

MODULARITY AND MEREOLOGY

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ABSTRACT

In the first section, ‘Morphology and Classification’, I give a brief account of the history of morphology and classification, examining the philosophical and theoretical basis of these disciplines. I criticise Darwin’s contribution, questioning whether the explanations he gives in *The Origin of Species* are valid. I favour the cladistic theory of classification, which rejects the need for evolutionary assumptions.

In ‘Genes and Modules’, I reject neo-Darwinism’s materialistic emphasis on genes. Nucleic acid genes rely on the infrastructure of the cell to carry out their role as replicators. The cell is a modular system of bounded compartments, on which the whole delicate balance of metabolism relies.

In ‘Parts and Wholes’, I contrast the mereology of Darwin with that of cladistics: historical groups comprising ancestor and descendants vs. relationships of organisms comprising common characters. These considerations of mereology lead on to a discussion of the appropriate theoretical basis of morphology and classification. In ‘Specifications and Instances’, I suggest such a basis is to be found in category theory.

1. MORPHOLOGY AND CLASSIFICATION

Pierre Belon, in his *La Nature des Oyseaux* (1555), places a skeleton of a bird alongside the skeleton of a human being. He shows that many of the bones in the two skeletons correspond and can be given the same names. This is simply a pragmatic exercise, he says, to save time explaining the parts (I, ch. 12, p. 38). It is easier to discuss the anatomy of a bird, if we follow the same plan as in human anatomy (I, ch. 12, p. 39). The parts of the bird and the human correspond, but nothing is said of the relationship of birds and humans themselves. Belon is dealing solely with morphology—comparative anatomy—rather than classification.

Carolus Linnaeus, the great eighteenth century Swedish naturalist, is hailed as the father of modern classification. He describes six classes of animals, namely mammals, birds, batrachians (reptiles and amphibians), fishes, insects and worms. With Linnaeus, comparisons do not simply yield a pragmatic scheme; they reveal the inner design of nature itself. Each class is a rung on the ladder of perfection, the *scala naturae*, starting at the worms and rising to the highest of animals, Man. Birds carry some of the perfect characters of mammals, but not all. They correspond in many ways, but they occupy one rung lower down on the ladder than mammals.

The classification of animals without backbones has changed much since Linnaeus' time. The arrangement of backboned animals, excepting the split of the batrachians, has changed little until recently and remains the popular understanding. Fishes are cold-blooded, have scaly skins and lay eggs in the water. Amphibians live out of the water but must return to lay their eggs. Reptiles have a watertight skin and watertight eggs, and are thus able to live entirely on land. Birds and mammals are warm-blooded, birds being covered by a protective layer of feathers and mammals by fur. Birds have the power of flight. Most mammals bear live young that they continue to nourish by suckling. If we arrange nature as a scale of perfection, then it makes sense to classify living beings partly by the presence of characters, marking their perfection, and partly by the absence of characters, signifying imperfection. Thus, fishes are all backboned animals except amphibians, reptiles, birds and animals. They live permanently in water and do not have four limbs. They lack the characters of their increasingly perfect cousins.

Towards the end of the eighteenth century, Johann Wolfgang von Goethe applies a very different approach to living things. He looks not for perfection and imperfection, but for unity. He sees in individual plants, the One Plant that brings forth the many and yet remains always itself. The plants in their organs, leaf, stem and root, emerge as a multiplicity from the unity of the leaf. Looking one day on the shattered skull of a sheep, he sees a unity among the backboned animals: they are transformed vertebrae. Goethe's followers, Carl Gustav Carus (1828) and Richard Owen (1848) develop the type of all backboned animals (see Figure 1). The archetype is a series of vertebrae repeated along the long axis of the body. Simply, the unity of type is a common architectural plan, or *Bauplan*. Thus, we may recognise common elements in the type through their relative positions: 'The archetype skeleton represents the idea of a series of essentially similar segments succeeding each other in the axis of the body; such segments being composed of parts similar in

number and arrangement' (Owen, 1866: xiii). Geoffroy Saint-Hilaire (1818) understands the ear ossicles—the bones that lie in the middle ear in mammals, namely the malleus, incus and stapes—as the same as the opercular bones—the bones that cover the gills in fishes. Both lie behind the lower jaw and below the ear region of the braincase. Today, we would not accept Geoffroy's conclusion, but instead a similar one, made by Reichert in 1837. The ear ossicles correspond to bones at the back of the lower jaw, in fact lying beneath the opercular bones, namely the articular, the quadrate and the hyomandibular. Geoffroy espouses a principle of the constancy of relative position and connections. The generative process acts in such a way as to preserve the connections of elements invariant. A more subtle understanding of unity of type is therefore a unity of generative principle. Common plan manifests from common process, as an invariant. The generative principle is the source of multiplicity, not in a historical but in a rational, imaginative sense.

