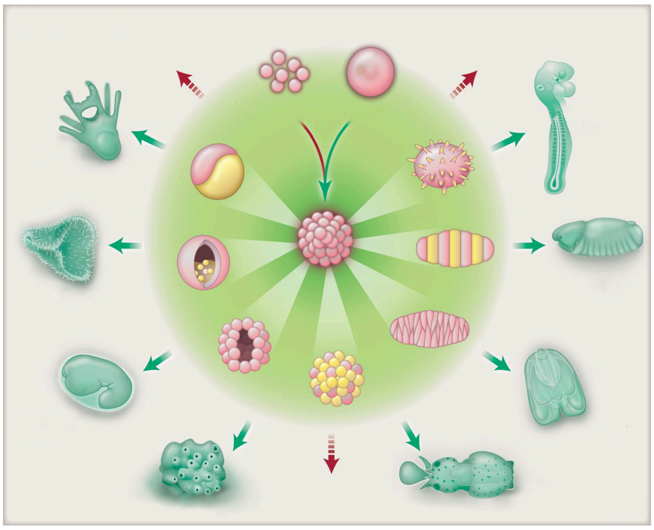


Table 3.

Theories	principle of inherency
Concepts	generic physical mechanisms
Examples	egg development cell adhesion evolution of body forms myxobacteria and dictyostelids development

When phenotypic plasticity guides evolution

When organisms exhibit different shapes, sizes, or any number of other traits and features in different environments, this phenomenon is called “**phenotypic plasticity**.” The study of plasticity falls under the field of “**ecological developmental biology**” (eco-devo).

We can visualize phenotypic plasticity by plotting the different phenotypes an organism can exhibit across different environments. This plot is called a “**reaction norm**” or “norm of reaction” (Figures 8, 9).

A problematic interpretation of reaction norms is to take only one of those phenotypes as the “true phenotype” adapted to one of the environments (Figure 9). The rest are seen as minor, transient deviations that do not affect evolution. Plasticity, from this perspective, is the noise that obscures the signal.

This view is challenged by work showing that plasticity is an integral part of evolution (Schlichting and Pigliucci 1998). Sonia Sultan argues that plasticity is an ecologically important trait that varies, evolves, and impacts future evolution (Sultan 1987, 1992, 2003, 2007, 2015). Plastic responses are not “noise” obscuring the single, true adaptation, but ecologically significant traits that interpret and respond to the environment through signal transduction processes. These adaptive traits can alter the environment an organism is exposed to and experiences.

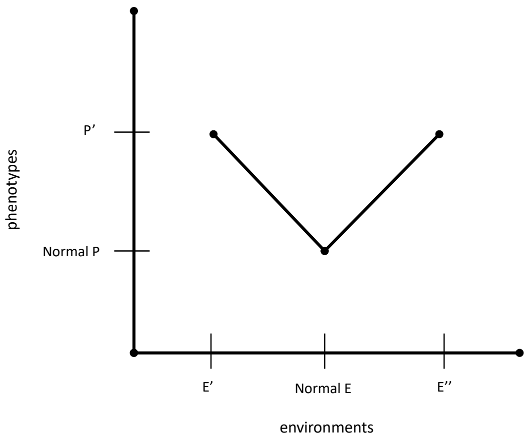


Figure 8. A problematic way of understanding a reaction norm across three different environments

example

Phenotypic plasticity is an ecologically significant trait that can vary between species. For example, an important plastic trait is the way certain plants can adjust to environmental conditions by selectively investing energy in leaf as opposed to root tissue growth (and vice versa). Under shade, the species *P. persicaria* will divert more energy to leaf production (as evidenced by an increase in biomass), an adaptive response that helps it collect more sunlight under lower light conditions. Another species, *P. hydropiper*, does not reallocate its resources as prominently under shade. This variation in plasticity probably explains why *P. persicaria* can expand into shady areas while *P. hydropiper* is limited to areas with more sunlight (Sultan 2003). The entire reaction norm is thus a property of the organisms (Sultan 2021). Plasticity is a feature, not a bug.

The plastic responses can be passed on as acquired traits. In a new study, *P. persicaria* plants were placed under competition with each other (Waterman and Sultan 2021). Intense competition between parents (i.e., close neighbors, which creates shade) triggered plastic responses to shade. Interestingly, they found that this competition had apparent influence on the growth, size, shape, and development of offspring plants. The offspring of competing parents had more total biomass and greater total leaf surface area than those from noncompeting parents. Intriguingly, these beneficial traits only appeared when the offspring were also grown under shade! The parents did not just transmit their plastic response to their offspring, they somehow conferred a beneficial, improved plastic response that is triggered only in the relevant environment. It is an environment-dependent trait expression.

514. Polygonum Persicaria.

Surprisingly, these transgenerational effects disappeared when the offspring plants were grown in sunny, dry soil conditions. The plastic trait is thus conditional on multiple environmental circumstances. We now know that organisms inherit not just genes, but also extra-genetic factors that regulate the expression of genes (such as cytoplastic small noncoding RNAs or epigenetic DNA methylation). In *P. persicaria*, DNA methylation changes are known to be associated with the inherited effects of shade (Baker et al. 2018).

Recommended podcast: Episode 60 of "The Naturally Speaking Editors," *Extending Evolution, an Interview with Prof. Sonia Sultan*.

Plasticity is a complex phenomenon. **Adaptive plasticity** refers to plastic responses that are complex, coordinated, and adaptive to brand new environments. Collating a wide array of evidence, leading scholar of phenotypic plasticity Mary Jane West-Eberhard argues that novel phenotypes can arise from the integrated reorganization of preexisting developmental processes induced by environmental triggers (West-Eberhard 2003).

example

An iconic example of complex, adaptive plasticity from West-Eberhard's book (2003) is Slijper's famous two-legged goat. Goats are not meant to stand on two legs and thus do not have the evolved adaptation to do so. Yet in this goat with only two legs, when it started to stand up and walk, a complex suite of adaptions developed in response to its new standing posture.

This is a novel trait that came from preexisting phenotypes, coordinated through developmental mechanisms in response to the environment, but were not meant for the purpose of upright walking. Adaptive plasticity is not always the outcome of prior evolution. The modular connections between traits seem to emerge from developmental plasticity as a universal, biological feature, not selection (West-Eberhard 2019).

Yoev Soen and his team proposed an organization principle that explains how organisms can respond to novel, stressful conditions with adaptive phenotypes, and more importantly, how this "**adaptive improvisation**" drives evolutionary processes. The hypothesis is that when organisms generate random changes in response to environmental stress, this can trigger a suite of self-organizational processes that end up being adaptive for the organism. These beneficial changes can then be further reinforced and entrenched through evolution by natural selection. The ability to harness randomness for adaptive traits is an active area of exploration (see Nobel 2017).

More generally, developmental plasticity and environment-dependent trait expression generate innovation in evolution (Moczek et al. 2011). After novel traits appear and spread through the population as adaptive responses ("**phenotypic accommodation**"), natural selection might favor the genetic mutations that can further reinforce the trait's expression and transmission ("**genetic assimilation**") by changing the sensitivity threshold of the system to the environment.

example

An example is a study about how ancestral beetles may have shaped the evolutionary trajectories of current species by plastically adapting to temperature changes. Current species have "settled" into different degrees of plasticity and thus different tolerable temperature ranges (Casasa and Moczek 2018). New adaptations do not always start with new genetic mutations. Instead, they might have started with phenotypes triggered by environmental changes.

As West-Eberhard put it, this mode of evolution is a "**phenotype-first**" style of evolutionary thinking, with genes probably more often "followers than leaders in evolutionary change" (West-Eberhard 2003).

Advanced readings: West-Eberhard's masterpiece, *Developmental Plasticity and Evolution*, is a foundational work for many theories on the role of phenotypic plasticity in evolution.

Table 4.

Theories	eco-devo
Concepts	reaction norm adaptive plasticity adaptive improvisation phenotype-first evolution
Examples	inheritable plasticity in plants Slijper's goat

Individual-level adaptation like the kind Seon works on can complement the emergence of adaptations due to natural selection (Soen et al. 2015).

Taking plasticity seriously requires us to re-conceive the genome not as a pre-fixed program tinkered by selection, but a repertoire of potential developmental outcomes that can impact the novel appearance of selectable variation, influence what is inherited, and furthermore, affect how the organisms are exposed to natural selection (Sultan 2015, 2017). The genome is conditioned by multiple types of inherited information about the environment, which is itself determined by how the parental organisms engaged with their environments (Sultan 2019). The entire reaction norm is an intrinsic property of the organism (Sultan 2021) (Figure 10).

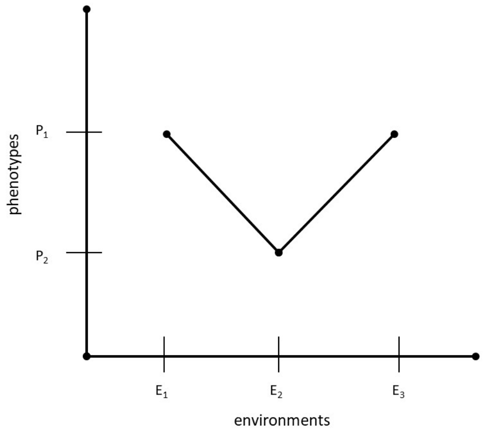


Figure 9. The entire reaction norm is a property of the genome and the organism.

Advanced readings: Rich examples of the role of plasticity in evolution can be found in Sultan's *Organism and Environment: Ecological Development, Niche Construction, and Adaptation* (2015). *Phenotypic Plasticity & Evolution: Causes, Consequences, Controversies* (ed. Pfennig 2021) presents the latest work in this area.

Evolution in a microbial, symbiotic world

Standard evolutionary theory is largely based on metazoan biology. In the microbial world, the concepts of species, lineages, and mechanisms of inheritance are radically different from the multispecies animals (and plants) we are most familiar with (Sapp 2009; O'Malley 2014). For instance, since microorganisms exchange genes and molecules horizontally between individuals and "species," the Darwinian "Tree of Life" is not a suitable representation of the evolution of life in general. In the microbial world, evolution is represented by a "**Web of Life**" (Figure 10).

Microorganisms are a particularly important ecological environment for all kinds of organisms. Multicellular organisms originated from a soup of microorganisms and thus their evolution is deeply interlinked with the constant presence of microorganisms (Margulis 1981; Sapp 1994; Gilbert 2014). Symbiosis with microorganisms in the broad sense, that is, the deep dependency between species, is thus a ubiquitous source of evolutionary change.

"Macro-organismal" evolution under the light of microbial interactions and symbiosis may look very different from that of the traditional, standard evolutionary theory framework. Lynn Margulis (1938–2011) is famous for her work on symbiosis (especially endosymbiosis). She argued that symbiosis presents significant challenges to neo-Darwinism and the Modern Synthesis (Margulis 1970, 1991). Specifically, the tools of population genetics cannot handle how fitness and selection work in other types of symbiotic arrangements, where the genetic materials from different species are intertwined dynamically and in widely diverse ways.

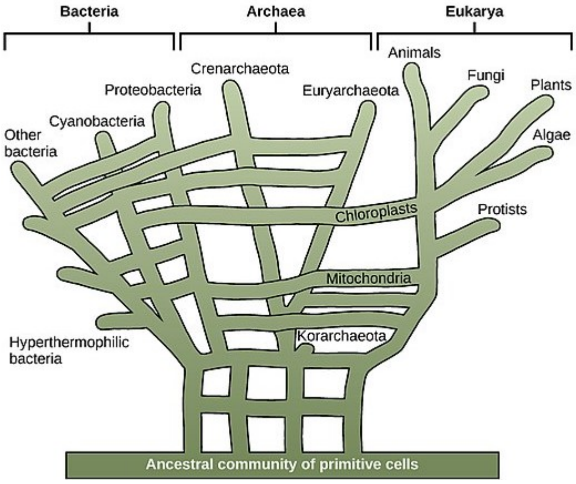


Figure 10. The microbial web of life

In the past decades, it's become increasingly clear that Margulis is right about the deep impact of microorganisms (Gilbert et al. 2015): they are a source of new phenotypic variants (it can generate novel traits beyond that from random genetic mutations and recombination), a part of the selective environment, a source of reproductive isolation and thus speciation, a part of the inheritance package transmitted across generations, and a constant partner in organismal developmental, physiological, psychological, and reproductive processes.

Ecological developmental biology ("**eco-evo-devo**") examines how developmental processes and phenotypes arise from the processing of environmental signals and cues (Gilbert et al. 1996; Gilbert 2000b, 2002, 2003a, 2012, 2016; Gilbert and Epel 2009). **Symbiotic co-development** is an instance of eco-evo-devo, where organisms have evolved to rely on each other for their development and shape each other's developmental stages (Gilbert and Epel 2009; Gilbert 2016).

example

An example of the role of the microbiota in development can be found in Armin Moczek’s extensive work on inherited microorganisms in dung beetle brood balls, which affect adult growth size, digestion, temperature response, and sexual dimorphism (Schwab et al. 2017).

Widely diverse examples of novelty-through-symbiosis can be found in the symbiotic relationship between a “macro-organism” host and resident inner microorganisms (collectively called the “**holobiont**”).

example

Consider the domestic cow. Baby calves still reliant on their mother’s milk do not have developed rumens. The rudimentary rumen is nevertheless seeded with microorganisms coming from and cultivated by the ingested milk. Once the calves wean off and start to eat vegetation, these microbes will begin to metabolize the incoming fibers, thus producing a range of by-products. In particular, the production of short-chained fatty acid stimulates the growth of the rumen so that it starts to develop the groves and finger-like polyps that enable rumination, fermentation, and intriguingly, an environment suitable for further bacterial growth. In this case, symbionts are involved in the construction of an organ that creates the herbivory niche for the cow (Gilbert 2020; Chiu and Gilbert 2020).

example

Yoav Soen and his colleagues found that microorganisms can break the Weismann barrier by directly influencing the germ line (Elgart et al. 2016). Working on fruit flies, they found that gut bacteria *Acetobacter* is involved in the process of making female eggs (oogenesis). When these bacteria were removed, oogenesis was repressed.

A Darwinian framework assumes that singular, autonomous individuals compete for their own survival and reproduction. Notably, this “selfish” perspective is taken to the extreme with Dawkins’s “selfish gene” perspective, where the unit of selection is genes instead of individual organisms.

