Philosophy of Science (2023), **90**, 21–38
doi:10.1017/psa.2022.11

PSA PHILOSOPHY OF SCIENCE ASSOCIATION
PHILOSOPHY OF SCIENCE

ARTICLE

A Chemostat Model for Evolution by Persistence: Clade Selection and Its Explanatory Autonomy

Celso Neto[1] and W. Ford Doolittle[2]*

[1]Department of Sociology, Philosophy, and Anthropology, Centre for the Study of Life Sciences (EGENIS), University of Exeter, Exeter, UK and [2]Department of Biochemistry and Molecular Biology, and Department of Philosophy, Dalhousie University, Halifax, Nova Scotia
*Corresponding author. Email: ford@dal.ca

(Received 28 April 2021; revised 17 November 2021; accepted 21 February 2022; first published online 25 April 2022)

Abstract

Many contemporary biologists and philosophers of biology admit that selection occurs at any level of the biological hierarchy at which entities showing heritable variation in fitness are found, while insisting that fitness at any level entails differential reproduction, not differential persistence. Those who allow that persistence can be selected doubt that selection on nonreproducing entities can be reiterated, to produce "complex adaptations." We present here a verbal model of subclones evolving in a simple idealized chemostat that calls into question these suppositions and is usefully explanatory when taken as an analogy to selection for persistence of clades.

> "Williams' Principle, as we will call it, says that adaptation at a level requires selection at that level."
>
> E. Sober and D. S. Wilson (2011, 462)

1. Introduction

Clades by most definitions (including that of cladists) cannot reproduce (de Queiroz and Gauthier 1990; Okasha 2003), and the idea that clades might undergo evolution by natural selection (ENS) as a result of *differential persistence* remains unpopular among Darwinian philosophers (Okasha 2003, 2006, 212–17; Godfrey-Smith 2009, 105; but see Doolittle 2017; Wilson and Barker 2019). Such philosophers do acknowledge that some entities persist longer than others but argue that without a mechanism like reproduction to *replace* entities that have gone extinct, populations necessarily dwindle and complex multistep adaptation is precluded. Natural selection might explain the

distribution of higher-level persistence-conferring traits but cannot explain their *origin* (Okasha 2006, 212–17; Godfrey-Smith 2009, 42). Still, among palaeontologists something very similar to ENS by differential persistence is often used to explain the longevity of higher taxa in the fossil record. Making sense of this through the use of an analogy is our goal here.

The paleontologist David Jablonski (1986) surveyed Late Cretaceous marine bivalves and gastropods and found that mass extinctions favored clades whose constituent species are broadly distributed geographically, while concluding that "During background times, traits such as planktotrophic larval development, broad geographic range [within] constituent species, and high species richness enhanced survivorship" (1986, 130). Much more recently, in a study of 30,074 genera of living marine animals and 19,992 genera of fossil marine animals, Knope et al. (2020) found that "ecologically differentiated clades became taxonomically diverse over time because they were better buffered against extinction, particularly during mass extinctions, which primarily affected [drove to extinction] genus-rich, ecologically homogenous clades" (2020, 1035).

Species richness (number of species), ecological diversity of species, their geographical distribution, and tendency to aid (or not) the survival of other species in their own clade are unquestionably persistence-related traits of clades more inclusive than species, not of species or organisms (Doolittle 2017, 2019). Nevertheless, one typically argues that the relative survival of clades is not ENS: There's no "clade fitness" *because clades do not reproduce* (de Queiroz and Gauthier 1990; Okasha 2003) and cannot meet the criteria of "Lewontin's Recipe" (Lewontin 1970, 1985).

Here we argue that clades can undergo ENS in which fitness is cashed out as differential persistence. This treatment of fitness and selection was initially proposed by Bouchard (2008, 2011) as pertaining in particular to clonal macro-organisms and has been gaining some attention ever since (Charbonneau 2014; Bourrat 2014; 2015a; Doolittle and Inkpen 2018; Papale 2020; Lenton et al. 2021). This article uses this "persistence-based selection" framework to vindicate clade selection. We hope to persuade unconvinced readers by drawing an analogy between clades and another nonreproducing entity, a bacterial clone in a chemostat. Our idealized chemostat model makes apparent the relationship between differential reproduction as a lower-level phenomenon and differential persistence at a nominally higher level, with selection on both playing an explanatory role. When used in an analogy to the evolution of clades in nature, the notion that these too can be units of selection through differential persistence becomes more interesting and plausible.

Multilevel selection theory (MLST) *is* gaining in acceptance as an explanatory tool for groups as inclusive as species, for which speciation can be cast as a kind of "reproduction" (Godfrey-Smith 2009, 105). MLST is seldom extended to nonreproducing entities such as clades (taxa more inclusive than species), however. Clades only "grow" (increase in number of species) or go extinct (death of all contained species), persisting or not. So, one of the novelties of this article is to extend MLST, by including differential persistence as a plausible fitness variable. Bouchard and others defending ENS by differential persistence seldom situate it in the larger context of MLST.

Here we argue that evolutionary explanations at different levels are often a matter of what Sterelny (1996) would consider *ontological dependence* coupled with *explanatory*

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

autonomy. Higher-level phenomena and processes do supervene on lower-level traits, such that causes and levels of selection are ontologically intertwined and hard to distinguish. Nevertheless, even in cases in which the distinction between levels of selection is unclear, we will argue that *explanations* of macroevolutionary patterns in terms of differential persistence are independent from and not inferior to *explanations* of the same patterns in terms of differential reproduction at lower levels. We hope that the analogy drawn in this essay between selective forces on bacterial clones in an idealized chemostat and clades subject to extinction in nature is useful in establishing this explanatory independence and in legitimizing evolutionary explanations based on selection by differential persistence.

Frequently, the persistence-based view of ENS is motivated by the claim that selection does not require reproduction (Bourrat 2014; Charbonneau 2014; Papale 2020).[1] We in contrast see reproduction and persistence as two sides of the same explanatory coin: The former has to do with how lower-level entities—cells or species in the example here—come to be *replaced*, but the latter has to do with how long the clones or clades derived from them last. While the connection between persistence and reproduction has been noticed before, our model aims to clarify and legitimize the nature of this connection (Bourrat 2015c; Papale 2020).

We describe our chemostat model in section 2, and in section 3 address certain difficulties with this account, arguing that we, with Sterelny (1996), assert explanatory autonomy in MLST. In section 4, we indicate how clones in our chemostat might be "units of selection" as well as "units of evolution" *sensu* Hull (1978). In section 5 we flesh out relevance of our chemostat model to clade selection, concluding and mapping out future investigations in section 6.