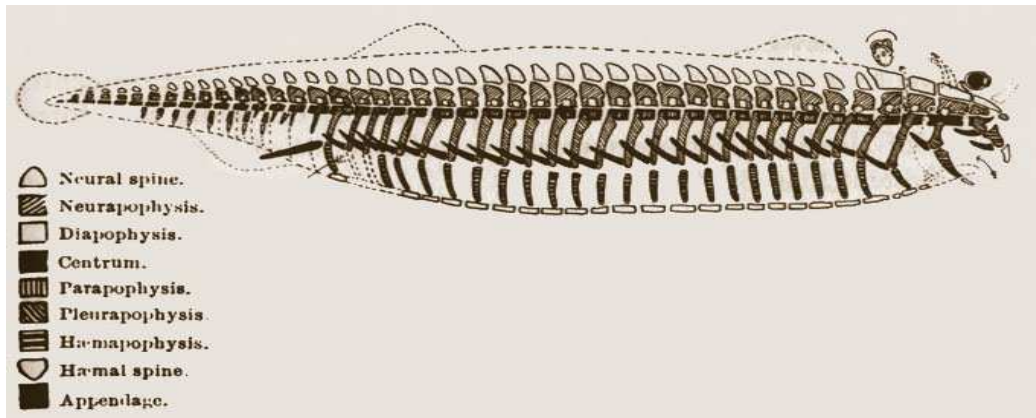


Figure 1: The vertebrate archetype from Owen (1848), constructed as a series of vertebrae.

Unity of type among living things of different modes of life is morphology's great claim. (The term 'morphology' owes to Goethe.) Darwin seeks to explain unity of type, in the thirteenth chapter of *The Origin of Species*. 'What can be more curious than that the hand of man, formed for grasping, that of a mole for digging, the leg of the horse, the paddle of the porpoise, and the wing of the bat, should be all constructed on the same pattern, and should include the same bones, in the same relative positions' (Darwin, 1859 [1968: 415]). The mole lives underground, the horse above it; the porpoise lives in the sea and the bat in the air. Yet, we may discern the same pattern of bones among these animals adapted to such different lifestyles. Darwin's explanation for the common plan lies not in a common generative principle but in a common historical origin. 'If we suppose that the ancient progenitor, the archetype as it may be called, of all mammals, had its limbs constructed on the

existing general pattern, for whatever purpose they served, we can at once perceive the plain signification of the homologous construction of the limbs throughout the whole class' (*loc. cit.*, p.416).

Morphological classification reveals a hierarchy of types within types, so for example, mammals are vertebrates and vertebrates are animals. Classification is 'the grand fact in natural history of the subordination of group under group, which, from its familiarity does not sufficiently strike us' (*loc cit.*, p.398). Darwin's explanation of classification is common descent: 'descent is the hidden bond of connexion which naturalists have sought' (*loc. cit.*, p.414). Humans, moles, horses, porpoises and bats are all descended from the common ancestral mammal, yet have all undergone modifications for adaptation to different modes of life. This is Darwin's theory of descent with modification caused by natural selection.

In a more modern classification of the backboned animals (Forey, pp. 30-31, pp. 128-143, in Burn, 1980), there are ten classes, six of which are devoted to fishes. The different types of fishes are as different from each other as they are from amphibians, reptiles, birds and mammals. The features that some fishes lack are striking. Hagfishes lack a fully developed backbone, instead the notochord, which is normally the embryonic precursor of the backbone, remains in the adult to form the main means of bodily support. (Indeed, hagfishes lie outside the backboned animals, and to include them we should talk of the craniates, animals with skulls.) Bone and cartilage are alien to the earliest fossil forms, the heterostracans. They have a different kind of skeletal tissue, aspidin, which lacks cells. Hagfishes, lampreys and the extinct heterostracans do not have jaws. Instead, hagfishes and lampreys have a muscular tongue with which they rasp at their prey, sucking blood. Neither do these three have paired fins, which arrive with another jawless group, the extinct cephalaspidomorphs. (For a fuller discussion, see Forey and Janvier, 1993, and the section on craniates at the Tree of Life website, <http://tolweb.org/tree?group=Craniata&contgroup=Chordata>).

