

Who put the class into classification?

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Abstract

Essentialists have recently argued that species and other taxa are classes not individuals, in opposition to the biologically nominalistic Species-As-Individuals thesis of Ghiselin and Hull. I argue that species are sets and might conceivably be classes, and that the S-A-I thesis is picking out the fact that species in evolution are bounded by space and time, but not that they are functional individuals. Classes cannot change their defining characters, but transformations between classes can be understood in terms similar to Hamming Distance measures in systematics and genetics, and I sketch how class change might be expressed.

In the Linnean system of classification of animals and plants a species was a set or class, in fact it originally meant a smallest named class in the system. But a class or set is an abstract entity and thus has neither beginning nor end in time. We cannot, therefore, speak of the origin of species if we are conceiving species in the Linnean manner. The doctrine of evolution is not something that can be grafted, so to speak, onto the Linnean system of classification. The species of Darwin and the species of Linneus are not at all the same thing – the former are concrete entities with a beginning in time and the latter are abstract and timeless. (Woodger 1952: 19)

Introduction

Since modern biology began at the end of the eighteenth century, there has been dispute over the nature of the kinds of organisms that make up what we now call biodiversity. This has largely been a metaphysical debate, with a strong tendency to propose unitary and exclusive “solutions”. Since Linnaeus, following Ray, established the scholastic term *species* to mean the diagnosable groups to which organisms belong, formal ontology has been an issue in discussions of metabiology.

As Mayr and others have made clear (Mayr 1970, 1982, Hull 1988), the predominant view of species and the other taxa of biology until comparatively recently has been that they are classes or types. However, the revival of “natural kinds” by Kripke and Putnam again raised these metaphysical conundrums in biology. Ghiselin and Hull argued in a number of influential essays that species were actually individuals, about which no general laws could be formulated. This view has been very influential amongst cladists, who view terminal taxa as singular objects, and also amongst evolutionary systematists who, like Mayr, Simpson and Dobzhansky, view species as the units of the evolutionary process.

The Ghiselin-Hull proposal is to treat species not as kinds, but instead as spatiotemporally restricted individuals, with proper names not type names, and therefore as objects. Just as there can be no sociopolitical laws that could only apply to Russia and no other country present, past or future¹, neither can there be a natural law about a single species, for example *Canis familiaris*. This proposal has been called the *Species-As-Individuals* thesis (SAI) because each species is ontologically equivalent any individual with a history and a name, no matter whether it is a single organism like Lewis’s cat Possum, or a large complex object like the Matterhorn, a geopolitical entity like Russia, or a historical sequence like World War 2. Mahner and Bunge (1997) have somewhat misleadingly called this thesis *bionominalism*.

The more traditional and opposing view is that species are kinds, which is taken to mean that they are types or essences or both. Species are on this account treated as universals, although this is not often the motivation for the view. For proponents of the species-as-universals thesis, an organism is a member of its species because it approxi-

1. As opposed to rules of thumb, or statutes and regulations that apply only to Russia. We are seeking natural laws here.

mates a type or because it either has, or evinces, the necessary and jointly sufficient properties that are essential to being of that species. Species are in this case classes or sets, because membership of the species is satisfied just so far as some set of criteria are satisfied for that organism. And so the species debate is framed between historical individualist and atemporal Platonist or Aristotelian positions about biological kinds.

Some call for a metaphysical pluralism about species, eg, Nelson (1989), Kitcher and Sterelny (Sterelny 1995, Sterelny and Kitcher 1988), but more often than not, disputants claim that species “are just” classes (eg, by Ruse 1987, 1998), or individuals (Ghiselin 1974, 1997), or some other specific and exclusive metaphysical category (cf. de Sousa 1989). Recently, Ruse (1998) stridently claimed that the notion of species as individuals has been passed by in the developments of biology since the 1960s, and that it is time to try again the notion that species are classes, if indeed it was ever abandoned (cf Hull 1988:213n), and he, along with others (Mahner and Bunge 1997), identifies classes in this case with natural kinds.

In an attempt to make clear what is being discussed, I turn to the resources of set theory and formal metaphysics. What exactly is being said if we say that species are classes, and that to classify one must needs have a class concept? How does it differ to say that X is a class, or a set, or an individual (or even a type)? Are there clear and distinct notions of these ontological categories? What is an individual that it is exclusive of being a set or a class?² I conclude that the metaphysical notion of a species is context dependent, and that there is no single notion that covers all the sorts of cases biologists want to see covered. I cannot deliver any novel solutions, but I hope this clarifies the problems being debated.

2. It should be clearly noted that Ghiselin and Hull are aware that their use of these terms is not exactly according to some standardised uses in logic. I believe that, disclaimers notwithstanding, this is confusing and at the root of some criticisms (such as Ruse's).

Summary of the argument

In Zermelo–Frankl set theory (ZF) and recent metaphysical formal languages like Zalta’s (1983, 1988, unpublished) theory of abstract objects (ZAO), there are only two categories: objects and sets. A set is an aggregate, or group, object, and has as its components other objects that may be either sets or elemental objects. A class is the set of properties that may be predicated of objects - it is the intension of the properties in that set. Not all sets are classes. An individual object is just some distinct and definite set, or some element that is primitive to the domain of discourse (the “universe” of that language, Machover 1996, or Reality in Lewis 1991).

To avoid antinomies like Russell’s paradox, sets and classes are technically distinct, but most writers mention this distinction and then use the terms “class” and “set” interchangeably. Likewise “object” and “individual” – not all objects are elements of the language.³ In this paper, I am being somewhat non-standard myself with terms such as “set”, “class” and “individual”, which I justify by noting the variability of these terms in the literature. I have picked the eyes out of those definitions that seemed to me to most closely answer to the distinctions that are implicit in or required by the biological debate over taxonomy. I take classes to be sets of properties or propositions. Of course, others make similar idiosyncratic distinctions – Lewis (1991) defines a proper class as anything that does not have an individual as a part, what I take here to be sets as classes *sensu lato*. The translation can be made with relative ease. I prefer Zalta’s terminology to Lewis’s largely because my interest here is the problem of grouping concrete biological objects (Lewis’s individuals) under abstract terms (Lewis’s classes), and the approach taken by Lewis’s mereology would confuse the issue.⁴

