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Evolvability

A Unifying Concept in Evolutionary Biology?

Edited by: Thomas F. Hansen, David Houle, Mihaela Pavličev, Christophe Pélabon

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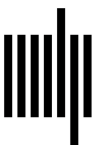
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Evolvability as a Disposition: Philosophical Distinctions, Scientific Implications

Ingo Brigandt, Cristina Villegas, Alan C. Love, and Laura Nuño de la Rosa

A disposition or dispositional property is the capacity, ability, or potential to exhibit some outcome. Evolvability refers to a disposition to evolve. This chapter discusses why the dispositional nature of evolvability matters—why philosophical distinctions about dispositions can have scientific implications. To that end, we build a conceptual toolkit with vocabulary from prior philosophical analyses using a different disposition (protein foldability) and then apply this toolkit to address several methodological questions related to evolvability. What entities are the bearers of evolvability? What features causally contribute to the disposition of evolvability? How does evolvability manifest? The various possible answers to these questions available from philosophical distinctions suggest implications for why the concept of evolvability as a disposition is useful in evolutionary research. These include (1) securing scientific virtues (e.g., explanatory depth and generalization, prediction or retrodiction, and control or manipulation) and (2) fostering interdisciplinary collaboration through the coordination of definitional diversity and different types of inquiry. Together these implications facilitate concentration on a variety of research questions at different levels of organization and on distinct timescales, all of which should be expected for a complex dispositional property such as evolvability.

4.1 Introduction

A disposition or dispositional property is the capacity, ability, or potential to exhibit some outcome. Since something can possess an ability without currently displaying it, dispositions are attributed when it makes sense to distinguish between something having a property and manifesting that property. For example, the fragility of a window is its disposition to break under certain conditions (e.g., on impact from a rock). The window is fragile even if it never breaks, and we can make claims about its degree and kind of fragility despite its manifestation not being directly observed. This kind of property contrasts with nondispositional or so-called categorical properties of the window, such as size or shape, for which a distinction between the property and its manifestation is irrelevant. Dispositional properties are common in biology (Hüttemann and Kaiser 2018), including the foldability of proteins or the differentiability or pluripotency of cells. The most recognizable example in evolutionary biology is fitness, where the general capacity to survive and reproduce is distinct from actual reproductive success (Mills and Beatty 1979). There also is an abundance of dispositional notions in the field of evolutionary developmental biology (evo-devo), such as forms of phenotypic plasticity, including the capacity to exhibit different morphological traits in seasonal polyphenisms (Austin 2017; Austin and Nuño de la Rosa 2021).

Evolvability—the core notion of this volume—is a disposition. Scientific definitions make this dispositional character plain by construing evolvability as the “*ability* to respond to selection” (Houle 1992, 195), the “*capacity* to generate heritable phenotypic variation” (Kirschner and Gerhart 1998, 8420), or the “*ability* to produce adaptive variants” (G. Wagner and Altenberg 1996, 970, emphasis added in all quotes). Evolvability can but need not manifest in a higher rate of evolution, because two populations with an identical ability to evolve may come to exhibit different evolutionary outcomes due to chance—just as in the case of fitness as a capacity to reproduce—or due to the two populations being exposed to different environmental conditions with different regimes of natural selection. Twenty-seven years ago, G. Wagner and Altenberg (1996) noted that *evolvability* and *variability* are dispositions and should be distinguished from actual evolutionary outcomes and observable variation (see also Hansen 2006). This distinction encourages making the dispositional property of evolvability a target for scientific investigation, especially how this capacity has changed through the history of life (i.e., the evolution of evolvability). Indeed, the increasing prominence of the notion of evolvability marks an important change in recent scientific theorizing (Brigandt 2015; Nuño de la Rosa 2017; and chapter 2¹), and its dispositional character may be part of the reason that the concept of evolvability nowadays enjoys widespread use in a variety of biological fields investigating evolution.

One task of this chapter is to argue that the dispositional nature of evolvability matters—to explain why philosophical distinctions about dispositions can have scientific implications—and to show what is distinctive about evolvability compared to other dispositions in evolutionary biology. However, as the limited array of evolvability definitions described above makes plain, different conceptions of evolvability are used by different disciplines, from quantitative genetics and evo-devo to evolutionary systems biology and paleontology. We therefore address what kind of disposition evolvability is in these different contexts, and how these conceptions and disciplinary approaches to such a complex disposition are related. To this end, we first build a philosophical toolkit related to dispositions, before deploying it both to make sense of the plurality of evolvability definitions and to draw implications for its scientific significance and explanatory value as a dispositional concept. Importantly, our analysis does not provide definitive claims about specific cases of evolvability but rather generates resources for more nuanced interpretations relevant to further empirical and theoretical evaluations.

4.2 Vocabulary: Building a Toolkit for Evolvability

To analyze evolvability as a disposition, it is useful to build a conceptual toolkit based on vocabulary from prior philosophical discussions. Although there are different, often non-overlapping bodies of literature in philosophy that reflect on dispositions (e.g., metaphysics, philosophy of science, and philosophy of probability), it is possible to identify some core ideas that are helpful (see Choi and Fara 2021 for an overview). To do so, we focus on a different disposition—protein foldability—so that the basic distinctions are laid out in advance of their application to evolvability. Although protein foldability provides sufficient biological details to illustrate the value of most of the dispositional vocabulary (see box 4.1),

1. References to chapter numbers in the text are to chapters in this volume.

Box 4.1

Philosophical vocabulary for dispositions

Background conditions: The various circumstances present when a disposition is manifested, may or may not be relevant (e.g., temperature while glass shatters).

Bearer: The entity that has a disposition or exhibits a dispositional property. This entity can be an individual or an aggregate and can be considered as either a token or a type (i.e., an individual or a class of similar individuals; a single population of entities or a class of similar populations of entities).