The features that some fishes share with the tetrapods, or four-legged vertebrates, are just as surprising. Lungfishes cannot breathe in water. If they are held under water, they will drown. Young lungfishes have external gills, just like young amphibians. In the same way as amphibians, they lose their gills and gas exchange then takes place at the lungs. Lungfishes possess a double circulation, just like we do, blood from one half of the heart supplying the lungs, blood from the other half supplying the rest of the body. Look, next time you go to the aquarium at London Zoo. You may see a lungfish rise to the surface to breathe!

How have scientists arrived at the conclusions summarised above? Let's look at the modern process of classification. The data of classification are the characters. Examining a study group, the systematist will make a list of characters and their states, scoring the specimens in the study group as to which state they possess. Through some method, usually codified in a mathematical algorithm, such scorings are converted into the classification.

Willi Hennig's method is based on Darwin's theory of descent with modification: 'Evolution is a transformation of organisms in form and mode of life through which the descendants become different from their ancestors' (Zimmerman, quoted in Hennig, 1966: 88). Limbs are transformed fins; fins are primitive, yet limbs are derived. Fishes share the primitive character, fins, whereas tetrapods share the derived character. In Hennig's method, only the tetrapods are a genuine historical group; the fishes are not.

Consider the salmon, the lungfish and the cow. The cow may seem the most different, and the salmon and the lungfish most similar. However, as we have seen, the lungfish shares derived characters with the tetrapods that are not found in the salmon. The external gills and the two-chambered heart are the most striking. Other characters that the lungfish and the salmon have in common, such as paired fins not legs, and cold not warm blood, are primitive characters (see also Gee, 2000).

Hennig explicitly ties his method to a model of the evolutionary process. The derived characters of the lungfish and the cow are hypothesised to have appeared in their ancestral species. The lungfish shares a more recent common ancestor with the cow than with the salmon. The species ancestral to all three split to give rise to the salmon and to the ancestral species of the lungfish and the cow. 'Evolution in this sense (transformation) is also connected with speciation: if a species (reproductive community) is split into two mutually isolated communities of reproduction ... there is always a change (transformation) of at least one character of the ancestral species in at least one of the daughter species' (Hennig, 1966: 88). Hennig's method generates binary classifications: at every fork, two branches result. The two branches so formed are 'sister groups' (Hennig, 1966: 139).

For Hennig, morphology is not enough for classification. We need to add the tenet of descent with modification, of the evolutionary transformation of characters. Why are morphological correspondences—special homologies—not enough? Hennig answers that evolutionary

transformations involve the loss, not only the gain, of features. 'In general, we speak only of the homology of organs, but a "character" may also be the absence of an organ' (Hennig, 1966: 95). The absence of wings in silverfish and springtails is a shared primitive character, whereas the absence of wings in fleas and lice is shared derived. 'This cannot be expressed in an equally unequivocal way by saying that the absence of wings is a "special homology"' in the fleas and lice, but not in springtails and silverfish.

Fleas are 'a well-defined and homogeneous group', according to Davies (p. 146 in Burton, 1980). 'They are wingless, with a brown, bristly, strongly sclerotised body compressed from side to side. Their eyes are greatly reduced and the antennae are short but the legs are well developed and in many species the hind pair is used for jumping.' To be a flea is not simply to be wingless, but to have a compressed body, short antennae and well-developed legs. We classify them together because of these positive characters. Fleas undergo complete metamorphosis (holometaboly), where they pass through a pupal stage between larva and adult. In the pupa, the larval tissues die and break down, and the adult tissues grow from special zones of persistently embryonic tissues, known as the imaginal discs. Since most insects that completely metamorphose have wings, then it is likely that fleas have lost their wings. The position of fleas within the winged insects is based on characters they possess, not on characters they lack. The fact that fleas lack wings just makes the business of classification more frustrating.

