The holobiont is not a useful model for most host-microbiome interactions

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Abstract

The holobiont concept refers to a host and associated microbes. It has been critiqued over the last decade, primarily based on the argument that individual holobionts are not an appropriate level for analyzing multi-generation host dynamics, as most microbes are acquired from the environment. Several responses were given to this and other criticisms. The main response has been that the holobiont concept, even from its initial conception, allows for a more holistic, and realistic, model of host biology. This is regardless of one's evolutionary concerns, since hosts are always in association with microbes and phenotypes change in response to these associations. Taken further, it has been argued that allele frequencies shifting across host populations and microbes shifting in composition across hosts exist on the same conceptual continuum. We highlight that this analogy equally applies to entire communities of macro-organisms, and that there is no principled reason to privilege hosts and microbiota specifically as a holobiont. We also highlight the conceptual confusion surrounding host genetic variance when the holobiont concept is employed, and how this relates to the "missing heritability" debate. More generally, we discuss the social and practical impacts of this model, particularly in terms of its implicature and how it relies on interest-relativity. We argue that while biological categories are often fuzzy, we should strive for categories that are both informative and unambiguous. An individual host represents such a category, while a holobiont does not.

Keywords: Holobiont; microbiome; hologenome; metaorganism; unit of selection; organism boundary

Holobiont terminology

A holobiont refers to a host and microbes living on or within this host (Theis et al. 2016). This term is increasingly used (Stencel and Wloch-Salamon 2022), in keeping with a general increase in microbiome-related publications (**Figure 1**). The closely related terms hologenome (Jefferson et al. 1997; Zilber-Rosenberg and Rosenberg 2008), all genomes within a holobiont, and metaorganism (Bell 1998; Bosch and McFall-Ngai 2011; Bang et al. 2018; Jaspers et al. 2019), a host and associated microbes that have functional impacts within a specific environment, have also become more frequent (**Figure 1**). For instance, recent initiatives and institutional titles explicitly highlight these terms, particularly hologenomes (Leonard et al. 2024; Gaun et al. 2025). Here we assess the purported benefits and costs of this terminology and its use as a biological model. Previous critiques primarily addressed the issue of whether the holobiont was a unit of selection (Moran and Sloan 2015; Douglas and Werren 2016; Skillings 2016; Doolittle and Inkpen 2018). However, not all holobiont theorists used the term in this way, and some holobiont theorists have, in any case, responded to this charge (Theis et al. 2016; Lloyd and Wade 2019). Here we consider their key responses. The primary challenge they face, as we see it, is to develop language that is informative and biologically distinctive—that describes, in a fruitful and non-arbitrary way, biological entities not already covered by more common terminology—as we expand on below. We argue that framing host-microbiome interactions with the above terms is unnecessary and undesirable: though there may be benefits for cross-disciplinary or public-facing communication and interaction, it primarily creates confusion rather than promoting useful and unambiguous communication.