When Ghiselin and Hull (Ghiselin 1974, 1975, Hull 1976) introduced the notion of species as individuals (SAI) they did so explicitly to capture the idea that species are spatiotemporally bounded – that they are segments of phylogenetic lineages with a more or less delimited beginning, end and duration, ranging over geographic locales and existing in ecotypical environments. Is this an individual? While it follows Strawson’s (1959, 1964) analysis, this is not how an individual needs to be formulated in mereology or set theory. In set theory, a set may be an individual, and may function as

3. Under Lewis’s formulation for example, proper classes are those classes that have only classes as members, while under Zalta’s theory, classes are objects that have zero-place predicates as their members. In both cases, species are not proper classes/classes because species have individuals/objects as their members. It matters little if we use the term “individual” or “concrete object” for organisms, except that Zalta’s approach makes the point more directly. For Lewis, individuals are unmembered objects or fusions of unmembered objects in Reality, which transports the notion of the spatiotemporality of these objects in any case.
4. Attempts are under way by Barry Smith and his colleague Berit Brogaard to develop a mereology that is sufficient to evolving species. However, so far it requires a functionally cohesive notion of species/individuals, which I argue below is not relevant to an SAI thesis as such.

an object in another set or in a class. I propose that what the SAI thesis is trying to capture is another distinction altogether, and should instead be understood as a meta-physical species-as-ordinary-objects thesis.

Zalta distinguishes between ordinary objects and abstract objects in ZAO, either of which may be ZF sets. Ordinary objects are those sets or objects that “exist in space and time”. Abstract objects are those that do not, and a set of abstract objects is a class. Another way to express this distinction, and one that matches the SAI thesis quite well, is that ordinary objects are bounded by space-time coordinates, and that such coordinates are part of the specification of those objects. Species are ensembles that are spatiotemporally bounded under this interpretation.

When Ruse says that species “are” classes, it seems that he wants to say that species are sets of objects – organisms – that satisfy sets of predicates (the “extension of a class” concept of a species). In this way a classification is made possible. Is this exclusive conception necessary, though? Can a species be spatiotemporally bounded, and still be a set of objects that satisfies some set of predicates? Whatever may suit one’s interests, species must be natural sets if they are not to be arbitrary constructs of convenience alone. So they do not satisfy just any set of predicates, and they must contain, either as members or as class inclusions, ordinary objects; that is, species must be of actual spatiotemporal biological objects. There are too many *possible* species otherwise, rather like the question of the number of possible bald fat men.

So, a species, while it may be an “exemplification” or “realisation” of a class relation, and while it certainly is a set, or collective (ensemble, group, and so forth), must be comprised of ordinary objects. Set out this way, the SAI is *not* in opposition to the conception of species as the *extension* of classes, but it is of species *as* classes (as the *intension* of predicates). Neither does the SAI preclude some notion of species as sets, which may or may not be conceived as individuals.

Is this pluralism? I rather think of it as an observation that the mental furniture of classification permits a range of diverse functions. The problem of natural classification is to find as general a set of descriptors of naturally occurring phenomena while still capturing the extensions of the causal processes. This sets up a tension between diagnostic and determinant properties. So to conceive species as sets is inevitable since they are groups or aggregates; as ordinary ensembles essential, since the things that comprise them are real not abstract; and as classes a possibility that depends on one’s theoretical and explanatory needs (ie, whether one wants to classify based on patterns or processes, Smith 1994).

I therefore think that we should do more than just separate species definitions into taxa (the members) and categories (the class), as Mayr does (1982: 254), but into

species_{object}, species_{set}, species_{class} (or species_{category}), and the particular species as ontologically either an *ordinary object* or an *abstract class*, or both, and in either case as a set. This is not novel. Woodger (1937) and Gregg (1954) made this very point, albeit in the logical positivist interpretation of set theory of the time.⁵

The problem with conceiving species as sets, and in particular as classes, is that species change, and the logic of set transformation is not very clear. If a class changes its predicates, how is it the same class? This is, of course, Hobbes' Ship of Theseus identity problem (Hull 1988, 1992). I propose an asymmetric "delta" relation that permits us to map two distinct sets in terms of the "distance" of the changes in predicates. This is called Hamming distance in systematics and information theory (Farris 1970, cf Panchen 1992). The delta transformation permits us to determine affinities (relationships) of selected sets or classes in what is called a Wagner tree (Wagner 1961), and to specify when two sets represent the "same" object or transformation series.

However, if the change is continuous – that is, not discrete or saltative – then the choice of what points in the Wagner tree to select for comparison and classification (ie, the selection of which sets) is arbitrary, and so also is the classification. For objective classification, the terminal nodes on the tree must be "forced", either by the discrete steps of a punctuated transformation, or by selecting simultaneous states (if the transformation is a time series, then synchronous states) as the relata. For instance, DNA sequences are forced by the DNA-to-amino acid "code", and comparisons generally tend to be commensurate. But as the phenetics debate showed, selection of just any old trait leads to wildly differing classifications according to the traits chosen (Hull 1988, Nelson and Platnick 1981).

5. Interestingly, given the influence Hennig has had upon this topic, Woodger is mentioned with some approval several times in Hennig's (1966): "We consider the investigations of Woodger and Gregg extraordinarily important because they clarify, with methods that exclude all confusion and contradiction, the peculiarities of the hierarchic system, as so create exact prerequisites for investigating the questions of whether and why it deserves the favor it enjoys in biological systematics." 17. Cladistic systematics is founded upon set theoretic considerations, and treats taxa as objects in sets, although characterising taxa as sets tends in practice to be applied to so-called "higher taxa". See also Nelson 1985.

Species as sets

We can perhaps begin with the notion that species (and other taxa⁶) are sets. There is a lot of confusion in the literature about this. Some seem to think that if a species is a set, it is also a class. Some think that a set can be a class or an individual but not both. To unravel this, we have to make some stipulative definitions. I will distinguish between *epistemic* and *ontological* sets, classes and individuals.

Ontological objects are objects *en soi*, independent of the knowledge cognisers may have of them or their potential to be known. They are what a natural classification wants to capture and represent, to reflect the causal processes which result in the observed distributions of properties, and to present natural relationships for theoretical explanation, rather than deriving them *from* theoretical considerations. Species are, to most of biology, data, not outcomes of models.