2. The chemostat model for the differential persistence of subclones

Consider a simple density and frequency independent model. This model is an idealized 1-liter chemostat maintained at a constant temperature and with growth control on cell density in the presence of excess nutrients (figure 1). That is, cell density is allowed to reach only 10^6/ml (say) and there is no effective competition between cells for any resource present in the medium. Imagine that this idealized chemostat is initially seeded with a single cell of some recombination-deficient (exclusively asexual) strain of *Escherichia coli*, this being allowed to multiply to the specified low density. The chemostat is then held at that density by balancing fresh medium input and draining of cell-containing contents at appropriate and equal rates. Thus, after each cell division, on average one-quarter of the cells will have contributed two cells to the contents of the chemostat, half will have contributed one, and one-quarter

[1] For instance, Bourrat (2014) argues that a population of entities that survive but do not reproduce can evolve by natural selection, sometimes even resulting in adaptations. This is a version of a persistence-based view of ENS (so-called *weak* ENS) that does not assume reproduction or any other mechanism for the replacement or renewal of members in a population. In contrast, Charbonneau (2014) argues that ENS involves this replacement, but reproduction is not necessarily responsible for it. Hence, ENS is a combination of survival and population renewal. Papale (2020) argues that minimal ENS does not require this renewal, but paradigmatic ENS does. In this article, we do not take sides on this debate. We discuss persistence-based selection *with* replacement because this is the type of selection present in the case of subclones and clades.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

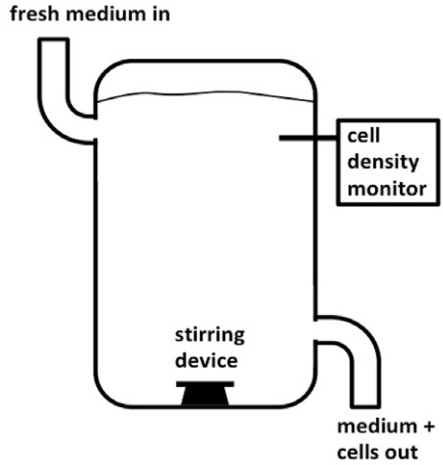

Figure 1. Our idealized 1-liter chemostat. Cell density is continuously monitored and kept at a constant low level (say 10^6/ml) such that no supplied nutrient is limiting. Fresh medium is pumped in, and medium containing cells is pumped out.

will have contributed none, although each will have had exactly two progeny. The missing cells would have been discarded through the outflow.

As indicated in figure 2, it is a consequence of both neutral and coalescent theory (Kingman 2000) that *one* of the billion cells contained in our idealized chemostat at any time after it reaches the maintained density is destined to become the ancestor of *all* cells in the chemostat at some future time. When this happens, the subclone founded by that cell has achieved "fixation." A subclone by the definition used here is an arbitrarily designated portion of a clone (or of a more inclusive subclone), consisting of one of the cells in that clone (or more inclusive subclone) and all this cells' descendants. Hence, at any time in the operation of a chemostat, every cell has the potential of founding a subclone some of whose cells will still live in the chemostat in the near future, and every subclone has the potential of occupying the whole chemostat in the distant future, thus comprising all surviving members of the clone from which the chemostat was first inoculated.[2] The average time for achieving such fixation might be long, although there is wide variance (Greenbaum 2015). Of course, all the *other* billion-minus-one cells present in the chemostat at any time after it has reached the maintained density are *potential* ancestors of all cells in the chemostat at some future time, but all are destined to found subclones that go extinct before that. By "extinction" we mean discharge through the outflow: When a subclone goes extinct, it means that there are *no* cells *in* the chemostat descended from the ancestor that gave rise to it (figure 2).

We see the ultimately fixed subclone, if its member cells are indistinguishable from those of the others, to have *differentially persisted* simply by chance. Those other subclones are spatiotemporally continuous entities with definite beginnings and persistence. Such entities are what Hull and Ghiselin called *individuals*

[2] The distinction between clone and subclone parallels the distinction between a clade and a subclade. While the clone is formed by all cells that ever existed in the chemostat plus their most recent common ancestor (the first cell in the chemostat), the subclone is any set of cells in the chemostat and their most recent common ancestor.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

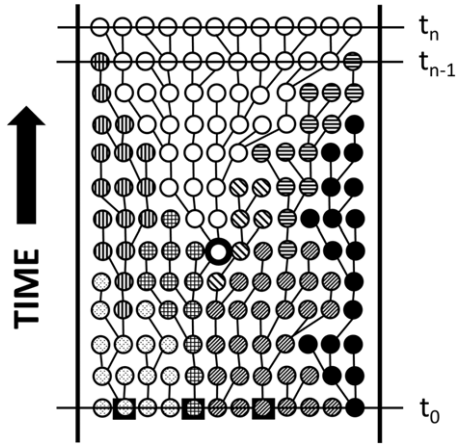

Figure 2. Fixation of subclones in our idealized chemostat. A subclone, like a clone or a clade, is defined as any ancestor plus all its descendants, living or dead (expelled from the chemostat or extinct). Designation of cells as ancestors and thus as founders of subclones is arbitrary. A subclone is "dead" if none of its descendants are living in the chemostat. In our model, the number of living subclones at t_n is defined as the number having distinct common ancestors at t_0, so this would be one for t_n as shown but would be three if t_n were one "generation" earlier, at t_{n-1}. Founder (ancestor) of subclone present at t_n is indicated by a circle and founders (ancestors) of subclones present at t_{n-1} are indicated by squares. That at some time t_n sufficiently distant from t_0, the number of living subclones will be one is a consequence of both neutral and coalescent theory (Kingman 2000). If a mutation favoring differential growth (increase in number of organisms) of a subclone (indicated as changes in pattern of fill in this figure) occurs, then the probability of fixation increases and the number of generations between t_0 and t_n will likely be reduced.

(Ghiselin 1974; Hull 1976, 1978). So too is the fixed subclone, which becomes potentially immortal as the sole living representation of "the clone" comprising all cells living or dead (expelled from the chemostat) descended from the cell with which we first inoculated the chemostat. Individuals can be nested within individuals, subclones within clones (and sub-subclones within *them*; Mariscal and Doolittle 2018).

Now consider scenarios that introduce natural selection in the chemostat. If, for instance, a mutation arises in some cell after the chemostat reaches a billion cells and this mutation results in mutant cells having more progeny per unit time, then the subclone comprising that cell and all its descendants has a better chance of achieving fixation than does any of the other billion cells, and the expected time to fixation will be reduced. We could see this as resulting in *differential reproduction* of the mutant cell and its progeny—but equally we could see it as resulting in *differential persistence* of the subclone that it founds—as a result of the latter's enhanced propensity to grow (acquire member cells). In the first perspective, the selected type of cell increases in number until it comprises all billion cells in the chemostat, this being the size of the relevant population. In the second, the subclone founded remains (as an individual) present only once, but the relevant population—which comprises competing subclones—dwindles in size from a billion to only one, as the *selected-for* subclone grows.

