

absolute space and its velocity with respect to absolute space can never be detected, it *is* possible to tell when an object is *accelerating* with respect to absolute space. For when an object rotates then it is by definition accelerating, even if the rate of rotation is constant. This is because in physics, acceleration is defined as the rate of change of velocity, and velocity is speed *in a fixed direction*. Since rotating objects are constantly changing their direction of motion, it follows that their velocity is not constant, hence they are accelerating. The water's curved surface is just one example of what are called 'inertial effects' – effects produced by accelerated motion. Another example is the feeling of being pushed to the back of your seat that you get when an aeroplane takes off. The only possible explanation of inertial effects, Newton believed, is the acceleration of the object experiencing those effects with respect to absolute space. For in a universe containing only the accelerating object, absolute space is the only thing that the acceleration could be relative to.

Newton's argument is powerful but not conclusive. For how does Newton know that the water's surface *would* curve upwards, if the rotating bucket experiment was done in a universe containing no other material objects? Newton simply assumes that the inertial effects we find in this world would remain the same in a world bereft of any other matter. This is obviously quite a substantial assumption, and many people have questioned Newton's entitlement to it. So Newton's argument does not prove the existence of absolute space. Rather, it lays down a challenge to the defender of Leibniz to provide an alternative explanation of inertial effects.

Leibniz also faces the challenge of explaining the difference between absolute and relative motion without invoking absolute space. On this problem, Leibniz wrote that a body is in true or absolute motion 'when the immediate cause of the change is in the body itself'. Recall the case of the hang-glider and the observer on earth, both of whom are in motion relative to the other. To

determine which is 'really' moving, Leibniz would say that we need to decide whether the immediate cause of the change (i.e. of the relative motion) is in the hang-glider, the observer, or both. This suggestion for how to distinguish absolute from relative motion avoids all reference to absolute space, but it is not very clear. Leibniz never properly explains what it *means* for the 'immediate cause of the change' to be in an object. But it may be that he intended to reject Newton's assumption that an object's motion, whether relative or absolute, can only be a fact about the object's relations to something else.

One of the intriguing things about the absolute/relational controversy is that it refuses to go away. Newton's account of space was intimately bound up with his physics, and Leibniz's views were a direct reaction to Newton's. So one might think that the advances in physics since the 17th century would have resolved the issue by now. But this has not happened. Although it was once widely held that Einstein's theory of relativity had decided the issue in favour of Leibniz, this view has increasingly come under attack in recent years. More than 300 years after the original Newton/Leibniz debate, the controversy rages on.

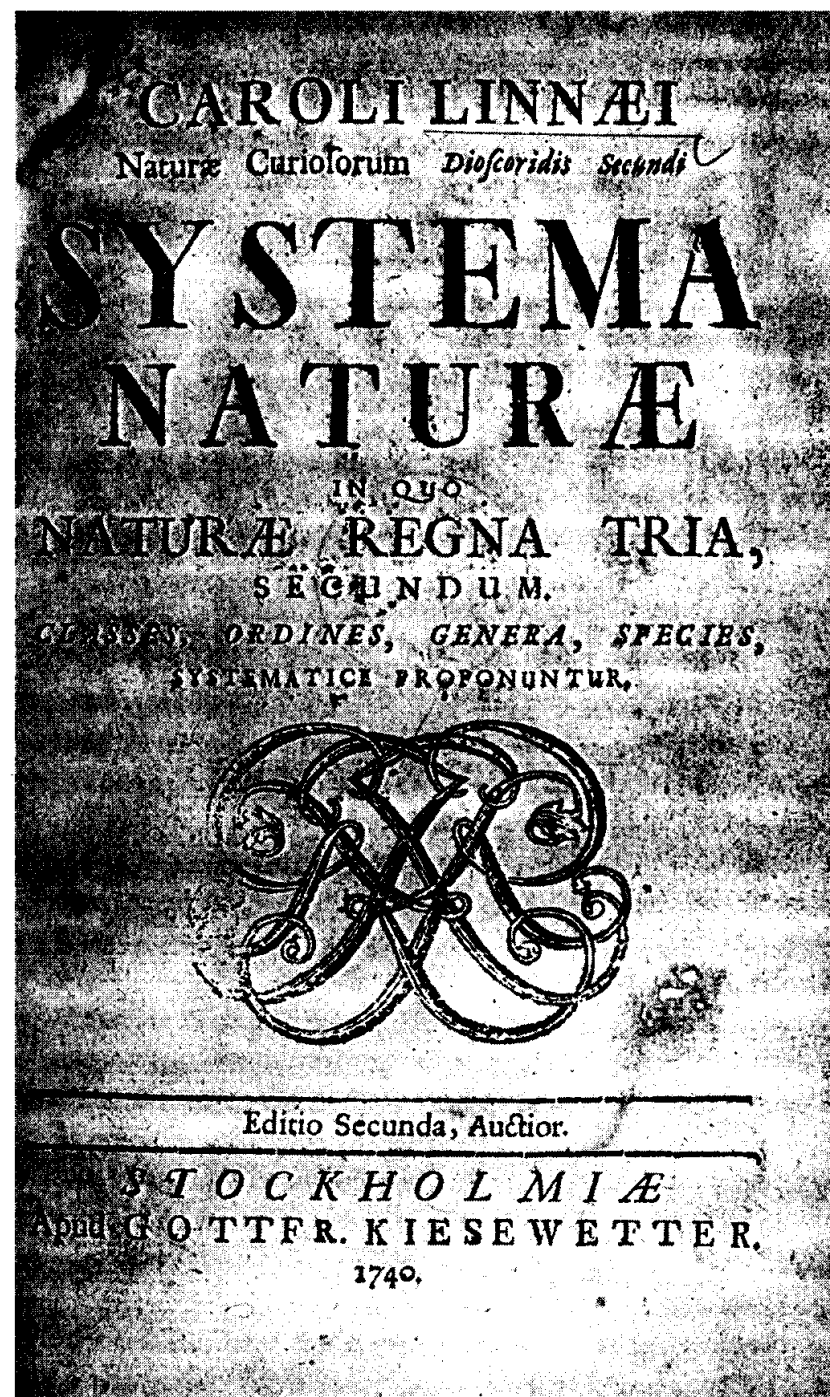
The problem of biological classification