Causal basis: The underlying properties determining that the capacity applies (e.g., amino acid sequence in a foldable polypeptide).

Disposition or Dispositional property: The capacity itself (e.g., fragility, foldability, or evolvability).

Explanatory depth: The aim of an account of a disposition that demonstrates how the causal basis contributes to the process of disposition manifestation, why a particular manifestation is regularly achieved and relatively stable, or what effects might arise from various possible stimulus conditions.

Intrinsic/Extrinsic: Whether the causal basis that determines the disposition is fully internal to the disposition's bearer (e.g., its parts and their interactions) or whether features external to the bearer (e.g., environmental components) also contribute to the capacity obtaining.

Manifestation: The actual display of the disposition (e.g., the glass breaking or the protein folding correctly), which might vary in rate (slower or faster), intensity, or number (e.g., different correct conformations of an intrinsically disordered protein).

Probabilistic/Deterministic: Whether a disposition manifests always (deterministically) or only some of the time (probabilistically, as a propensity) under the appropriate stimulus conditions.

Single-track/Multitrack: Whether a disposition always has a single outcome (manifestation) or whether there are several distinct outcomes, depending on the stimulus condition.

Stimulus (Triggering) conditions: The circumstances leading to the disposition's manifestation (e.g., a solid object hitting glass).

Token/Type: Dispositions can be ascribed to single entities (tokens) or to classes/kinds of entities (types).

there are limitations to the example as a template that we note in section 4.3 before turning to evolvability.

Foldability is the disposition of a protein to have its linearly arranged structural components—amino acids—rearranged (“folded”) into higher-order, 3-dimensional configurations to accomplish cellular functions. Biologists attribute this disposition to proteins because proteins adopt one or more 3-dimensional (tertiary) structures or conformations that are typically necessary for them to be functional. (These conformations exhibit variation that can be represented with probability distributions.) The process of achieving a 3-dimensional structure is sometimes described as spontaneous (Campbell and Reece 2002). This appeal to spontaneity denotes something happening as soon as certain conditions arise. Just as glass shatters on projectile impact (fragility), a protein has a disposition to fold (foldability) into one or more conformations with functional properties under appropriate *stimulus conditions* in its chemical environment. The display of a tertiary structure and corresponding function is a *manifestation* of the disposition. The capacity of foldability *explains* the resulting patterns of folded-and-functional proteins (the manifestation). Such a dispositional property

can be ascribed to an individual macromolecule (a *token*) or to a class of the same polypeptides (a *type*). However, predicting how this folding occurs and understanding mechanistically why a specific functional outcome is achieved have been refractory questions. Some of the empirical details making these questions difficult to solve serve to further build a toolkit for talking about dispositions.

Initially, protein folding was understood to result from physical properties of the component amino acid residues in a polypeptide (e.g., hydrophobic residues avoid interaction with surrounding water by segregating to internal regions). These components and their interactions were thought to constitute the *causal basis* of foldability: “the native conformation is determined by the totality of interatomic interactions and hence by the amino acid sequence” (Anfinsen 1973, 223). Some of the strongest evidence for this idea came from experiments on the denaturation and refolding of ribonucleases in vitro. These experiments suggested that the causal basis was *intrinsic* to the linear polypeptide; that is, the polypeptide’s primary structure contains all the information required for achieving a 3-dimensional, functional conformation. This causal basis provides increased *explanatory depth* (Weslake 2010) to our understanding of protein folding, accounting for both how the process of folding occurs and why one or more functional conformations are regularly achieved and relatively stable.

However, the proteins investigated in these experiments did not fold as rapidly as in their cellular context (a discrepancy in the *rate* of expected manifestation). This suggested that there were *background conditions* (Hüttemann and Kaiser 2018) to be considered for protein folding, such as particular environmental factors that enhanced folding speed. For example, Anfinsen’s group found that folding was faster when the in vitro solution contained an enzyme from the endoplasmic reticulum. Some proteins do not fold functionally (i.e., the disposition fails to manifest) or do not fold functionally as commonly under in vitro conditions. Such background conditions can therefore be relevant by modulating the disposition’s manifestation (e.g., its rate), even when they are not stimulus conditions that initiate a particular manifestation in the first place.

Another conceptual issue arises from the frequency of successful manifestation: whether a disposition is *deterministic* (always manifesting under a stimulus condition) or *probabilistic* (manifesting under a stimulus condition with some quantitative frequency). The existence of the unfolded protein response in cells (Hetz 2012), where only some proportion of a protein species folds functionally, points toward foldability as a probabilistic disposition or *propensity*. A further complication relates to the assumption that proteins have a single native conformation. Intrinsically disordered proteins highlight that the sequence-structure-function relationship for foldability is not universal; many proteins do not form stable and static 3-dimensional configurations but instead assume many structural conformations over time under different stimulus conditions (Tompa 2010). The same disposition can yield multiple outcomes (i.e., a *multitrack* disposition), and these outcomes can be quantified with a probability distribution over the possible manifestations. Most dispositions are probabilistic in nature, manifesting only with a certain probability, but the multitrack foldability of intrinsically disordered proteins reminds us that there can be several probabilities of manifesting in different ways.

These additional issues with the manifestation of foldability prompted detailed studies of the background conditions, which revealed the importance of distinct chaperone pro-

teins that guide protein folding during *de novo* synthesis, quality control, and the response to stress in the crowded environments of cells. Sometimes chaperones provide a sequestered domain and at other times actively facilitate folding. Even when mutations are introduced that lead to altered amino acid components in a polypeptide, functional folding can be induced by the overproduction of chaperones (Maisnier-Patin et al. 2005). Depending on how foldability is modeled, this role of chaperones can be understood differently, either as appropriate background or stimulus conditions or as *extrinsic* components of (or contributors to) the causal basis of the disposition (Hüttemann and Love 2011). At a minimum, the causal basis of foldability is more complex and relationally intertwined than previously thought (see section 4.3.2).