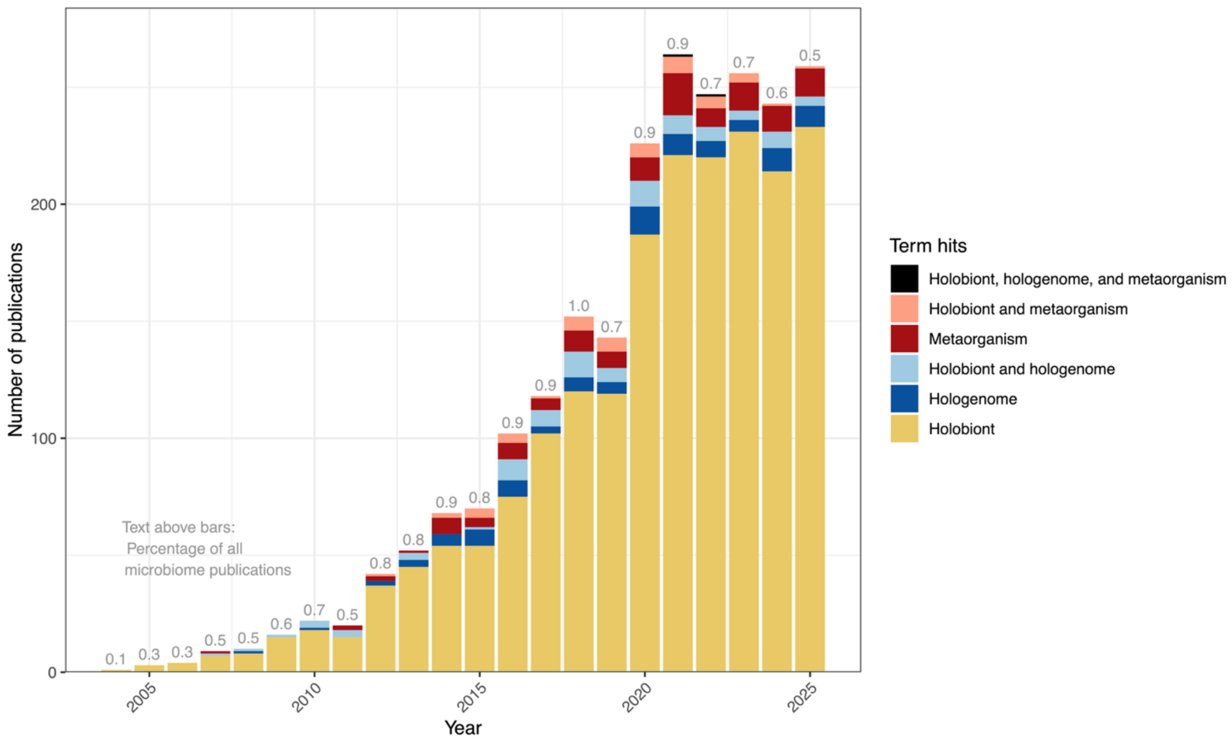

Figure 1: The number of articles and reviews that prominently contain holobiont-related terms from 2004-2025. These data were downloaded from Scopus on April 20, 2026. Matches were only considered within the title, abstract, or keywords of publications. The considered terms are indicated in the legend, and correspond to cases where only those terms were identified. The grey text indicates the percentage of microbiome publications (defined as matching “microbiome”, “microbiota”, "microbial community", or “metagenome” in the title, abstract, or keywords, or which matched the above holobiont-related terms) that each bar represents. Only matches to articles and reviews were considered here, but there are additional matches to other formats. We show these values to give context relative to the overall field, but readers should not over-interpret changes in this percentage over time, as there are many possible driving factors.

Recent criticisms

The holobiont concept was first proposed as a means of describing certain symbioses (Margulis and Fester 1991; O’Malley 2017; Baedke et al. 2020). The formulation of this concept focused on host-microbiome interactions, which was structural rather than requiring an evolutionary link, was first presented in the context of corals (Rohwer et al. 2002; Rosenberg et al. 2007). The concept was then expanded to describe host-microbiome interactions across diverse animals and plants, including humans, and in some of these cases it was argued that the holobiont is a unit of natural selection (Zilber-

Rosenberg and Rosenberg 2008; Gilbert et al. 2012). Calling the holobiont a unit of selection in this context generally referred to the claim that populations of holobionts, and not just their components, showed heritable, including vertically transmitted, variation in fitness differences . This claim, which was not made by all holobiont proponents, was strongly criticized (Moran and Sloan 2015; Douglas and Werren 2016; Skillings 2016), primarily because critics believed it requires exact organism lineages to be heritably co-transmitted across generations. This is the case for entities with obligate co-vertical transmission, such as for human egg cells and their mitochondria. However, this is not the case for most microbes, as they are not vertically transmitted with high fidelity and can be gained and lost over a single host generation (Douglas and Werren 2016).

Holobiont proponents have argued that this criticism ignores the long-running pluralistic perspective underlying the concept, which does not depend on this strict formulation of a unit of selection. Here we focus on two general paths of defense of the holobiont concept, and related ideas, which were in some cases refined in response to these critiques, but also in response to the historical use of the holobiont concept. The first has been to argue that the holobiont concept (or a related and updated concept, "metaorganism" (Bosch and McFall-Ngai 2011)) picks out an important and distinctive category of biological entities, regardless of whether those entities primarily evolve by natural selection as a unit (Theis et al. 2016; Stencel and Wloch-Salamon 2022; Hazelwood 2025). This work fits with older uses of the holobiont label to refer to physiological or ecological units, rather than evolutionary units (Rohwer et al. 2002; see, e.g., O'Malley 2017 for the complex history of this term).

The second path has been to answer the criticism more directly, by explaining how some host-microbe communities evolve as a unit of selection despite organism turn-over and lineage instability. This work overlaps with several recent developments in evolutionary theory (**Box 1**), which represent exciting new theoretical areas, but which do not require the holobiont concept to function. In the context of the holobiont concept and the above criticisms, Elizabeth Lloyd's work is particularly noteworthy (see summary in Lloyd (2020)). Building on work by Hull (1980), Lloyd has demonstrated that recurring debates over the proper “unit of selection” are ambiguous. There are at least four different senses in which a biological entity has qualified as a “unit of selection”: as a replicator/reproducer (an entity that is faithfully copied across generations), as an interactor (an entity that interacts with its environment and is subject to direct selection), as a beneficiary of selection (an entity that benefits from a selection process), or as a manifestor of adaptation (an entity that exhibits adaptation to a local environment) (Lloyd 2020). Lloyd, and others, have argued that some holobiont systems can act as units of selection in at least one of these four senses, and that the early criticisms of the holobiont concept merely showed that very few holobionts were lineage-forming, reproducing entities (i.e., most holobionts are not reproducers).

Lloyd’s helpful framework provides much needed clarity to debates about units of selection. But we do not think it exonerates the holobiont concept. The problem is that each of the four senses of units of selection systematically cuts across holobiont boundaries. Consider the interactor concept. An interactor is the entity interacting with the environment and experiencing selection, as opposed to the replicator which is the actual material replicated (typically DNA), but usually does not experience selection directly. In the context of individual organisms and their genomes this dynamic can be summarized as: selection acts on phenotypes, not genotypes. Many host phenotypes arise partially from host-microbiome interactions (McFall-Ngai et al. 2013; Lynch and Hsiao 2019), such as immune system development (Belkaid and Hand 2014), nutrient metabolism (Russell et al. 2009; Rowland et al. 2018), and certain behaviours (Nguyen et al. 2024; Suzuki et al. 2025). Due to these phenotypic impacts, proponents of this view argue that the holobiont is a defensible concept under the interactor model (Theis et al. 2016; Lloyd and Wade 2019).