Epistemic objects, on the other hand, tend to be conventional and pragmatically delineated. One major justification of a classification scheme is the operational justification: that it permits researchers to jointly reference data sets (Buffon's view), and ensure that apples are compared to apples, not oranges. Epistemic objects are "subjective" in the sense that they depend upon the state of observer systems and the relationship that obtains between observers and the phenomena observed. For example, bee purple is not an epistemic object until the ability to "observe" in ultraviolet was developed.⁷

Sets, according to Cantor's original definition, are phenomenal collectives – groups that are observed to be separate aggregates or individuals comprised of many parts. Membership of a set is often arbitrary, but can be objectively defined, and perhaps also may reflect natural realities. Classes are not identical with sets – some sets are classes (the set of all as that are *P*) but not all classes are sets, to avoid the Russell paradox (a class may be a class of classes,⁸ and class inclusion can operate on abstractions). In modern usage, sets can be epistemic *or* ontological, and the distinction is often glossed over, so it is worth making explicitly here. Simply because an aggregate presents itself to our perceptions is no guarantee that the aggregate reflects the underlying causal processes.

If sets are held to be aggregates of individuals⁹, then we must further distinguish between the different kinds of things that get called individuals:

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6. I make this qualification in order to include clonal and secondarily asexual lineages, as well as quasispecies in single celled organisms and viruses, and superspecies of mutually interfertile species. In other words, all taxa.
 7. In my opinion, epistemic objects can also be objective to the extent they adequately represent ontological relationships. However, this is to assume a representational epistemology that is irrelevant to this discussion.
 8. The sense of "proper class" in Z-F.

- *phenomenal* individuals – observer-dependent, scale-relative, individuality,
- *functional* individuals – the least ensemble required to generate a given result. The complexity of that least ensemble is the *cohesion* of the aggregate – the ratio of the minimum to observed structure; for example, a slime mold like *Dictyostelium* is less cohesive than a metazoan, and plants are less cohesive than animals, (Buss 1987)¹⁰, and
- *spatiotemporally restricted* individuals – Hull-Ghiselin individuals, Hull 1988, 1992. This could also be called the *contiguity* definition, and is directly analogous to the Hobbesian notion of identity exemplified in his Ship of Theseus thought experiment.

These three senses of *individual* also give rise to three senses of *set*:

- *phenomenal* sets – morphological ensembles that, *at some scale*, appear to be similar to each other,
- *functional* sets – sets of functionally-related individuals, that is, individuals that satisfy some function, and
- *contiguous* sets – sets of adjacent individuals, or neighbours¹¹.

These relations are summarised in Table 1.

Overall, the differences between biological sets, classes and individuals may be expressed in terms of the part–whole relations they have (Hull 1988): sets are *differentiated*, classes are *diagnosed*, and individuals are *identified* or *ostensively named* (Ghiselin 1997). It may also be expressed in terms of the labels that delineate each one: sets have parts (the set of all *Xs*), classes have inclusions or members (all *Xs* that are *P*), and individuals have proper names (*X*).

Biological aggregates have been divided in the literature in several ways, generally into *morphological*, *phyletic* and *genetic* kinds (respectively, the metrics of structure, historical differentiation, and lineage topology).

Structural (morphological) sets are either *monothetic* (unified by a necessary and sufficient set of conditions) or *polythetic* (unified by a cluster of conditions, ownership of most but not all being sufficient for inclusion, Sokal and Sneath 1971). Artificial sets

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9. A set is distinct from a *bag*, for the latter may have identical and duplicate copies of the same individual, whereas a set either includes an object or it doesn't. In other words, clones are the same object in genotypic sets, but distinct in a bag.
 10. Ruse is arguing against the notion that species are individuals *because* they are kept cohesive by gene flow, a view proposed by Mayr (1971) and accepted by numerous others but more recently tending to be rejected in favour of the notion that species have a shared developmental system that buffers them against change and keeps them distinct. As I argue below, this is not the core argument of the SAI thesis.
 11. "Adjacent" here means bordering in some metric space – it may be physical space, but it may also be morphological space – that is, the metric space of morphological variables. Note also that bordering depends upon the grain of the spatial scale (see Rosenzweig 1995, Kunin 1998 for discussions of the geographical sense of neighborhood of species, but the point can be extended to cover metrics other than locale).

	<i>Epistemic</i>	<i>Ontological</i>
<i>Set</i>	Phenomenal aggregate (Cantor set)	Extension of individuals, a system
<i>Class</i>	Diagnosable properties	Inherent (essential) properties
<i>Phenomenal individual</i>	Perceptual object	Grain of partition of space
<i>Functional individual</i>	Hypothetical cause of observed outcome	Vera causa
<i>Contiguous individual</i>	Historical evidence of contiguity (eg, biogeographic distribution)	Causal contiguity (ie, no discontinuities)

of structure would (by analogy with Hennigian terminology) be *parathetic* (incomplete clusters on some list of conditions, eg, all triangular shapes except those that are red).

Historical (phyletic) sets are divided by phylogenetic (Hennigian, or cladistic) systematics into *monophyletic* sets (all subsequent branches from and including a given node in a cladogram), *polyphyletic* sets (sets of nodes and branches that are not monophyletic because they have more than one ancestral node), and *paraphyletic* sets (sets of some, but not all, subsequent branches and nodes from an ancestral node). Paraphyletic sets are artificial because they do not reflect the real causes of differentiation (Wiley, *et al* 1991).

Genetic (lineage) sets: Hennig also extended the definitions of lineage topology. Prior to his (1966) there had been *phylogenetic* lineages (sets of nodes in the lineage) that were considered to be *anagenetic* (the gradual change of one set or taxon into another) – Hennig introduced the term *cladogenetic* to denote lineages that split and do not recombine, and the term *tokogenetic* to denote lineages that do regularly recombine. Within-species lineages (that is, sexual recombination) are tokogenetic, between-species lineages are cladogenetic. As is well-known, Hennigian systematics de-emphasises the relevance of anagenesis to classification.

The terms used in Ghiselin's and Hull's SAI papers and Mayr's earlier discussions (eg, Mayr 1970, cf Hull 1965) leads one to conflate the notions of essentialism (the view that species are monothetic sets) and typology (which, as far as I can make out, is best understood as the view that species are polythetic sets, or modal approximations to a coordinate in a metric space) – indeed Mayr uses the term “typological essentialism” continuously (Mayr 1982, 1988, 1991, Mayr and Ashlock 1991).