Classifying, or sorting the objects one is studying into general kinds, plays a role in every science. Geologists classify rocks as igneous, sedimentary, or metamorphic, depending on how they were formed. Economists classify taxation systems as proportional, progressive, or regressive, depending on how unfair they are. The main function of classification is to convey information. If a chemist tells you that something is a metal, that tells you a lot about its likely behaviour. Classification raises some interesting philosophical issues. Mostly, these stem from the fact that any given set of objects can in principle be classified in many different ways. Chemists classify substances by their atomic number, yielding the periodic table of the elements. But they could equally classify substances by their

colour, or their smell, or their density. So how should we choose between these alternative ways of classifying? Is there a 'correct' way to classify? Or are all classification schemes ultimately arbitrary? These questions take on a particular urgency in the context of biological classification, or taxonomy, which will be our concern here.

Biologists traditionally classify plants and organisms using the Linnean system, named after the 18th-century Swedish naturalist Carl Linnaeus (1707–1778) (Figure 13). The basic elements of the Linnean system are straightforward, and familiar to many people. First of all, individual organisms are assigned to a *species*. Each species is then assigned to a *genus*, each genus to a *family*, each family to an *order*, each order to a *class*, each class to a *phylum*, and each phylum to a *kingdom*. Various intermediate ranks, such as *subspecies*, *subfamily*, and *superfamily* are also recognized. The species is the base taxonomic unit; genera, families, orders, and so on are known as 'higher taxa'. The standard Latin name for a species indicates the genus to which the species belongs, but no more. For example, you and I belong to *Homo sapiens*, the only surviving species in the *Homo* genus. Two of the other species in that genus are *Homo erectus* and *Homo habilis*, both now extinct. The *Homo* genus belongs to the Hominid family, which belongs to the Hominoid superfamily, which belongs to the Primate order, which belongs to the Mammalian class, which belongs to the Chordate phylum, which belongs to the Animal kingdom.

Notice that the Linnean way of classifying organisms is hierarchical: a number of species are nested in a single genus, a number of genera in a single family, a number of families in a single order, and so on. So as we move upwards, we find fewer taxa at each level. At the bottom there are literally millions of species, but at the top there are just five kingdoms: Animals, Plants, Fungi, Bacteria, and Protocists (algae, seaweed, etc.). Not every classification system in science is hierarchical. The periodic table in



13. Linnaeus' most famous book *Systema Naturae*, in which he presented his classification of plants, animals, and minerals.

chemistry is an example of a non-hierarchical classification. The different chemical elements are not arranged into more and more inclusive groupings, the way species are in the Linnean system. One important question we must face is *why* biological classification should be hierarchical.