In the first case, what would be *selected for* would be whatever the mutant trait causing *differential reproduction* turned out to be—more efficient substrate use, better adaptation to the temperature at which the chemostat is maintained, the jettisoning

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

of genes rendered superfluous by conditions in the chemostat, or indeed many others. In the second, what would be *selected for* is the faster growth rate (more rapid acquisition of members) of the mutationally favored subclone, regardless of how that mutation worked. The faster acquisition of members by the mutationally favored subclone is *ontologically dependent* on the precise mutation that occurred, but evolutionary *explanations* at the level of the cell and of the subclone are *autonomous*, or so we will argue.

This is always the right way of thinking in circumstances like our chemostat model, at least. What is *selected for* in individual cells is *the trait* causing differential reproduction (over the short or long term as in Bourrat [2015b]), not that differential reproduction *itself*, which can be seen as the *consequence* of individual cell-level trait-specific selection. This consequence, however, can also be interpreted as a trait that is selected for at the next higher level. The differential reproduction of cells can thus be interpreted as differential growth rate of subclones. In that respect, subclones represent the next higher level in our model, which is in that sense an MLST model. One can describe this model as selection for differential persistence of subclones. Such subclones could be selected based on growth rate alone, which is a subclone level trait resulting from many possible mutations. The constant outflow of the chemostat and consequent population limitation establishes a selective regime in which subclone growth rate (regardless of its lower-level cause) is a selectively advantageous trait of subclones.

To us, the following words of Daniel Rabosky and Amy McCune (2010), while relating specifically to species selection, drive home the same general point about selection operating at different levels in MLST:

> Selection at the individual level contributes to trait variation between species by transforming intraspecific variation into species differences that might result in species selection. However, the mechanism by which a trait becomes fixed within a species, whether through selection or drift, need not be the same as the mechanism by which the trait influences diversification. (2010, 70)

In this passage, species diversification is defined as rate of speciation minus species extinction over time. So, while species diversification is a species-level trait that might be determined by individual-level traits (intraspecific variation), it does not follow that species selection can be fully and satisfactorily explained in terms of individual-level selection. It is of course easier to notice this explanatory irreducibility when higher-level selection is *opposite in direction* to lower-level selection, as in the case of the species selection rationale for the maintenance of sexuality (Maynard Smith 1978). Okasha (2006, 209) admits that such species selection favoring sexuality is at least "plausible." Arguments are easier too when at both levels differential reproduction is at stake, which Okasha also admits. Still the "critical issue" for Okasha in multilevel selection is that *fitness* (which Rabosky and McCune describe as the "mechanism by which the trait influences diversification") at one level is not simple a function of fitness at another level. Okasha writes:

> [T]here are plausible examples of species selection by differential extinction, for example the hypothesis that species selection favored sexual reproduction, mentioned above. This hypothesis says that sexual lineages had better survival prospects than asexual ones, not that their intrinsic rate of cladogenesis was

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

> higher. So while it is true that extinction occurs when all the organisms in a species die, and so in that sense can be "expressed in organismic terms", this does not mean that a species' probability of extinction is solely a function of organismic fitness, which is the critical issue. (Okasha 2006, 209)

The arguments for clone and clade selection presented here are similar in form to this. The key difference is that Okasha intends to make an ontological claim about the occurrence of selection at different levels, while we intend first and foremost here to make a claim about the epistemic relevance of distinguishing those levels. Additionally, Okasha anticipates the possibility of clade selection by differential persistence only to quickly dismiss it as "not very interesting" (2006, 214). The arguments in this article aim to convince the reader that Okasha's dismissal is premature and perhaps unwarranted.[3]

So far, the chemostat model illustrates how subclones are selected for persistence based only on their growth rate. Nonetheless, there are at least three other *independent* ways, analogous together with growth to the four clade-specific traits listed near the beginning of this essay (namely, the number of species in a clade, their ecological diversity, geographic dispersal, and level of intraclade cooperation), in which a subclone might generally survive longer than competing subclones. It is not necessary that selected subclones grow relative to others to last longer in either absolute or relative terms than they do.

A second and more interesting way to differentially persist would be one analog of ecological diversity among a clade's species, the possession by a subclone of a mutation conferring greater phenotypic plasticity. Some bacterial species exhibit "wall growth" in chemostats, the wall population constantly contributing "migrants" to the free-living population and undermining turnover and fixation due to selection or drift in the nonwall environment (Dykhuizen and Hartl 1983). Mutant subclones more prone to facultative wall growth would out-persist those not so prone, even if more slowly reproducing.

Third and even more interesting would be the possession of a mutator allele, increasing the frequency of heritable *genetic* variation, mutations being mostly detrimental but very occasionally beneficial. Such mutator mutations have been uncovered in Richard Lenski's Long Term Evolution Experiment (LTEE; Good et al. 2017), which as well provides evidence for the dependence of selected mutations on previous *unselected* mutational events (Blount et al. 2008). Although some individual lineages within a subclone will have benefited by virtue of "hitchhiking" on

[3] Bourrat (2015b) argues that Okasha's analysis of fitness across levels is inexact because it does not account for timescales. According to him, once one treats fitness as relative to timescales, one can properly compare fitness at different levels. This comparison might reveal that two levels of fitness are not opposed, but rather that one and the same process of selection changes direction over time (2015b, 11). We do not think Bourrat's analysis raises a problem for our argument. First, our goal is simply to show that we are justified in claiming that subclones have subclone-level traits under selection. We are not committed to Okasha's analysis here. Moreover, Bourrat offers a few pragmatic reasons for keeping the distinction between lower and higher (particle and collective) level fitness (2015b, 12). This appeal to pragmatics and his view of multilevel selection as epistemic models is good enough to our purpose here, which is arguing for epistemological autonomy of selective explanations at different levels. We articulate our argument in the next section.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

specific favorable mutations so created, a mutator-bearing subclone might be said to benefit as a differential *persister* from its standing genetic diversity per se, which is a subclone property, not the property of any individual cell. We might even call this diversity "evolvability" because it is in such a mutator-bearing subclone that selectable favorable mutations ("evolutionary innovations") are more likely to occur. Indeed, even though cells in any subclone with such a high mutation frequency might be at a *selective disadvantage* in terms of differential reproduction they would not necessarily be able to "revert" to a lower rate (if resulting from a deletion for instance), and a subclone of such cells might be differentially persistent as a higher-level individual because different favorable mutator-caused mutations keep saving it from extinction. This would be like "species selection" for sexual reproduction and selection on organisms *within* species for that trait being opposed in direction (see preceding text and Vrba and Gould 1986; Okasha 2006; Jablonski 2007, 2008).

