



# Can communities cause?

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## Abstract

Lynch et al. (Biol Philos, 2019) propose an extremely useful framework to assess microbiome research. By utilising advances in the causation literature, they argue that many of the claims in microbiome research are ‘weak or misleading’ as these claims lack stability, specificity, or proportionality. In the final paragraph before the conclusion they entertain and rapidly dismiss the ‘ecological version’ of microbiomes, in which microbiome properties are emergent from their constituent populations and can fulfil Koch’s postulates. I assess the possibility of microbiomes having emergent causal efficacy on host health and suggest they can.

**Keywords** Ecological communities · Causation · Philosophy of ecology · Microbiome

## Microbiomes as communities

Lynch et al. (2019) make a strong case for reconsidering the role of microbiomes on health. Health outcomes originally ascribed to functional or compositional microbiomes have been identified as the product of narrow population subgroups, often only a couple of species of bacteria. This indicates that we should be reductive in our causal explanandum. That is, rather than consider the role of a microbiome on health, we should consider the role of specific microbial species on health, just like in the case of *Helicobacter pylori* and stomach ulcers.

The authors, in my view, correctly argue that there is no reasonable sense in which the entire microbiome could have a specific effect on a host. The microbiome is dispersed across the host organism, occupying the many different environments a macro-organism produces. Many of these microbes exert no discernible influence

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on each other or the host. The microbiota of the inner ear will have very little causal association with the microbiota of the lower intestines. There is, however, a plausible case to be made for a multispecies ecological unit to cause health outcomes. This will not be a whole microbiome but instead will be a smaller association, often contained within a biofilm structure or one of the modular compartments of a multi-cellular organism.

Microbes form ecological communities, which possess some analogies and dis-analogies to macrobial communities. The extent to which these are similar should allow us to utilise conceptual resources originally built for macrobial ecology. In microbiome research we are searching for ecosystem effects that influence human health. This search can be treated as analogous to the search for how large-scale ecosystems provide humans with goods in the form of ecosystem services. Previously, I provided a template for identifying the means by which ecological communities provide goods, like ecosystem services (Lean 2018). I describe two different general causal patterns that result in ecological systems robustly producing goods of human interest: *ensemble robustness* and *machine robustness*. Ensemble robustness occurs when we have many different causal actors that can fill the same functional role in the system, their combined marginal or redundant action maintains the ecosystem output. Machine robustness occurs when a system output is the result of a particular sequence of required populations that strongly co-vary. These different causal patterns affect the stability, proportionality, and specificity of microbiome effects on human health; ultimately resulting in microbial communities being units of causal interest. While these microbial communities will be smaller than the whole microbiome units often mentioned in microbiome research, they will still be multispecies assemblages.

## Specificity and health outcomes

The integration and diversity of microbiome populations is crucial for health outcomes. Health outcomes are often described as human physiological capacities, that are predicated on whole organ systems, and encompass a range of physical states. Health is not a static state; it requires the maintenance of functional capacities across a range of internal conditions. The body contains many mechanisms to maintain function and homeostasis. Different microbes within a single microbiome can play different roles in responses that maintain biotic function. If we focus on individual microbes there will be a mismatch between the wide grain explananda of health outcomes and the finer grained explanandum of the physiological influences derived from individual populations of bacteria.

To explain the stability of human health outcomes we will need to consider how the diverse network of populations produce these health effects. It has long been known that ecosystem outcomes in macroecology are not so much the product of homeostatic systems, with tightly integrated causal structure, but rather through the aggregation of the properties in diverse local systems. Ecosystem outputs are often the product of statistical averaging effects, where an ecosystem effect is maintained due to independently fluctuating species maintaining that effect, or biological

insurance, where an ecosystem effect is maintained in the face of instability due to diverse modes of realising this good (Sterelny 2005). Aggregational properties of the microbiome community could maintain health outcomes under the many fluctuations the body undertakes through these mechanisms.

Common environmental problems are likely to produce varied evolutionary responses in different lineages. When these lineages are co-located we will find cases of biological insurance. For example: diverse mechanisms exist within bacteria for responding to other bacteria, yielding different antibiotics. Biological insurance is key in maintaining important functions in other organisms which cultivate microbial communities. Leaf cutter ants live in highly symbiotic relationship with the microbes they house and feed. These microbes produce antibiotics and fungicides that protect the leaf cutter ants' fungal gardens. The antibiotic and fungicidal effects appear to be the product of diverse actinobacterial species, which have different molecular pathways to produce these functional molecules (Scheuring and Yu 2012). Diverse antibiotic responses mean that if one antibiotic fails to protect their fungal garden another will. Therefore, to explain why the fungal garden is protected we should describe not just the population that acted as the immediate cause of repelling a bacterial invasion but the populations that counterfactually would have as well. This system may have analogues in human cases. Bodily functions that maintain health, like defences against specific pathogens, will likely be the product of complementary actions of microbiota through differing mechanisms.