The Linnean system served naturalists well for hundreds of years, and continues to be used today. In some ways this is surprising, since biological theories have changed greatly in that period. The cornerstone of modern biology is Darwin's theory of evolution, which says that contemporary species have descended from ancestral species; this theory contrasts with the older, biblically inspired view that each species was created separately by God. Darwin's *Origin of Species* was published in 1859, but it was not until the middle of the 20th century that biologists began to ask whether the theory of evolution should have any impact on the way organisms are classified. By the 1970s two rival taxonomic schools had emerged, offering competing answers to this question. According to *cladists*, biological classifications should try to reflect the evolutionary relationships between species, so knowledge of evolutionary history is indispensable for doing good taxonomy. According to *pheneticists*, this is not so: classification can and should be totally independent of evolutionary considerations. A third group, known as the *evolutionary taxonomists*, try to combine elements of both views.

To understand the dispute between cladists and pheneticists, we must divide the problem of biological classification into two. Firstly, there is the problem of how to sort organisms into species, known as the 'species problem'. This problem has by no means been solved, but in practice biologists are often able to agree about how to delimit species, though there are difficult cases. Broadly speaking, biologists assign organisms to the same species if they can interbreed with each other and to different species otherwise. Secondly, there is the problem of how to arrange a group of species into higher taxa, which obviously presumes a solution to the first

problem. As it happens, cladists and pheneticists do often disagree about the species problem, but their dispute primarily concerns higher taxa. So for the moment, we ignore the species problem – we assume that organisms have been allocated to species in a satisfactory way. The question is: where do we go from there? What principles do we use to classify these species into higher taxa?

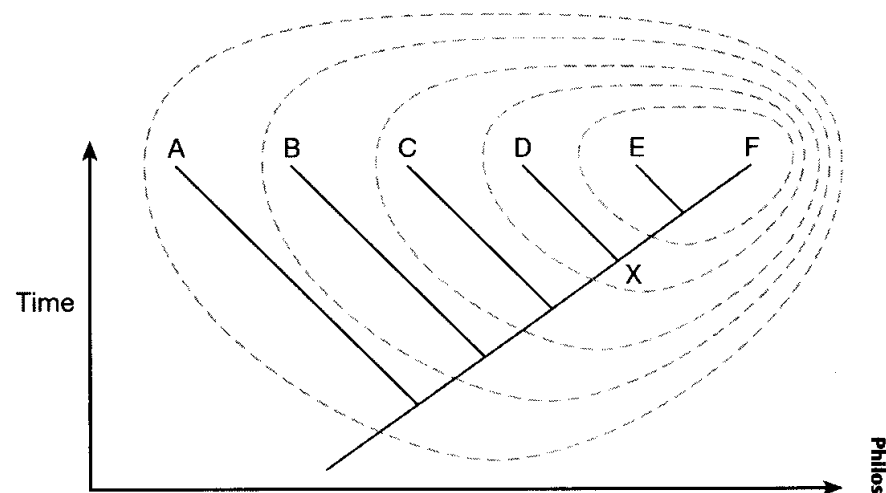
To focus the issue, consider the following example. Humans, chimpanzees, gorillas, bonobos, orangutans, and gibbons are usually classed together as members of the Hominoid superfamily. But baboons are not counted as Hominoids. Why is this? What is the justification for placing humans, chimps, gorillas, etc. in a group that doesn't also contain baboons? According to pheneticists, the answer is that the former all have a number of features that baboons do not, for example the lack of a tail. On this view, taxonomic groupings should be based on *similarity* – they should bring together species that are similar to each other in important ways and leave out ones that are dissimilar. Intuitively, this is a reasonable view. For it fits neatly with the idea that the purpose of classification is to convey information. If taxonomic groups are based on similarity, then being told which group a particular organism belongs to will tell you a lot about its likely characteristics. If you are told that a given organism belongs to the Hominoid superfamily, you will know that it doesn't have a tail. Furthermore, many of the groups recognized by traditional taxonomy do seem to be similarity-based. To take an obvious example, plants all share a number of features that animals lack, so placing all the plants in one kingdom and all the animals in another makes good sense from the phenetic point of view.

However, cladists insist that similarity should count for nothing in classification. Rather what matters are the evolutionary relationships between species – known as their *phylogenetic* relations. Cladists agree that the baboons should be excluded from the group that contains humans, chimps, gorillas, etc. But the justification for this has got nothing to do with the similarities and

dissimilarities between the species. The point is rather that the Hominoid species are more closely related to each other than are any of them to the baboons. What exactly does this mean? It means that all of the Hominoid species share a common ancestor that is not an ancestor of the baboons. Notice that this does *not* mean that the Hominoid species and the baboons have no common ancestor at all. On the contrary, any two species have a common ancestor if you go back far enough in evolutionary time – for all life on earth is presumed to have a single origin. The point is rather that the common ancestor of the Hominoid species and the baboons is also an ancestor of many other species, for example the various macaque species. So cladists argue that any taxonomic group that contains the Hominoid species and the baboons must also contain these other species. No taxonomic group can contain *just* the Hominoid species and the baboons.