Fourth and most interesting still would be "cooperation," slower to evolve, perhaps, but consistent with many observations on laboratory-maintained and natural populations, and often difficult to distinguish from frequency-dependent interactions of any sort. The recently developed "Black Queen Hypothesis" (Morris et al. 2012) imagines such a scenario, in which different strains or species lineages have lost genes involved in the production of essential metabolites that can be provided by other strains or species present locally, as do schemes for the evolution of symbioses and societies (Strassman and Queller 2010). Lenski's LTEE experiment involving the serial dilution of *Escherichia coli* cultures for more than 60,000 generations shows evidence of quasi-stable existence of subclones that *may* reflect such cooperation (Good et al. 2017) as might the genomic characteristics of wild populations of *Prochlorocccus* (Domingo-Sananes and McInerney 2021), and the pangenome phenomenon in general (Fullmer et al. 2015). The propensity to lose genes could be selected for through the differential persistence of mutualistic interactions between members of a subclone.

Relationships between selection processes can be cashed out in terms of the Price equation in each case and at each level. According to it, selection involves the covariation of character trait and fitness (Okasha 2006, 62–71). Fitness cashes out differently at the level of the individual organism, where it is in the end measured as differential reproduction, and at the level of the subclone, where it is in the end measured as differential persistence (survival). These fitnesses may, though they need not, be opposite in sign or direction, and of course there need not be selection or definable populations at one level or another (Jantzen 2017). Hence, the covariation between individual organismal trait and differential reproduction at the lower level (positive or negative) underwrites a higher-level covariation (positive or negative) between individual subclone trait and subclone persistence. The two processes are ontologically intertwined in the sense that there would be no higher-level persistence without lower-level reproduction and no higher-level trait without a lower-level trait. As a result, fitness at one level might be recast as temporally adjusted lower-level fitness (Bourrat 2015b). But despite this ontological dependence those two processes are not easily reducible to one another and give rise to *autonomous explanations*.[4] To further understand why, we next address some potential problems with our model.

[4] Hence, our argument for explanatory autonomy stands even if one adopts a conventionalist view of levels of selection (Waters 2011; cf. Bourrat 2021).

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

3. Problems with the model and explanations involving differential persistence

We have consistently described individual cells in our chemostat and the multicellular subclones they make up as existing at different levels. Readers might nevertheless still be suspicious about interpreting our chemostat model as a case of *multilevel selection* because the "higher" level, though clearly composed of entities at a lower level, *only* evolves through differential persistence rather than differential reproduction, and lacks the internal integration of a multicellular organism. Some comfort might be derived from the fact that some models of species selection, those dealing with the evolution of sex for instance (Maynard Smith 1978), are also based largely on the differential *extinction* of selected-against species. Species *do* remain capable of a reproduction-like process (speciation), but that capacity is superfluous in such explanations (Okasha 2006; see preceding text). Additional comfort might be derived from paleontological practice as sketched at the beginning of this essay. Clade selection is understood by many paleontologists in an MLST framework, though often only implicitly (Jablonski 2007, 2008) and clades need only be "integrated" in a genealogical sense.

Suspicious readers might also argue that multilevel selection has to involve "emergence" or ontological independence (Vrba 1980, 1983). This requirement is controversial among proponents of MLST (Okasha 2006, 207–8). Regardless, our more modest goal here is to establish the *explanatory autonomy* of clade selection models through using the analogy to subclone selection, while conceding *ontological dependence* in both cases. That is, there are no traits of clones or clades that are *not dependent* on lower-level properties, but selection on subclones and clades addresses higher-level–specific traits that lower-level entities cannot be said to have, and there are many possible lower-level causes (e.g., cell level mutations). In other words, subclone-level traits are *multiply realizable*, that is, they can be equally determined by different, alternative lower-level traits (Sterelny 1996; Sober 1999) and under different conditions.[5] To explain why a particular subclone eventually took over the entire chemostat as a result of selection, not drift, one only has to understand that that subclone differentially persists because of some subclone-level trait, irrespective of its actual lower-level cause. There are important reasons why one should favor explanations involving the subclone-level trait rather than or in addition to its lower-level cause. In what follows, we consider this point in more detail.

When explaining why a subclone became fixed in a chemostat, one might claim that this was more or less likely without knowledge about the actual lower-level mutation that drove the subclone to fixation. Implicit in this claim is the possibility that there could have been many other plausible ways to instantiate the same advantageous subclone-level trait and, thus, to drive that subclade to fixation or promote its

[5] A similar argument is given recently by Chalupka, Perona, and Eberhardt (2014, 2015) in the context of understanding machine learning as a process of selection. According to them, properties like temperature are causal macrovariables corresponding to a set of microvariables (e.g., gas molecules with certain position and momenta). Explanations in terms of causal macrovariables are valuable because they preserve information about how the system will behave under intervention. One might also use this and similar arguments to vindicate the ontological independence of higher-level (usually multiply realizable) traits. Our focus in this article is evolutionary (selective) explanations though, so we do not need to go into this debate.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

differential persistence. Explaining the persistence of the subclone in terms of growth, for instance (a subclone-level trait) captures that modal information, while reference to a particular lower-level mutation misses it. After all, growth rate and other persistence promoting properties are multiply realizable and, thus, can be instantiated by different mutations. If one explains subclone persistence (including fixation in the chemostat) by merely citing one of these mutations, one gives no indication that other mutations could have produced the same result. Hence, this explanation misses the fact that subclone persistence was likely because it could have been achieved by several different plausible means.

So, focusing on multiply realizable subclone-level traits is relevant at least in certain explanatory contexts. Such traits are relevant in contexts in which one wants to know, explain, or predict the likelihood of a certain evolutionary outcome (e.g., fixation) at the level of subclones. Similarly, clade-level properties help to explain why certain clades differentially survived "background" and "mass" extinction events, as discussed at the beginning of this essay. Certain clades were more likely to survive than others due to their advantageous multiply realizable properties (see Jablonski 2008 and section 5).

Thus, focusing on subclone-level traits is justified in two interrelated ways. First, these traits are distinct from their lower-level causes because they are multiply realizable. Second, explanations referring to such traits convey modal information that is useful in certain explanatory contexts. The explanation involving selection of the subclone level trait is independent from lower-level selective explanations. In this sense, the *explanation* is autonomous.