The problem, as we illustrate below, is that, in most cases, the causally relevant interactor is not limited to host-microbiome interactions. A grouping of entities relevant to the interactor concept would nearly always include those outside of the holobiont and would nearly always exclude some of those internal to it (e.g., microbes with negligible influence on the host). Thus, if we were to accept the interactor framework as valid, the holobiont would be a poor proxy for the causally-relevant interactor. Thus, the “holobiont” directs attention to the wrong grouping, and thus might obscure, rather than clarify, the selection process occurring. But before addressing this point further, we will first attend a simpler point: some researchers may find the holobiont concept useful, regardless of whether it is defensible from an evolutionary perspective.

Box 1: Novel developments in evolutionary theory that relate to changing researchers’ perspectives

Several novel developments in evolutionary theory have challenged the field’s traditionally skeptical position towards the possibility or strength of natural selection acting on multi-species systems. These include: approaches to evolution by natural selection that reformulate fitness as differential persistence rather than differential reproduction (Bouchard 2011; Bourrat 2014; Doolittle and Inkpen 2018); approaches that decouple heredity from the formation of species lineages (Charbonneau 2014; Papale 2021; Veigl et al. 2022); mathematical models that bridge vertical and horizontal transmission dynamics (Roughgarden et al. 2018; Roughgarden 2020; Week et al. 2025); the development and application of community genetics frameworks to show, in particular, that vertical inheritance is not required for evolution by natural selection (Whitham et al. 2006; Lloyd and Wade 2019; Lean et al. 2022); simulations demonstrating the role of ecological scaffolding in the evolution of individuality (Black et al. 2020); multi-level selection theory and related reformulations of Price’s equation (Sober and Wilson 1998; Lean and Jones 2023; Doolittle 2024; Week et al. 2025). There is now an interest in developing these and related frameworks in ways that lend themselves to empirical testing (Week et al. 2025). These and other frameworks do not require holobiont terminology or categorization to function, and indeed using the holobiont concept could oversimplify interactions in nature, as exemplified by our honeybee example presented below.

Utility of the holobiont concept

The main response from proponents of holobiont terminology to the original criticisms regarding the lack of co-transmission between host and microbiome was to argue that these critics were misunderstanding the concept, as the term is not meant to specify a unit of selection (Theis et al. 2016). Instead, they argued, a holobiont refers solely to a host and their associated microbiome, which can be but is not necessarily a unit of selection. These host-associated microbes can be involved in any type of symbiotic relationship (beneficial, deleterious, or neutral) and can be acquired horizontally (from the environment, including other hosts) or vertically (parent to offspring, typically during reproduction). This rightly addresses the concern that there are very few holobionts under the early critics' interpretation of the holobiont concept, but it presents other issues.

This way of defining the holobiont concept is often justified because it is helpful: it highlights the previously unappreciated complexity of host-microbiome associations (Bordenstein and The Holobiont Biology Network 2024). Metagenomics sequencing has indeed revealed widespread microbial diversity (Handelsman 2004; Gilbert and Dupont 2011), and raising awareness of the complexity and nuances of host-microbiome dynamics is important. For instance, understanding the role of host-microbe interactions underlying speciation events (Brucker and Bordenstein 2012; Miller et al. 2021) and the myriad impacts of microbes on host fitness (Franche et al. 2009; Zheng et al. 2020) is valuable. However, critics have pointed out that appreciating these dynamics does not require the holobiont concept: these exciting observations are entirely consistent with existing eco-evolutionary frameworks for inter-species co-evolution and wider interactions (Moran and Sloan 2015; Douglas and Werren 2016; Skillings 2016). For instance, a recent review described frameworks for modelling and understanding host-microbiome interactions (Week et al. 2025), describing complex interactions, including multi-level selection, but without invoking the holobiont concept. So, the immediate question is why we need this term, given that we have terminology that already covers this biological ground.

One might argue that if some researchers find holobiont terminology useful, then it is a useful concept for biological practice. On one hand, this makes sense because all biological categories are somewhat arbitrary and imprecise, and as a result there will always be disagreement over the correct scope and use of key terms and concepts (Dupré 1993). However, this does not imply that all concepts are equally useful for describing the natural world. In science, we should strive for terms, concepts, and categories that are unambiguous and informative (Corter and Gluck 1992), which will help the scientific communication required for knowledge production. Of course, attaining this ideal for all scientific terms and concepts is impossible; even terms like gene and species can be interpreted ambiguously. However, such terms are highly entrenched and nearly necessary to sensibly discuss biological units in everyday biological practice, and they capture causal structures in nature. Arguing that we should abandon such concepts is not unprecedented, but it is contentious (Ereshefsky 1992; Brigandt 2003). In contrast, the holobiont concept is not needed to discuss microbiome dynamics and provides insufficient information to justify using an ambiguous term. The holobiont and related terms are commonly misunderstood and applied in diverse ways (Douglas and Werren 2016; Morris 2018; Madhusoodanan 2019), and so can clearly be interpreted ambiguously. But even if we solve the concerns about ambiguity (that is, stick to one and only one definition), there are still issues about informativeness: we should strive for a concept that (i) tracks causally important structures in nature and (ii) supports novel explanation and prediction.