Types are construed in this paper as fuzzy sets with a unimodal distribution (the mode being the type¹²), essences are single point distributions. In classical usage, being of a type is construed as approximation to an Idea or a Form (Lovejoy 1936, Stevens 1994).

However, if aggregates are clusters that are merely neighbours in a metric, then there is no essential set of characters required for being a type, and we should separate the two categories.

A type may be a diagnostic ideal or it may be a causal kind (Stevens 1994). As a diagnostic ideal, it represents the mode of the state of a population, with the distribution curve representing the spread of properties members of that population exhibit. For each trait or character, including genetic characters, there will be a metric axis, so there will be a hyperspace or state space with as many axes as there are measured variables, and the population will cluster about the mode in that space. The older sense of type, to which Mayr objects, is the causal variety. This is the sense that the type somehow *causes* the cluster to remain where it is in that state space. It gives ontological priority to a diagnostic idealisation, and forms the basis for antievolutionary objections, since if a type has causal power, then it resists change. We can safely ignore that sense of type here.

Ghiselin-Hull species under the SAI conception are epistemic and ontological phenomenal and contiguous individuals. They are not, despite the tenor of Ruse's criticisms (1987, 1998), necessarily functional individuals. So when Ruse criticises the SAI because species do not have the requisite functional cohesion from gene flow or population structure, he is attacking the SAI for not being what it doesn't have to be.

However, even under the SAI conception, particular species – monotypic species – may be classes in the epistemic sense, and may even be classes in the ontological sense, for they represent the actual extensions of diagnosable (and sometimes diagnosed) properties (or key characters), and inherent properties, even though the extensions are in polythetic clusters most of the time. As aggregates of individual organisms, species are ontological sets, and as aggregates of phenomenal characters they are epistemic sets. We can conclude from these distinctions that the objections Ruse has to the SAI thesis do not carry his conclusion, even leaving to one side his intuitions regarding temporal contiguity.

The Ghiselin-Hull argument rests on the claim that taxa are not universals – they do not feature in laws of nature (cf Ghiselin 1997: 129). Taxa are objects that are related by descent (minimally monophyletic tokogenetic lineages, Kornet 1993). The objection is that we derive this relationship rather than starting with it in subsequent classification, which makes taxa classes just insofar as their extension is specified by the predicability of phenomenal or endogenous properties.¹³ So, which is it? Are species objects or cate-

12. Sober (1994) has argued that typologies deriving from Aristotelian conceptions are Natural State Models. This would make the mode some kind of attractor in the metric space.

gories, sets or classes, individuals or universals? Let us consider two cases: Red the reborn Neandertal, and Possum the actual cat.

The many statuses of Red the Neandertal

The metaphysical categories listed in the table above can, in my opinion, all be applied to taxa, and there is no in-principle conflict between them, subject to the caveat that each category depends on the appropriate context. To illustrate, suppose that cells from a Neandertal are found mummified, from which DNA is extracted, fed into a sequencing computer which is later used to generate the DNA inserted into the oocyte of a *H sapiens*,¹⁴ and a viable individual is born (let us call him Red, from *H neanderthalensis redivivus*). Is Red a member of the taxon *H neanderthalensis*? Ruse's intuitions are that he would be¹⁵, but intuitions aside, it depends on the categories in play.

If one asks "is Red a member of the **phylogenetic lineage** *H neanderthalensis*?", and we may reply that he is not, for the relevant causal links of sexual reproduction do not apply (the contiguity criterion for inclusion in the set *H neanderthalensis*). We may answer that he is, in the sense of phenomenal identity (he looks and perhaps behaves like a member of *H neanderthalensis*) or of functional identity (the relevant genetic and cytological identity obtains). We may ask if he is a member of the **class** *H neanderthalensis*. In both the epistemic and ontological senses, the answer might be yes, for all biological properties (apparent and real) endogenous to a member of *H neanderthalensis* are also endogenous to him.

Is Red also a member of the **set** *H neanderthalensis*? Here we equivocate upon the notion of phenomenal aggregates. Red is certainly not contemporaneous with his putative conspecifics, but there is nothing in a simple notion of set extension to rule him in or out, either. And so forth – depending on what relation criteria are used for inclusion or exclusion, Red is, or is not, or cannot be said clearly to be, a *H neanderthalensis* specimen. *Mutatis mutandis*, Red will also be, not be, or be vaguely or indefinitely, human, or mammalian, and so on.

In the normal course of biological systematics, taxonomy, and classification in general, there are no such difficulties. Animal taxonomists identify species without trouble, plant taxonomist identify species with a bit more ambiguity, bacterial and viral taxono-

13. Jo Assher notes in conversation that this raises a "grue" problem – the predicates of the class must be projectable. This is not merely a thought experiment, since the defining characters of species often turn out not to be projectable – the classic example is "swans are white". A better example is *Arctocephalis pusillus*, the "little" South African Fur Seal, which grows to around 2.5m and can weigh as much as 350kg. The holotype was a pup. See also (Griffiths, In press, 1999).

14. The use of the computer overcomes the objection that a physical contiguity between the mummified Neandertal and Red makes Red the descendent of the mummy. Inasmuch as information must be stored physically, there is contiguity, but not of the kind that automatically licenses species inclusion. I am grateful to Michael Ghiselin for this point.

15. Ruse mentions revived dinosaurs to bolster his arguments in his 1998.

mists make discriminations about strains and taxa (quasispecies) all the time. Red is an interesting case just *because* he tests “intuitions” developed in the normal course of events. When we leave Kansas for Oz, we soon reassess our intuitions and common-sense assumptions. When Ruse challenges the SAI thesis on the basis of *his* intuitions, he is ignoring the exceptional cases, which, however, turn out to be a lot less exceptional than one might expect if we are working from folk taxonomy – what “everybody knows” about living kinds (Atran 1990).