Sterelny (1996), in an important article that in many ways prefigures this essay, makes a general case for clade selection similar to that we make here based on the chemostat analogy. He asserts that "Evolvability—the capacity of a lineage to respond to change—will count as a lineage property if, but only if, it is multiply realized" (1996, 205). (Similarly, Jablonski [2008] argues that traits deemed selectable at the species level must be multiply realizable at the organismal level.) Sterelny's argument, which we repeat, is equivalent to the claim that *if* there were not alternative possible ways to instantiate a subclone level trait (e.g., growth rate, diversity, cooperation), then it would be very hard to make the case that such traits are subclone-specific, rather than just relabeled cellular ones. Multiple realizabilty may be essential to any explanatory invocation of higher-level selection.

Sterelny (1996) also argues that explanatory autonomy of higher-level selection is sometimes appropriate because it embodies "robust-process" rather than "actual-sequence" explanation (Jackson and Pettit 1992; Sterelny 1996; Brown 2014), and we think that is relevant here too. He considers the example of World War I. One way to explain the beginning of the war is to detail Gavril Princip's accuracy as a marksman, the several consequences of his behavior and how they triggered a sequence of events leading to the declaration of war. This type of explanation is an "actual sequence" explanation because it informs us about the order of events that led to World War I.

Another way of explaining the origins of this war is by presenting general facts about the system of armed alliances and conflicting interests among European nations in the early twentieth century. This type of explanation involves a different set of modal information. It informs us that general circumstances make an outcome

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

most *likely* to happen. So, given the sociopolitical context in Europe at the time, World War I was "a war waiting to happen." The war was likely to happen one way or another regardless of the actual order of events. This type of explanation is called "robust process" explanation and it is fully independent from the actual-sequence explanations.

In our chemostat model, the differential persistence of one subclone (e.g., the fixation in the chemostat) is a *robust process* waiting to happen. To explain why one subclone would likely outlast others, one should describe how the chemostat works and how subclone level selection for growth rate or phenotypic/genotypic diversity or "cooperation" would likely happen and lead to subclone persistence. This type of explanation does not require knowledge about the actual sequence of mutations that led a subclone to fixation. Hence, the robust process explanation of subclone persistence is independent from the actual sequence explanation of the same phenomenon.

In summary, the chemostat model describes conditions under which there is a selection for persistence at the subclone level. There is *ontological dependence* but *explanatory autonomy* between individual-level selection and subclone-level selection. Individual-level mutations are selected and result in subclone-level traits such as growth rate and diversity. Subclones are selected for persistence based on such traits. Dependence is not reductionism, though. Growth rate and other subclone-level traits are multiply realizable. For this reason, explanations of subclone persistence in terms of subclone-level traits are autonomous and frequently preferable to ones cashed out in terms of individual-level traits. We offered several examples of cell level traits (due to cellular mutations) that might result in differential subclone fitness and thus persistence, but neither these traits nor fitness can be reduced to (or always be taken to be a mere average of) individual traits and fitness (Okasha 2006).

4. The clone in our chemostat as a "unit of evolution" and, in some circumstances, a "unit of selection"

Our designation of subclones was arbitrary, and it meant to distinguish individual cells and their descendants in the chemostat from "the clone," by which we mean *all* descendants, living or dead (expelled), of the initial (single) inoculating cell. As we have shown, any of the billion cells present in our idealized chemostat at any time after reaching the maintained density is a *potential* founder of a subclone and, also potentially, the ancestor of *all* cells living in the chemostat at some future time, that is to say the ancestor of all living cells in "the clone." All but one subclone eventually will go extinct (if differential growth, even when the result of drift, underwrites differential persistence), and our model in its simplest form presents a case in which there is selection for persistence at the subclone level. Insofar as the chemostat is held at a constant density, selection at the subclone level might be said to be competitive. That one subclone "succeeds" means that others fail. Hence, subclones are "units of selection" insofar as there are reasons other than drift (at the subclone level) for their success.

In contrast, the single chemostat-housed "clone" might be cast as a relevant "unit of evolution" not a "unit of selection." It would be comparable to a species in the words of David Hull (1976), who writes:

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

> Evolution, as it is usually characterized, results from mutation and selection. According to one time-honored formula, genes mutate, organisms compete with each other and are selected, and species evolve. To put the matter dogmatically, the gene is the unit of mutation, the organism is the unit of selection, and the species is the unit of evolution. (1976, 181)[6]

Units of evolution in Hull's sense are spatiotemporally continuous entities that can change over time as a result of selection operating on the elements that compose them (Hull 1978, 1980). So, populations and species are paradigmatically units of evolution. As organisms are selected, they transmit genotypic and phenotypic changes over generations. These changes drive the evolution of a population or species, contributing to the change of its gene pool, phenotypic profile, speciation, and the likelihood of extinction. Hence, at different moments in time, a population or species will display several traits that have been continuously subject to change in the past.[7]

Similarly, the clone in the chemostat is a unit of evolution. This clone changes over time as a result of successive events of selection operating on its components. Subclones will be under selection for differential persistence, which can be dependent on but distinct from selection at the level of cells (section 2–4). Selection explanations might be formulated at both the subclone and the individual cell level. Hence, while clones (as in the contents of our chemostat since the first inoculation) are units of evolution, subclones and individual cells can be units of selection, albeit at different levels and with different outcomes (Lewontin 1970).

Now consider an extension of the chemostat model. Distribution of the clone into many separate chemostats would make a noncompeting population of chemostats not different from the noncompeting population of cells in our chemostat. Whether or not the differential survival of chemostats would then also count as ENS depends only on how we define "population" (Millstein 2010; Stegenga 2016).[8] Supposing a generously inclusive definition, extending the chemostat model in this way might create a scenario of selection between clones. Clones would then be units of selection. Any clone in any chemostat can go extinct through the operation of selection on cells and subclones that make it up, just as any species (apocryphally the "Irish elk"; Stuart et al. 2004) might go extinct if selection at a lower level (including sexual selection) is opposed to selection at a higher level. For instance, in our chemostat, one can imagine

[6] Hull does not claim that genes are the only units of mutation, the organism is the only unit of selection, or the species is the only unit of evolution. His point is that there is an important distinction between three types of units in evolution by natural selection. In later works (1980), he rephrases this distinction and argues that evolution by natural selection can be understood as an interplay between replicators (akin to units of mutation), interactors (akin to units of selection), and lineages (units of evolution).

[7] This meaning of "units of evolution" here is very different from the one attributed by Griesemer (2001) and related to the work of Maynard Smith. According to Griesemer, "units of evolution" refer to entities that multiply, vary, and present heredity (2001, 68). So, units of evolution are entities that can participate in ENS. In contrast, Hull's notion of units of evolution refers to entities whose genotypic and phenotypic profile change over time *as results* of ENS (see also Neto 2019). Here we rely strictly on Hull's notion because it better fits our purposes.