4.3 Methodological Questions: Putting the Toolkit to Use

This philosophical toolkit for studying dispositional properties orients us to several methodological questions that frame research on evolvability. For example, at what rates and on what timescales does evolvability manifest? Are the contributors to the causal basis of evolvability only intrinsic to the bearer of evolvability? What is being measured when studying evolvability empirically (causal basis, disposition, manifestation, or something else)? Additionally, further questions not directly addressed in the example of protein foldability must be explored, such as the difference between an individual entity versus an aggregate of entities having a disposition, the quantitative measure and comparison of dispositions, the distinctive behavior of dispositions at different timescales, or the evolutionary transformation of dispositions. We now turn to these and allied questions with special attention to the variety of definitions of evolvability, including why different definitions need not be in conflict and how different construals of evolvability are related.

4.3.1 What Are the Bearers of the Dispositional Property of Evolvability?

In the case of complex dispositions, it is useful to clarify what the *bearer* of a disposition is. For evolvability, the bearer is whatever entity is evolvable and thus possesses the capacity to evolve. Once we have specified a particular bearer of evolvability, we are better positioned to examine the constituents of its causal basis (section 4.3.2). In addition to common cases where an *individual* object possesses a disposition, we need to consider that an *aggregate* of individual objects also can have a dispositional property (which also matters for protein foldability; Invernizzi et al. 2012). Both options appear in scientific definitions of evolvability. When evolvability is interpreted as a population-level capacity, it is an aggregate of individual organisms that bear the disposition: “the ability of a *population* to respond to selection” (Houle 1992, 195, emphasis added; see also Flatt 2005; G. Wagner 2014). In contrast, the bearer of evolvability appears to be an individual object if the disposition is construed as a property of an organism: “evolvability is an *organism’s* capacity to generate heritable phenotypic variation” (Kirschner and Gerhart 1998, 8420, emphasis added; see also Yang 2001). For accounts that focus on the evolvability of a species or a higher taxon (Hopkins 2011; McGuire and Davis 2014; see also Jablonski, chapter 17), both options are utilized: Sometimes a lineage is conceptualized as an individual (an entity persisting as the same thing across time even while its constituent parts change; Rieppel 2007), and sometimes as an aggregate of organisms that compose an evolvable taxon.

How should we interpret these divergent viewpoints about what possesses evolvability? One possibility is to adopt a more abstract definition, such as by understanding evolvability as the “ability of a *biological system* to produce phenotypic variation” (Payne and Wagner 2019, 24, emphasis added). A “biological system” could be an individual (an organism is a biological system) or an aggregate of individuals, including a whole population of conspecific organisms or an interacting microbial system consisting of individuals from various species. However, it is practically necessary for many scientific investigations to have an account that more concretely specifies the bearer of evolvability. In population and quantitative genetics, it is typically populations of individuals (or their traits) that are assumed to be the units of evolutionary change: Populations (as aggregates) possess evolvability in the sense of having the ability to respond to selection. In evo-devo, the focus is on how the configuration of development for organisms biases phenotypic evolution. In such a context, evolvability is conceptualized as a property of organisms in the sense of the ability to generate functional phenotypic variants. These different definitions of evolvability need not be in conflict: They can refer to different aspects of the evolutionary process or be useful tools that have appropriate uses in the context of different approaches.

At the same time, the notion that an organism would be evolvable appears misguided; only a population or lineage of individuals evolves, not an organism. This issue can be resolved by making use of the toolkit distinction between types and tokens. One token organism cannot evolve, but a type or kind of organism exemplified in a population of individuals can undergo evolutionary change. This type or kind is representative, sometimes only implicitly, of a population or aggregated unit. Thus, the above definitions that refer to an organism’s evolvability can be read as referring to a *type* of organism, such as organisms from a particular species or exhibiting shared constellations of traits. Likewise, when a developmental system is seen as the bearer of evolvability—“evolvability, the capacity of a *developmental system* to evolve” (Hendrikse et al. 2007, 394, emphasis added)—it is not a token developmental system of one individual organism, but the type of developmental system that is evolvable (Nuño de la Rosa and Villegas 2022). An analogous bearer of evolvability is the genotype-phenotype map: “evolvability as a property of the *genotype-phenotype map* (the genetic system) and not as a population property” (Hansen 2006, 129, emphasis added). As noted above, another prominent bearer of evolvability is a *trait*, given that phenotypic traits (Roseman et al. 2010; Opedal et al. 2017) or characters (G. Wagner and Altenberg 1996) evolve. Traits on quite different levels of organization can exhibit evolvability, from molecular traits (e.g., protein domains and transcription factor binding sites) and physiological traits (e.g., metabolic rates and immune responses), to complex morphological traits (e.g., insect wings and vertebrate limbs) and life-history traits (e.g., size at maturity and clutch size).

Although different interpretations concentrate on a variety of relevant bearers, it is possible to navigate among these interpretations. The same researcher may offer a generic or abstract characterization of evolvability as well as a specific or concrete characterization of evolvability, and then use them for distinct purposes. For instance, from the perspective of quantitative genetics, Houle (1992) construes evolvability generally as “the ability of a *population* to respond to natural or artificial selection” (195, emphasis added), while also providing a quantitative measure for the evolvability of a specific *phenotypic trait* (in terms of the trait’s coefficient of additive genetic variation). The latter permits a comparison of the abilities of

different specific traits in the same population to respond to selection; a generic definition only stating that evolvability is a capacity of a population would not accomplish this. A specific definition focusing on traits also facilitates comparisons of the same trait in different populations. Although different bearers often yield different evolvability dispositions, which are relevant for different purposes or in different scientific fields, in section 4.4 we also point to interrelations among these different construals of evolvability.