The analogy between host and microbial genetic variation

A holobiont is defined as a host and its microbes that can be labile or stabile components of the hologenome (Theis et al. 2016). This is a novel way of envisioning genome variation: the traditional view of a (mainly) static genome over an individual's lifetime is strongly contrasted by a dynamically changing hologenome in typical mammals, for instance. This is particularly interesting as microbial genes can drive phenotypic shifts within a single host generation. This dynamic has been referred to as having elements of Lamarckian evolution (Rosenberg et al. 2009; Bordenstein and Theis 2015; O'Malley 2017), and can include both changes in the presence and absence of microbes, as well as shifts in microbe relative abundances. This has been framed as genetic variation that selection can act upon to drive adaptations (Bang et al. 2018). More generally, evolutionary changes in terms of microbial composition and host genetic variation have been argued to be conceptually equivalent (Bordenstein and Theis 2015) (**Figure 2**). The claim is that microbiota (and/or their composite genes) with beneficial, deleterious, or neutral fitness impacts of the overall holobiont fitness should be thought of as a broader extension of nuclear genetic alleles, which also have varied fitness impacts. Although microbes are more frequently lost from hosts than host genetic alleles are from a population, the argument is that these processes are similar on a conceptual continuum, and that microbes can be likened to alleles, albeit often with extremely high (and within-generation) rates of recombination (Bordenstein and Theis 2015).

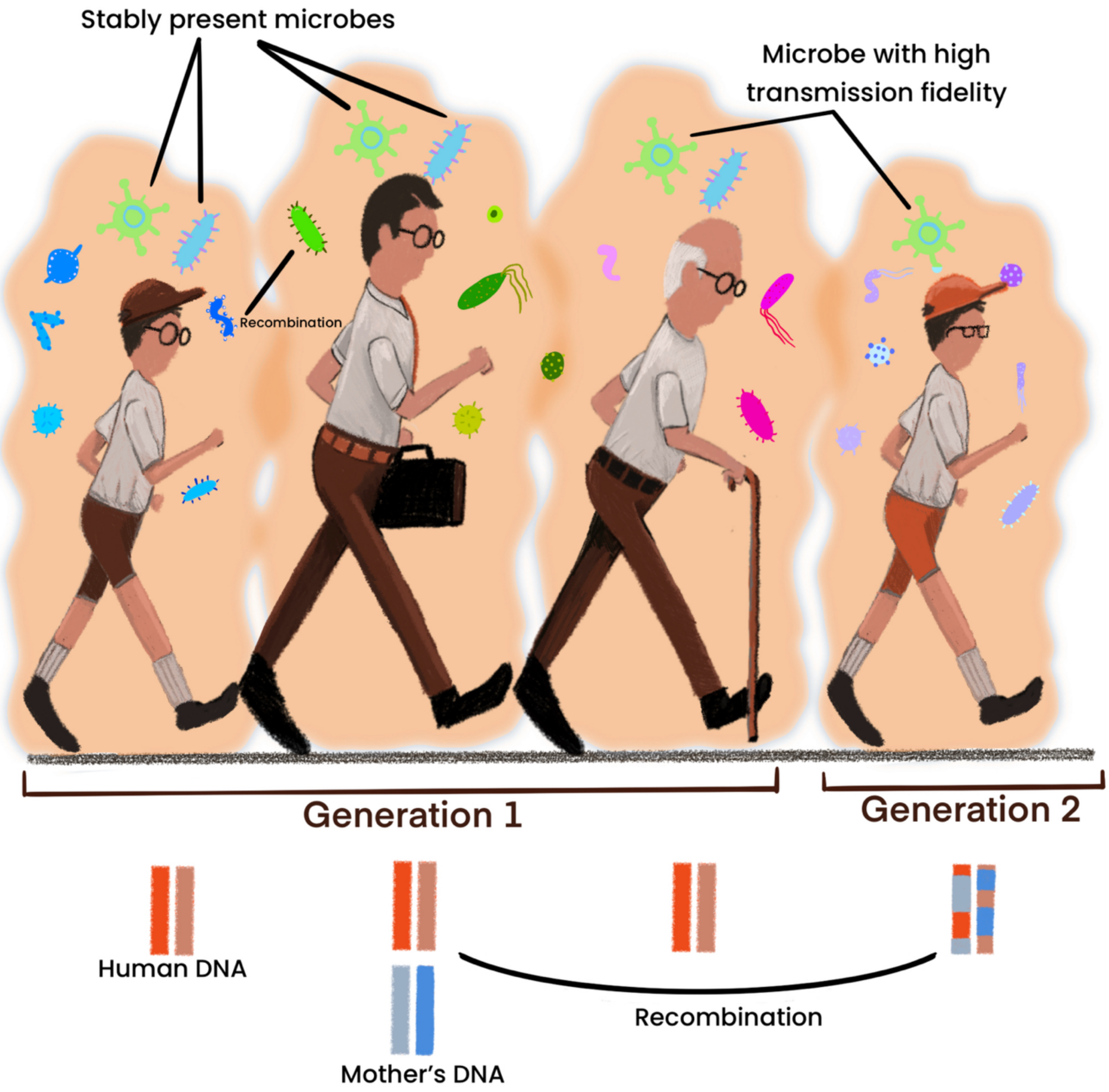

Figure 2: Key analogy between variation between host genes across generations and microbial strains within generations that has been presented previously, and that is closely related to the hologenome model of evolution. These types of variation have been argued to be part of the same continuum of genetic variation, albeit with differing rates of recombination, that contribute to an overall hologenome. Artwork: Morgan MacPherson.