[8] This arbitrariness is not a problem. For instance, it is present when paleontologists and other scientists divide high-level clades.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

that cells that gained advantage by lysing and metabolizing the contents of other cells might ultimately go extinct and lead to the demise of the whole chemostat-contained clone.

In summary, differential persistence of clones might depend on how selection operates at the individual and subclone level. In this section we entertained the possibility that our model chemostat is just one of many, that these define a population, that some "survive" longer than others, and that the reasons that they do are under selection for persistence. Depending on how the chemostat model is implemented, clones can be units of evolution, units of selection, or both. The same idea applies to clades, as we show next.

5. Relevance to clade selection

What are usually called clades (such as Mammalia or the ammonites) are, in this view and for many purposes relevant here, similar to the subclones of our model (Doolittle 2017). In fact, clade selection might be easier to accept than clone selection were it not for the historically contingent linking of ENS and differential reproduction. Neither can "reproduce" (*as* a subclone or a clade; Okasha [2003; 2006, 212–17]), though their constituent parts (cells/organisms for subclones, or species [reproducing by speciation] for clades) can, and as a result subclones and clades can "grow" in size (number of parts), differentially persisting as an indirect result. Differential reproduction at the level of cells *resulting from* mutation to more efficient substrate use and *resulting in* differential representation among a billion cells in our simple chemostat model compares directly to differential species diversification (speciation rate—extinction rate) in clades leading to more species-rich and thus less easily extinctable clades. Similarly, persistence-promoting properties not explanatorily reducible to differential reproduction at a lower level can be found in both clades and clones.

If we define as the living component of "the clone" all the cells in our chemostat, then its subclones at any given time comprise an ever-dwindling population in "competition" to differentially persist. Similarly for clades in nature, we might argue that there is only one all-inclusive clade, which is elsewhere called life, defining it as LUCA, the last universal common ancestor, together with all its descendants (Hermida 2016; Mariscal and Doolittle 2018; Doolittle 2019). Presumably LUCA was not the only cell or species present on Earth at its time, and presumably many of these other cells or species gave rise to clades that went extinct sometime in the last four billion years—a dwindling population of internally diversifying clades (Doolittle 2019). Monophyletic groups such as the mammals or ammonites now make up life's living parts (we might instead call them less inclusive clades or even subclades), composed of species in place of individual cells in a chemostat.

That these less-inclusive clades are not effectively in competition to become ancestral to all life is because they are (at least for now) so distinct ecologically that one replacing the other in all its niches is unimaginable. Thermophilic archaea embedded in the Earth's crust do not compete with albatrosses flying above them. Our chemostat model (in its simplest but not more complex forms), arguably boasts only one niche. We have suggested some ways in which one might complexify it further of course, and chemostat environments do support diversification into subclones occupying various metabolic and spatial (e.g., "free-living" vs. wall-clinging) niches

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

(e.g., Maharjan et al. 2006). And, of course, many of us *do* think that life once existed as a thermophilic archaean, which, in about 4 billion years, gave rise to albatrosses!

Clades in nature compete in that one can out-persist the other, and much of the paleontological literature (Jablonski 2007) is devoted to considerations of why and how some groups designated clades (the ammonites, e.g.) have gone extinct while other have survived (Mammalia, e.g.). Some examples were given at the beginning of this essay. Ecological diversity is surely a clade-level "emergent" property, though ontologically dependent on lower-level causes. To predict and explain why certain clades dominate the oceans, one appeals to clade-level properties. These properties abstract from their multiple possible lower-level causes. For this reason, the prediction and explanation contain counterfactual information (Sterelny 1996; Jablonski 2007). It indicates that, even if lower-level causes were different, the clade-level pattern would be the same: As long as clades are ecologically diverse, they tend to dominate the oceans. This point corresponds to the idea that higher-level properties are multiply realisable and, thus, they result in the *explanatory autonomy* of evolutionary explanations at higher levels (see section 3). Ecological diversity depends on lower-level traits, but these traits are irrelevant in many explanatory contexts. In particular, if we want to explain why a clade has dominated the ocean, arguing that such domination was likely to happen, no reference to lower-level traits is required, and we use a *robust process*, not an *actual sequence*, explanation.

Clades are persisters only, not reproducers, and the only possible long-term fates for them are growth in size, constancy in size, decrease in size or extinction (loss of all species). Clades that lack properties conferring persistence are more likely to meet that last fate. In the simplest translation of the model presented for subclones, clades might be seen as *directly* subject to ENS only based on properties they, and not their parts, can be said to have. Minimally (again), these "emergent properties" include the number of species, their diversity (physiological/phenotypic or ecological, so that they are not all vulnerable to a single environmental change), their geographic distribution (so that they are not all vulnerable to a local extinction event), and the extent to which they can help each other and/or specifically attack parts of other clades or subclades. An example of helpfulness at the clade level would be the *exchangeability* of genes based on a common genetic code and regulatory signals (Jankovic and Cirkovic 2016; Doolittle 2019).

As well as "emergent properties," there can also be "aggregate traits," easier to imagine for clades than clones, maybe (Lloyd and Gould 1993). For instance, as in the preceding text, it might be that being larger is selectively advantageous within species so that there come to be more and more species of large individuals, even if there is no effect of average individual size on rates of speciation or species extinction. But largeness of individuals *could* also affect, positively or negatively, rates of speciation and extinction. A positive effect might be that larger individuals more easily invade new territories, there to speciate. A negative one would be that larger individuals might form smaller populations (because of local food supply limitations) lacking the genetic diversity to avoid extinction. Though selective explanations at two levels (within and between species, in this case) are more easily made when selections are in opposition, it is not necessary for selection at different levels to *be* opposed. Even when they are not opposed, we should invoke both levels in explaining why there are so many (or so few) species with such large individuals, as in this example.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

Intraspecies competition hardly explains the difference in speciation rate among species.

It is tempting (as mentioned previously) to think of emergent properties as more directly associated with higher-level selection than aggregate causes, but a full embrace of MLST renders such thinking unnecessary, perhaps even wrong. Depending on how one formulates MLS theory, the discussion pertaining to "emergent" and "aggregate" traits is a red herring. Vrba (1980, 1983) holds that selection at a particular level requires *emergent properties* at that level.[9] In contrast, Okasha (2006, 207–8) drops this requirement, and we tend to agree with him on this point. Unfortunately, however, Okasha falls short of recognizing the explanatory relevance of selection by persistence and clade selection. Our discussion in the concluding section of this article vindicates this relevance.

6. Conclusion

Even those who admit that selection for persistence matches Lewontin's Recipe (Lewontin 1970) would often deny that such selection can produce "complex adaptations" because differential persistence entails decreasing populations of persisters: There is no "replacement." But we argue here that clones and clades are in a sense self-replacing, continuously generating populations of potential persisters. Moreover, we would expect some clones (*pace* "cheaters") to become progressively *better* at occupying the chemostat, by successive mutations conferring more rapid growth, "ecological diversity," or cooperation with each other. Each of these "adaptations" could comprise several steps, so the clone will acquire "complex adaptations" to the conditions of the chemostat: Such adaptations would be the sum of all those individual innovative lower-level steps.