Abstract and ordinary cats

In his theory of abstract metaphysical objects (ZAO), Zalta (1983, 1988, unpublished) distinguishes between ordinary and abstract objects. Being *ordinary* (“O!”) is the state of being possibly located in spacetime – that is, of having boundary coordinates, while being *abstract* (“A!”) is not to be possibly located in spacetime:

$$O! =_{df} [\lambda \hat{\diamond} E! . x] \quad [1]$$

$$A! =_{df} [\lambda \neg \hat{\diamond} E! . x] \quad [2]$$

where “ λ ” is a predicate of complex n -place relations and “E!” denotes the state of being concrete, that is, located in spacetime. This is tolerably close to the Ghiselin-Hull claim that individuals are spatiotemporally restricted and classes are not. No object is both ordinary and abstract and every object is either one or the other. Ordinary objects *exemplify*, or *instantiate*, properties, while abstract objects *encode* them. Zero-place λ relations, or predicates, range over the domain of propositions. In this formalisation, an extension of Zermelo-Frankl set theory (ZF), relations without variables generate propositions; with free variables they generate classes; with bound variables they generate sets.¹⁶

In ZF, the appropriate “gathering” relationship for sets is “membership” (\in), for classes it is “inclusion” (\subset or \subseteq) and we can add that for individuals it is “part of a whole”¹⁷ (Hull 1976, 1980, 1988, 1992, Ghiselin 1974, 1997, Pollock 1990). Lewis defines a set as either a class that has (includes) a singleton, or as the null set. *Singletons* are unit sets, ie, those containing one member. Proper classes for Lewis have no singletons as members. Something is a *part* of some other thing iff it is *included* in that other thing. *Membership* pertains to classes *sensu* Zalta, while *parthood* pertains to sets *sensu* Zalta.

16. Sets are either extensional or intensional; the latter are classes, but as we observed above, to avoid the Russell paradox, not all sets are classes and vice versa. The class of all objects (the universe of discourse) and the class of all sets are proper classes (classes that are not sets). According to Machover (theorem 1.3.10), in ZF a proper class is not an object and therefore cannot be a member of any class. In ZF, an individual is not a set and has no member objects (Machover 1996: 13). In the ZF universe of discourse, the objects are either sets or individuals (ibid, 16): “Classes are admitted as extensions of properties: if P is a definite property of objects, then we admit the class $A = \{x: Px\}$ to say that $a \in A$ is just another way to say that Pa (the object a has the property P).

17. Mahner and Bunge (1997: 25) introduce the part operator \sqsubset in their mereology, where $\{x \mid x \sqsubset s\}$ is the *composition*, or *constituent class* of a concrete system s .

Under neither system must classes that are Zalta sets (ie, not proper classes) have any kind of coherence, cohesion or functional composition. This is significant for those criticisms of the SAI that require individuality to be integrated. This is why I mean by “class” that it is defined by intension, and an ordinary set that it is delimited by extension.

In this essay, the terms “class”, “set”, “individual” are not used exactly as they are in standard logic, mainly because it suited me to pick the eyes out of those definitions that are implicit or required in the biological debate. So, I mean by a *class* a set of propositions or properties or predicates. Others have their own idiom: Lewis (Lewis 1991) defines a *proper class* as anything that does not have an individual as a part. I prefer to treat “classes” as a sort of set, as Zalta does, rather than a set as a sort of class as Lewis does, because I am interested in the problems of grouping concrete (biological) objects – Lewis’ individuals – under abstract objects (Lewis’ classes). In Lewis’ terminology, proper classes have only classes as members, not individuals. Under Zalta’s theory, classes are objects that have zero-place predicates (propositions). In both interpretations, species are not proper classes under the standard interpretations in taxonomy. It matters little if we use the terms “individual” or “concrete object”, except that Zalta’s approach makes the point more directly. Lewis defines an *individual* as unmembered objects of Reality¹⁸, or “fusions” of unmembered objects, which transports the notion of spatiotemporality in any case. So I am not being technically exact in how these and other terms are used here. It seems to me that Lewis’ and Zalta’s treatments can be turned to the same general conclusions in the biological arena.

Zalta’s ontology of abstract objects rests on a division of the domain of discourse (Lewis’ Reality) into sets and objects, with the proviso that sets can be, but need not be, objects and vice versa. Lewis expresses this as his Division Thesis:

Division Thesis: Reality divides exhaustively into individuals and classes; in other words, everything is an individual, a class, or a mixed fusion of individuals and classes. (p99)

Bearing in mind that for Lewis “individuals” are atoms of Reality or fusions of atoms, we might investigate the possibility that species are mixed fusions of classes (set or class in ZF/Zalta) and individuals. However, I do not see how to proceed with that idea.

Let us now consider the various group properties attributed to natural taxa in general and species in particular.

The SAI thesis has as its basic initial insight that species *are* spatiotemporally bounded groups of objects. In ZAO terms, they are sets of ordinary objects. If the sets are extensionally defined (for instance, as just those objects that are contiguously related by lineal descent, which requires exogenous n -place properties¹⁹ where $n \geq 2$) then the

18. The fusion, or sum, of all individuals, in (Lewis 1991).

sets are ordinary complex objects. If the sets are intensionally defined as just those objects that satisfy some criteria $F1 \dots Fn$ (where n is ≥ 1) then the sets are not ordinary objects but are instead classes, where the functions F happen to denote. If taxa are sets, then they may contain objects. Taxa as sets may be objects but they are not individuals. Taxa as individuals have no members, but they are still objects.

To illustrate: I am the **set** of all my cells. I am the **class** of all genetically monophyletic cells (ie, which have the properties of genetic identity and lineal descendancy) derived from a fertilised oocyte. I am also an **individual** (indivisible object) in one domain of discourse. In another, I am a group object (a set). Objects bear properties. Individuals bear properties primitively, while sets bear them compositionally, from the properties of their parts. How I am characterised – as a bearer of primitive or compositional properties – is a matter of the universe of the discourse.