In symbiosis, however, individuals with different genetic makeup come together as “teams” or “consortia” to form a new developing and evolving entity (Gilbert et al. 2012). The “holobiont” unit can go beyond a single host to an entire colony of hosts. For instance, an analysis on the microbiome of fruit bats found that colonies have coordinated microbial change within their groups (Kolodny et al. 2016).

The **hologenome theory of evolution** is the idea that the collective genomes of the holobiont constitute an important unit of natural selection (Bordenstein and Theis 2015; Lamm 2017; Lloyd 2017).

Recommended lecture: *You Complete Me: A Symbiotic View of Life* by Scott F. Gilbert.

Table 5.

Theories	eco-evo-devo symbiotic evolution hologenome theory of evolution
Concepts	web of life holobionts
Examples	rumen development dung beetle microbial impact on the germline during oogenesis

Inclusive inheritance beyond the DNA

The neo-Darwinism Weismann barrier excludes the possibility of "soft inheritance," that is, inheritance beyond the mere transmission of genes through the germ line. Since the 1970s, however, an explosion of knowledge has accumulated about epigenetic mechanisms as well as the **epigenetic inheritance** of these mechanisms.

At the cellular level, epigenetic mechanisms can maintain cellular identity and heredity through self-sustaining feedback loops (such as in metabolic networks), by the copying of structural templates (such as prion proteins), through the silencing of genes with chromatin markers (such as DNA methylation), or via the transmission of small RNAs (Jablonka and Lamb 2014). These factors, along with the genome, are often collectively referred to as the "epigenome."

Extra-genetic factors are evolutionarily relevant because they can determine phenotype expression, developmental processes, and the generation of new variations. They also permit the transmission of impactful life experiences and environments organisms may encounter, as these experiences can reverberate across generations through epigenetic inheritance.

Under the Modern Synthesis, epigenetic factors are often assumed to be unstable and fleeting, with little evolutionary relevancy. There is now robust evidence that they are stably transmitted across generations and ubiquitous in a wide range of taxa (see Jablonka and Raz 2009 for review), with important consequences for evolution in areas such as adaptive variation, reproductive isolation, macroevolutionary change, etc. (see reviews by Richards and Pigliucci 2020 and Jablonka and Lamb 2020). Epigenetic inheritance asks us to go beyond the neo-Darwinian model of evolution (Jablonka 2017).

Eva Jablonka and Marion Lamb argue that we need to broaden our conception of what is inherited. They proposed **an inclusive conception of inheritance** that includes a wide variety of **extra-genetic inheritance** such as the genetic, the epigenetic, the behavioral (learning and copying mechanisms), and the symbolic (linguistic, cultural) (Jablonka and Lamb 1999, 2005, 2014, 2020; Jablonka et al. 2005) (Figure 11). What we think of as "heredity" should be

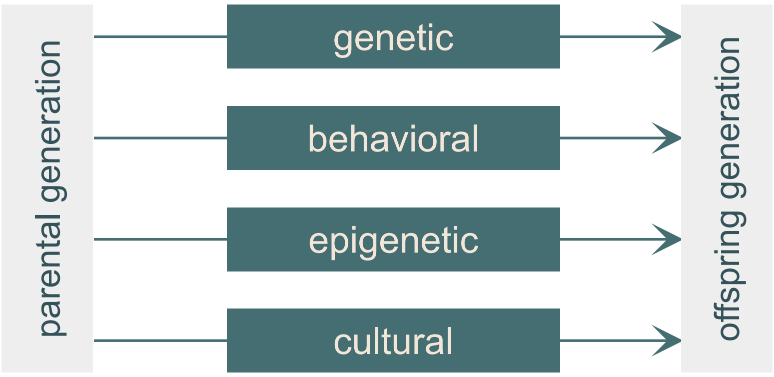


Figure 11. Multiple channels of inheritance

understood as an **extended heredity** instead of mere genetic heredity (Bonduriansky and Day 2018).

Recommended video: short interview with Eva Jablonka, "*Epigenetics in Evolution*"

example

One of the most exciting advances in this field is the inheritance of small interference RNAs (small RNA inheritance). Oded Rechavi's team studies the transmission of small RNAs in the model organism *C. elegans*, a nematode (Rechavi and Lev 2017; Houri-Zeevi et al. 2020). Small RNAs can function as a source of immunity against viral infection, as they can stick to and silence viral RNAs. They can also adaptively regulate nutrition-related genes to mitigate against starvation. Rechavi found that small RNAs are transmitted across generations through the germ cells and, most importantly, are physiologically relevant in the offspring (Posner et al. 2019; Lev et al. 2019; Lev and Rechavi 2020). They can effectively "vaccinate" offspring if they are formed in response to infections (Rechavi 2020). They can also "pre-adapt" offspring against starvation if they are formed in response to starvation (Rechavi et al. 2014).

Transgenerational inheritance happens when the following generation exhibits an adaptive phenotype without prior exposure to the same environmental stimuli. While DNA methylation is erased frequently, small RNAs can pass down three to five generations. The inheritance of small RNAs doesn't follow a Mendelian pattern nor does it eventually get diluted. Instead, a genetic network sets a "timer" that terminates the transmission after several generations (Houri-Zeevi et al. 2020, 2021).

From a neo-Darwinian perspective, memory is part of the somatic line and thus not transmitted across generations. The Weismann barrier prohibits it. Since DNA does not transmit from the somatic cells of an organism to its germ cells, what happens in the brain and bodily cells of organisms should stay in those cells. Yet small RNAs formed in parents can be found in the brains of the next generations. Interestingly, they are passed through the germ line, not directly into the next brain. These small RNAs are also physiologically relevant, changing the behaviors of these worms (e.g., influence on mating behavior, see Posner et al. 2019).

Another type of inheritance is the transmission of microorganisms from parents to offspring. There are at least three ways microbes can be inherited across generations, from soma cells to soma cells, from the soma to the germline, or from soma to the germline and then the soma again (Elgart and Soen 2018). Using a computational model, Soen examined some of the evolutionary consequences of microbial inheritance. For instance, when a host and its microbe are selected for their resistance to a toxin, the persistence of toxin-resistant microbes across generations can increase the toxic tolerance of host offspring, leading to an emergent adaptation in the host-microbiome system (Osmanovic et al. 2018).

example

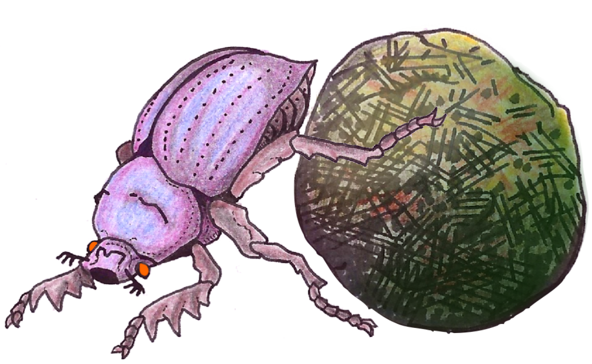


*Figure 12. A dung beetle rolling a dung ball. *Note that these are not the specific species analyzed in Moczek's lab.*

example

Finally, an incredible example of microbial inheritance is the dung beetle (superfamily *Scarabeoidea*). Some beetles roll balls of animal feces around as sources of food and bury them deep in underground tunnels as breeding chambers for the young (Figure 12). Others dig tunnels underneath dung pads, moving pieces of dung to shape into underground brood balls. These brood ball is not just a ball of fecal matter, but a carefully constructed shelter. The larvae must persist on the nutrients within the brood ball for their development.

When Moczek and his team teased apart the brood balls, they found that young beetles inherit more than just the genes of their parents. The mother deposits its own dung in the dung ball, a fecal pellet called the "pedestal" on which she lays a single egg. This pellet contains species-specific microorganisms that are consumed by the newly hatched larva, seeding it with maternal microbes that greatly influence its development, size, and mass as well as protects it from fungal infection (Schwab et al. 2016).

Furthermore, the team uncovered the presence of symbiotic nematode worms in the brood ball (Ledón-Rettig et al. 2018). The worms actively co-construct the microbial composition of the ball, with major effects on beetle development. They then latch onto the grown beetles when they finalize metamorphosis and are transmitted into new brood balls after sex. Worms are part of the transmitted package as well.

Recommended reading: *What a Beetle's Genital Worms Reveal About the Concept of Individuality*.

Figure 13. The niche constructors of brood ball ecology: larvae, nematodes, mothers.

Therefore, the mother transmits the constructed brood ball, the microbes, and the worms to the larvae (Figure 13). The offspring receives an ecological inheritance from the mother that is actively constructed by these actors, which becomes their developmental environment. As the larva defecates and works its own excrement into the ball, repairing and eventually restructuring it into a pupae chamber, it cultivates an "external rumen" with microbes that can digest diverse sources of carbon outside the larval body. By re-eating this mixture, larvae then take advantage of this predigested food source .

Inclusive inheritance challenges a gene-centric view of evolution because extra-genetic types of inheritance can influence the rate and direction of genetic evolution, generate adaptations, and affect macroevolution as well as evolutionary transitions.

Table 6.

Theories	inclusive inheritance extended heredity
Concepts	epigenetic mechanisms epigenetic inheritance behavioral inheritance symbolic inheritance ecological inheritance microbial ecological inheritance
Examples	small RNA inheritance microbial inheritance of toxin resistance dung beetle microbial inheritance

Evolution through the construction of niches and cultures

In standard evolutionary theory, the behavior of an organism is a proximate cause that does not affect evolution. Proponents of the Modern Synthesis have always given a small evolutionary role to behavior, for instance, as a way for organisms to "hold the strain in" and maintain a stable environment (Huxley 1942) or as a way to expose oneself to new niches and selective pressures (Mayr 1960, 1974, 1982). However, the evolutionary roles of behavior and learning are seen as minor, rare, or the result of prior evolution.

Later explorations have sought to integrate behavior as a core component of evolutionary dynamics (Plotkin 1988; Weber and Depew 2003). **Niche construction** is one way behavior can make a difference to evolution. Niche construction occurs when organisms (plants and animals alike) affect their evolution or that of others by modifying environments through their metabolism, activities, choices, or behavior (Odling-Smee et al. 1996; Laland et al. 2016). While biology has long acknowledged that organisms can construct or even engineer their environments, niche construction was not an evolutionary force from the neo-Darwinian or Modern Synthesis perspective (Scott-Phillips et al. 2014). If a niche construction activity is complex, adaptive, and repeated across generations, it is considered an evolved trait.

If it is not, then niche construction is seen as too insignificant to make a difference or too random for sustained evolutionary change. Niche construction is not considered a direct evolutionary cause under standard evolutionary theory because it does not directly alter the frequency of genes.

Proponents of **Niche Construction Theory** synthesized a wide range of previously disconnected evidence in ecology, developmental biology, physiology, and anthropology to show that niche construction is a ubiquitous, nonrandom, and in many cases, sustained and substantial evolutionary process (Odling-Smee 1988; Odling-Smee et al. 2003; Laland et al. 2019). It is evolutionary for multiple reasons.

Recommended reading: *Deconstructing Niche Construction: A Conversation between Gordon Burghardt and Kevin Laland*

First of all, niche construction provides an alternative evolutionary route to adaptations: instead of "matching" organisms to environments through natural selection, niche construction matches environments to organisms. The constructed environment can be passed on to future generations as an ecological legacy ("**ecological inheritance**"), thus impacting multiple generations. A classic figure contrasts the traditional view (Figure 14A) with the niche construction view (Figure 14B).

example

Termite mounds, beaver dams, earthworm tunnels, nests and burrows, etc., are all classic examples of niche construction. Other examples include the manipulation of penguin group temperature through huddling, the maintenance of stable food sources through migration, or as mentioned before, the manipulation of light intensity on plant leaves through plasticity.

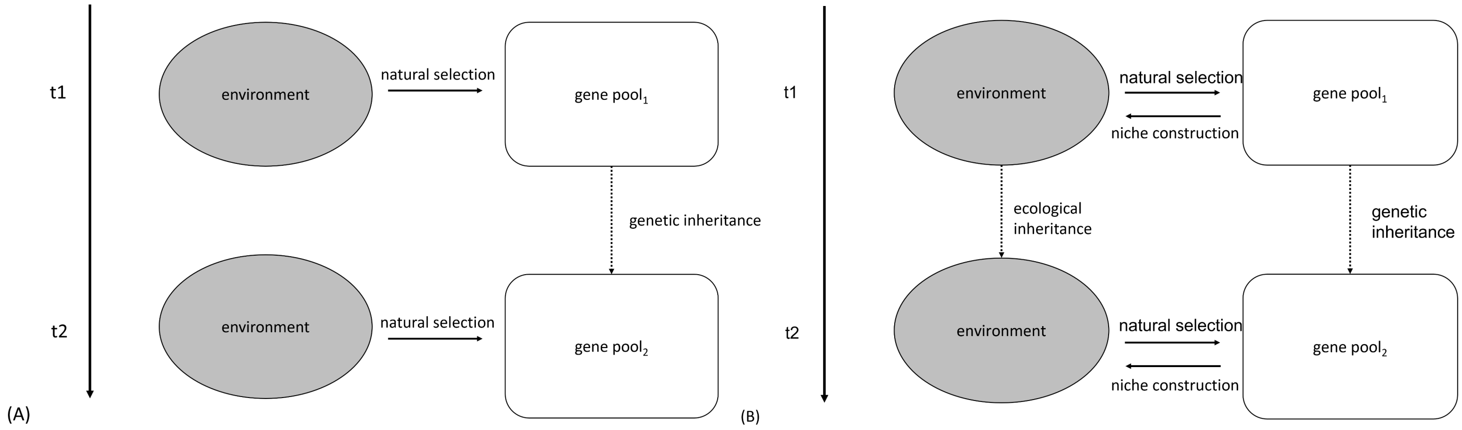


Figure 14. The traditional view (A) versus the niche construction (B) perspective

Further reading: More examples can be found in Odling-Smee et al. 2003, Sultan 2015, and the website: *www.nicheconstruction.com*

Second, niche construction coupled with natural selection provides a more complex picture of evolution. Examining multiple published studies on niche constructing behavior and evolutionary outcomes, Clark et al. (2020) found that niche construction affects the strength and variability of natural selection. As the environment also evolves as it takes input from organisms through niche construction while the organisms evolve by being selected by the environment, models have shown that the causal reciprocal feedback between organism and environment generates novel evolutionary dynamics (Laland et al. 1999; Uller and Helanterä 2019; Tanaka et al. 2020).