Most importantly, some of the increasingly complex adaptations generated by selection at lower levels emerge as *increasingly complex clade-level properties subject to ENS at the clade level, and only at that level*. Following our epigraph, the *complexity* of an adaptation must be evaluated at the level in which it *is* an adaptation. Vertebrate eyes, wings and fins, and similarly complex organismal-level traits might be taken as the standard of what a "complex adaptation" looks like. But if that is the standard, what could a species or clade have that would count as a complex adaptation in the first place? We end this article with two plausible candidates for a high-level *complex adaptation*, within and between species.

Maynard Smith (1978) suggested that prevalence of sexual reproduction might best be explained as selection at the species level through differential persistence (resistance to extinction) of sexual organisms with more variable gene pools. We have discussed this interpretation in the preceding text. Unless such variability was fully beneficial at the first inkling of lower-level sexual activity, it has gotten better (more complex) as sex has evolved. So genetic variability is a higher-level adaptation that has "improved" as a complex trait by *reiterated selection* at a higher level. More obviously and even more globally, the ecological diversity ("biodiversity") and interconnectedness of life as the most inclusive clade, achieved through countless evolutionary "innovations" (Dawkins 2009) and in the face of numerous near-total

[9] Whether our model qualifies as MLS in Vrba's account depends on how one defines "emergence."

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

extinction events, is surely one of the reasons that life is still with us, 4 billion years after it started (Erwin 2008). If there had only ever been a single living species it would have long since gone extinct.

Acknowledgments. This work was supported by the Gordon and Betty Moore Foundation (GBMF9729, https://doi.org/10.37807/GBMF9729) and the New Frontiers in Research Fund (grant NFRFE-2019-00703). We thank Christopher Lean, Christopher Jones, Letitia Meynell, Joe Bielawski, Ed Susko, Tyler Brunet, Rose Novick, Andrew Inkpen, Carlos Mariscal, Stefan Linquist, and anonymous reviewers for comments on various versions of this manuscript.

References

Blount, Zachary D., Christina Z. Borland, and Richard E. Lenski. 2008. "Historical Contingency and the Evolution of a Key Innovation in an Experimental Population of *Escherichia coli*." *Proceedings of the National Academy of Sciences USA* 105 (23):7899–906.

Bouchard, Frédéric. 2008. "Causal Processes, Fitness, and the Differential Persistence of Lineages." *Philosophy of Science* 75 (5):560–70.

Bouchard, Frédéric. 2011. "Darwinism without Populations: A More Inclusive Understanding of the 'Survival of the Fittest.'" *Studies in the History and Philosophy of Science Part C* 42 (1):106–14.

Bourrat, Pierrick. 2014. "From Survivors to Replicators: Evolution by Natural Selection Revisited." *Biology & Philosophy* 29:517–38.

Bourrat, Pierrick. 2015a. "How to Read 'Heritability' in the Recipe Approach to Natural Selection." *British Journal for the Philosophy of Science* 66 (4):883–903.

Bourrat, Pierrick. 2015b. "Levels, Time and Fitness in Evolutionary Transitions in Individuality." *Philosophy and Theory in Biology* 7:1–17.

Bourrat, Pierrick. 2015c. "Reconceptualizing Evolution by Natural Selection." PhD diss., University of Sydney.

Bourrat, Pierrick. 2021. *Facts, Conventions, and the Levels of Selection*. Cambridge: Cambridge University Press.

Brown, Rachel L. 2014. "What Evolvability Really Is." *British Journal for the Philosophy of Science* 65 (3): 549–72.

Chalupka, Krzysztof, Peitro Perona, and Frederick Eberhardt. 2015. "Multi-level Cause-Effect Systems." arXiv:1512.07942 [cs, stat]. arXiv: 1512.07942.

Chalupka, Krzysztof, Pietro Perona P., and Frederick Eberhardt. 2014. "Visual Causal Feature Learning." arXiv:1412.2309 [cs, stat]. arXiv: 1412.2309.

Charbonneau, Mathieu. 2014. "Populations without Reproduction." *Philosophy of Science* 81 (5):727–40.

Dawkins, Richard. 2009. *The Greatest Show on Earth: The Evidence for Evolution*. New York: Simon and Schuster.

De Querioz, Kevin, and Jacques Gauthier. 1990. "Phylogeny as a Central Principle in Taxonomy: Phylogenetic Definitions of Taxon Names." *Systematic Zoology* 39 (4):307–22.

Domingo-Sananes, Maria R., and James O. McInerney. 2021. "Mechanisms That Shape Microbial Pangenomes." *Trends in Microbiology* 29 (6):493–503.

Doolittle, W. Ford. 2017. "Making the Most of Clade Selection." *Philosophy of Science* 84 (2):275–95.

Doolittle, W. Ford. 2019. "Making Evolutionary Sense of Gaia." *Trends in Ecology and Evolution* 34 (1):889–94.

Doolittle, W. Ford, and S. Andrew Inkpen. 2018. "Processes and Patterns of Interaction as Units of Selection: An Introduction to ITSNTS Thinking." *Proceedings of the National Academy of Sciences USA* 115 (16):4006–014.

Dykhuizen, Daniel E., and Daniel L. Hartl. 1983. "Selection in Chemostats." *Microbiological Reviews* 47:150–68.

Erwin, Douglas H. 2008. "Macroevolution of Ecosystem Engineering, Niche Construction. and Diversity." *Trends in Ecology and Evolution* 23 (6):304–10.

Fullmer, Matthew S., Shannon M. Soucy, and J. Peter Gogarten. 2015. "The Pan-genome as a Shared Genomic Resource: Mutual Cheating, Cooperation and the Black Queen Hypothesis." *Frontiers in Microbiology* 6:Article 728.

Ghiselin, Michael T. 1974. "A Radical Solution to the Species Problem." *Systematic Biology* 23 (4):536–44.