Does this approach yield informative groupings about nature? Does it track causally important structures? We do not think so because there does not seem to be a reason to limit holobionts, nor hologenomes, to hosts and their microbiome. Holobiont proponents often argue that a holistic approach to studying biological complexity is needed, and that the holobiont concept encourages this. But if this is true, the holobiont concept must be too limiting. If one is interested in phenotypic outcomes, such as under the interactor model, then the holobiont boundary should not be limited to the host and microbiota. A complete understanding of the biotic interactions that can (or that potentially can) impact phenotypes clearly requires a broader view of community interactions (**Figure 3**). A host interacts with and is often interdependent with many other organisms beyond members of its microbiome. Simply stating that, for example, interactions between a pollinator and a flower represent separate holobionts interacting, because a holobiont is defined solely as a host and microbiota (Bordenstein and Theis 2015), deals with the issue by assertion, rather than providing reasons why the holobiont should be so limited. A holobiont based on the interactor concept from a causal perspective would have no basis for drawing these boundaries. In other words, although the holobiont concept is often presented as an expansive view, from the perspective of remaining open-minded about the potential factors and interactions causing host phenotypes, it is restrictive.

Holobiont and hologenome boundaries can be seen to be especially arbitrary when neutral microbes are considered. The holobiont is meant to include the host and all their associated microbes, including those with a neutral relationship. But this means that we can include as parts of the holobiont entities that have no effect on the host simply because they are microbes, and not include biological entities that do interact with the host simply because they are either not microbes or not co-located. In other words, causally unrelated elements are grouped by arbitrary boundaries. The severity of this issue may depend on how frequently persistent contact encourages coevolution, and eventually, vertical transmission. While it is true that neutral genes are present in host genomes, those are still part of a shared inheritance system, whereas many neutral microbes will not be vertically transmitted with high fidelity, as part of the larger trend of microbes often being horizontally acquired (Douglas and Werren 2016). Is persistent contact enough to justify the inclusion, for many holobionts, of the large fraction of resident microbes that are likely neutral, even though they would be excluded on the grounds of causal irrelevance?