Niche construction changes how we should use common conceptual and formal (mathematical) models for evolution.

For instance, a common visual metaphor under adaptationism uses an "**adaptive landscape**" to model evolution by natural selection (Wilkins and Godfrey-Smith 2009; Pigliucci 2012a; see also articles in Gissis et al. 2018).

example

Adaptationism assumes that the environment (the landscape) remains constant as organisms are driven by natural selection to climb fitness peaks. Niche construction, however, implies that as organisms climb the peaks, they are also shifting the landscape under them. This is because they are also changing their environments as they evolve. Evolution should thus be modeled as a dynamic landscape, a "trampoline" that is continuously molded by the evolving population (Walsh 2012, 2015). Recently, Tanaka et al. (2020) proposed such a "dual landscape" model to show how niche construction and natural selection simultaneously change their landscapes as populations evolve.

example

Another example is proposed revisions to the **Price Equation**, a formal model of natural selection. Uller and Helanterä (2019) argue that the Price Equation can be dissected into component parts that correspond with aspects of niche construction. Laland and Chiu (2020) used a concrete example, earthworms, to illustrate (Figure 15). Earthworms have created wide-scale environmental impact beyond the fertilization of our backyard gardens. The Price Equation

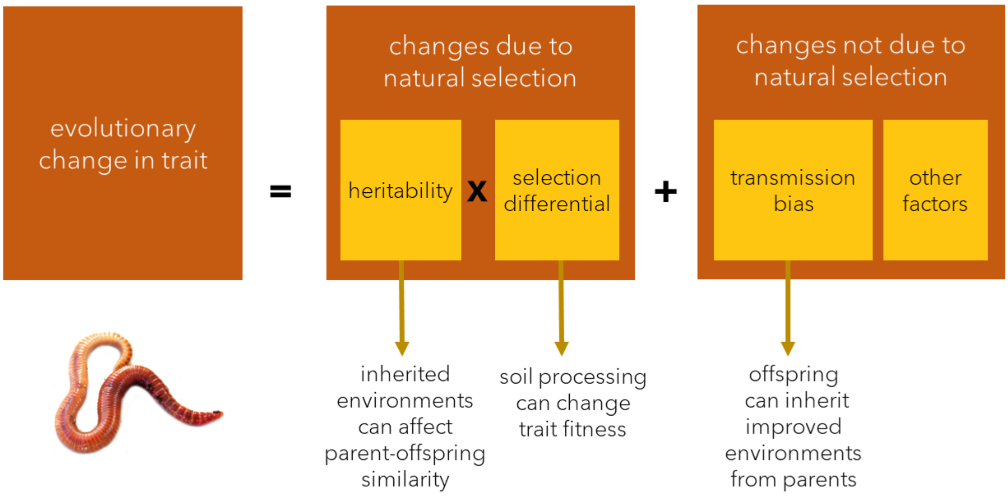


Figure 15. Niche construction can affect all three components of the Price Equation.

models evolutionary change as a result of natural selection and nonselection factors such as transmission bias. The former can be further decomposed into two components, heritability and the selection differential. Earthworm niche construction creates environments that are inherited, thereby affecting the similarity between parent and offspring, the processing of soil can alter the selective environment, and finally, offspring with niche constructing parents are biased toward inheriting an improved environment.

Increasingly, new conceptual developments argue that niche construction is not just a process interacting with natural selection, but a constitutive part of natural selection ("constitutive niche construction") (Walsh 2015). On this view, organisms can construct new experienced environments without changing the physical features around them (experiential niche construction), often through processes of phenotypic or developmental plasticity (Sultan 2015; Chiu 2019; Aaby and Ramsey 2020).

Behavior can also have an evolutionary impact through the creation and maintenance of culture. The ways cultural evolution can affect biological, organic evolution, and vice versa, are usually understood under the theory of **gene-culture co-evolution** (Feldman and Laland 1996; O'Brien et al. 2021).

example

Two famous examples of human gene-culture co-evolution are the origin of lactose tolerance in populations with dairy farming traditions and the evolution of sickle-cell genetic variants. The prevalence of dairy created a selective environment that favored the prolonged persistence of lactose tolerance (whereas adults in other cultures lose lactose tolerance as they wean from mother's milk) (Simoons 1970; Beja-Pereira et al. 2003, though also see Evershed et al. 2022). The complex feedback between the mosquito vectors of malaria, the medical and agricultural management of the disease and its consequences on mosquito populations, and the rise of sickle-cell alleles and anemia in those human populations is also another fascinating example of human gene-culture co-evolution (Laland and O'Brien 2012).

Gene-culture co-evolution also occurs in animals. Killer whales and dolphins, for instance, are societies where daughters stay in the same pod as their mothers (these are called matrilineal societies). Since mitochondrial DNA (mtDNA) is transmitted purely from mother to daughter through the female line via the egg cell of the mother, we can track the pod communities through their mtDNA. There is strong evidence that cultural differences are contributing to the evolution of diverging communities (Whitehead 2020).

example

Kopps et al. (2014) showed that some bottlenose dolphins in Western Australia created and transmitted the cultural trait of using sponges as foraging tools, which protects them against more harmful prey and thus led to a shift in their diet and food sources. Since these traditions are socially transmitted between parents and offspring, they tend to "stay within the family" thanks to the matrilineal structures of dolphin societies. As a result, these researchers found that those with and without sponge tools are genetically diverging from each other. Those with sponge traditions had a distinct mtDNA type. This indicates that cultural differences are shaping genetic differences. In these examples, we can see that culture allows for the transmission of behaviors that can give rise to adaptive phenotypic variation. These behaviors also modify selective pressures and population structures (niche construction). As a result, culture instigates genetic evolution, including those that reinforce traits related to culture. Genetic evolution thus feeds back into cultural transmission (Figure 16) (Whitehead et al. 2019).

example

Cultural specialization has also led to the genetic, morphological, and behavioral divergence between killer whale pods through reproductive isolation (Riesch et al. 2012; Whitehead et al. 2017; Whitehead and Ford 2018). There is only one species of killer whales, but there is an astonishing diversity of diet-based "ecotypes." Each ecotype has its own preferred food source based on its hunting traditions, which are passed on as cultural traits within each pod. Most importantly, killer whales strongly prefer to mate with those that share the same cultural diets. As a result, each ecotype is becoming increasingly distinct. Within each ecotype, adaptations can be found that evolved to better handle their own habits and food sources. This is an example of cultural transmissions creating ecological niches with different selective pressures.

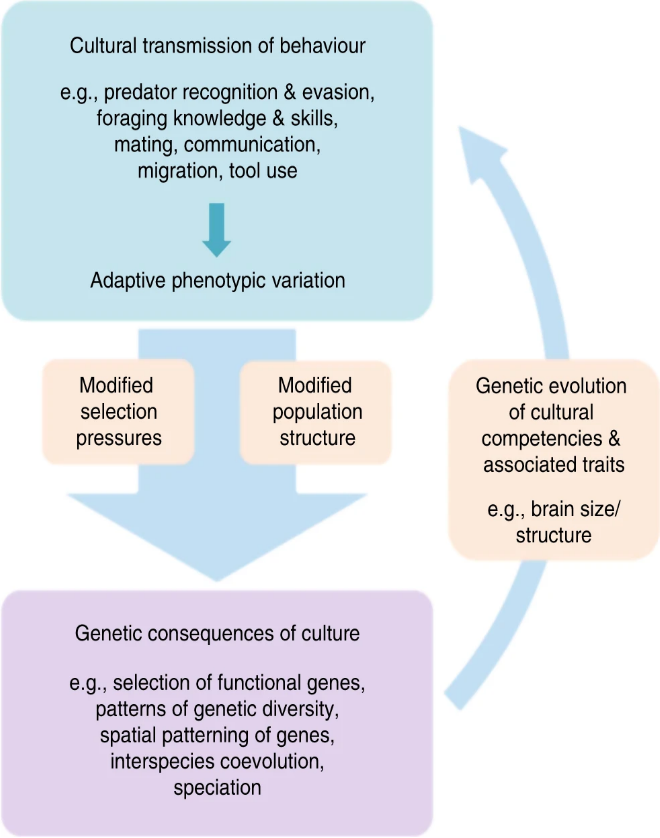


Figure 16. Animal gene-culture co-evolution

Culture is a fast, adaptive route to phenotypic change. Cultural evolution and biological evolution share some similarities, but in the former, there is not just parent to offspring vertical transmission, but also **horizontal transmission** (through learning) between peers as well as **"oblique" inheritance** from one generation to unrelated following generations. Culture involves different mechanisms of inheritance, such as copying rules (e.g., copying the majority). Furthermore, transmission can be constantly fine-tuned throughout the lifetime of organisms. Culture often involves exploratory behavior and developmental processes "that are powerful agents of phenotype construction, as they enable highly diverse functional responses that need not have been prescreened by earlier selection" (Laland et al. 2015, p. 6). The cultures of humans and nonhumans can go beyond Darwinian evolution to form unique dynamics of evolutionary change (Ram et al. 2018).

Table 7.

Theories	niche construction theory gene-culture coevolution
Concepts	niche construction ecological inheritance
Examples	niche constructing traits niche construction models dolphin and whale cultures

Putting it all together: Common themes

In the previous subsections, we offered a selective review of the ways organisms develop, operate, behave, and interact that can influence evolution. Each of these factors participates in the generation of novel variants, transgenerational inheritance, and the way selection works.

These cases are far from exhaustive. Physiology, for instance, is also a crucial proximate cause with evolutionary consequences. **The physiology of an organism**, that is, the organizational principles that maintain its homeostasis, extends beyond the internal mechanisms of the organism to include its external world (Turner 2000). Scott Turner argued that organisms manage their homeostasis and adaptations emerge from the process (Turner 2007, 2017). Using "music" as a metaphor for life, Denis Noble argued against a gene-centric theory of evolution. Instead, the genome is a passive instrument (like a pipe organ) that is played by the organismal system as a whole (Noble 2008, 2017), which in turn constrains the parts.

Advanced reading: The recent anthology *Challenging the Modern Synthesis: adaptation, development, and inheritance* (2017b).

A few common themes emerge from these studies.

(1) They situate genetic evolution within a broader context of evolutionary factors.

Genetic evolution (defined as changes in gene frequencies) is a special case situated within a diverse range of evolutionary modes. The channels of inheritance go beyond mere genetic inheritance. Inheritable phenotypic variation arises not just from genetic variation, but from the dynamics of gene regulatory networks and the interaction with biophysical processes and tissue mechanics as well as the microbial and larger environment. Natural selection can arise from environmental selection but also from the relationship between organisms and their social, cultural, and physical environments as they construct and alter the selective environment.

(2) They mostly concern biological phenomena left out or excluded from standard evolutionary theory.

Many are, for instance, soft inheritance and environmental influences, proximate causes, developmental causes of macroevolutionary change, and niche construction. From the standpoint of standard evolutionary theory, these phenomena are either interpreted as insignificant for evolution or mere outcomes of prior evolution. They are not treated as having an active, constitutive role in evolutionary processes. By paying attention to these proximate causes, we now realize that they do play a role in evolutionary processes.

(3) They challenge some core commitments of standard evolutionary theory.

Cases like the examples we've covered challenge many of these commitments. For instance, against gradualism, the speed of evolution may vary, and the outcomes might be discontinuous. Against atomism, traits might not evolve independently. Against adaptationism, natural selection is no longer the only or most prominent creative source of evolution. Processes other than natural selection can explain how adaptive capacity is acquired and passed on across generations.

Finally, breaking through the Weismann barrier, inheritance is more than just the transmission of genes. Developmental and plastic responses might be responsible for macroevolutionary events.

These cases also suggest principles of evolution that differ from the standard theory. A prominent line of reasoning is the principle of "phenotype-first" or "plasticity-led" evolution, that is, the idea that genetic evolution can follow significant adaptive phenotypic and developmental change (Figure 17). Other examples include environmentally induced adaptation and the reciprocal evolutionary processes of niche construction and natural selection.

(4) They show that evolution is not fractionated into different autonomous components.

Instead, processes such as variation, inheritance, selection, and development interact and overlap (Figure 18). These processes are not independent, but interdependent. The concepts of organisms and environments are not autonomous but instead intermingle (Lewontin 1983; Levins and Lewontin 1985). Proximate causes and ultimate causes are not distinct causes but reciprocally connected (Laland et al. 2011, 2012; Laland 2015).

Furthermore, these cases show that the mapping between genotype and phenotype is not straightforward (Brun-Usan et al. 2022). On the standard view, there is a simplifying assumption concerning the relationship between the genotype and the phenotype of a trait. The phenotype is a particular variation of a trait, a function, structure, or behavior of the organism. The genotype refers to the gene(s) that underlie(s) the phenotype. Standard evolutionary theory assumes that there is a linear relationship connecting the two (Figure 19, top). Yet there is no clear genotype-phenotype map because developmental processes determine how genes are and can possibly be involved in phenotypes. Thanks to developmental processes, different genotypes may generate the same phenotypes (canalization) while the same genotype might produce different phenotypes (plasticity). Taking the role of development in evolution seriously requires us to take developmental processes and phenotypes as the starting points, not the genotype (Figure 19, bottom).