4.3.2 What Is the Causal Basis of Evolvability?

Once the bearer of evolvability is defined (whether it be traits, organisms, populations, or taxa), a subsequent concern is to understand the disposition's causal basis: What makes a particular bearer evolvable? For example, G. Wagner and Altenberg (1996, 967) focus on the evolvability of characters and argue that what determines this is the structure of the genotype-phenotype map. This structure governs the way in which random genetic mutation translates into nonrandom, structured, and possibly adaptive phenotypic variation for characters (Nuño de la Rosa and Villegas 2022). Many accounts point to the genotype-phenotype map and similar features of development underlying the variational properties of phenotypes as the disposition's *causal basis*: “evolvability . . . is largely *a function of* the developmental system's ability to generate variation” (Hendrikse et al. 2007, 394, emphasis added).

As noted (section 4.3.1), the genotype-phenotype map can itself be the *bearer* of evolvability. This bearer is operative in models of how the genotype-phenotype map as an entity evolves or can evolve, including discussions of whether a particular genotype-phenotype map is an adaptation (Pavličev and Hansen 2011; see also Hansen and Wagner, chapter 7). This point is a reminder of the value of the philosophical toolkit. What is a *bearer* in one analysis of evolvability can be a *causal basis* in another analysis. It is crucial to be explicit about whether a feature, such as the genotype-phenotype map, is considered the disposition's bearer (the entity possessing the ability to evolve) or the causal basis (of some other bearer of evolvability, e.g., a character). Keeping this in view can facilitate the identification of connections across different interpretations as well as possible ambiguities in how researchers are using evolvability. For example, Hansen (2006) claims that he “follow[s] Wagner & Altenberg (1996) in defining evolvability as *a property of* the genotype-phenotype map (the genetic system) and not as a population property” (129, emphasis added). Although this claim appears to assert that the genotype-phenotype map (and not a population) is the disposition's bearer, Hansen also states that the genotype-phenotype map “*determines* the variational properties of the phenotype” (123, emphasis added). The latter suggests that the genotype-phenotype map is the causal basis, while the phenotype is the bearer (which aligns with our earlier reconstruction of G. Wagner and Altenberg 1996). More generally, equivocal statements like “evolvability is a property of X” could be intended to mean either “evolvability is a capacity of X” (which refers to the *bearer* X) or “evolvability is a function of X” (which refers to the causal basis X; see the quote earlier in this section from Hendrikse et al. 2007). In addition to clarifying potential ambiguities, the distinction we are making here serves as a reminder of distinct research tasks: The genotype-phenotype map needs to be investigated both as a bearer of and the causal basis for evolvability.

Focusing on the genotype-phenotype map as the causal basis of evolvability tends to accent features *internal* to organisms: “The evolvability of an organism is its *intrinsic* capacity for evolutionary change. . . . It is a function of the range of phenotypic variation

the genetic and developmental architecture of the organism can generate” (Yang 2001, 59). These internal properties can then be examined in more detail, such as how modularity is conducive to evolvability (G. Wagner and Altenberg 1996; Kirschner and Gerhart 1998; Pavličev and Hansen 2011; Pavličev et al., chapter 8; Hallgrímsson et al., chapter 9; Jablonski, chapter 17). Additionally, we can ask whether evolvability is always an intrinsic capacity. Our formulation of the toolkit using protein foldability raised the possibility that biological dispositions can have an *extrinsic* causal basis in the sense that some features external to the bearer are relevant to the disposition being present (Hüttemann and Kaiser 2018; Love 2003). A protein’s foldability is not always due to its internal amino acid sequence but can depend on the presence of chaperones.² If so, such external factors are not just stimulus conditions that can trigger the disposition’s manifestation (e.g., directional selection in the case of evolvability) or mere background conditions: They would need to be included in models of the disposition’s nature (see box 4.1).

In the case of evolvability, the distinction between internal and external is ultimately a matter of theoretical perspective: A methodological choice should be made about whether to investigate some factors external to an evolvable entity because they impact evolvability or to relegate them to the background conditions under which evolvability takes place. Consider several scenarios where evolvability may not be an intrinsic disposition but also can be seen as contingent on external factors. If the focus is on a phenotypic trait as the bearer of evolvability, then it may be the case that extrinsic features compose at least part of the causal basis of this trait’s evolvability, such as pleiotropic relations to other traits or the frequency of the trait in the whole population. Regarding another bearer, a taxon, there are a variety of considerations that point to an extrinsic basis, including interactions with entities in the environment that have an impact on evolvability (Love 2003; Sterelny 2011; Jablonski, chapter 17). From a paleontological perspective, species and higher taxa can possess evolvability also in terms of having lower extinction rates and the ability to undergo adaptive radiation and diversify. A taxon’s extinction rate can depend on its geographic range (Jablonski 1987), but this is not primarily an intrinsic, internal property of the organisms making up a taxon, because it can include landscape topography or ecological diversity across the range (Love 2003). In cases of ecosystem engineering, a taxon’s ability to undergo radiation and diversification is dependent on transformed ecological conditions, where the resulting ecological feedback can yield self-propagating radiations (Erwin 2012). A classic example is the radiation of mammals due to empty niches left by the extinction of non-avian dinosaurs (Alroy 1999). Such abiotic conditions as well as ecological interactions with other taxa would causally contribute to the basis of a taxon’s evolvability relationally or extrinsically.