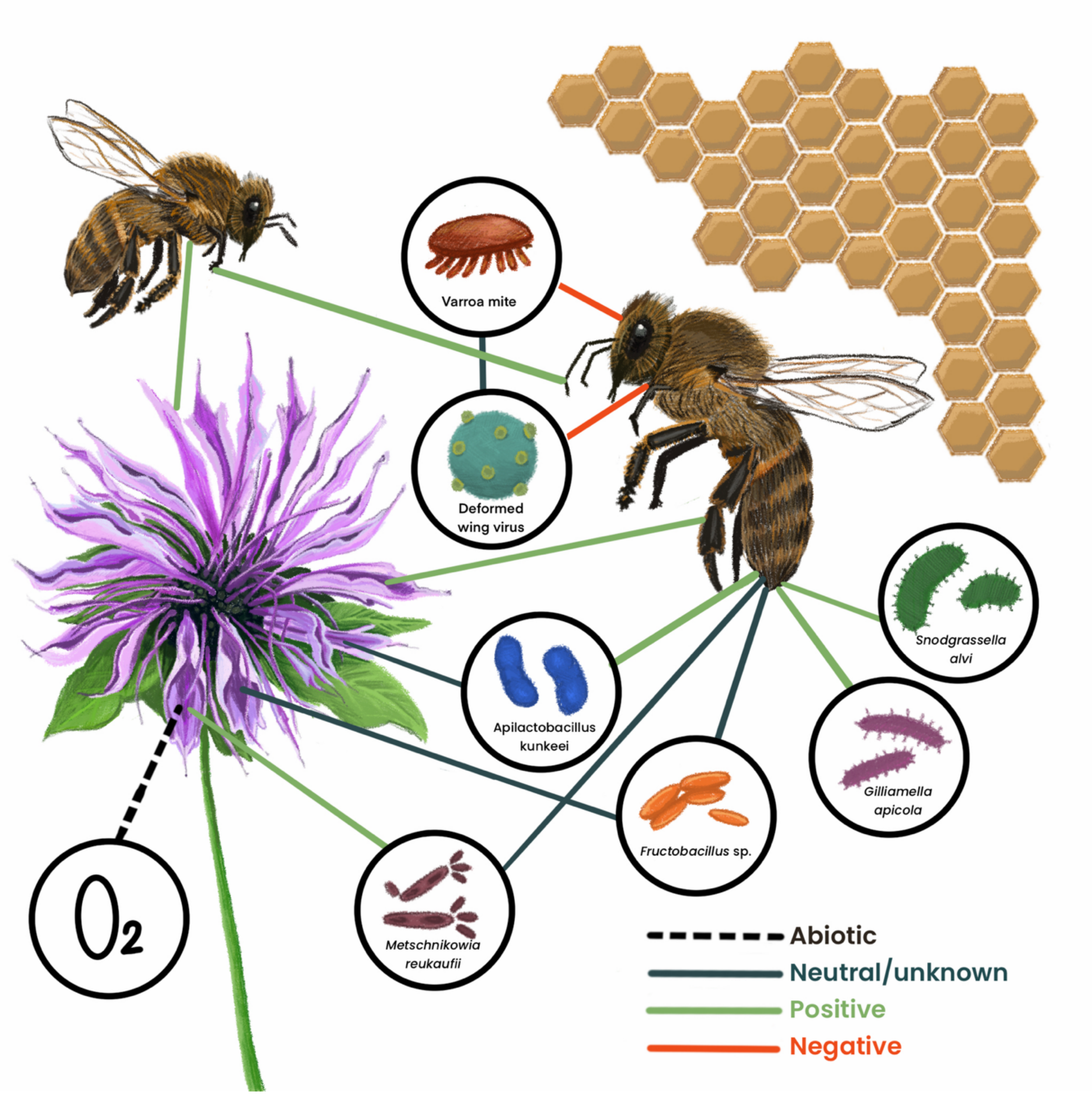

Figure 3: Interactions between honeybees, a flower, and interconnected microbes. This example is meant to highlight that there is no principled reason why these entities should not all be part of the same holobiont, particularly under the interactor model. In the most extreme case, an interactor would include interactions of all magnitudes, including indirect interactions through environmental modulation (as through oxygen production). We are not arguing that this should be the case, and instead simply argue that the

holobiont concept suffers from clear boundary issues. Importantly, if the response to this critique is that the holobiont requires physiological integration, then this conflicts with how the holobiont concept has been repeatedly defined to include transiently present and neutral microbes. Artwork: Morgan MacPherson.

Claims about the distinctiveness of the holobiont as a host and its microbes sometimes rely on arguments about co-localization and the strength of interactions. We agree that co-localization is denoted by the term holobiont, however this is already redundant with the simpler terms of host and microbiota, which are unambiguously interpreted. Indeed, the issue of deciding which interactions are spatially close enough to be considered part of the holobiont compared to the external environment has been raised previously (Morris 2018).

Defenses of the concept based on the strength of interaction or metabolic integration face two challenges. First, many symbiotic interactions between macro-organisms share this feature (Boucher et al. 1982): this is not unique to host-microbe interactions. Secondly, the holobiont concept has been defined to include neutral symbionts, who need not be metabolically integrated with any other entities, or at least do not impact host fitness. In other words, stating that a host and microbiota are a holobiont does not imply that they are metabolically integrated, only that they are co-localized. This discussion highlights the mix of concepts under the umbrella of “holobiont”. Referring to either a host and microbiome, including neutral microbes, or to an interactor entity could each be useful, but using the term holobiont to represent both creates unnecessary ambiguity.

One way to avoid the above criticisms is to be more specific about what is included in the holobiont, which is what the “metaorganism” concept does. Jaspers et al. (2019: 82) define the metaorganism as, “the sum of a eukaryotic host and its associated species in a narrower context as compared to the holobiont, with the focus on those associates for which function, i.e. any form of contribution (beneficial or detrimental) to the metaorganism, is known or implied [and ...] whether a specific function/microbe is functionally relevant can depend on host developmental stage, age, reproductive state, or physiological condition." So, unlike the holobiont concept which includes a host and all of its microbes, the metaorganism concept does not include microbes without functional effects.

Although the metaorganism concept deals with some of the above concerns, it suffers from a different issue that is related to the fact that it is interest-relative, meaning it depends on a researcher's specific interests and goals rather than only intrinsic properties of a host-microbiome system. Consider that, often, hosts harbour many microbes that contribute in many different ways to many different physiological processes. Say we are researching the role of microbes in pollen digestion in the honeybee gut (Motta and Moran 2024). If our interest is in studying how waste nitrogen is recycled in the pylorus section of the gut, then the metaorganism we are studying will be constituted by the host bee and a specific set of microbial species that give rise to a particular phenotype. But if on the other hand our interest is in digestion of pollen wall components in the ileum section of the gut, then our metaorganism will be constituted by the host bee plus a different set of microbial species. But which is *the* metaorganism we are studying? And why is that worth articulating rather than simply stating the phenotype of interest and the interacting organisms that are involved? There are nearly as many metaorganisms as we have different interests. So, the specificity of the metaorganism concept solves some of the issues of the holobiont concept, but at the cost of generality. Should we not drop this language and instead use the common language of host-microbiome interactions that does not risk reifying what we do not intend to reify? In other words, we are worried that host-microbiome systems will be seen as entities, rather than as sets of interactions, even though the latter seems more apt given the diversity of such systems.

In summary, existing categories used in ecological and evolutionary modelling, such as individual genome, host, organism, and community are much more informative in terms of the characteristics the constitutive entities within each share. In contrast, there is nothing distinctive, in terms of causal interactions, about the entity chosen as the holobiont: it is arbitrary whether to draw the boundary around a host and its microbes rather than some other way.

Epistemic complications of the hologenomic view

Beyond the fundamental issue of there being no convincing reason for defining holobionts with clear boundaries around a host and microbiota, there are clear examples of conceptual confusion that arise from using the framework. If one accepts the hologenome view, many aspects of how host genetics are conventionally studied can seem simplistic. After all, for example, human microbiota encode more unique protein-coding genes than the human genome (Qin et al. 2010; Rosenberg and Zilber-Rosenberg 2018). If microbial genes are excluded, then any studies of human genetic variation are missing a large proportion of meaningful data from the hologenomic perspective. This insight has been the basis for some to argue that heritability estimates of human traits are systematically biased downwards due to this problem (Sandoval-Motta et al. 2017; Marques 2018; Huitzil et al. 2020). These points have been raised in the context of genome-wide association studies finding lower heritability estimates compared to pedigree-based studies across many organisms, which is referred to as the "missing heritability" problem (Maher 2008). There are many possible explanations for this observation, including that larger sample sizes and including rare genomic variants are needed to capture trait heritability (Wainschtein et al. 2025).