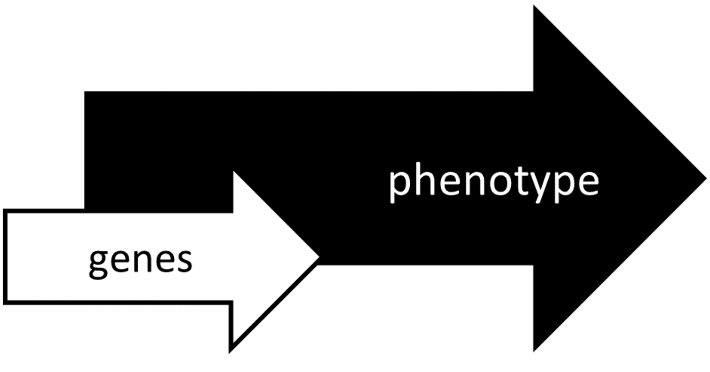


Figure 17. Phenotype-first evolution: genes as followers rather than leaders of evolution

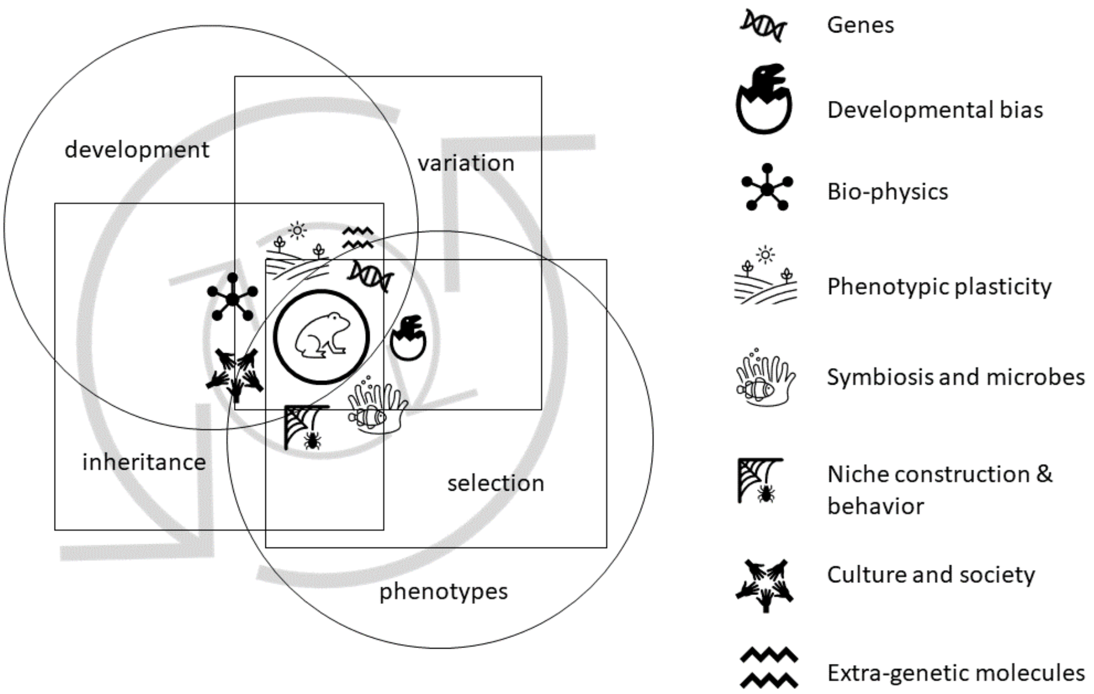


Figure 18. An intermingled perspective of evolution, with examples of non-genetic factors (right). Causation is reciprocal (gray arrows).

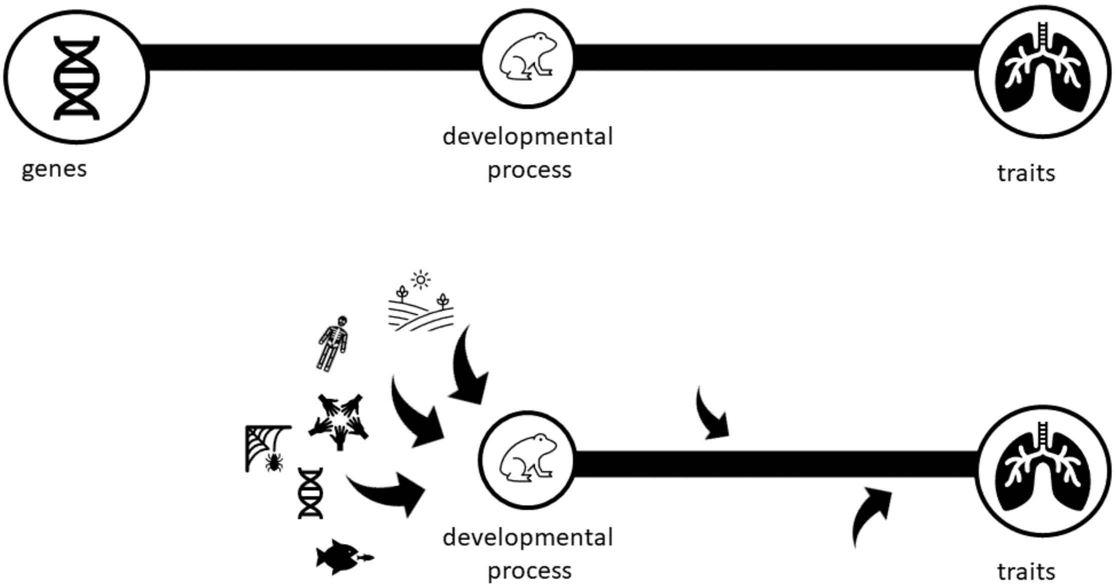


Figure 19. The role of development in the generation of traits.
Top: the standard evolutionary theory point of view.
Bottom: a development-centric perspective.

We can examine how the causal arrows change when we revisit the dung beetle case. How do dung beetles evolve? Standard evolutionary theory assumes that the only informational inputs from the parents that are passed to the next generation are genes, contained in the nucleus of the egg cell (Figure 20B). If the adult that emerges in the next generation has a different phenotype (e.g., having horns and more ornate antennae), the only possible explanation is that either it has suffered a mutation on its DNA, or that pre-existing genes have been re-arranged in novel ways (Figure 20C).

The reality, however, presents a much richer view of inheritance (Figure 20D). First, it recognizes that inheritance always involves more than genes. These epigenetic elements are necessary for development to occur and, crucially, they play an active role. That is, they affect the development of the larvae, but they are also affected by the larval development: the way it hollows the ball, the way it defecates, its movements, metabolism, and behavior. This reciprocal, dynamic causation is represented in the figure by the different crisscrossed arrows symbolizing causal flows. Red arrows symbolize processes that involve organismal "agency," that is, the action from the organisms. Organisms do not develop in a fixed, static, and passive medium. Rather, organisms can to some extent control, or at least play an active role in, their own development.

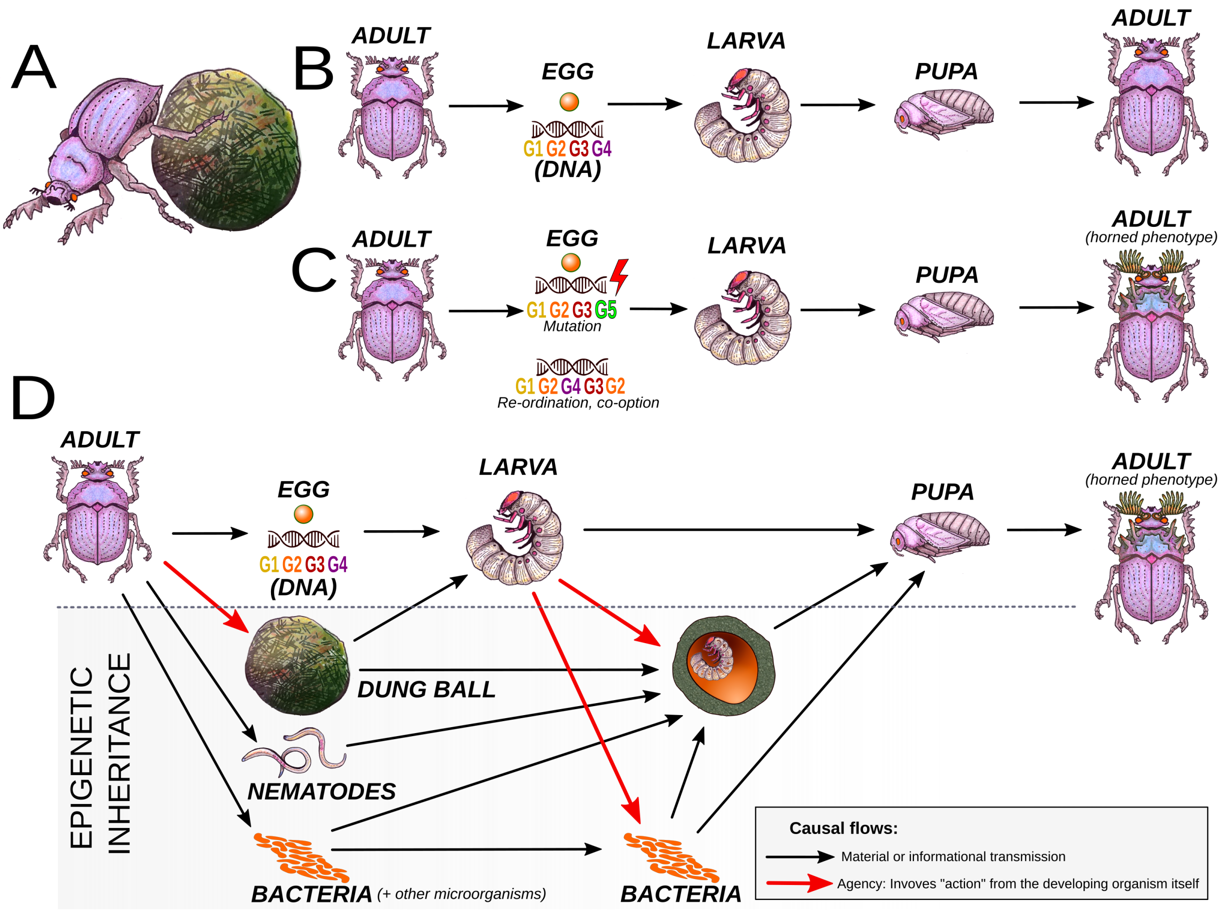


Figure 20. Different perspectives of dung beetle development and evolution.

Part III

Restructuring evolution: An extended evolutionary synthesis

The selected examples covered in Part 2 are sampled from a wider range of studies that focus on the ways organisms can affect their evolution. These examples expose the limitations of the standard evolutionary theory as an explanatory framework and challenge core theorems of neo-Darwinism and the Modern Synthesis.

In light of these challenges, many have sought to restructure evolutionary theory beyond genetic and selectionist explanations. “Epigenetic systems” that described how non-random variants can arise from development, plasticity, behavior, etc., and subsequently direct evolution were proposed, for instance, by Waddington (1959a, 1959b) and Ho and Saunders (1979).

Toward the beginning of the 20th century, scholars from multiple disciplines started a concerted effort to propose what evolutionary biology should look like as an “extended” synthesis, or “extended evolutionary synthesis” (EES) (Pigliucci and Müller 2010; Laland et al. 2015).

This version of the EES will be the final focus of our review. We will address the following questions:

What is the EES?

How does the EES make progress?

Is the EES new? What does adopting an EES perspective mean for the gene-centric standard evolutionary theory—should one abandon the latter or heavily restrict its scope?

Short history of key workshops and publications on the EES

Following early calls for an extended synthesis (Müller 2007; Pigliucci 2007), the first EES meeting was held in 2008 as an Altenberg Workshop *Towards an Extended Evolutionary Synthesis* at the Konrad Lorenz Institute for Evolution and Cognition Research (KLI) . The workshop led to the first anthology on the then-emerging EES: *Evolution: The Extended Synthesis* (Pigliucci and Müller 2010). In 2015, Laland et al. (2015) proposed the EES as an empirical research program, complete with a suite of concepts, assumptions, hypotheses, and predictions. These predictions were put to the test under the grant project, *Putting the Extended Evolutionary Synthesis to the Test* (2015–2018).

In the last few years, multiple conferences and special issues sought to explore the EES and what it meant for evolutionary theorizing. These include the 2016 conference at the Royal Society *New Trends in Evolutionary Biology: Biological, Philosophical and Social Science Perspectives* and its special issue (see Bateson et al. 2017); the 2018 conference *Talking Evolution* at the MPI for Evolutionary Biology, Plön; the 2019 workshop at Ruhr University Bochum, *The Extended Evolutionary Synthesis: Philosophical and Historical Dimensions* (see Fábregas-Tejeda 2019); and the 2019 workshop, *Evolution Evolving: Process, Mechanism and Theory* at Cambridge.

What is the EES?

The EES research program can be characterized by its core concepts, assumptions, structure, and predictions (Laland et al. 2015).

Two core EES concepts

Constructive development: The EES seeks to overcome the predominant idea that development is the passive unfolding of a predetermined, inherited genetic program (Figure 21). Instead, development is continuously and actively shaped by interactions and adaptive responses driven by the organism with itself, others, and the environment. Developmental processes are constructed throughout the lifetime of an organism from diverse resources across multiple levels of organization (e.g., genetic, molecular, cellular, organismal, environmental, etc.) (Figure 22). These heterogeneous resources are inherited across generations, some facilitated by the organism's actions.

Reciprocal causation: This term refers to the bidirectional feedback and interaction between two types of causes: the proximate causes that explain how organisms function and develop, and the ultimate causes that explain how they evolve. Standard evolutionary theory does not treat proximate causes as candidates for ultimate causes.