Statistical averaging effects act in ecological systems to maintain aggregational outcomes, such as resource processing or the production of some common good. Many studies in macroecology have focused on the relationship between biomass production and species diversity (e.g. Tilman and Downing 1994). One prominent explanation of this relationship is that the different populations in the community occupy different niches, their slightly differing adaptations allow them to have asynchronous responses to environmental fluctuations (Doak et al. 1998). Differing responses to environmental change allows the ecological system to maintain a stable aggregational output, as when one populations density reduces another's will rise. Microbial communities have been found to maintain productivity in the face of fluctuations in salinity through having diverse compositions (Matias et al. 2013).

A macro-organism may require microbes to play a critical function, requiring a highly specific mutation. If the individual microbial population that serves this function dies out, then this key function is lost. But if niche differentiated populations all possess this mutation then the critical function will be maintained in the face of environmental fluctuation. This situation is made likely in microbial communities due to the high amount of lateral gene transfer found in the microbiome (Liu et al. 2012). If there is a gene that facilitates the utilisation of a resource, it can be passed across microbial lineages rapidly allowing for diverse populations to utilize this resource. In such cases, the statistical averaging effects of the whole communities aggregational productivity will be an important factor in maintaining the health outcome of interest.

Many different mechanisms maintain a macro-organism's functional states. The causal relationship that yields a healthy function state, or range of states, can be the result of the contributions of many populations within the system. Given this, our

grain of causal description may be better represented by a community of microbes rather than individual populations. To put this in the language that Lynch et al. (2019) so helpfully provided: to explain the *stability* of a health outcome we will be forced to look at the ensemble effects of an ecological arrangement, rather than individual populations, as otherwise the cause will not be *specific* (2) to the effect we are looking for.

## Microbial integration and proportionality

Metabolic integration between microbial populations necessitates the causal variable, which influences health, be the ecological unit rather than an individual population. A health outcome could be the product of multiple populations dividing the biochemical processing into distinct steps. In such cases, the causal mechanism which influences a health state is itself the product of a specific sequence of populations acting in complimentary manners. Microbial communities are better suited to creating tightly integrated units than communities made of macrobes due to their ability to rapidly shed or gain coding DNA. Macrobial organisms do not have the ability to rapidly form these types of dependencies, long-term co-evolution is required for such integration.

These strong co-dependencies between microbes can be seen prominently in black-queen dynamics (Morris et al. 2012). This is when microbes shed genes for essential functions when there are other populations that perform these functions in their local environment. In the original version, Morris et al. (2012) consider populations of *Prochlorococcus*, which require other populations to take on the costly role of breaking down toxic hydrogen peroxide. Given this type of co-dependency, even if a necessary biological function for human health is the product of a single microbe, there may be a network of microbial populations that are required for this focal population to survive and produce their health-giving function.

It is widely believed that complex metabolic functions are dispersed through multiple microbial lineages, with each population doing a single step in a multistep process (Fischbach and Sonnenburg 2011). This can be seen in the way microbes process complex polysaccharides. Initially, cellulolytic bacteria act to break down plant walls before other microbes act to break down complex sugars into smaller and smaller molecules that can be more easily processed (Flint et al. 2012). Similarly, biofilms are the product of co-ordinated and sequential actions by communities of microbes and may similarly require us to consider them as causal units (Ereshefsky and Pedroso 2013). These sequential relations mean that there are community outputs that influence human health, resulting from many microbial populations acting in tandem.

Strong dependencies between sequences of populations alters the causal unit being examined. The *proportionality* (1) of the causal unit influencing the effect of health interest will need to be widened in such cases, depending on the causal strength involved. While we want our causal variable to be as discrete as possible, causal integration will at times force a wider variable description. The causal chain could be cut off at the point of a single population but the necessity of the other

populations for the health outcome will make a microbial community the appropriate cause.

We can explain the way ecological communities stably produce ecosystem services through ensemble robustness and machine robustness (Lean 2018). Both biological insurance and statistical effects can result in ensemble robust ecosystem outputs. In such cases, the stability of the ecosystems effect will be specific to the range of contributing populations rather than individual populations. In the cases where populations are strongly co-dependent, or metabolites are the product of sequential processing, we will find machine robust ecosystem dynamics. In these cases, the proportionality requires us to widen the causal variable to include the multiple populations necessary for the effect. As a result, ecosystem outputs which are robust in these two different ways will require us to represent the community as a cause.

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