Species (taxa) have some properties primitively: ranges, durations, variability, resistance to extinction. They have some other properties compositionally: the typical member is thus and so (fast, long, adapted, has a certain developmental system, etc)²⁰. However, it should be clearly understood that their phenotypic properties are properties of organisms not taxa. Organisms and taxa change in different ways: organisms develop through a life-cycle, while taxa evolve through gradual change (anagenesis), splitting (cladogenesis), and movement (allopatry, demic isolation, drift). Relative to the domain of lifecycles, for example, organisms exhibit particular dynamics and trajectories through the metric of the discourse. They can be points in a fuzzy set, or even in a polyphyletic set. And if populations can merge to form novel populations (as in the case of allopolyploidy in plants), then organisms can even form paraphyletic sets. Organisms themselves, though, are always monophyletic.²¹

The “gathering” relations above have to do with the way we are treating biological classes and groups. It is appropriate to be more exact now. Concrete objects are members of abstract classes only if there is some abstract object in the class that denotes, or maps on to, that concrete object and only that concrete object. This is what Lewis calls the singleton of that object – the set of which that object is the only

19. Such as “is descended from” or “is parent to”.

20. Cf. Williams’ 1966 distinction between fleet groups of deer and groups of fleet deer.

21. This is not really so clearly true (cf Nelson 1989). Organisms shed dead and living cells. Moreover, in one famous case – HeLa cells – cells from a single organism (Mrs Henrietta Lacks, a sufferer from cervical cancer in the 1960s) not only live on after her but now reproduce in the “wild”, in the cell cultures of cancer laboratories the world over (often unintentionally). This goes to bolster the claim that individuality is not an intuitively simple idea in biology. Either HeLa cells are a new genus, or even phylum, in which case *H sapiens* is a polyphyletic taxon (that is, not a natural taxon on cladistic criteria) along with all the taxa it is part of (eg, Mammalia) or HeLa cells are members of the *H sapiens* taxon, a “counterintuitive” result if there ever were one.

member. If we visualise the matter as follows, it might make the connection to biology clearer:

Lewis' cat Possum is the sole member of the set of all objects that are Lewis' cat Possum. There is an abstract object ("Possum") consisting of three predicates – {*is called uniquely Possum, is a cat, belongs to Lewis*} of which the concrete object Possum is the sole and only possible member. Having the predicate *is a cat* as part of the definiens of that singleton set means that it (the singleton) is also a member of the set "Cats", and so Possum is one of a number of actual objects that are denoted by singletons in "Cats". So, this predicate *is a cat* explodes out to the definienda of the set "Cat", and the singleton set "Possum" is a member of the set "Cats". Is the actual concrete object Possum a member of the abstract set "Cats"? Not on Zalta's account, for the abstract set "Cats" comprises predicates (abstract objects) not pussycats (concrete objects). If "Cats" is named *Felis domesticus*, then "Possum" is a member of it, but Possum is not (Figure 1)

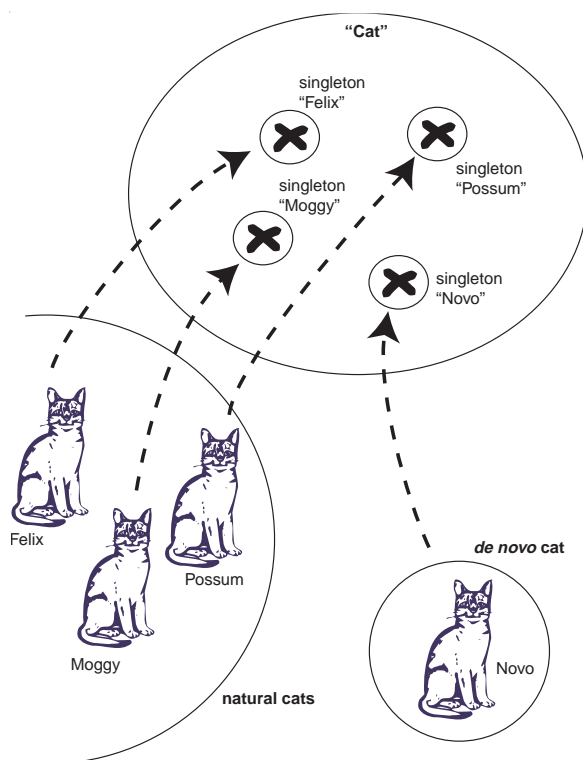


Figure 1 – Old Possum's Set of Natural Cats, and the set of de novo Cats

This would mean that the set of all cats (actual snarling, purring, reproducing cats) is not identical with the proper set *Felis domesticus*. Suppose the obligatory demon – a super scientist, alien intelligence, djinn, or movie producer – creates an object *de novo* that is in all respects save history a Cat; that is, it satisfies all predicates contained within *is a cat*. This, congruent with Ruse's intuition, would *be* a Cat because its single-

ton would be a member of “Cats”. However, it would not be a member of the set of cats, not being reproductively, that is, concretely and causally, connected to any actual cat.

We might extend the set “Cats” to include *de novo* cats, but to do this would make the abstract class prior to the concrete set – a form of idealism which has abandoned pretensions to natural classification and grouping in favour of arbitrary or conceptual classification (cf Mahner and Bunge 1997, who seem to take this approach explicitly).

We therefore are presented with the following mutually exclusive alternatives: classify natural groups, or treat taxa as classes. Short of taking Mahner and Bunge’s approach, which they call Conceptualism, we must treat taxa as sets, and therefore on appropriate occasions, as individuals.

How classes can change

But suppose that we persist in calling taxa classes. A recurring objection to the notion that classes are the correct metaphysical category to cover species is that species evolve, and classes do not. A species' set of characters is always in a state of some change, while classes may only change their extensions, and not their intensions. It will not do, as Gasking did, to think that because the *members* of a set change, that the set changes. No matter how many singletons are included in "Cats" or how they may be replaced, the predicate *is a cat* and its defining criteria do not change. But perhaps there is a way in which we can allow change from one class to another. Let us treat it as the replacement of criteria, or predicates in the case of a class, and of objects in the case of a simple set.

If we allow that classes and sets can change, what is the process, function or relationship between antecessor and successor classes? The succession relationship may be temporal, but it must involve some transformation function before we can count it as segments of a sequence, temporal or otherwise. Let us call this the *delta transformation* of class A into class B and represent it as $\partial(\{A\} \rightarrow \{B\})$ ²². This transformation may consist of *replacement* of predicates of A by predicates of B, or of *modification* of predicates of A to form B, either by varying the scope, value or modality of A-predicates, or by adding predicates to or eliding predicates from A to form B. Class A transforms into class B by the operation of some ∂ , and the distance between A and B is the modulus of the difference: in information theory and taxonomy this is called the *Hamming distance*, although it is usually calculated as the difference in integer values (mostly presence/absence) rather than real values.