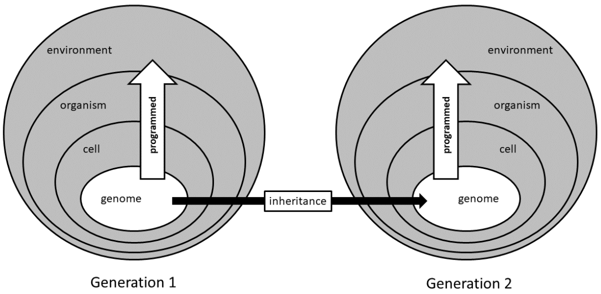


Figure 21. The traditional "genetic blueprint" perspective (figure adapted from Fig 1 of Laland et al. 2015)

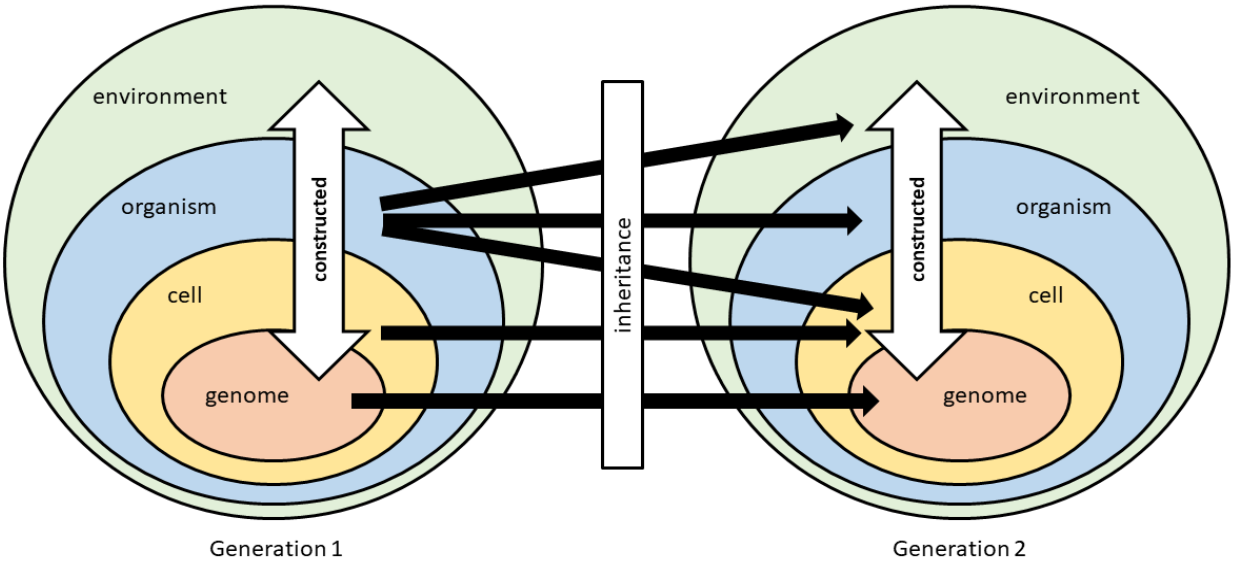


Figure 22. The constructive development perspective (figure adapted from Fig 1 of Laland et al. 2015)

EES core assumptions

A comparison of the core assumptions of standard evolutionary theory (SET) versus that of the EES can be found in Table 8.

Table 8. SET versus EES core assumptions

SET assumptions	EES assumptions
The pre-eminence of natural selection	Reciprocal causation
Genetic inheritance	Inclusive inheritance
Random genetic variation	Nonrandom phenotypic variation
Gradualism	Variable rates of change
Gene-centered perspective	Organism-centered perspective
Macro-evolution is explained by microevolutionary processes	Macro-evolution is also explained by additional evolutionary processes, e.g., developmental bias and ecological inheritance

The EES structure of evolution

Standard evolutionary theory is a theory of genetic evolution. Evolution occurs only when the relative frequencies of genetic variants change. Only four forces can directly cause such change, therefore, only they can be considered as evolutionary processes or causes (Figure 23).

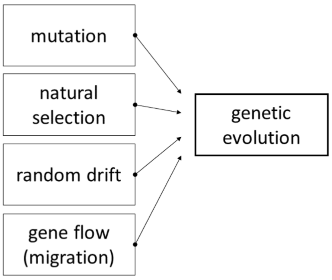


Figure 23. The four forces of evolution according to standard evolutionary theory

From the EES perspective, evolutionary theory should be a theory of phenotypic evolution. The causes that can affect phenotypic evolution can be divided into three types (Figure 24), with the four evolutionary forces of the standard theory belonging to just one category.

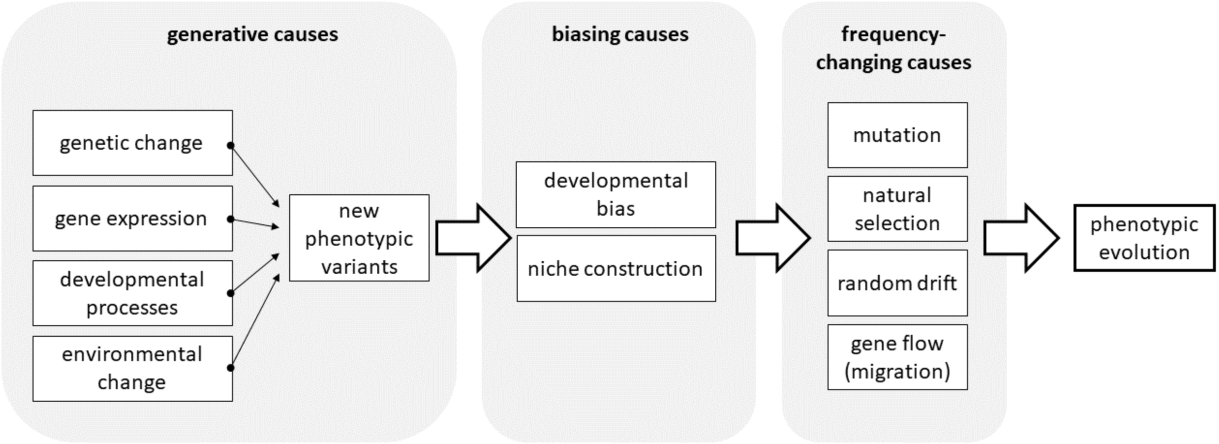


Figure 24. The causes of evolution, according to the EES

The first type of causes are **generative causes**. They are the processes that can generate novel phenotypes (e.g., developmental, epigenetic, environmental, etc.).

The second type of causes are **biasing causes**. They are the processes that can limit or facilitate the direction of evolution (developmental bias and niche construction).

The third type of causes are **frequency-changing causes**. These processes change the relative numbers of inheritable variants in each generation. These are mutation, natural selection, random drift, and migration, aka the four processes traditionally accepted by standard evolutionary theory.

The EES presents a more extensive understanding of evolution in two ways: in terms of the diversity of scientific fields and phenomena it covers but also in terms of the diversity of fundamental causes that go into evolutionary processes. Population genetics is but one part of evolutionary biology.

The EES as a phenotypic-oriented, organism-centered theory of evolution.

The EES is a research program centered on organisms as the core causes of the evolution of their phenotypes.

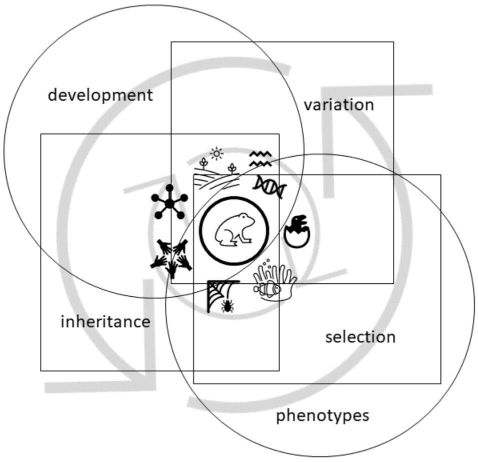
Standard evolutionary theory is a gene-centric theory that defines evolution as the micro-changes of genetic frequencies in a population, pushed around by the four forces of evolution. The organism was treated as a mere vehicle for the transmission of genes under the Modern Synthesis.

The EES, on the other hand, is an organism-centric theory of evolution that redefines evolution as *"transgenerational change in the distribution of heritable traits of a population"* (Laland et al. 2015).

Looking carefully, we'll see that, most of the scholars under the EES framework are clustered around the areas of developmental biology and animal behavior, as well as cognition, learning, and culture. The common thread between these fields is the organism, which some connect to the earlier movements such as organicism (Baedke 2019). As Günter Wagner put it, the concept of "organism" was "reinvented" for evolutionary biology under evo-devo in the 1980s (Wagner 2015).

Examining EES research, we will find that, first, the phenotypes and traits of organisms return to the central stage as the focus of evolutionary explanations. Genetic evolution is but one part of organismal evolution and part of the explanation of organismal evolution.

Second, evolutionary causes go beyond the four forces that alter genetic frequencies. Any cause that can alter the transgenerational frequencies of



heritable traits are also deemed evolutionary, even if they do not directly change gene frequencies. As a result of incorporating new causes of macro-evolution, the evolution of higher taxa, clades, and species may not be reducible to micro (genetic) evolution.

Finally, genetic inheritance is not the only inheritance system in evolution. Epigenetic, cultural, behavioral, physiological, and ecological inheritance, etc., are all channels of inheritance that can pass traits on to the next generations.

The EES thus situates genetic evolution as one part of a much more complex organismal and ecological system. The EES leans toward an **organism-centered biology.** Organisms can be both the subject (cause) and the object (effect) in their evolution (Lewontin 1983). Through their behaviors and movement, developmental processes, and plastic responses to the environment, organisms can generate new variations for selection, variants that are sometimes direct responses to environmental pressures. Organisms can also directly bias the process of natural selection by constructing and altering selective and experienced environments or by shaping the trajectory of evolution through their developmental architecture.

Organisms are not mere passive objects at the mercy of environmental selection and genetic programs. They are active "agents." Many proponents of the EES thus seek to naturalize the notion of "**organismal agency**," that is, as agents that purposefully explore and carry out their goals in response to their interpretation of the environment (Sultan et al. 2021). Altogether, these new causes and processes of evolution work alongside the causes and processes of genetic evolution to present a fuller, more comprehensive picture of evolution.

Further reading: The foundational paper of the EES is Laland et al.'s 2015 *The extended evolutionary synthesis: its structure, assumptions and predictions*. *The Extended Evolutionary Synthesis project website* contains extensive resources and documentations of the projects carried out between 2015-2018. *The final report* summarizes key outcomes and publications, including the anthology *Evolutionary Causation* (2019).

Advanced reading: Baedke's (2021) review of *Evolutionary Causation* situates the EES within a broader debate landscape and philosophical context.

EES predictions

Finally, the EES research program has proposed testable hypotheses that can adjudicate between the EES and standard evolutionary theory. Table 9 contrasts several hypotheses proposed by Laland et al. 2015.

Table 9. SET versus EES predictions (according to Laland et al. 2015)

SET expectations	**EES predictions**
What comes first? On the logical order evolution.	
Genetic change causes, and logically precedes, phenotypic change in adaptive evolution	Phenotypic change can precede, rather than follow, genetic change, in adaptive evolution
On the generation of novel variations	
Genetic mutations, and hence novel phenotypes, will be random in direction and typically neutral or slightly disadvantageous	Novel phenotypic variants will frequently be directional and functional
Mutations generating novel phenotypes will occur in a single individual	Novel phenotypic variants will frequently be environmentally induced in multiple individuals
On the evolution of adaptive variants	
Adaptive evolution typically proceeds through selection of mutations with small effects	Strikingly different novel phenotypes can occur through mutation of a major regulatory control gene expressed in a tissue-specific manner, or through facilitated variation
Adaptive variants are propagated through selection	Adaptive variants are also propagated through repeated environmental induction, non-genetic inheritance, learning and cultural transmission
On the causes of rapid phenotypic evolution	
Rapid phenotypic evolution requires strong selection on abundant genetic variation	Rapid phenotypic evolution can also result from the simultaneous induction and selection of functional variants
On the causes of taxonomic diversity	
Taxonomic diversity is explained by diversity in the selective environments	Taxonomic diversity will sometimes be better explained by features of developmental systems (evolvability, plasticity) than features of environments
Is heritable variation biased?	
Heritable variation is unbiased	Heritable variation will be systematically biased, often towards variants that are adaptive and well-integrated
Are constructed environments special?	
Environments modified by organisms are not systematically different from other environments	Niche construction will systematically create environment factors well-suited to the constructor's, or its descendants' phenotype, and that enhance fitness
On the evolution causes of phenotypic similarities	
Parallel evolution is explained by similarity in environmental conditions	Parallel evolution may also be due to niche construction
Convergent selection is the main cause of repeated evolution in isolated populations	Developmental bias and convergent selection together cause repeated evolution in isolated populations

How does the EES make progress?

Many of the results from the "Putting the EES to the Test" grant were described in Part 2 of this review. Here are some further examples that demonstrate how evolutionary biology can proceed under the guidance of an EES research program.

Reanalyzing empirical studies to find new clues.

EES hypotheses can be tested by revisiting previously collected data with an alternative research angle. Previously collected data from a large number of independent studies can be systematically collected and analyzed to tease out patterns that were not explicitly studied before.

Niche construction theory predicts that niche constructing behavior can affect the way natural selection acts on organisms. Pouring over hundreds of previously published studies on natural selection in the wild, **Clark et al. (2020)** conducted a meta-analysis to see whether the strength and direction of natural selection was different when niche construction was involved. They found evidence that niche construction can indeed buffer organisms from the effects of natural selection by lowering its strength and variability.

Plasticity-first evolution is the hypothesis that novel complex traits can first arise as a plastic response to environmental stimulation, then natural selection can act on the genetic elements that favor this plastic response.

Noble et al. (2019) did a meta-analysis on preexisting literature and found that plastic traits do seem to have a greater potential to evolve in the direction of their environmentally induced adaptations.

Radersma et al. (2020) also carried out a meta-analysis on studies that transplanted plants into different environments. They uncovered strong evidence that current, local adaptations indeed mirror ancestral plastic responses to similar environments, indicating that ancestral plasticity "took the lead," resulting in strong selection for the adaptive traits in offspring generations.

Learning from unexpected results.

Putting EES hypotheses to the test also means that one should be open to negative outcomes concerning EES predictions. These cases provide the opportunity to further reflect on the nuances of the systems at hand, instead of merely defaulting to the standard model or fully refuting the EES.

Feiner et al. (2020) examined *Anolis* lizards, which on multiple islands have diverged into a similar set of ecological niches with similar specialized adaptations (ecomorphs). They found that in bone morphology, evidence did not support that the ecomorphs started out as ancestral plastic responses to those environments, which were then stabilized later. In other words, they did not find evidence for plasticity-led

evolution. A lesson for the EES is to create more detailed plasticity-led evolution hypotheses by analyzing the conditions under which it will be expected. One could shift focus to how plasticity-led evolution has long-lasting effects on evolutionary trajectories and outcomes.

Developing new models and principles.

Zeder (2017, 2018) argues that the human domestication of plants and animals can offer a useful model system to test EES ideas of reciprocal causation, constructive development, niche construction, etc.

Computer modeling can also analyze how evolution would turn out in the far future. A way to test EES hypotheses is to explore the consequences of models that incorporate ESS assumptions. Adaptive plasticity is the capacity to respond to a new environment with beneficial, "pre-adaptive" traits.