Methodologies in evo-devo make it natural to view evolvability as a disposition with an intrinsic basis, where evolvability resides within an organism whose developmental architecture yields its ability to generate phenotypic variation. At the same time, some evo-devo and eco-devo phenomena relevant to the generation of novelty are difficult to fit into an intrinsic causal basis framework. For example, symbiosis has contributed to the origin of multicellularity as well as to multiple origins of herbivory (Gilbert 2020). In

2. Other dispositional properties exhibit a similar context dependence. For example, the “stemness” (a dispositional property) of a cell can depend on the cell being situated in an appropriate stem cell niche (Laplane and Solary 2019).

niche construction, organisms not only encounter a given environment to which they adapt, but their physiological and behavioral activities also modify the environment in an adaptive fashion, resulting in feedback loops and organism-environment coevolution (Scott-Phillips et al. 2014; Clark et al. 2020). Examples include the evolution of lactose intolerance in humans influencing the rate and direction of evolution (Scott-Phillips et al. 2014) and horned dung beetle larvae manipulating the surrounding dung, which influences morphological development, sexual dimorphism, and life history (Schwab et al. 2016). In both symbiosis and niche construction, ecological interactions between the organism and some of the biotic or abiotic entities in its environment have undergone adaptive evolution and increased the evolvability of organisms in the lineage. Such ongoing evolutionary interactions transform features internal as well as external to organisms, exhibiting an iterative dynamic between “internalization” of environmental factors and “externalization” of an organism’s structures (Laubichler and Renn 2015).

Organism-environment interactions, theoretically captured as $G \times E$ (gene-environment interaction), likewise matter for quantitative genetics (Hansen, chapter 5; Houle and Pélabon, chapter 6). As additive genetic variance determines the response to selection, one common quantitative measure of a phenotype’s evolvability is $I_A = V_A/\bar{X}^2$, where V_A is the phenotype’s additive genetic variance (the proportion of phenotypic variance due to additive genetic effects), and \bar{X} is the phenotype’s mean value in the population (Hansen et al. 2003). A trait’s V_A in a specific population—with a fixed genetic composition—can change when the environment changes (just as the trait’s heritability is environment dependent; Rice 2012). Due to $G \times E$, a phenotype’s value can change together with the environment, in turn changing the phenotypic variance across the population. Similarly, the phenotype’s mean value \bar{X} can be subject to change when the environment changes—without the population and its genetic composition changing. Therefore, the evolvability $I_A = V_A/\bar{X}^2$ for a trait in a given population can be different if this population is in two different environments (see also Pélabon et al., chapter 13). Thus, evolvability as construed in quantitative genetics might not be solely an intrinsic property of a population but might also be dependent on the population’s environment; so the disposition’s causal basis is partly extrinsic.

An overarching lesson that emerges from these considerations of why or when evolvability might have an extrinsic, relational causal basis is that these judgments depend on the specific definition of evolvability being used. If on some definition the manifestation is not just phenotypic variation, but also stipulates that the phenotypic variation must be *adaptive*, then the external context of individual organisms or populations of organisms has to be considered, because a trait’s adaptiveness is relative to the environment. In a similar vein, the relevant causal basis also varies depending on the bearer of evolvability. For example, population size is an intrinsic factor for the ability of a *population* to respond to selection, but population size is obviously external to an *organism’s morphological structure*, which forms the core of evo-devo models of evolvability. If the bearer possessing evolvability is not an organism with its developmental structure, but instead is understood as a larger biological system (which contains organism-environment interactions), then this system exhibiting evolvability would also be the complete causal basis, rendering the disposition intrinsic (Nuño de la Rosa and Villegas 2022).

Because of these different possible methodological choices and explanatory strategies, it may be preferable to talk in terms of *causal contributors to evolvability* rather than one

unique causal basis. This explicitly acknowledges the diversity of individual causal factors involved: from the internal properties of individuals (e.g., the genotype-phenotype map and developmental architecture) to population-level features (e.g., genetic variance), from aspects of the abiotic or biotic environment of the individuals composing a population to organism-environment interactions. Which of these causal contributors are actively investigated with respect to evolvability is a *methodological choice*. Some biologists may consider environmental features as a causal background condition and focus on the genotype-phenotype maps of different taxa as the primary driver of evolvability; others will take some environmental factors (e.g., selection regimes) as stimulus conditions for the manifestation of evolvability. Still others may incorporate organism-environment reciprocal interactions in their explanatory frameworks in cases where niche construction or ecosystem engineering yield evolvability. In some situations, examining specific causal contributors (while relegating others to background conditions) may be a standard methodological preference adopted by some research groups; in other cases, an adjudication of what contributors must be included to yield an adequate explanation of a specific instance of evolvability may be required (Baedke et al. 2020).

4.3.3 How Does Evolvability Manifest?

Given this plurality of bearers and causal contributors, what characterizes evolvability as a distinct property? Dispositions are defined by their manifestation—and sometimes by their stimulus conditions, too—regardless of the variety of possible causal mechanisms that bring about this manifestation. For example, foldability is individualized as a disposition by a folding behavior under certain conditions (such as being in a solvent), despite the many distinct amino acid compositions that can be the causal basis of foldability. Therefore, even if evolvability can be instantiated by many diverse causal contributors in different contexts, it is a single dispositional property because it is defined by a manifestation: evolving in a certain fashion. Importantly, many if not all living systems are trivially evolvable or have been in their evolutionary history. However, when foldability is invoked, the aim is to specify a tendency of certain amino acid sequences to fold in a specific way as compared to other sequences. The same is true for evolvability: Evolvability is invoked to specify that some living systems (or configurations thereof) tend to evolve more readily than others (e.g., to diverge more or to evolve at a higher rate). These comparisons might include vertical contrasts with the ancestors of those systems or horizontal contrasts with other lineages (see also Jablonski, chapter 17). This is a restricted, comparative sense of evolvability that is distinct from the less informative and quasi-universal capacity to evolve (Love 2003).