Godfrey-Smith, Peter. 2009. *Darwinian Populations and Natural Selection*. Oxford: Oxford University Press.
Good, Benjamin H., Michael J. McDonald, Jeffrey E. Barrick, Richard E. Lenski, and Michael M. Desai. 2017. "The Dynamics of Molecular Evolution over 60,000 Generations." *Nature* 551:45–50.
Greenbaum, Gili. 2015. "Revisiting the Time to Fixation of a Neutral Mutant in a Finite Population—A Coalescent Theory Approach." *Journal of Theoretical Biology* 380:98–102.
Griesemer, James. 2001. "The Units of Evolutionary Transition." *Selection* 1 (1-3):67–80.
Hermida, Margarida. 2016. "Life on Earth Is an Individual." *Theory in Biosciences* 135:37–44.
Hull, David L. 1976. "Are Species Really Individuals?" *Systematic Biology* 25 (2):174–91.
Hull, David L. 1978. "A Matter of Individuality." *Philosophy of Science* 45 (3):335–60.
Hull, David L. 1980. "Individuality and Selection." *Annual Review of Ecology and Systematics* 11:311–32.
Jablonski, David. 1986. "Background and Mass Extinctions: The Alternation of Macroevolutionary Regimes." *Science* 231 (4734):129–33.
Jablonski, David. 2007. "Scale and Hierarchy in Macroevolution." *Paleontology* 50 (1):87–109.
Jablonski, David. 2008. "Species Selection: Theory and Data." *Annual Review of Ecology, Evolution and Systematics* 39:501–24.
Jackson, Frank, and Philip Pettit. 1992. "In Defense of Explanatory Ecumenicalism." *Economics and Philosophy* 8 (1):206–7.
Jankovic, Srdja, and Milan M. Cirkovic. 2016. "Evolvability Is an Evolved Ability: The Coding Concept as the Arch-unit of Natural Selection." *Origins of Life and Evolution of Biospheres* 46:67–79.
Jantzen, Benjamin C. 2017. "Kinds of Process and the Levels of Selection." *Synthese* 196:2407–33.
Kingman, J. F. C. 2000. "Origins of the Coalescent: 1974–1982." *Genetics* 156 (4):1461–63.
Knope, Matthew L., Andrew M. Bush, Luke O. Frishkoff, Noel A. Heim, and Jonathon L. Payne. 2020. "Ecologically Diverse Clades Dominate the Ocean via Extinction Resistance." *Science* 367 (6481):1035–38.
Lewontin, Richard C. 1970. "The Units of Selection." *Annual Review of Ecology and Systematic* 1:1–18.
Lenton, Timothy M., Timothy A. Kohler, Pablo A. Marquet, Richard A. Boyle, Michel Crucifix, David M. Wilkinson, and Marten Scheffer. 2021. "Survival of the Systems." *Trends in Ecology and Evolution* 36 (4):333–44.
Lewontin, Richard C. 1985. "Adaptation." In *The Dialectical Biologist*, edited by Richard Levins and Richard C. Lewontin, 65–84. Cambridge, MA: Harvard University Press.
Lloyd, Elisabeth A., and Stephen Jay Gould. 1993. "Species Selection on Variability." *Proceedings of the National Academy of Sciences* 90 (2):595–99.
Maharjan, Ram, Shona Seeto S., Lucinda Notley-McRobb, and Thomas Ferenci. 2006. "Clonal Adaptive Radiation in a Constant Environment." *Science* 313 (5786):514–17.
Mariscal, Carlos, and W. Ford Doolittle. 2018. "Life and Life Only: A Radical Alternative to Life Definitionism." *Synthese* 197:2975–89.
Maynard Smith, John. 1978. *The Evolution of Sex*. Cambridge: Cambridge University Press.
Millstein, Roberta. 2010. "The Concepts of Population and Metapopulation in Evolutionary Biology and Ecology." In *Evolution since Darwin: The First 150 Years*, edited by M. Bell, D. Futuyma, W. Eanes, and J. Levinton, 61–85. Sunderland, MA: Sinauer.
Morris, J. Jeffrey, Richard E. Lenski, and Erik R. Zinser. 2012. "The Black Queen Hypothesis: Evolution of Dependencies through Adaptive Gene Loss." *MBio* 3 (2):e00036-12.
Neto, Celso. 2019. "What Is a Lineage?" *Philosophy of Science* 86 (5):1099–110.
Okasha, Samir. 2003. "Does the Concept of 'Clade Selection' Make Sense?" *Philosophy of Science* 70 (4): 739–51.
Okasha, Samir. 2006. *Evolution and the Levels of Selection*. Oxford: Oxford University Press.
Papale, Francois. 2020. "Evolution by Means of Natural Selection without Reproduction: Revamping Lewontin's Account." *Synthese* 198:10429–55.
Rabosky, Daniel L., and Amy R. McCune. 2010. "Reinventing Species Selection with Molecular Phylogenies." *Trends in Ecology and Evolution* 25 (2):68–74.
Sober, Elliot, and David Sloan Wilson. 2011. "Adaptation and Natural Selection Revisited." *Journal of Evolutionary Biology* 24 (2):462–68.
Sober, Elliott. 1999. "The Multiple Realizability Argument against Reductionism." *Philosophy of Science* 66 (4):542–64.

https://doi.org/10.1017/psa.2022.11 Published online by Cambridge University Press

Stegenga, Jacob. 2016. "Population Pluralism and Natural Selection." *British Journal for the Philosophy of Science* 67 (1):1–29.
Sterelny, Kim. 1996. "Explanatory Pluralism in Evolutionary Biology." *Biology & Philosophy* 11:193–214.
Strassman, Joan E., and David C. Queller. 2010. "The Social Organism: Congresses, Parties and Committees." *Evolution* 64 (3):605–16.
Stuart, A. J., P. A. Kosintev, T. F. G. Higham, and A. M. Lister. 2004. "Pleistocene to Holocene Extinction Dynamics in Giant Deer and Woolly Mammoth." *Nature* 431:684–89.
Vrba, Elisabeth S. 1980. "Evolution, Species and Fossils: How Does Life Evolve?" *South African Journal of Science* 76:61–84.
Vrba, Elisabeth S. 1983. "Macroevolutionary Trends: New Perspectives on the Role of Adaptation and Incidental Effect." *Science* 221 (4608):387–89.
Vrba, Elisabeth S., and Stephen Jay Gould. 1986. "The Hierarchical Expansion of Sorting and Selection: Sorting and Selection Cannot Be Equated." *Paleobiology* 12 (2):217–28.
Waters, C. Kenneth. 2011. "Okasha's Unintended Argument for Toolbox Theorizing." *Philosophy and Phenomenological Research* 82 (1):232–40.
Wilson, Robert A., and Matthew J. Barker. 2019. "Biological Individuals." In *The Stanford Encyclopedia of Philosophy*, edited by Edward N. Zalta. Stanford: Stanford University Press. https://plato.stanford.edu/archives/fall2019/entries/biology-individual/.

Cite this article: Neto, Celso and W. Ford Doolittle. 2023. "A Chemostat Model for Evolution by Persistence: Clade Selection and Its Explanatory Autonomy." *Philosophy of Science* 90 (1):21–38. https://doi.org/10.1017/psa.2022.11