The key cladistic idea is that all taxonomic groups, be they genres, families, superfamilies, or whatever, must be *monophyletic*. A monophyletic group is one that contains an ancestral species and all of its descendants, but no-one else. Monophyletic groups come in various sizes. At one extreme, all species that have ever existed form a monophyletic group, presuming life on earth only originated once. At the other extreme, there can be monophyletic groups of just two species – if they are the only descendants of a common ancestor. The group that contains just the Hominoid species and the baboons is not monophyletic, for as we saw, the common ancestor of the Hominoid species and the baboons is also ancestral to the macaques. So it is not a genuine taxonomic group, according to cladists. Groups that are not monophyletic are not permitted in cladistic taxonomy, irrespective of how similar their members may be. For cladists regard such groupings as wholly artificial, by contrast with 'natural' monophyletic groups.

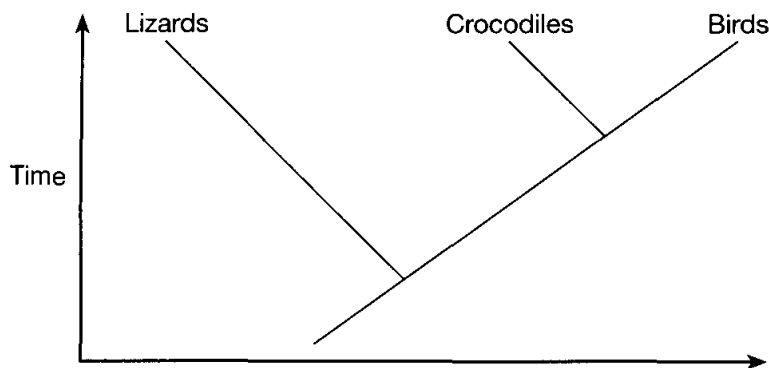
The concept of monophyly is easily understood graphically. Consider the diagram below – known as a *cladogram* – which shows the phylogenetic relationships between six contemporary species,



14. Cladogram showing the phylogenetic relations between six contemporary species.

A–F (Figure 14). All six species have a common ancestor if we go back far enough in time, but some are more closely related than others. Species E and F have a very recent common ancestor – for their branches intersect in the quite recent past. By contrast, species A split off from the rest of the lineage a long time ago. Now consider the group {D, E, F}. This is a monophyletic group, since it contains all and only the descendants of an ancestral species (not named), which split into two at the node marked 'X'. The group {C, D, E, F} is likewise monophyletic, as is the group {B, C, D, E, F}. But the group {B, C, D, F} is not monophyletic. This is because the common ancestor of these four species is also an ancestor of species E. All the monophyletic groups in the diagram have been ringed; any other group of species is not monophyletic.

The dispute between cladists and pheneticists is by no means purely academic – there are many real cases where they disagree. One well-known example concerns the class Reptilia, or the reptiles. Traditional Linnean taxonomy counts lizards and crocodiles as members of Reptilia, but excludes birds, which are placed in a separate class called Aves. Pheneticists agree with this traditional



15. Cladogram showing the phylogenetic relations between lizards, crocodiles, and birds.

classification, for birds have their own unique anatomy and physiology, which is quite different from that of lizards, crocodiles, and other reptiles. But cladists maintain that Reptilia is not a genuine taxonomic group at all, for it is not monophyletic. As the cladogram above shows, the common ancestor of the lizards and the crocodiles is also an ancestor of the birds; so placing lizards and crocodiles together in a group that excludes birds violates the requirement of monophyly (Figure 15). Cladists therefore recommend that traditional taxonomic practice be abandoned: biologists should not talk about Reptilia at all, for it is an artificial not a natural group. This is quite a radical recommendation; even biologists sympathetic to the spirit of cladism are often reluctant to abandon the traditional taxonomic categories that have served naturalists well for centuries.

Cladists argue that their way of classifying is 'objective' while that of the pheneticists is not. There is certainly some truth in this charge. For pheneticists base their classifications on the similarities between species, and judgements of similarity are invariably partly subjective. Any two species are going to be similar to each other in some respects, but not in others. For example, two species of insect might be anatomically quite similar, but very diverse in their feeding habits. So which 'respects' do we single out, in order to

make judgements of similarity? Pheneticists hoped to avoid this problem by defining a measure of 'overall similarity', which would take into account all of a species' characteristics, thus permitting fully objective classifications to be constructed. But though this idea sounds nice, it did not work, not least because there is no obvious way to count characteristics. Most people today believe that the very idea of 'overall similarity' is philosophically suspect. Phenetic classifications do exist, and are used in practice, but they are not fully objective. Different similarity judgements lead to different phenetic classifications, and there is no obvious way to choose between them.