Soen et al. (2015) asks what happens when microorganisms are a heritable part of the organism's developmental system, especially the parts that stabilize phenotypic traits against disruptions. His models showed that perturbations can destabilize the cooperation between host and microbes, leading to changes in the phenotype and thus releasing variability for evolutionary change. Microbes can help organisms restabilize into an alternative phenotype down the road, thus constricting future evolutionary opportunities.

Richard Watson is working on new principles that depart from the Modern Synthesis focus on counting genes. One of them is "evolution by natural induction." He argues that things (e.g., genes) and their frequencies are not the drivers of adaptive transformations. Instead, adaptations come from the way relationships between things change, by the way they induce each other (Watson and Szathmáry 2016; Brun-Usan et al. 2020).

Recommended podcast: Richard Watson on *Natural Induction, Cooperation and Where Survival of the Fittest Is Wrong*

Kouvaris et al. (2017) created evolutionary models to explore how plasticity and development can influence evolution. Their EES-driven hypothesis is that the developmental systems can evolve to become better at generating adaptive responses to new environments. In their models, developmental systems with the deep ability to learn from past regularities were able to generate pre-adaptive responses even to brand new environments. Without this learning principle, evolution could only evolve traits that are adaptive to environments they've experienced before.

In their models, **Rago et al. (2019)** found that learning principles can enable the evolution of adaptive plasticity even when there is no selection for plasticity (or even selection against!).

The standard theory of evolution can explain how evolutionary individuals can further evolve, but cannot explain their origins. **Watson and Thies (2019)** theorized that the evolution of major transitions, which concerns the origin of evolutionary individuals, cannot occur without niche construction and plasticity.

Furthermore, they argue that evolution—the actual process—is itself also constantly "evolving." Under the Modern Synthesis, even though species change, the causes of their change remained unaltered. Watson and Thies (2019) argue that as new types of individuals evolve, they establish new relationships and redefined selective pressures. Mechanisms of inheritance and development are subject to change. Almost all components of the evolutionary process are evolving as they evolve.

Rather than overly complicate things, **Brun-Usan et al. (2022)** propose that a theory that includes extra-genetic sources of phenotype variation in a single representation can open the way for a more coherent and elegant evolutionary theory.

Using current tools to address EES questions.

Adopting an EES approach means that one can use the powerful molecular tools we have to investigate phenotypic evolution, instead of just genetic evolution. For instance, developmental genetics is now fruitfully used to investigate the evolutionary origin of novel, complex traits and the role of developmental bias (Hu et al. 2019b). In Part 2, we saw how developmental genetics was used to uncover that the prothoracic horns of beetles in part originated from the genetic networks that develop wing tissues (Hu et al. 2019a).

Linz et al. 2019 also found that the tibial teeth on the legs of dung beetles, a crucial adaptation for their digging behaviors, in part came from preexisting gene networks that had nothing to do with the formation of legs.

Using the EES framework to address current issues

The EES can help breathe new life into areas that traditionally drew on Modern Synthesis ideas of evolution. For instance, **Sarto-Jackson (2019)** argued that evolutionary epistemology, the study of the evolution of knowledge mechanisms, traditionally relied on Modern Synthesis ideas. Yet the EES, with its interest in the role of individual development in evolution, can provide a better research framework for the discipline.

Another issue concerns the evolution of the modern human. Some fields in human anthropology, such as human behavioral ecology and cultural transmission theory, are heavily influenced by the Modern Synthesis (Prentiss 2021). However, a neo-Darwinisan approach tends to sideline the evolutionary roles of social institutions, cultures, as well as the way humans perceive construct them (Fuentes 2016). This is because it focuses on selectionist explanations concerning the natural or sexual selection of human traits (e.g., aggression, body size dimorphism, fire use) (Kissel and Fuentes 2021).

An EES approach can enable us to focus on organisms and their constructive roles in their own evolution (Fuentes 2016). **Kissel and Fuentes (2021)** argue that by going beyond pan-selectionism, evolutionary anthropologists can explore how multiple evolutionary processes (e.g., niche construction, plasticity, individual phenotypic variation, etc.) interact with each other and contribute to human evolution. For instance, **Antyn and Kuzawa (2017)** argue that we can generate new hypotheses about the diversification of early humans if we adopt an EES approach and take plasticity-induced variation seriously (instead of thinking of it as noise around a normal phenotype).

Disciplines such as cultural macroevolution and evolutionary cognitive archaeology are already closely aligned with EES ideas (Prentiss 2021). We should ask how the EES can help us better understand human origins (Murray et al. 2020).

Is the EES new?

Across multidisciplinary fields in biology, history, and philosophy, scholars debate what an extended synthesis would look like (see, for instance, Pigliucci 2007; Love 2010; Craig 2010b; Brooks 2011a, b; Danchin et al. 2011; Dickins and Rahman 2012; Martinez 2013; Pigliucci and Finkelman 2014; Huneman 2014; Müller 2014; Futuyma 2015; Laubichler and Renn 2015; Huneman and Walsh 2017b), and whether it's needed (Scott-Phillips et al. 2014; Wray et al. 2014; Futuyma 2017).

So what's new about the EES? How radical or revolutionary is the EES position?

To make progress on these questions, we can evaluate the novelty of EES by categorizing the responses into five types of positions (Table 10). The extreme ends beyond this spectrum are not viable positions. Given the evidence, it is extremist to maintain either that there is nothing new or everything new about the EES. In between, there are multiple positions that situate these two research programs in different ways.

Table 10. Is the EES new? Five positions on the conservative-progressive spectrum

Positions	**Relation between EES and gene-centric evolutionary theory**	**Is the EES new?**
The reactionary: The EES is already part of standard evolutionary theory.	The EES is already part of the central concerns of standard evolutionary theory. It can be fully explained by a gene-centric theory of evolution.	EES findings and concepts are not novel.
The conservative: The EES is a rare, special case of standard evolutionary theory.	The EES is a rare exception. It is more complicated to explain EES findings with a gene-centric theory, but still feasible.	EES findings and concepts are new as optional "add-ons" to the standard theory.
The moderate: The EES is the latest expansion of an evolving standard evolutionary theory.	The EES is the latest expansion of standard evolutionary theory. New concepts and principles are needed to explain EES findings, but they are compatible with a gene-centric theory of evolution.	EES findings and concepts are novel, important, necessary additions to the standard theory.
The progressive: Standard evolutionary theory is instead a part of the EES.	Gene-centric evolution is a restricted, special case of a broader view of evolution. The EES is a restructured evolutionary theory with different conceptual grounds and commitments.	EES is the new standard framework that in turn assimilates gene-centric evolutionary theory.
The radical: The EES is an alternative framework that will replace standard evolutionary theory	The EES is fundamentally incompatible with a gene-centric theory of evolution. It is a brand new evolutionary theory with new conceptual grounds and commitments.	EES is a radical, novel framework that excludes gene-centric evolution.

For instance, many scholars in evolutionary genetics argue that the extended synthesis does not threaten the centrality of standard evolutionary theory. It is either as a topic already covered (reactionary) or a special case that can be explained by the same research tools (conservative) (Dickins and Rahman 2012; Scott-Phillips et al. 2014; Wray et al. 2014; Charlesworth et al. 2017; Futuyma 2017).

A conservative position, for instance, would admit that organisms exhibit some sensitivity to the environmental conditions (i.e., phenotypic plasticity), and that some nongenetic factors are transmitted, in addition to genes, to the next generation (i.e., parental effects). These phenomena are conceptualized as add-ons to the prevailing gene-centered paradigm. That means that they are often considered as genetic, or genetically controlled, properties and thus analyzable with preexisting conceptual and mathematical tools.

We will now focus on the moderates and the progressives.

The Moderates

That standard evolutionary theory itself can continue to grow and expand should come as no surprise, as it itself is an expansion of the Modern Synthesis. A clear case is the assimilation of the neutral theory of molecular evolution. Even though it contradicts a core tenet of Darwinian thought, it became a powerful "null hypothesis" of genetic evolution and is now widely used as a benchmark to estimate evolutionary relationships, distances, and to detect the presence of natural selection. Therefore, one could reasonably hold that even if the EES did introduce something different, this is the normal kind of progress to be expected from the evolution of any scientific theory.

Massimo Pigliucci, one of the early figures of the EES, offers a moderate option. He does not think that the EES is "revolutionary" in the sense that scientific revolutions can instigate paradigm shifts.

This is because there has only been one true paradigm shift in biology, argues Pigliucci, and that was Darwin's revolutionary contribution to the world (Pigliucci 2007, 2009, 2012b). All the other changes to evolutionary theory—neo-Darwinism, the Modern Synthesis, etc.—are shifts in emphasis (Pigliucci 2007, 2009, 2012b).

Pigliucci maintains that the EES is still a novel endeavor bringing in evo-devo and epigenetic inheritance studies that were not parts of the Modern Synthesis. More importantly, the target phenomenon of EES shifts away from the traditional focus of standard evolutionary theory. EES is concerned with the bigger picture of phenotypic evolution, not just the current focus on the evolution of genes.

However, none of these shifts depart from Darwinian evolution. The EES is the latest extension (an "extended" synthesis) of Darwin's theory, and even the Modern Synthesis. In their most recent appraisal on the evolutionary role of epigenetic inheritance, Christina Richards and Massimo Pigliucci (2020) disagree that it undermines Darwinism or the Modern Synthesis. Instead, they double down on the position that the EES is an *"enlargement of the original Darwinism, building on the Modern Synthesis, not replacing it."* (p. 467)

Drawing on philosopher of science Imre Lakatos instead of Kuhn, Telmo Pievani also argues that the EES is a continuous revision around the same hardcore Darwinian "belt" of commitments (Pievani 2012). It is not revolution in the Lakatos sense.

Advanced reading: Baedke (2021) and Baedke et al. (2020) warn against using simplistic frameworks of theory change to evaluate the EES. They offer a more nuanced list of explanatory criteria to help adjudicate the positions.

A promising approach is to treat biology as clusters of "problem agendas" that call for specific types of solutions (Love 2010; Kaiser and Trappes 2021). Others propose to look at the shifting conceptual landscape as changes happening in epistemic networks that are not always internally consistent (Callebaut 2010; Fábregas-Tejeda and Vergara-Silva 2018b).

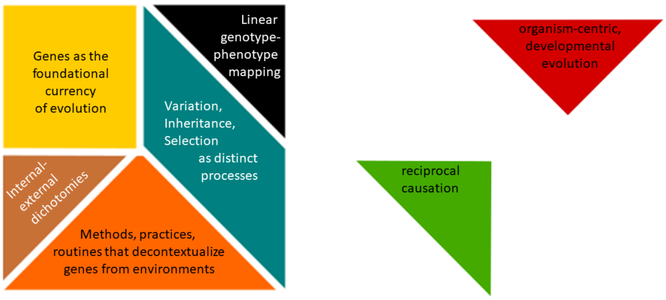


Figure 26. New shapes that don't seem to fit into the standard evolutionary theory tangram.

Recall our evolution tangram?

The acquisition of new data or the performing of new experiments may reveal new facts or principles that cannot be adequately fitted into the original tangram of standard evolutionary theory (e.g., reciprocal causation, organism-centered evo-devo) (Figure 26).

The moderate way forward is to reframe the new pieces into the original tangram. One can expand

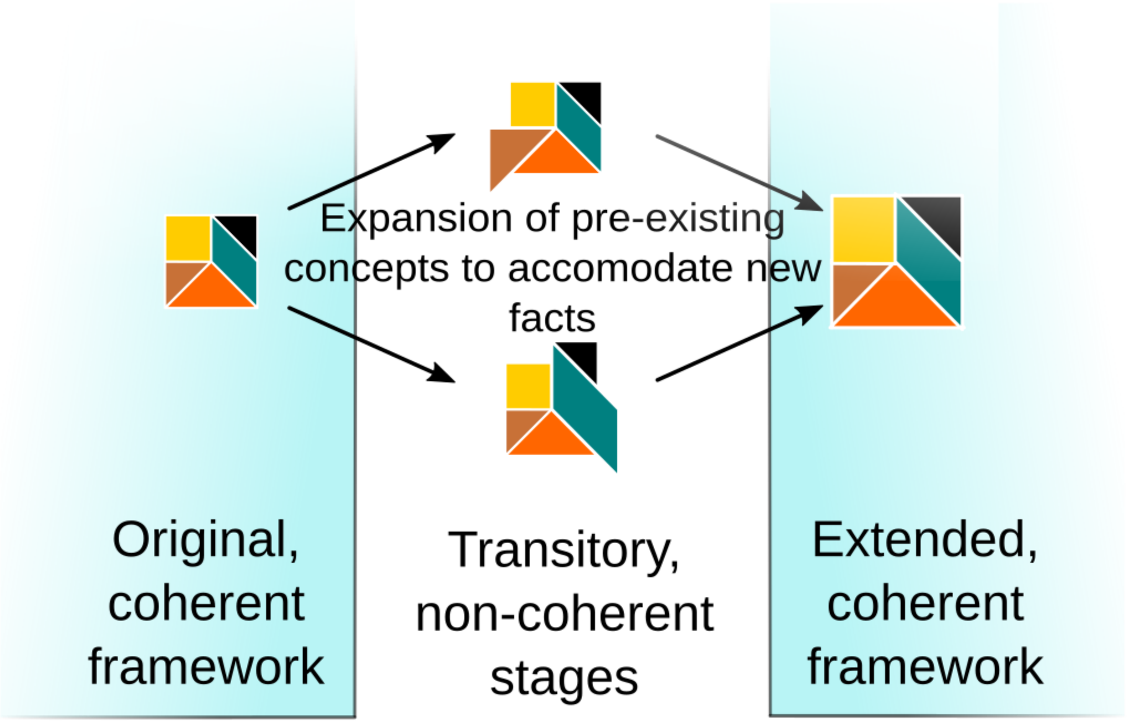


Figure 27. One way to "extend" standard evolutionary theory is to use the same pieces but broaden the scope of each to accommodate new phenomena.