Norman Platnick applies a similar argument to the absence of limbs in fishes: 'if we form a group Pisces, we have based it not on a character, but on the absence of a character. The group Pisces includes those organisms with fins that also happen to lack modified fins (limbs). Such use of the absence of a character is one of the hallmarks of an artificial group' (Platnick, 1980: 544). Paired appendages unite the cephalospidomorph fishes with the gnathostomes (backboned animals with jaws). Tetrapods have these paired appendages manifesting as limbs and are one type of gnathostome. Sharks, lungfishes and codfishes are others. There is level in the hierarchy of types where the presence of paired appendages is relevant: allying the cephalospidomorphs with gnathostomes and not, for example, the lampreys or the hagfish. However, with the Cephalospidomorpha + Gnathostomata, we cannot pull together as Pisces all those animals which have paired appendages but not limbs. In this context, the presence of paired appendages is no longer relevant. Colin Patterson (1982) points that every shared primitive

character is just a shared derived character considered at the wrong hierarchical level.

Morphology is the study of the affinities between parts of organisms; classification is the study of the affinities between organisms as a whole. According to Hennig, we bridge the gap by considering transformations between corresponding parts. According to Patterson, we bridge the gap simply by considering the hierarchical level of correspondences. Every homology is a shared derived character somewhere in the hierarchy of life. We either assume a *process* of transformation, or a hierarchically branching *pattern*. Cladistics is the study of branching diagrams (Nelson 1979) and the approach of Nelson, Platnick and Patterson is known as pattern cladistics.

2. GENES AND MODULES

There are difficulties in morphological classification, in the delimitation and correlation of characters, which have led some systematists to genetics instead. Where does one character start and another stop? Do we consider a suite of features, which make up a coherent functional whole, one character or many? What are the dependencies between the states of one character and the states of another? These correlations could be functional or pleiotropic. For example, all the different adaptations to endothermy (“warm-bloodedness”) in birds and mammals are functionally correlated, whereas a mutation that causes both blindness and a deformity of the skeleton in mice is known as a pleiotropic correlation.

Much of the literature on morphological classification deals with disagreements over the conceptualisation of characters. Often such disagreements arise because living things vary continuously rather than discretely. Many of the algorithms employed for morphological classification require discrete characters. So, systematists need to find a way to divide the range of continuous variation into a number of relatively distinct states. Also, the processes of morphological change are only just becoming understood. How can we classify when we know so little about the possibilities of character state transformation? For example, we may reason that it is unlikely that lice and fleas are unlikely to be related by the loss of wings, because in evolution it is easier to destroy than to create (Mayr, 1942: 278-279). However, it would be better if we had a testable model of morphological change to back up such reasoning.

What about gene sequences? Do we have more success here? The base pair is the character and it is possible to construct tractable, statistical models of genetic change. The model can take account of dependencies between characters. For example, base pairs in the first codon position are more likely to be constrained by function than base pairs in the third position. This is because the base pair in the third position often makes no difference to the amino acid into the ribosomes translate the gene sequence.

Base pairs are the units of replication, mutation and recombination, the material cause of genetic evolution. They are the hereditary atoms that are passed on from generation to generation, ensuring material continuity. In this mechanistic approach, statistical models of genetic change represent the efficient cause of evolution. Models may simply describe a certain probability for base pairs to be miscopied. (Imagine a machine running down.) Alternatively, models can be increased in complexity by considering the external forces of natural selection. (Imagine billiard balls pushed here and there.) So to avoid the problems with delimitation and correlation of characters we may turn to a material approach.

In Darwin's account, form is reduced to matter. Form is preserved from generation by generation, through the material connection of descent. Darwin does not say why form should be preserved from a common ancestor, and this seems a little at odds with 'descent with modification'. To explain the unity of type, we have to assume 'descent *without* modification'! If we bring natural selection into the equation, then we can say that form is preserved as long as it is not disadvantageous and removed by selection. So instead of 'descent with modification caused by natural selection', we have 'descent without modification caused by the absence of natural rejection'. Rather than explaining morphology and classification, Darwin explains them away!

We may have doubts about the present inability of a genetic approach to account for all the subtleties of morphology. Is it only a matter of time before genetics fully explains the riddles of organic form, or is there some fundamental impediment to its progress? Today all life is based on nucleic acid, but life could not have started that way. Graham Cairns Smith (1982) raises 19 objections to the synthesis of nucleic acids in the early oceans. There are difficulties with the purity, the concentration and the instability of intermediates. The replication of nucleic acids requires processes and structures that are too complex to take place outside a living cell: intricate metabolic pathways, delicately synthesised enzymes, organised structures such as ribosomes. Much more likely, life started with materials that were common in the early Earth. The origin of life

was 'low-tech' rather than 'hi-tech', unlikely to have been based on sophisticated, manufactured components.