To specify the transformation (but not necessarily to specify the function that describes that transformation) we require a common metric for all predicates of both classes. In the usual case of presence/absence instance matrices, each trait or property is some objectively measurable phenomenal property, which can be marked as present above some value or absent below it ("long" and "short" being examples). It doesn't matter if the defining predicates of the class include the reaction threshold to some antigen marker, the mean length of a feather, or some gross morphological or behavioural trait (such as "stotting" behaviour), so long as they can be marked commensurately between taxa or organisms as present or absent. The binary state is the common metric. In the case of the "DNA code", sequences are commensurate because the "encoding protocol" is effectively (but not quite universally) imposed on the analysis. However, no matter what the categories and their alternate states may be, the result is a message string, one that is presented to analysis as a row in a matrix (figure 2).

22. I am indebted to Allen Hazen for this suggestion

Hamming distance is the modulus of the number of single state changes required to transform one message string into another message string – that is, the absolute minimum number of changes between the two strings. It can be expressed as the bit difference between the original and transformed message, although such characterisations tend to confuse more than elucidate. In taxonomy it is the number of trait differences, and in molecular genetics the number of point mutations in a nucleotide sequence. More broadly, in molecular biology it can also be applied to the amino-acids that make up protein primary structures. It is, in other words, a generalised notion of measurable difference.

Once the objects under study are described by the relevant instance matrix (a matrix formed by aligning the message sequences, figure 2, from Wiley, *et al* 1991), then a relationship diagram known as a Wagner groundplan divergence tree is drawn (figure 3, from Wiley, *et al* 1991). Through the choice of an outgroup in the matrix (ie, the message that is known or most likely to be least related), this tree is then “rooted” to form a cladogram (figure 4, from Wiley, *et al* 1991).

Figure 2: An instance matrix

Taxon	Transformation series						
	1	2	3	4	5	6	7
X (outgroup)	0	0	0	0	0	0	0
A	1	1	0	0	0	0	0
B	1	1	1	1	0	0	0
C	1	1	1	1	1	1	1

Figure 3: A Wagner groundplan divergence diagram, or unrooted tree

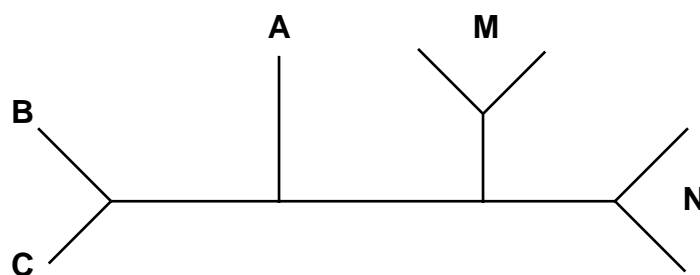


Figure 4: A cladogram, or rooted tree.

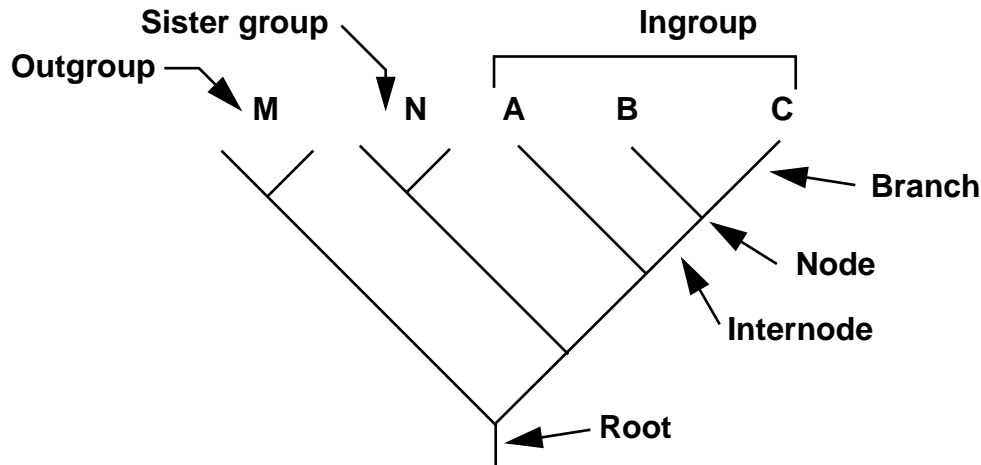
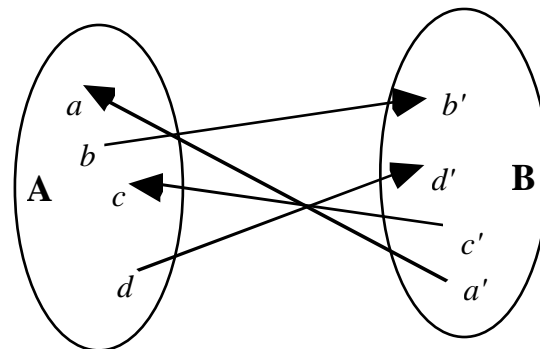


Figure 5: Differences between sequences in an instance matrix (using DNA symbols)

	A	B	C	D	...	W	X	...
Seq1	A	G	-	T	...	G	T	...
Seq2	A	C	C	-	...	G	T	...

Figure 6: Hamming distance of 4 between unordered sets



When two messages are aligned²³, any given *locus* in the strings will exemplify one of the following delta relations between the messages: they will be the same (figure 5, locus A), they will be different (figure 5, locus B), a locus will have been inserted (figure 5, locus C) or deleted (figure 5, locus D). This is clearest when the array of the string is simple and linear (ie, an ordered set), as it is in nucleotide sequences, but it can be represented as the transformation between two unordered sets (figure 6), so long as we can identify the homologies (the loci of the message strings) on other grounds, itself a form of ordering.²⁴

23. Elisions and additions in nucleotide sequences are determined by isomorphisms further down or up stream from the matched sequence (columns W and X in figure 5). In this simple example, we would be justified in saying that a T had changed to a C at the third locus, if Seq1 were the earlier of the two sequences and those isomorphisms did not exist.