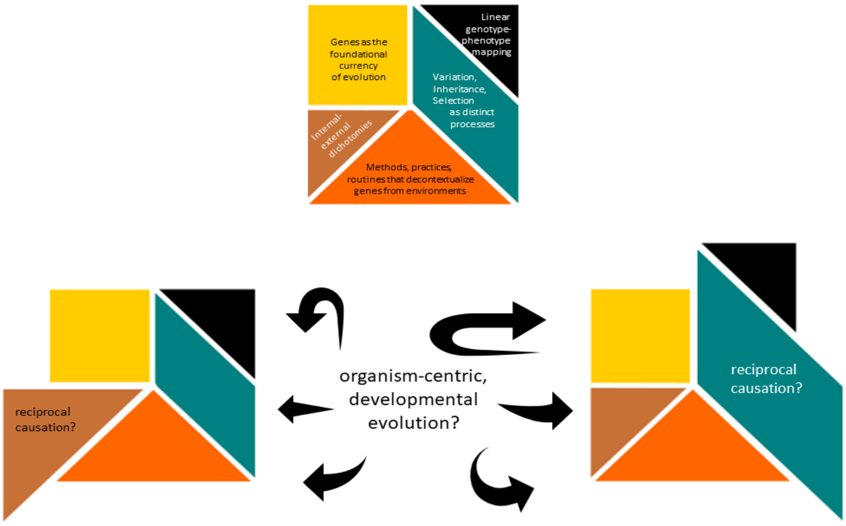


Figure 28. Yet not all aspects of EES can fit into the standard evolutionary theory tangram

on preexisting concepts to accommodate new phenomena. This solution is one way of extending the current synthesis—by expanding the scope of each component piece (Figure 27). Yet not all EES ideas can fit in. Furthermore, in the process, we also eliminate key concepts–e.g., the organism (Figure 28).

There is another kind of moderate. The molecular era did not merely reinforce the Modern Synthesis. It also introduced new findings that go beyond it. The genetic study of morphological (Carroll 2008) and developmental evolution (Carroll 2000) uncovered the presence of vast **genetic regulatory networks** (GRNs) responsible for the origin and transformations of major body forms and modular body parts.

Recommended reading: Carroll wrote many accessible pieces about evo-devo and gene regulatory networks. A starting point is *Endless Forms Most Beautiful* (2006) and the 2000 review, *Endless forms: the evolution of gene regulation and morphological diversity*.

Furthermore, the study of genomics, which examines the entire genome and not just protein-coding DNA regions, transformed our assumptions about the role of genes in evolution. Genomics enabled us to go above single genes to analyze the genetic regions and mRNA structures that regulate gene expression.

These studies show that genes evolve in the context of the entire genome in developmental processes, not in isolation nor independently from each other (Wray 2007, 2010). Evolutionary innovations can arise from mutations that alter the way genes are regulated (see Shapiro 2017 for more ways genome context can be affected and expressed), not merely through the generation and accumulation of new genetic variants. Even neutral mutations can affect the genetic background of genes and thus facilitate the potential appearance of novel traits (Zheng et al. 2019).

These new developments in genomics and molecular developmental biology are intriguing. On the one hand, they still count as genetic theories of evolution. The target of research is still genetic, e.g., genetic regulatory networks and the genome. Yet we can no longer describe this type of work as a gene-centric theory of evolution. Physiological and developmental genetics are not about the counting and tracking of gene frequencies; they cannot be fully captured by the models of the Modern Synthesis. The result is a moderate position with a progressive flare: a focus on genetic theories of evolution that are not gene-centric.

The Progressives

Müller, Laland, Uller, Jablonka, etc., are firm progressives (Laland et al. 2015; Müller 2017; Uller and Laland 2019; Jablonka and Lamb 2020). They argue that the extended set of evolutionary concepts, processes, and findings are not mere expansions of standard evolutionary theory. They restructure it.

Most crucially, the EES is an organism-centric and phenotypically oriented biology. The EES is a *"distinctively different framework for understanding evolution"* (Laland et al. 2015, p. 3) that can guide different aims and means of scientific investigation and offers different interpretations of scientific findings.

Analyzing the work done by Laland et al. (2015) and beyond, Tim Lewens (2019) argues that the EES is philosophically distinct from the standard theory. It offers a different understanding of the basic components of evolution (ontology) and also uses novel concepts and principles to explain evolutionary processes (epistemology).

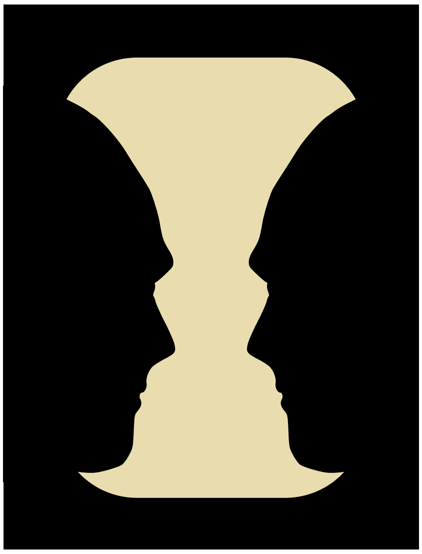
Ontologically, the EES assumes that organisms and their developmental, behavioral, etc., properties are foundational to evolutionary theory. Compare this to the "ground floor" of standard theory, which is instead centered on genes and their variants. Epistemologically, the EES offers different kinds of explanations, methodological approaches, and testable hypotheses.

Progressives seek to redefine "evolution" so that a new, expansive framework can assimilate gene-centric evolution as a special case. For instance, Laland et al. (2015) define evolution as *"transgenerational change in the distribution of heritable traits of a population,"* which includes gene-centric evolution in the definition. Another example is Marion Blute (2019), who expanded the definition of microevolution into *"any change initiated by inheritance, ecology, or development that alters the relative frequencies of (genetic or other) hereditary elements in a population beyond those expected of randomly chosen variants."*

Progressives tend to lean toward **pluralism** when they speak of the relationship between standard evolutionary theory versus the EES. They call for open-mindedness, to resist dogmatism, and hope that scientists can allow for the exploration of multiple co-existing perspectives and explanations (Laland et al. 2015; Fábregas-Tejeda and Vergara-Silva 2018b). This camp often advocates for "bottom-up" and pragmatic approaches (Love 2010; Lewens 2019).

On the slightly more radical side, other progressives like Emily Herrington and Eva Jablonka (Herrington and Jablonka 2020), however, use the metaphor of a "Gestalt switch" to describe what it would mean to completely shift from the standard view to an EES framework. Gestalt switches are visual illusions where one can switch between two incompatible perspectives (see, for instance, the rabbit-duck illusion and vase-face illusory figures). It is nearly impossible to see both perspectives at the same time. The switch, in this case, is from a gene-centered view to one that is organism and development centered. Instead of starting an evolutionary analysis with genes and treating phenotypes as mere evolutionary outcomes, on

Is this a vase or two faces?



the phenotype-first and organism-centered perspective, the physiology and development of organisms are the main sources of phenotypic innovation. Gene-centric evolution drops out of the picture.

Back to the tangram, the progressive way forward is to take the new phenomena as new pieces of the tangram and figure out a different way of solving the puzzle (i.e., creating a new coherent framework) (Figure 29).

The transitory, noncoherent stage takes time. In the process of trying to fit in the new data, the whole theoretical framework can seem to lack its internal consistency and elegance. The new principles will still be confronted with most of the theoretical foundations of the paradigm, or, at best, will be assimilated as inelegant add-ons to the main body of the theory.

The EES is still at this transitory stage.

Moving beyond this state to return to a coherent theory (but to a bigger, more comprehensive and complete one) might require either retweaking and rethinking all the subfields within the existing framework (so that each subfield is more inclusive and able to take into account disruptive facts), or redeveloping a truly overarching theory to make all the observations sense again.

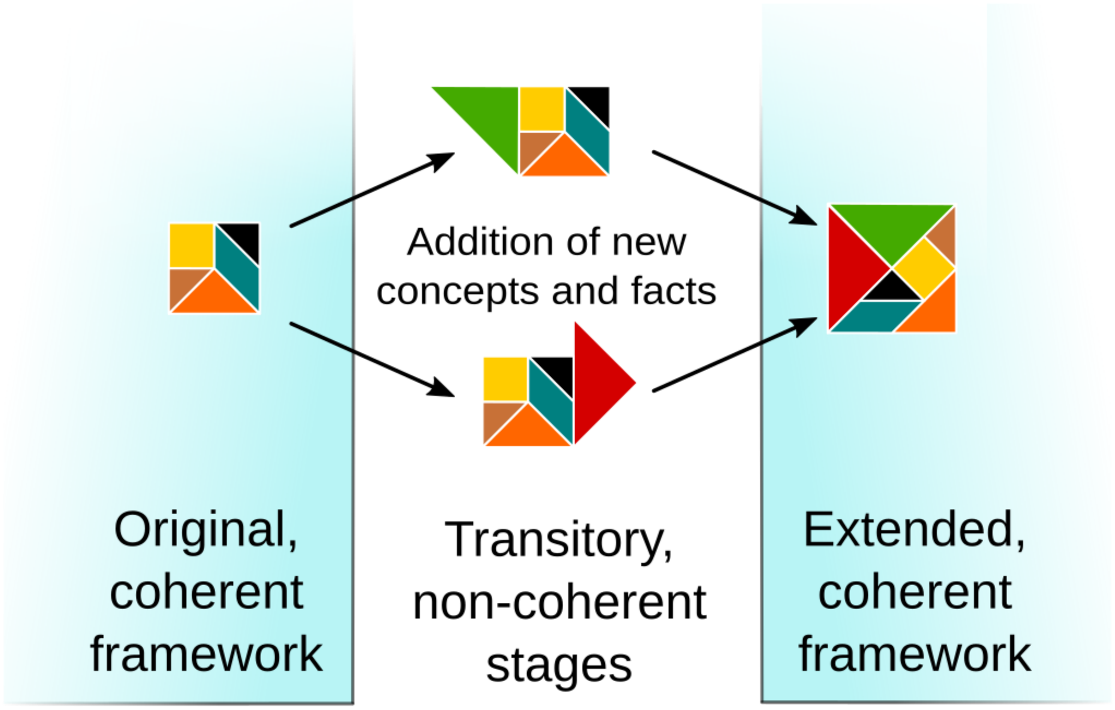


Figure 29. Solving the puzzle by reorganizing the pieces into a new tangram.

Putting it all together: Restructuring evolutionary theory

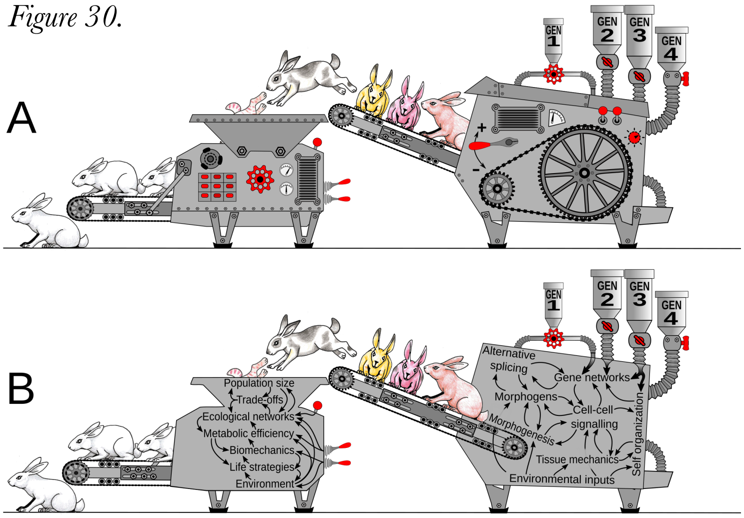
Let's take stock.

Mainstream evolutionary theory is dominated by the idea that evolution is ultimately about the evolution of genes. The extended synthesis, on the other hand, puts value on the evolution of phenotypes, in part driven by features of the organisms.

Under standard evolutionary theory, what matters is the statistical association genotype and phenotype. Everything else is put into a black box. In Figure 30A, genetic variation translates into phenotypic variations (different colored rabbits in the middle) that are then filtered by natural selection (white rabbits at the end). Each process is handled by a distinct set of mechanisms. Proximate causes are hidden away from the ultimate causes.

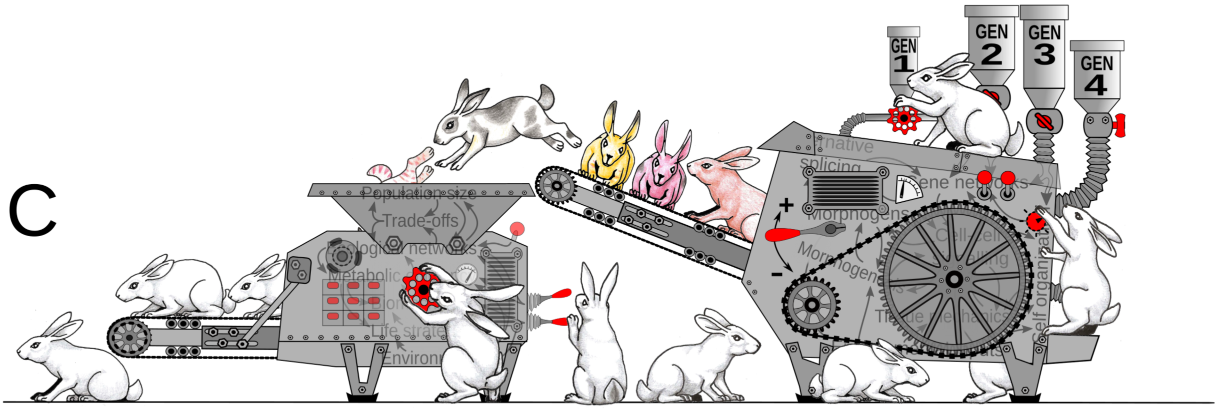
As we open up the developmental black box, the proximate causes have important roles to play. In Figure 30B, the mechanisms of how organisms work and the causal pathways of ecological systems now figure into ultimate, evolutionary explanations. A causal story, not just the statistical story, is now part of evolutionary theorizing.

Figure 30.



Yet a crucial ingredient is still lacking. The missing ingredient is the interdependency between these processes facilitated by organismal agency. Organisms are constructing their environments, constructing the conditions of their development, and thus constructing their evolutionary future.

In Figure 30C, this is illustrated by the rabbits themselves playing with the controllers of the evolutionary processes. Variations and selection depend on not only the genetic makeup of the population, but also on developmental processes and constructed environments. Organisms play central and active roles in manipulating each part of the evolutionary process.



The following figures fit together the findings reported in Parts 2 and 3.