Cairns Smith's controversial suggestion is that life started as clay crystals—replicators that were not DNA. Clay crystal layers grow one on top of another. Dislocations propagate through the crystal lattice like mutations in a lineage of bacteria. Some time after the origin of life, there was a genetic takeover, where DNA replaced clay in its role as replicator. All today's life is likely to have been descended from a common ancestor with nucleic acid as the replicator. This does not mean that all life that has ever lived replicated through nucleic acid.

Apart from being the first replicators, clay crystals would also have had to provide the first cellular morphologies. Clays are inert, not readily reacting with organic molecules in aqueous conditions. They would not have interfered with complex, drawn-out synthesis of organic molecules. Clays can form the structured compartments necessary to concentrate reactants and to purify products in a metabolic pathway. Halloysites form membranous tubes and vesicles. Zeolites and sepiolites pack together as bundles of grooved rods, with well-defined pores.

Cells and their compartments must have been present to allow DNA replicators to evolve. 'These complex structures, we are beginning to suspect, hold much of the secret of how cellular processes are controlled in both space and time: the secret may consist, at least in part, of isolating and maintaining the different cellular constituents—mainly enzymes, together with their substrates, products and modifiers (activators, inhibitors)—in different compartments; sometimes allowing, sometimes denying mutual accessibility' (Mahler and Cordes, 1971). Clays would have formed the 'glassware' for early organic reactions.

The neo-Darwinian definition of life is to replicate with error: 'We shall regard as alive any populations of entities which has the properties of multiplication, heredity and variation' (Maynard Smith, 1975). However, this cannot be the whole story. Living cells are bounded and themselves contain bounded components. This is vital to metabolism. Living cells are stable to resist error catastrophe, forestalling the build-up of deleterious errors. At the same time, favourable errors are accumulated and preserved over generations. Living cells are autonomous, bounded, stable entities, creating and maintaining the boundary between themselves and their surrounding world. 'Animals and plants are made out of homologous organelles like the mitochondria, homologous organs like the gills and lungs, homologous limbs such as

arms and wings. They are the stable holons in the evolutionary flux' (Koestler, 1967: 139).

Life is not simply a replicating system; it is an organised, modular system. Living organisation is the end of 'an ordered and structured inner movement that is essential to what things are' (Bohm, 1980: 12). Far from being explained away by theories of genetic descent, morphology, with the cell as the unit of morphology, lies at the centre of a theory of life, not DNA.

3. PARTS AND WHOLES

In the Darwinian picture, an ancestor and its descendants form a whole in the manner of an individual, with a unique origin, history and termination. The taxa discovered through classification are wholes, with organisms as their parts. If ancestry is not considered, taxa lose their claims to individuality and classifications are nothing more than diagrams of set membership (Friday, 1994). The taxa that emerge in a classification are, therefore, accidents of history. Species descended from a common ancestor form a historical group. There is no necessary—or rational—connection between them. Without common descent, the hierarchy of types is nothing more than an arbitrary nesting of sets. Ho (1990) and Goodwin (1994) complain that Darwin thus removes the scientific status of biology by replacing rational theories of biological organisation with purely historical narratives. Darwin changes the language of biology, away from talking about types—common generative principles—to historical groups of ancestral and descendant species.

Gary Nelson considers an alternative picture to Darwin. Taxa are not groups of organisms, but relationships. 'Conceived as relationships, taxa and homologies do not literally descend from one another. Taxa come into being with organisms that literally descend' (Nelson, 1989: 281)'. The unity of the tetrapod type, for example, consists in the homologies, or morphological correspondences, that tetrapods share. To justify the hypothesis of the tetrapod type, there is no need to propose that there existed a tetrapod ancestor, which possessed these features. No ancestral animals have been found and many evolutionary arguments are advanced to account for this. For example, if new species emerge in small, isolated populations, then it is unlikely that any members of the new species will die in circumstances suitable for their remains to be fossilised. The validity of the Tetrapoda does not depend on the ancestral tetrapod being found. To recognise a morphological correspondence is to make a

hypothesis, not about ancestry, but about the level in the hierarchy of life at which it applies. Every homology is part of some taxon, contributes to the unity of some type.