24. Arrived at in figure 4 by the upstream homologies at W and X

If these delta transformations occur between classes, the members of the loci are predicates, if between sets, objects of the set. We therefore have, in addition to identity ($A = B$, Hamming distance of 0), the following formal delta relations between classes (*m.m.* between sets if objects are changed instead of predicates):

- 1 $\partial(A \xrightarrow{n} B)$ A expands to B (n predicates difference/Hamming distance)
- 2 $\partial(A \xleftarrow{n} B)$ A elides to B (n predicates difference/Hamming distance)
- 3 $\partial(A \xrightarrow{m} \xleftarrow{n} B)$ m A predicates are elided and n B predicates are added ($m + n$ Hamming distance)

The *replacement* of an A predicate with a B predicate is clearly a special case of 3.

- 4 $\partial(A \xrightarrow{1} \xleftarrow{1} B)$ One A predicate is elided and one B predicate is added

There is also the case in which a predicate is slightly or greatly modified, but this just resolves to case 4, for if whether modification had occurred were not already at issue then we could simply stipulate that it was the “same” predicate. What this overlooks is the question of differences at the same locus in an ordered class. In an unordered class, or a partially ordered class where the predicates in question are not ordered, the Hamming distance is just the number of different predicates. In an ordered class, delta transformation 4 has a Hamming distance of 1 if the predicates occupy the same locus in the string, and 2 if they occupy different loci, and this affects transformation of types 1, 2 and 3 as well. Since the delta relation is asymmetric, we must be able to ascertain which is the “original” and the “later” sequence, or, in the Greek stems from which the terminology of phylogenetic systematics is constructed, which is the *plesion* (the primitive state) and which is the *apon* (derived state). Since cladistic instance matrices tend to be based on structural states (morphs), these are usually referred to as *plesiomorphs* and *apomorphs* respectively. In the usual course of events, the instance matrices of taxonomy are comprised of discrete values in each state locus (the “character code”) and the “direction” of change is called the *transformation series* (Wiley *et al.* 1991).²⁵ A transformation series that has a recognisable direction is termed *polarised*.

By generating a Wagner tree from the Hamming distances of a polarised transformation series (where the plesiomorphic row and apomorphic rows are predetermined) a classification follows. However, if the values are reals – that is, if there is some arbitrary precision or granularity – and the differences are imperceptible at different stages of the transformation (as in the case of anagenesis), then we cannot generate a *natural*

25. In Hennigian cladism, this transformation series is of course the time series of the change of state from plesiomorph to apomorph. This assumption is not made in pattern cladism.

classification, because any choice of end states is arbitrary. By this I mean that if we have discrete states in the instance matrix, like Galton's polyhedron that is stable in discrete phases but not intermediate phases, then each discrete state is an objective measuring point (which is why the DNA code generally works well as data).

If, on the other hand, we have a gradual differential (Darwin's "insensible series" of gradation between the incipient species of geographic variants and proper species), then the choice of points to measure against are arbitrary and so is the classification. Considerations such as these led some to argue that classifications may only be what Mayr called "non-dimensional": classifications at one time and restricted to a given geographical location (the *generic-speciemes* of Atran 1990), for otherwise (if all characters used as differentiae are gradually differentiated) all classifications are arbitrary, and therefore subjective, because the classes are arbitrary. This needs explication.

A biological class cannot be generated a priori – we cannot specify natural kinds as we will, because indefinitely many classes can be generated from indefinitely many possible collections of predicates. A class is generated by definition – the defining predicates (key predicates or characters) are stipulated. If at two points of a transformation certain predicates are deemed to differ indiscernably (they are effectively identical) then these predicates might be stipulated as keys for the class, and the transformation distance will be very low, giving a close relationship. Alternately, keys that differ greatly may be stipulated giving a large transformation distance. In either case, the classification may or may not be accurate, that is, natural. This is effectively the reason why phenetics (or numerical taxonomy) failed and why discrete data is used in cladistic taxonomy (but see Rae 1998).

Conclusion: Are species natural kinds?

Ruse wants to make species natural kinds, along with some others (eg, Mahner and Bunge 1997). Rosenberg 1993 and Dupré 1994, also take species to be natural kinds, although of a limited kind that are involved in low-level laws and generalisations]. In order to do this, Ruse, and Mahner and Bunge, characterise them as classes (but Rosenberg and Dupré do not) and therefore as abstract objects. However, it cannot be said that the aggregates of all individual organisms of a species are a class. These are just a set, because the objects incorporated in the aggregate are not predicates; that is, they do not encode properties, they exemplify them.

Specimens (even type specimens that ostensibly define a species) are not *members* of a class, they are at most *realisations* of one. This is non-standard in taxonomy, but consistent with ZF and ZAO. Taxa as aggregates are not categories, which is well understood by Mayr and Hull. These objects form the extension of the class of categories that might define the species.

Of course, accepting species as Z-F classes would also commit us to accepting that no one of us is a *member* of the class *H sapiens* (or perhaps that *H sapiens* is the name of an aggregate, and not a species, if species are classes). So, if the preliminary question is “Are the species of competent taxonomists classes?” then the answer is simply that they are not. Perhaps it would be better to use a different term – just to bite the bullet that species and natural kinds are two entirely different concepts.

The more subtle question “Are species defined by classes of concepts?” is still open to discussion. I think that it is a real alternative only if a class can be construed as a polythetic cluster of zero-place λ relational predicates (because most species are polymorphic; that is, they have many characters that are distributed multimodally). Species would then be fuzzy sets of abstract objects that satisfied all or most of the n -place λ relations defined by the predicates of the class. So, the SAI stands, in my view. It is the only way to conceive of evolutionary aggregates, although I would assert that it is not as individuals but as spacetime objects that species must be conceived, and individuality follows only if one’s metaphysics requires such objects to be individuals.

I do not think this requires arbitrary pluralism about species concepts. In each domain of discourse there appears to be a single basal taxon-type. The nature of taxa are context and discourse relative, but it seems that basal taxa generally exist at or about the same general level in the different biological hierarchies imposed by the different domains of discourse. What I am arguing is that the taxa of the classification of biological organisms are quite distinct and disjoint from the semantic, abstract, classes of definition.

Moreover, classes can change with the appropriate transformation relations only in the context of a common metric, and I do not think that “class” is an adequate way to characterise the evolving objects we call species. Although Gasking (1960), for example, thought that classes **could** change, he made it clear that he meant that the “members” of the class – the ordinary objects that instantiate the properties of the class – are replaced and added to, while the classes themselves remain as they were. But biological sets, especially cluster sets, change all the time.

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