In Figure 31A, inheritance is realized only by genes “isolated” from the organismal body thanks to Weismann’s barrier. The environment appears as a selective agent. While the environment can change over generations, the organism does not play an active role in environmental change.

Figure 31A

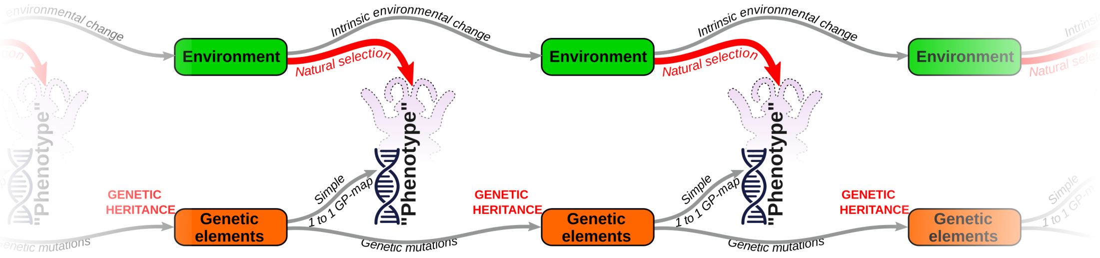


Figure 31B recognizes that phenotypic variation is much more complex, involving environmental input and complex developmental processes. However, the relevant processes are ultimately encoded in genes and passed on through genetic inheritance. They contain all the information required to orchestrate the organismal development within a given environment.

Figure 31B

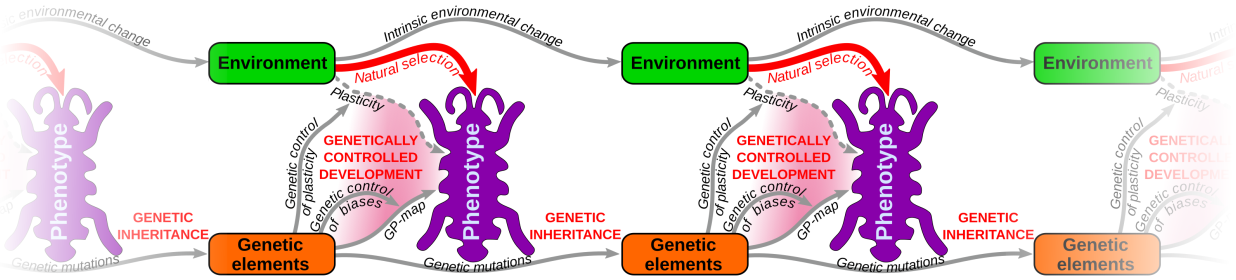
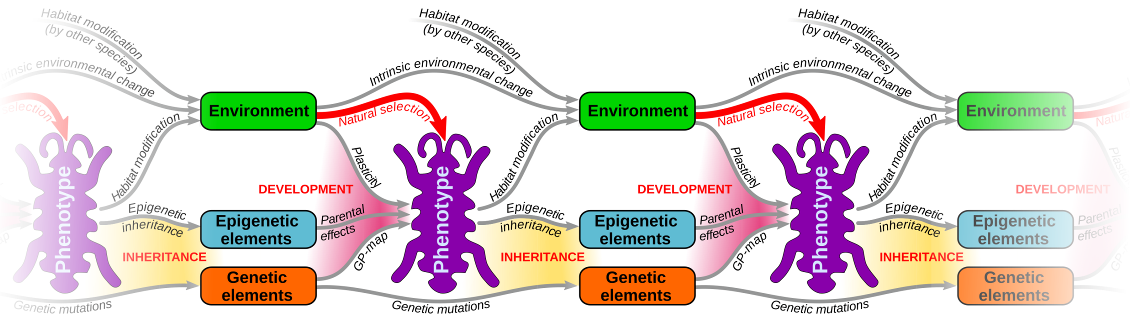


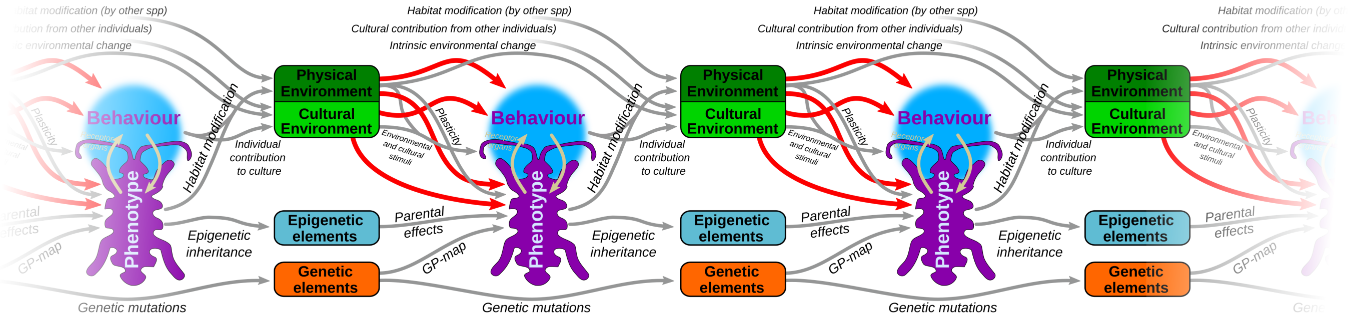
Figure 31C illustrates a multicausal, more inclusive view on development, inheritance, and thus evolution. It shows how development requires several different informational inputs (genetic, environmental, epigenetic...) to create phenotypes, and how all these elements need to be passed to the next generation for the inheritance of traits. It also shows how environment is influenced by organisms themselves (i.e., niche construction). Finally, it also shows that the intergenerational transmission of relevant sources of information depends on the organism. Organisms play an active role on their own mechanisms of variation, selection, and inheritance.

Figure 31C



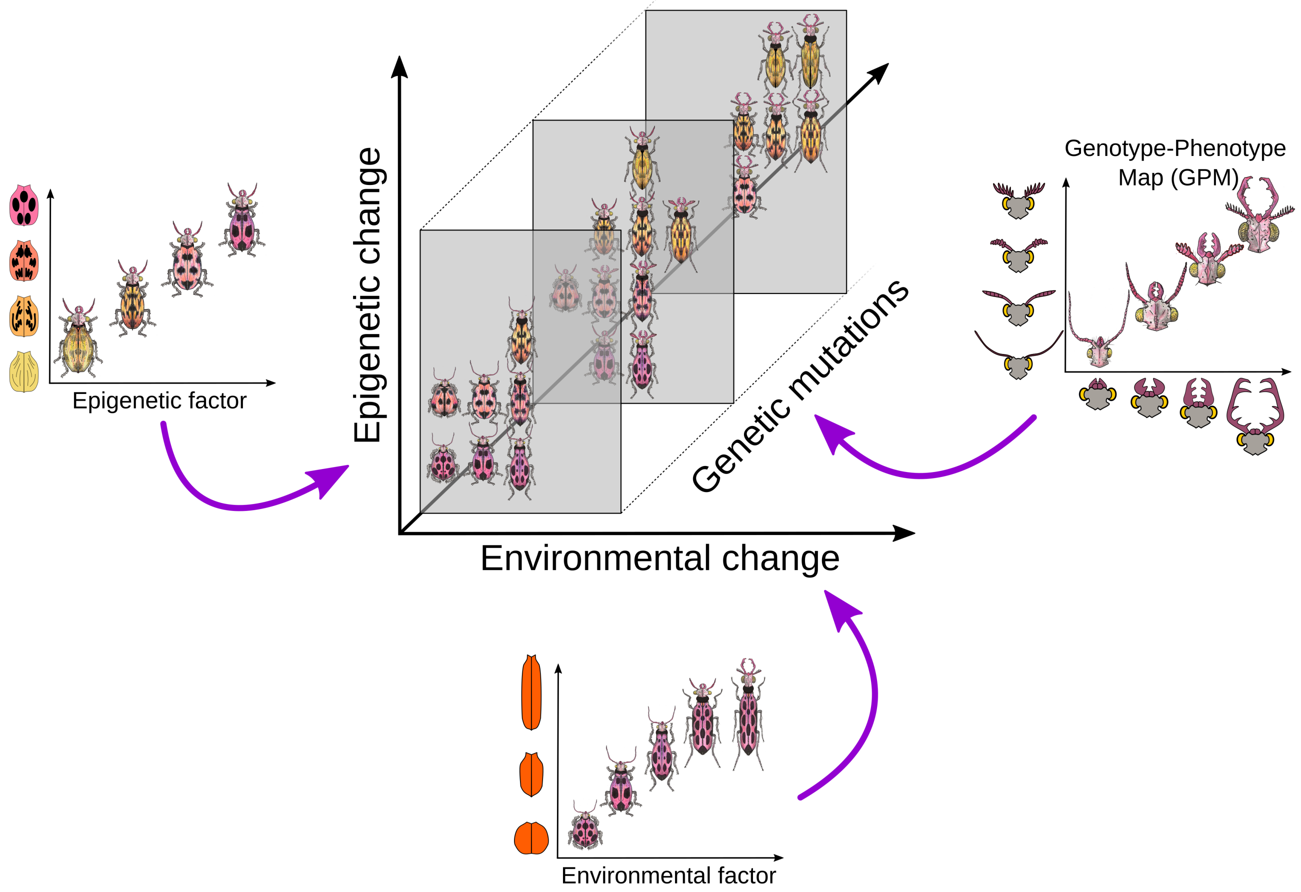
Culture adds an extra dimension in Figure 31D. Culture and its evolutionary dynamics are fast, adaptive sources of biological evolutionary change. They can be seen as a very complex informational environment co-constructed by the members of the society. Cultural transmission is related to niche construction. If the organism has the appropriate receptor, effector, and cognition organs, it will be able to receive, respond, and co-construct its cultural environment.

Figure 31D



Under the EES, the environment, the epigenetic elements, and the genetic elements are all involved in the co-construction, inheritance, and evolution of organismal phenotype. Genes are just one—albeit they are very important—of the necessary inputs required for development. Developing systems are also sensitive to environmental and epigenetic information, and the specific forms of sensitivity will depend on the specific developmental dynamics. This multicausality is what the final figure, Figure 32, represents.

Figure 32



Conclusion

Evolution is, by definition, “change.” As life on Earth continues to evolve, our evolutionary theorizing and our meta-commentaries evolve as well. New work under the wide umbrella of EES is coming at a rapid clip. Several new EES-related projects funded by the John Templeton Foundation are well underway, for instance, one on biological agency (*Agency in Living Systems*) (Sultan et al. 2021) and another on a naturalistic notion of purpose (*Agency, Directionality, and Function: Foundations for a Science of Purpose*). With the field rapidly moving forward, this review is best seen as a temporary road map.

Here are the key messages each part seeks to convey:

Part I– “Progress” in science is not merely the steady, slow accumulation of new findings (just as evolution itself is not just small gradual accumulation of minute mutations). Instead, humans play a large role selectively discarding, retaining, and merging our concepts and tools to reach specific goals. There is a story to tell behind each decision to exclude or include. Standard evolutionary theory is the result of one such set of decisions, in part as a reaction to the biology of the time. While taking this particular path helps us solve some problems (e.g., solving microevolutionary problems), it might blind us to others. With the benefit of hindsight and a stronger research toolkit, we can try to examine where alternative tracks can take us.

Part 2– Frustrations against the Modern Synthesis and neo-Darwinism were prevalent in numerous areas of study way before the current EES research program. While the concerns raised have independent origins, the common thread is the effort to reintegrate the organism into evolutionary biology. A broader solution is thus needed to unify the challenges against the core commitments of standard evolutionary theory and to provide a fruitful path forward.

Part 3– The EES research program arose as one such answer. The core concepts, principles, and predictions are distinct from that of standard evolutionary theory. Pitted side by side, they allow us to conceptually and empirically evaluate whether EES principles are new, true, and useful. However, contrary to the predominant narrative, this is not an either-or situation. This section characterized multiple possible interpretations of the relation between standard theory and EES, and there is space for more nuanced responses to develop. To reconcile the differences and move forward as a scientific community, we need to first acknowledge where we stand and why.

The length of this review reflects the challenge of finding a bird’s eye view while we’re still deep in the woods. It is impossible to provide an uncontroversial account of the historical turns that led up to the EES or to offer a fair appraisal of its current status.

Yet I hope that the reader will find that there are plenty of rich stories to tell about the EES beyond the question “is evolutionary theory overturned?” It is sobering to realize that there will not be any “slam dunk” finding that will revolutionize evolutionary theory as we know it.

– Lynn

About the author

Lynn Chiu is a philosopher of biology and science communicator based in Vienna, Austria. She is currently a postdoctoral researcher at the University of Vienna, working on a wide range of public engagement projects related to Gregor J. Mendel's bicentennial birthday.

Her research interests include the role of niche construction in evolutionary explanations and the nature of host-microbiome interactions. She is currently writing on the "gut mind" with collaborators in psychology, physiology, and philosophy.

In the last few years, she worked as a science communicator and visiting scholar at the Laland Lab, University of St. Andrews, and also as the communicator officer of the KLI at Klosterneuburg, Austria.

She holds a Ph.D. and M.A. in Philosophy, a M.S. in Psychology, and a B.S. in Life Sciences.

About the illustrator

Miguel Brun-Usan is an evolutionary biologist. After completing his PhD in the Universitat Autonoma de Barcelona, he joined the Extended Evolutionary Synthesis project (in UK and Sweden), where he conducted research on cell plasticity (with conceptual tools from learning theory) and on the relationship between phenotypic plasticity and developmental biases. He is currently working in the Universidad Autónoma de Madrid, where he is trying to build ever more comprehensive evolutionary models unifying developmental and ecological dynamics.

Besides his scientific research, he is a passionate artist, with more than a hundred of science-inspired drawings in different styles, from surrealistic ones to mathematical tessellations. He has organized several art exhibitions in Spain and UK, and he has also made several commissioned posters and covers, from PhD thesis works to some Q1 scientific journals.

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All mistakes, inadequacies, and omissions are mine alone.

Image credits

Miguel's illustrations

Figures 2, 5, 12, 13, 20, 26, 27, 28, 29, 30A, 30B, 30C, 31A, 31B, 31C, 31D, 32

Lynn's figures

Figures 1, 3, 4, 5, 6, 7. 8, 9, 11, 14, 15, 17, 18, 19, 21, 22, 23, 24

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