A horseshoe bat and I are organisms, and one of the parts of my body, my arm, is a homologue of the bat's wing. Following Darwin, we would say that the bat and I *belong* to the taxon Tetrapoda, as descendants of the ancestral tetrapod. However, Nelson says that the bat and I are *related* through the taxon Tetrapoda, and our arms/wings are related by the homology 'limbs'. This homology is part of the Tetrapoda. 'Taxa are homologies and have homologies for their parts. Organisms are homologues and have homologues for their parts' (Nelson, 1989: 279). Nelson describes homologies and taxa as 'phylogenetic parts of life', as opposed to homologues and organisms, which are 'ontogenetic parts of life'. Phylogenetic parts of life expose the hierarchical pattern of life, the pattern of common descent, if you will. Ontogenetic parts of life express the history of individual living things.

There are a number of subtle ideas here, which we will need to explore further:

1. The distinction between phylogenetic and ontogenetic parts of life, and the relationship between the two.
2. The distinction between homologies and taxa and the part-whole relationship between the two.
3. The relationship between taxa at different hierarchical levels.

All these ideas derive from Patterson (1982). To recognise a morphological correspondence is to make a hypothesis about the level in the hierarchy of life at which it applies, and thus to make a hypothesis of a taxon. My Ph.D. supervisor, Ken Joysey, commissioned this paper from Patterson. He hoped that, forced to consider the question of homology, Patterson would give up the pattern approach he had adopted from Nelson and Platnick. Instead, Joysey relates, 'Patterson gave up evolution'! In the same symposium volume, Alan Charig comments that, without evolution, pattern cladistics 'is without any proper theoretical basis' (Charig, 1982: 372). Statistics underpins genetic approaches to reconstructing evolutionary history. The likelihood of and support for a particular tree are well defined within the theory. The suggestion I make in this paper is that the appropriate mathematical language for cladistics is *category theory*, and in particular, colimits. I examine the application of category theory to hierarchies in computer science and explore its relevance to systematics.

4. SPECIFICATIONS AND INSTANCES

‘How do you build big, complicated things? Commonly, you put them together—or *configure* them—from smaller, simpler things, and this is as familiar in software development as it is in everyday life’ (Vickers and Hill, 2001: 32). This is Herbert Simon’s message (Simon, 1962), that the architecture of complexity—natural and artificial—is modular. Arthur Koestler (1967) draws extensively on Simon in his hierarchical theory of holons, which he applies to behaviour, language and morphology.

Software modules can be reused in contexts different to the one in which they originated. The internal implementation of the module can change as long as the services that it offers remain the same. Enhancements and bug fixes are limited in scope to one or a few modules. These are the principles of object- and component-oriented programming. They are related to Simon’s insight, that modular systems are more stable. Subsystems may change independently of one another, without affecting the integrity of the system.

The object-oriented programmer defines the services offered by a module as a class. The properties will generally be held internally, invisible to the outside world, and methods will be available to get and set these properties. A running program will create objects as instances of the class. Each object may have different data values, but conforms to the type of module specified in the class.

Steven Vickers and Gillian Hill address the problem of putting together systems from specified components and specified sharing. They contrast specifications with their instances. This is a very natural language to talk about classification. Taxa are specifications and organisms are instances. The horseshoe bat and I are instances of the tetrapod specification, which is composed of the homology ‘four limbs’. This defines the tetrapod type. The horseshoe bat and I possess instances of four limbs as parts of our body. Instances of homologies are homologues. Nelson’s phylogenetic parts of life are specifications; his ontogenetic parts of life are instances.

In a similar vein, Stanley Salthe reflects on the hierarchy of classification and concludes that it is a hierarchy of specifications. Hierarchies, say in ecology, are usually considered in scalar terms, where ‘components at different levels differ in size roughly by orders of magnitude ... Levels in the specification hierarchy mark the qualitative differences of different realms of being, as in ‘physical realm’ versus ‘biological realm’ (Salthe,

2001, http://www.nbi.dk/~natphil/salthe/Hierarchy_th.html). One of the tasks of the systematist, when presented with a specimen, is to give as precise a specification of its identity as possible. With fossils, which may not be complete, the identification may be carried only to family level, leaving the genus unspecified, or to genus, leaving the species unspecified. Levels in the specification hierarchy emerge in a generative process, starting with the most general and leading to the most specific. At each stage, the range of accessible states narrows irreversibly (Salthe, 1993: 64-65).