The microbiome will not help solve the "missing heritability" problem, at least not as a source of missing host genetic information (Douglas et al. 2020). For example, in humans the "missing heritability" problem is based on the observation of high heritability of traits inferred (primarily) through twin studies. In this study design, identical (monozygotic) and fraternal (dizygotic) twins are compared and heritability is defined as the extent of increased phenotypic similarity between identical vs. fraternal twins. Identical twins have more similar microbiomes on average (Goodrich et al. 2016), which, among other potential factors (Felson 2014), is likely due to shared genetic variation modulating exposure or colonization success of microbes. However, for this signal to be relevant to the "missing heritability" problem, a mechanism for why the same microbes are more likely to be directly transmitted to identical twins, compared to fraternal twins, is needed. Importantly, this mechanism cannot simply be that identical twins' higher genetic similarity increases their predisposition to acquire certain strains from the environment: this would be just standard genetic-by-environment interactions. Nor can it simply be that human genetics cause the presence of a microbe, regardless of the environment, as this would already be captured by host genetic variation, and thus including the resultant microbe would be double counting of this effect. Framing such interactions as (human) gene-by-(microbe) gene interactions that represent a component of missing human genetic variation is misleading to those seeking to understand trait heritability, as it conflates genetic and environmental variance.

Researchers who have recently argued in favour of the hologenome model (Bordenstein and The Holobiont Biology Network 2024) will likely disagree with our above characterization. They have rightly highlighted that more variance in host traits can be explained when both host genetic and microbial information is incorporated, compared to host genetic information alone. Similarly, host genetic variants associated with traits can depend on the host microbiome's composition. For instance, some quantitative trait loci associated with functional traits in bunch grass interact with the soil microbiome composition (Khasanova et al. 2023). In other words, the host genomic regions identified that likely contain causative variants driving functional traits can vary depending on the microbial context. These and related findings have been used to argue in favour of "a hologenomic view of life that does not prescribe prominence to either host or microbial genomic contributions to a given trait" (Bordenstein and The Holobiont Biology Network 2024). The role of microbiomes in modulating host traits has indeed been unappreciated historically. However, this broader view is consistent with standard quantitative genetics modelling: some traits are driven primarily by host genetics, while some are environmentally driven, and any inferences about the relative contribution of each, and their interaction or co-variance, is always environment-specific (Falconer and Mackay 1996). In addition, environmental variance can be split into more specific components, such as maternal effects (Kruuk and Hadfield 2007). When host genetic and microbial variation are uncorrelated, the microbiome can similarly be modeled as a separate component of variance (Difford et al. 2018). In some cases, such as when studying levels of methanogenesis in cow rumens, there is good reason to plausibly think microbes are causally connected to the host traits of interest, with a clear direct mechanism. However, applying this framework more generally, to any host trait, is much harder to interpret. Many environmental factors (e.g., diet) can impact both the microbiome and host traits. This means that microbial variation that statistically explains a high proportion of variation in a host trait can be, and likely often will be, due to independent impacts from an unmeasured environmental cause on both the microbiome and host trait. For example, it would be unsurprising to find that the nutritional content of an organism's diet affects both the host's growth rate and its microbiome. Uncritically assessing how microbial variation is associated with variation in growth rate would not provide insight into the causal factors involved, except as a proxy for a separate, unmeasured, environmental factor. More generally, it will often be unclear what information is provided by knowing the degree to which microbial variation is associated with a host trait, compared to estimating the overall environmental variance. The ultimate causal factors driving the association are often unclear in both cases. Of course, this does not mean that identifying associations between host traits and microbiota is not helpful: this can generate useful hypotheses. However, the same is true for any high-throughput profiling data that could be applied to hosts, such as gene expression and metabolic profiles. Leveraging these data would also result in a higher proportion of variation in host traits being explained, but would similarly not distinguish between cases where these data are causally important and where they are simply correlated with unmeasured environmental factors.

Social aspects of the hologenomic view

Recent work on the hologenome view (e.g., Bordenstein and The Holobiont Biology Network 2024) emphasizes the social benefits of the concept as well as the epistemic, which are important to consider but were often overlooked in earlier criticisms. If we are reviewing how to address contested terminology, we must consider these potential benefits as well. One benefit is in terms of interdisciplinarity. Using holobiont terminology means that host organisms are defined as containing microorganisms and their genomes, so there is no question of separating host biology from microbiology. This rejects the siloing of microbiology from, e.g., evolutionary biology, development, anatomy, and ecology, and might justify disciplinary transgressions as necessary for a full understanding of host-microbiome systems. A related benefit has to do with the historical context: before the 2000s, and despite the interest and arguments of Lynn Margulis and others (O'Malley 2017), macro-organisms were often studied without much thought to microorganisms. Part of the change was driven by technical advancements in sequencing, but concepts can also help, and the holobiont is an example.

Proponents also draw attention to potential benefits for public outreach and for developing ethical relationships with the rest of nature. There is some supporting social science evidence, e.g., that people with some exposure to the holobiont concept may feel greater connection to nature (Robinson et al. 2026). There is need of further empirical study here to determine the strength of this benefit of the holobiont concept. In addition, it remains unclear where existing "holistic" terminology (i.e., community, ecosystem, host-microbiome, etc.) has a similar effect.