Thus, to make sense of a comparative notion of evolvability in a specific context, it is crucial to specify the kind of evolutionary manifestation in view. Different definitions of evolvability focus on different possible manifestations. For example, if evolvability is defined as the ability of a population to respond to selection (Houle 1992), then this property will be manifested in a particular pattern of population-level phenotypic change across a certain number of generations (when under a selective regime), where that selection regime can be considered as the stimulus condition. If evolvability is understood as the ability to generate *new* phenotypic variants (A. Wagner 2005) or *novel* forms (Klingenberg 2005), then it will be expressed in the form of novelties or morphological disparity. In these cases, mutations are typically considered to be the stimulus conditions. If evol-

ability is conceived as the capacity to provide *adaptive* phenotypic variation (Payne and Wagner 2019), it will manifest in the alignment of new variants with the direction of selection, which contrasts with definitions focused on the production of heritable phenotypic variation without reference to its adaptive value. The meaning of “new,” “adaptive,” or “diverse” needs to be specified in each context for these manifestations of evolvability to be defined precisely.³ For example, a character can be considered new if it is not homologous to an ancestral character or provides novel potential for future variation (Brigandt and Love 2012).

It is not only the kind of evolutionary change (adaptive, new, diverse, etc.) that must be specified; in addition, an appropriate timescale needs to be chosen. The complexities mentioned so far should make it obvious that there is no unique, privileged timescale for evolvability. Instead, each different approach will require a timescale that is relevant to its methodological perspective and research question, while ensuring that the timescale used to measure the stimulus condition (e.g., the period during which an average selection differential applies) matches the timescale for the ensuing manifestation of a population’s or taxon’s evolvability (Houle and Pélabon, chapter 6). Theoretical models and field studies in quantitative genetics will typically choose shorter timescales than paleontological investigations will. An important question in this area is the extent to which results from microevolutionary timescales can be projected to mesoevolutionary or macroevolutionary scales; much of the information available for current populations, such as the genetic basis of variation or selective pressures, is inaccessible for evolution on longer timescales (see also Jablonski, chapter 17). Limitations to such projectability justify the need to use more than one timescale in evolvability studies, especially given that different approaches also might focus on a different kind of evolvability (e.g., a population’s evolvability in terms of changes in a phenotypic trait as opposed to a taxon’s evolvability in terms of differential phylogenetic branching and extinction rates).

Once a suitable type of and timescale for the manifestation of the disposition to evolve are specified, it becomes more meaningful to talk about biological systems being more or less evolvable and, importantly, some systems being more evolvable than others.⁴ In this sense, evolvability is a graded disposition, manifesting with different strengths in different systems, which in turn can show a capacity to evolve *more often* or at a *higher rate* than in other systems. To make such claims in a precise manner, however, there must be a way to measure evolvability (Houle and Pélabon, chapter 6). The dispositions of particular *tokens* are not directly measurable simply because, by definition, capacities as such are not observable properties. However, one can measure a disposition’s strength by other means. One straightforward way to do this is by measuring rates of manifestation in aggregates or *types*. Mutation rates, rates of short-term response to selection, or long-term morphological disparity may serve as a proxy for the evolvability of some biological

3. This point reveals an analogy to protein foldability as a disposition. Rather than understanding foldability as the generation of any tertiary structure, one might require that foldability involves the production of a specific functional protein.

4. Our conceptual distinctions align with how Houle and Pélabon (chapter 6) make evolvability and its measurement context specific. In their “evolvability of . . . under . . . over . . .” framework, the evolvability “of” designates what we call the bearer, the evolvability “under” (e.g., directional selection) specifies the stimulus condition, and the evolvability “over” (e.g., a few generations) is equivalent to our timescale.

systems. For example, Landry et al. (2007) measured mutation rates in gene networks and suggested that these rates can be a good estimate of the evolvability of gene expression under no selection. However, since evolvability is not always manifested, this approach has limitations. A population can be very evolvable and yet fail to evolve, because it has not experienced the appropriate stimulus conditions or encountered interfering factors, just like a potentially fit phenotype can fail to spread and reach fixation in a population due to genetic drift. A different way to measure evolvability indirectly is by measuring one or more of its corresponding causal contributors. This approach offers a basis for comparative claims in terms of the same properties constituting a causal basis for evolvability in different biological systems. For example, one trait of a population might have a higher evolvability *than* another trait in the same population (because it has more underlying additive genetic variation), or one taxon can be more evolvable with respect to a trait *than* another taxon is, because its developmental architecture permits the generation of more morphological variation in a specific direction.

This analysis brings us to a major distinction in our philosophical toolkit: deterministic dispositions versus probabilistic dispositions (propensities). Although some dispositions always exhibit their characteristic manifestation when the stimulus conditions obtain, there are cases in which the manifestation will occur with a certain probability. Probabilities are generally preferred for measuring propensities in science (Cartwright 1989). An atom's radioactive decay is probabilistic, just like biological fitness is when understood as the capacity of an organism to survive and reproduce. Evolvability is likewise a probabilistic disposition (Brown 2014; Nuño de la Rosa and Villegas 2022), because there is rarely a single effect that will necessarily follow whenever it manifests. Instead, changes in selective pressures or genetic alterations, as triggers of evolvability, can bring about a range of different results, resulting in a probabilistic pattern of possible evolutionary trajectories.

A related idea from our toolkit is *multitrack* dispositions. Consider evolvability in an RNA model with a genotype-phenotype map that relates primary RNA sequences to their folded secondary structure. In this type of model, evolvability can be measured as the probability of a point mutation yielding one among several possible novel secondary structures (Nuño de la Rosa and Villegas 2022). Each of those secondary structures is a different possibility—the secondary structures are different *tracks* that can be followed in the manifestation of evolvability. The same holds for the evolvability of a phenotypic trait. Due to the architecture of the genotype-phenotype map, different phenotypes will have different probabilities of arising from one phenotypic starting point, which can be captured by a *probability distribution* across outcome phenotypes, that is, by multiple tracks (Stadler et al. 2001). For the purpose of theoretical modeling, researchers generally have to assign probabilistic estimates, including for unlikely outcomes if the aim is to theoretically investigate a variety of potential outcomes. But the primary reason that evolvability is probabilistic and multitrack derives from evolutionary events being subject to stochasticity. Whether a new phenotype will occur or how common it will be in a population is, at least in part, a matter of chance with respect to a variety of processes: sexual reproduction, population composition, mutational events, developmental noise, and environmental fluctuation. This stochasticity is especially pertinent for the manifestation of evolvability on longer timescales, where accidental events also can result in the extinction of whole taxa (Jablonski, chapter 17). This issue highlights the role of *contingency* and chance in evolution (Blount et al. 2018).