So how does category theory fit in? A category is ‘a mathematical universe’, populated with certain objects, maps between these objects, and rules for how the maps can be added together (Lawvere and Schanuel, 1998). Maps between objects are often called morphisms.

Consider specifications, X and Y , to be objects in a category C : ‘... a morphism $u: X \dashrightarrow Y$ describes how the specification X can be considered a part of Y . In consequence, an implementation—or *instance*—of Y contains somewhere inside itself an instance of X , and we shall view this *reduction* of instances of Y to those of X as the most direct manifestation of morphisms. (Note the contravariance. The natural direction of morphisms for instances is the reverse of the natural direction for the syntax of specifications.)’ (Vickers and Hill, 2001: 32)

So, in Nelson’s category of life, specifications X and Y are phylogenetic parts of life, namely homologies and taxa respectively. The implementations, or instances, of X and Y are homologues and organisms. The map u assigns a homology X to the taxon Y of which it is a part. In consequence, an instance of taxon Y contains within itself an instance of the homology X . For example, $u: \textit{four limbs} \dashrightarrow \textit{Tetrapoda}$ means that tetrapod organisms possess homologues of four limbs, whether arms, legs, wings or flippers. The language of specifications and instances, framed in category theory, captures the subtlety of Nelson’s mereology.

‘Now suppose Y_1 and Y_2 both contain X , by morphisms $u_i: X \dashrightarrow Y_i$. Then the pushout Z , a simple colimit, configures a new specification out of Y_1 and Y_2 with sharing a common part X ’ (Vickers and Hill, 2001: 33). Let’s consider a concrete example (Vickers and Hill, 2001: 43-44). *Lift* is the class of instances of lifts in an office building. *CButton* is the class whose instances are series of call buttons. There is an instance reduction from *Lift* instances to *CButton* instances. Given any lift, we can point out its call buttons and so display a *CButton* instance. The category C of primitive specifications includes the objects *Lift* and *CButton* and a map

i: *CButton* --> *Lift*. If L_1 is a lift instance, then i_1L_1 will denote its call buttons. We would like to specify a *LiftSystem* with two lifts serving the same location. Naturally, they should share the same call buttons. We have two lifts instances L_1 and L_2 and a set of call buttons B , which is common, i.e. $i_1L_1 = i_2L_2 = B$. Identifying the pattern of call buttons common to the two lifts allows us to recognise a specification hierarchy. The lifts are at level n in the hierarchy, the lift system at level $n+1$.

This is exactly Patterson's insight that the hypothesis of a morphological correspondence between instances of two taxa is equivalent to the hypothesis of a taxon at a higher level. Indeed, the two taxa are sister taxa within the newly discovered taxon.

Consider an example where there are three taxa, hagfishes, lampreys and gnathostomes, or jawed vertebrates (see Figure 2, below). Hagfishes have a skull, but no backbone or jaws. Lampreys have a skull, a backbone, but no jaws. Gnathostomes have a skull, a backbone and a pair of jaws. The homology 'backbone' shows that lampreys and gnathostomes are sister taxa. This relation identifies the Vertebrata, which emerges as the colimit. In turn, the homology 'skull' shows that vertebrates and hagfishes are sister taxa, identifying the Craniata as a further colimit. Hierarchy bridges the gap between the morphology and classification and emerges naturally from the theory of categories.

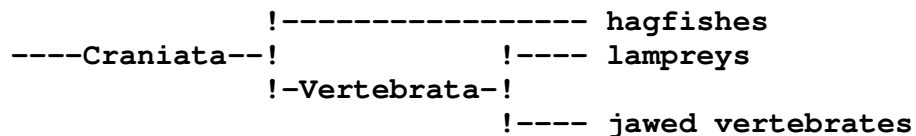


Figure 2: The classification of craniates.

So far, the algorithms employed in cladistic analysis require discrete characters. We have already mentioned that this raises a difficulty with continuous characters, which have to be split up into a number of discrete states. Ideally, data should be entered into the analysis in as raw a form as possible. Categories are abstract, wherein lies their power. If homology can be formalised in the way that the above discussion suggests, then we have a concept that applies to continuous characters as equally as to discrete characters. I am hopeful that new methods of cladistic analysis will emerge from the application of category theory.

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