Moving to social costs, a point of confusion introduced by the holobiont framing concerns health. Because of the now recognized role that microorganisms play in human physiological and psychological processes central to our health and well-being (Bäckhed et al. 2012; The Human Microbiome Project Consortium 2012; Lloyd-Price et al. 2016; Morar and Skorburg 2018), it has been suggested that the appropriate locus for assessing or treating health is the holobiont, rather than the individual human (Catania et al. 2021; Bosch et al. 2024). But this is problematic for two reasons (Inkpen 2024). First, if it is really the health of the whole holobiont that matters, then it is unclear why the human member of the holobiont cannot be replaced by another human, given that microbial members consistently turnover. This renders the idea unhelpful for most human medical contexts. Second, if instead the health of the holobiont is indexed to the health of the human host, then it is unclear why the holobiont concept is necessary. Studying interactions between hosts and their microbes that are relevant to the health of each member is more clearly tackled without the holobiont concept, and by instead employing already entrenched "ecosystem health" and "ecosystem services" concepts from ecology (Inkpen 2019).

The above conceptual issues point to an additional concern about the holobiont concept, which is with what the concept implies, rather than how it may be strictly defined. Readers will likely always be tempted to interpret a holobiont as something well-defined and "real" in nature. As something like a canonical organism, which is more than this vaguely-bounded and interest-relative concept should imply, and more than the evidence can support for the great majority of holobionts. This problem is made worse by the varying definitions for the holobiont, hologenome, and metaorganism that have been presented in the literature. If, as we have argued, these concepts are either too general or too interest-relative to support this implication, then this will always be a problem. It is thus also what the concepts imply, and not only how they are defined, that is costly.

Moving forward

We recommend researchers avoid the term holobiont, as well as the related terminology hologenome and metaorganism in most circumstances. All microbes on and in a host are not of equal impact or interest, and categorizing them all as the same unit is unhelpful. There is no principled biological reason to privilege the assortment of microbes on a host and the host itself as a single entity, without arbitrarily excluding more distant organisms. It is sufficiently clear to state "host and microbiota," if a researcher's focus is on these co-localized organisms, which does not risk misinterpretation. More generally, the holobiont framework is an oversimplification of biotic interactions in nature, as has been previously noted (Douglas and Werren 2016; Skillings 2016).

Importantly, our commentary is not meant to deter or criticize research into host-microbiome interactions, including research that has been presented under a holobiont framework. For instance, phylosymbiosis, the paralleled evolutionary divergence of hosts and symbionts in a lineage, has been well-documented and used as evidence for the holobiont concept (Bordenstein and Theis 2015). However, phylogenetic congruence can occur between non-microbial lineages through known co-evolutionary mechanisms that do not require the holobiont concept (Farrell and Mitter 1990; Farrell and Mitter 1998; Cruaud et al. 2012), or through host filtering (van der Sprong et al. 2026). Nonetheless, the evidence for co-speciation and phylogenetic congruence between microbial symbionts and hosts is highly consistent across lineages. Continued investigations of this topic and host-microbiome interactions in general will undoubtedly uncover more important insights; our point is simply that holobiont-related terminology is not needed to do so.

Collectively, we have argued that: (i) the holobiont is often a poor proxy for the causally-relevant interactor; (ii) its boundaries are interest-relative; (iii) it includes too many causally irrelevant elements (i.e., neutral microbes); (iv) it does not make clear predictions beyond what existing frameworks provide; (v) the term might encourage reification (treating a pragmatic grouping as a “real” cohesive unit); (vi) though there may be some social benefits, there are also social costs. Taken together, we conclude that the holobiont is not a useful model for most host-microbiome interactions.

Many concepts in biology are imprecise and ambiguous, even central ones like “gene.” And there is nothing inherently wrong with imprecision or ambiguity. It is when such terms become epistemically or socially costly, and this outweighs the benefits, that we should rethink our adherence to them. In the face of a critique like ours, there are many options. We have advocated for an eliminativist thesis here: that we abandon the holobiont concept in favour of unambiguous language. We believe this is the appropriate position given our above points, at least until evidence is provided that the holobiont concept provides value beyond existing categories. There are other options. One would be to use the holobiont label only for obligate symbiosis or those with very high transmission fidelity, which has some historical precedence (O’Malley 2017). In this case there will be few holobionts, as others have previously argued.

Another option would be pluralism in which we divide up the holobiont concept into subtypes, akin to other contemporary examples: developmental gene versus molecular gene, or biological species versus ecological species. We do not think this would be a worthwhile approach. There is a risk of confusing readers; one could simply explain the intended meaning in plain terms without the use of a near neologism. In addition, this pluralistic strategy seems more appropriate for terms that are practically indispensable (or highly entrenched) in biological thinking, such as species and gene. Ultimately, it is up to the biological community to decide what concepts and frameworks they employ.

Date and code availability

The raw data and a description of our methods and R code for creating Figure 1 are available on Zenodo (https://doi.org/10.5281/zenodo.19682360).

Acknowledgements

We thank Louis-Marie Bobay, René Malenfant, and Derek Skillings for feedback on this manuscript. We are especially appreciative to Seth Bordenstein and Kevin Theis for a collegial exchange and discussion on this topic, despite our differing opinions. We are grateful to Morgan MacPherson for her artwork in Figures 2 and 3.

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