Philosophers have typically assumed that the stimulus condition (triggering condition) and manifestation of a disposition are one-time *events*. In the case of glass having the disposition to break, the stimulus condition of being hit by an object and the manifestation of breaking are events with a short and well-demarcated duration. Only recently have some philosophers come to appreciate that, at least in the case of biological dispositions, the stimulus conditions or manifestation may be an *ongoing process* (Hüttemann and Kaiser 2018). This conceptual point is relevant for evolvability. The stimulus conditions for evolvability may be the occurrence of natural selection or some other ecological conditions, such as extinction events or factors producing random drift. Even if discrete changes in selective pressures prompt changes in the manifestation of evolvability for traits, neither selection nor the response of biological systems to it are time-point events; instead, they are best understood as ecological conditions or processes extended over longer durations of time. As a result, evolvability becomes a moving target. Not only are the stimulus conditions and manifestation of the disposition processes without a fixed termination point, but the biological system itself also undergoes modifications as evolvability manifests, which may entail a change in the system's evolvability (e.g., through modifications of one or more causal contributors). In this case, the original disposition has undergone modification before its manifestation could terminate. The evolutionary alteration of gene regulatory networks might reduce pleiotropy and thereby increase evolvability: The activation of a system's evolvability can result in increases to its longer-term evolvability.

4.4 Implications: Why Is the Conceptualization of Evolvability as a Disposition Useful?

Having surveyed how the philosophical toolkit related to dispositions applies to different aspects of evolvability, a natural question is how the dispositional character of evolvability matters for ongoing biological inquiry. For example, various efforts are dedicated to quantitatively measuring and representing evolvability (e.g., using G-matrices and M-matrices, or genotype networks) to make accurate evolutionary *predictions* (Hansen, chapter 5; Houle and Pélabon, chapter 6). Since evolvability is not merely a property of one specific population, it is desirable to establish *generalizations* across populations and taxa. In addition to the scientific aims of predicting some outcome under natural circumstances or generalizing conclusions from isolated investigations, evolvability is also useful for the purpose of *control* of or intervention in natural systems, including breeding and conservation efforts or for protein engineering (Villegas et al., chapter 3).

Knowing about evolvability permits one to manipulate natural systems because evolvability is a *causal capacity*. In general, dispositions are scientifically important because they embody causal potency—dispositions bring about their manifestations (Austin 2017). This points to their *explanatory* role because a disposition explains the occurrence of its characteristic manifestation. In addition to documenting phenotypic variation, a primary aim of evolutionary biology is to understand the very *ability* to produce variation, exhibit evolutionary transformation, and yield phylogenetic diversification, precisely because evolvability explains these evolutionary outcomes of interest. The same is true for other dispositions in evolutionary biology (Austin and Nuño de la Rosa 2021). Phenotypic plasticity (as the capacity to generate several phenotypes) explains the possibility of various phenotypes resulting from one

genotype, as well as why a particular phenotype resulted from environmental circumstances. Developmental robustness explains why a functional phenotype was maintained despite environmental or genetic perturbations during ontogeny. Likewise, phenotypic integration as the covariability of characters accounts for how a few genetic mutations can generate changes in many traits, often in a coordinated and functional fashion (see also Hallgrímsson et al., chapter 9). And modularity is the basis for the capacity of different organismal characters to vary quasi-independently of one another, which is instrumental to explaining the possibility of ongoing adaptation. However, evolvability may be distinctive as a disposition. For example, plasticity and organismal robustness to environmental perturbation primarily pertain to short-term effects, whereas evolvability also captures long-term evolutionary potential, thereby accounting for change and innovation across longer timescales.

One of the most important features of evolvability as a disposition is that it does not just explain one characteristic manifestation or the *actual* evolutionary outcome observed (see also Sterelny 1996; Brown 2014). Instead, the disposition of evolvability has *explanatory depth*, because a biological system's evolvability explains a whole *range of possible manifestations* under different potential stimulus conditions. This can be seen in quantitative genetics, where evolvability is understood as the ability of a population to respond to selection through phenotypic change. The stimulus condition of primary interest is the strength of selection acting on traits, and the manifestation is a change in the population's (mean) phenotypes. In the case of several phenotypic traits, evolvability can be captured by the additive genetic variances and covariances of traits (Hansen 2016; Hansen, chapter 5; Pélabon et al., chapter 13). This quantitative measure permits a prediction of how these phenotypic traits would change in each *possible* scenario if a particular strength of selection were to act on these traits. This general approach not only tracks one particular pattern of within-population phenotypic change to infer the selection pressures that obtained, but it also aims to predict the phenotypic change that would result from any of many different possible selection pressures. This type of prediction is useful for anticipating the effectiveness of a potential breeding strategy or ecological intervention (among other things). As a consequence of a population's evolvability (including trait covariances and different amounts of additive genetic variances for different traits), the phenotypic response may well deviate from the direction of selection (Hansen 2016). Unlike simply documenting actual phenotypic variation, this type of study of a disposition facilitates an understanding of how a population would respond to various possible situations.