Cladism faces its own set of problems. The most serious problem is that in order to construct a classification according to cladistic principles, we need to discover the phylogenetic relations between the species we are trying to classify, and this is very far from easy. These relations are obviously not discoverable just by looking at the species – they have to be inferred. A variety of techniques for inferring phylogenetic relations have been developed, but they are not fool-proof. Indeed, as more and more evidence from molecular genetics emerges, hypotheses about the phylogenetic relations between species get overturned rapidly. So actually putting cladistic ideas into practice is not easy. It is all very well to be told that only monophyletic groups of species are allowed in taxonomy, but this is of limited use unless one knows whether a given group *is* monophyletic or not. In effect, cladistic classifications constitute hypotheses about the phylogenetic relations between species, and are thus inherently conjectural. Pheneticists object that classification should not be theory-laden in this way. They maintain that taxonomy should be prior to, not dependent on, conjectures about evolutionary history.

Despite the difficulty of putting cladism into practice, and despite the fact the cladists often recommend quite radical revisions of traditional taxonomic categories, more and more biologists are coming round to the cladistic viewpoint. This is mainly because

cladism is free of ambiguity in a way that phenetic and other approaches are not – its taxonomic principles are perfectly clear, even if they are hard to implement. And there is something quite intuitive about the idea that monophyletic groups of species are ‘natural units’, while other groups are not. Furthermore, cladism provides a genuine rationale for why biological classification should be hierarchical. As Figure 15 above indicates, monophyletic groups are always nested inside each other, so if the requirement of monophyly is rigidly followed the resulting classification will automatically be hierarchical. Classifying on the basis of similarity can also yield a hierarchical classification; but pheneticists have no comparable justification for *why* biological classification should be hierarchical. It is quite striking that naturalists have been classifying living organisms hierarchically for hundreds of years, but the true rationale for doing so has only recently become clear.

Is the mind modular?

One of the central jobs of psychology is to understand how human beings manage to perform the cognitive tasks they do. By ‘cognitive tasks’ we do not just mean things like solving crossword puzzles, but also more mundane tasks like crossing the road safely, understanding what other people say, recognizing other people’s faces, checking one’s change in a shop, and so on. There is no denying that humans are very good at many of these tasks – so good, indeed, that we often do them very fast, with little if any conscious thought. To appreciate just how remarkable this is, consider the fact that no robot has ever been designed that behaves even remotely like a human being in a real-life situation, despite considerable effort and expense. No robot can solve a crossword, or engage in a conversation, with anything like the facility the average human being can. Somehow or other, we humans are capable of performing complex cognitive tasks with minimal effort. Trying to understand how this could be is the central explanatory problem of the discipline known as cognitive psychology.

Our focus is an old but ongoing debate among cognitive psychologists concerning the architecture of the human mind. According to one view, the human mind is a ‘general-purpose problem-solver’. This means that the mind contains a set of general problem-solving skills, or ‘general intelligence’, which it applies to an indefinitely large number of different tasks. So one and the same set of cognitive capacities is employed, whether the human is trying to count marbles, decide which restaurant to eat in, or learn a foreign language – these tasks represent different applications of the human’s general intelligence. According to a rival view, the human mind contains a number of specialized subsystems or modules, each of which is designed for performing a very limited range of tasks and cannot do anything else (Figure 16). This is known as the *modularity of mind* hypothesis. So, for example, it is widely believed that there is a special module for language acquisition, a view deriving from the work of the linguist Noam Chomsky. Chomsky insisted that a child does not learn to speak by overhearing adult conversation and then using his ‘general intelligence’ to figure out the rules of the language being spoken; rather, there is a distinct ‘language acquisition device’ in every human child which operates automatically, and whose sole function is to enable him or her to learn a language, given appropriate prompting. Chomsky provided an array of impressive evidence for this claim – including, for example, the fact that even those with very low ‘general intelligence’ can often learn to speak perfectly well.

Some of the most compelling evidence for the modularity hypothesis comes from studies of patients with brain damage, known as ‘deficit studies’. If the human mind is a general-purpose problem-solver, we would expect damage to the brain to affect all cognitive capacities more or less equally. But this is not what we find. On the contrary, brain damage often impairs some cognitive capacities but leaves others untouched. For example, damage to a part of the brain known as Wernicke’s area leaves patients unable to understand speech, though they are still able to produce fluent,