In a similar vein, paleontologists may try to understand a range of possible evolutionary trajectories in addition to explaining a particular trajectory of morphological change seen in the fossil record. Would a larger or different range of outcomes have been possible from an ancestral starting point? Would a particular evolutionary outcome known from the fossil record be likely to reoccur if evolution restarted from this ancestral point? Evolvability—as the capacity of taxa to generate specific patterns of morphological transformation and diversification—can account for the possibility or difficulty of obtaining alternative outcomes (Love et al. 2022). Paleontological research also can employ computer simulations to investigate these types of scenarios. For example, although extinction events have a destructive effect in the short run, one may explore whether it is possible (and under which conditions it is possible) for extinctions to accelerate evolution *in the long run*. Prior extinction events might have selected for taxa that can rapidly occupy vacated niches;

these taxa have a high evolvability with respect to future extinction events as a possible stimulus condition of evolvability (Lehman and Miikkulainen 2015). Studies of evolutionary novelty (including in evo-devo) may have one particular morphological transition in view, such as the origin of the nervous system. Considered from the vantage point of evolvability, this morphological transition can be investigated more broadly with respect to the range of possible evolutionary outcomes under different stimulus conditions in light of assumed developmental contributors to the causal basis.

A recurring research task for evolutionary biologists is to understand *how evolvability itself evolves* (G. Wagner and Altenberg 1996; Draghi and Wagner 2008; Hansen and Wagner, chapter 7). Yet the question of the evolution of capacities has been absent from the classical philosophical literature on dispositions. Here we encounter a seeming puzzle, given the dispositional nature of evolvability. Selection can act on actual variation but not on the potential for variation: “the basic problem with the evolution of evolvability is that selection cannot act on potentials or *abilities*—only on results.” (Watson 2021, 143) Once again, the philosophical toolkit suggests a way to get traction on this puzzle (see box 4.1). Selection acts on the *manifestations* of the evolvability disposition (resulting in evolutionary change), but this does not amount to selecting for the disposition itself. Importantly, selection can also act on the *causal basis* of a biological disposition. One relevant causal contributor to evolvability is the genetic architecture of organisms (Hansen 2006) and the structure of organismal development (Kirschner and Gerhart 2005). Genetic architecture and developmental mechanisms are concrete traits on which natural selection can act. As a result, even though selection does not act directly on a disposition, the evolution of the disposition to evolve can be understood in terms of selection on one or more contributors to evolvability’s causal basis. Modifications of development yielding a phenotype-genotype map with an altered modular or covariational structure among traits can result in substantial evolutionary changes in evolvability (see also Hallgrímsson et al., chapter 9; Hansen and Wagner, chapter 7). This issue is another important place where the dispositional nature of evolvability matters: it serves to clarify distinct ways in which it could evolve by pointing to its relevant causal basis or manifestation.

We noted above (section 4.1) the presence of various definitions of evolvability. Importantly, there need not be a single evolvability disposition; instead, different scientific fields can focus legitimately on different concrete dispositions. For example, the evolvability of a population in terms of changes in phenotypic traits can be a different disposition from the evolvability of a clade in terms of taxonomic diversification. Our toolkit helps clarify that there are different kinds of evolvability and that the corresponding dispositions can be subject to distinct investigative projects. Most importantly, in the face of definitional diversity, the philosophical toolkit illustrates that different definitions can be legitimate and need not be in competition. For instance, the bearer of a disposition can be an individual or an aggregate. Correspondingly, the capacity to generate novel morphological variation may be a property of an organism’s developmental system, but evolvability as the ability to respond to selection is a property of a population or aggregate of individuals.

We also distinguished between the disposition, its manifestation, and the disposition’s causal basis. One reason these distinctions matter is that the definition of evolvability (e.g., simply in terms of generating variation, or more specifically, in terms of adaptive variation) has implications for the corresponding manifestation and causal basis. Once the choice of a

particular definition with its bearer of evolvability is explicitly recognized, it increases clarity about the relevant manifestation and causal basis. An additional reason that these distinctions are useful is that different scientific activities can target different aspects of a disposition (see also Villegas et al., chapter 3). *Predicting* the outcome of evolvability concerns its manifestation, whereas *explaining* evolvability is about understanding the disposition's causal basis—an investigative context where developmental mechanisms are relevant, even if these do not suffice for the endeavor of making predictions for specific populations.

Although different definitions of evolvability may not be reducible to one another, and different fields may focus on different kinds of evolvability, there still can be systematic relations between them that are the subject of investigation. For example, individual organisms (as the bearers according to some definitions) have the disposition to generate adaptive variation, which in turn forms the causal basis for the evolvability of populations (the focus of other definitions). One can likewise reveal connections between different approaches to investigating evolvability. To the extent that the same kind of evolvability requires investigation from different perspectives because it is a complex phenomenon, studies of evolvability in evolutionary biology demand *interdisciplinary collaboration*. One biological field may address specific aspects of a disposition, such as paleontology elucidating phylogenetic patterns of diversification (the manifestation of taxon evolvability) or attempt to understand the ecological and biogeographical conditions that (as part of the causal basis) enabled high rates of diversification and reduced rates of extinction. One field might concentrate on the manifestation (or the disposition), while another is needed to uncover aspects of the causal basis. A case in point is when quantitative genetics measures realized phenotypic and genetic variation, whereas evo-devo seeks to characterize the developmental architecture of organisms that constitutes key aspects of the causal basis of evolvability. Insofar as different approaches investigate different aspects of evolvability, there are connections among such approaches that structure interdisciplinary collaboration (see Villegas et al., chapter 3). Because evolvability occurs on multiple timescales and is exhibited by entities on different levels of organization, contributions from different biological fields are needed to dissect its multifaceted complexity. And given the diversity of causal contributors to evolvability—from the internal constitution of organisms to organism-environment interactions and various ecological conditions—an interdisciplinary strategy seems most appropriate for understanding it. Keeping in view that evolvability is a disposition and utilizing the resources of the philosophical toolkit described in this chapter are critical to accomplishing this task.

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