

# Cladistics:

## Identifying Branching Points in Evolutionary Pathways

For a biological classification system to be most useful, it should reflect current ideas about *evolutionary relationships* among the creatures it organizes into groups.

Organizing creatures into groups is usually based on shared anatomical or biochemical features. Determining which features reveal what about evolutionary relatedness falls under the discipline of phylogenetic systematics. There are several major systematic approaches, but the one favored by most modern biologists is called *cladistic phylogenetics*, or '*cladistics*' for short.

In 1950, German entomologist Willi Hennig published a short book in which he proposed the basic ideas that revolutionized systematics and launched the new science of cladistics. Cladistics takes its name from Hennig's concept of a "clade", which he defined as a group of organisms related by common descent. Hennig argued that only groups that include all the descendants of a common ancestor represent 'natural' units. He termed such natural groups "*monophyletic*" (meaning one tribe or lineage). Many of the animal 'groups' in common use - such as invertebrate, coral, fish, and reptile - are not monophyletic, as they either include descendants of several ancestors or exclude some of the descendants of a common ancestor. Hennig also devised new criteria for "*characters*" useful for determining the ancestry of living creatures. Using Hennig's system, taxonomists are able to develop classifications that are less subjective than those produced following previous methods. Hennig's basic method is being refined continually by new generations of taxonomists using high-tech tools like powerful computers and molecular genetics. Modern cladistic classifications thus reflect the evolutionary relationships of organisms with increasing accuracy and precision.

The *essence of cladistics* is simplicity itself: if two organisms share a given feature, it's a fair bet their common ancestor did too. But not all features are equally revealing of ancestry. For example, unique features may be useful for defining a given species or group, but are more-or-less useless for tracing ancestry. Features which are widely shared by virtue of having extremely long histories are also not all that useful for tracing ancestry; they are evolutionary 'hangers on', fundamental features that have persisted in several lineages that have continued to diverge and are no longer closely related. For example, a two-opening gut (with a mouth at one end and a cloaca or anus at the other) is an ancestral character. Both you and a cockroach have a two-opening gut, but you would probably take offense if I were to suggest that you and a cockroach are closely related - unless, of course, you happen to be Franz Kafka.

The features that are *most revealing* of a species' ancestry are modifications of long-standing characteristics shared by two or more species. For example, many animals have digits on their forelimbs, but only humans, apes and monkeys have opposable thumbs. No other animal has this feature. This is a strong piece of evidence that humans, apes, and monkeys form a natural group: the mammalian order Primate. Tree shrews, which used to

be considered primates are now placed in their own order, Scandentia, based - in part - on their lack of opposable thumbs. Such shared derived characters are termed "synapomorphies". Under the basic paradigm of cladistics, the greater the number of synapomorphies between two species or groups, the more recent their common ancestor and the more closely they are related.

Cladistics has *revitalized the study of evolutionary interrelationships*. Dinosaurs, for instance, were traditionally thought to be dull, lumbering - and ultimately unsuccessful - experiments in reptilian evolution. Yet dinosaurs were the dominant terrestrial vertebrate for some 150 million years. Impressive lists of skeletal synapomorphies have been proposed for both theropod dinosaurs and modern birds. Cladistic analysis of these characters has persuaded many (but by no means all) paleontologists that dinosaurs and birds are not merely adjacent sidebranches of reptilian evolution, but that modern birds are actually feathered theropods. Whether or not this startling conclusion is eventually borne out indisputably, the cladistic perspective has injected fresh new ways of thinking about both dinosaurs and birds. In many paleontological circles, dinosaurs are now perceived as active, warm-blooded, socially complex animals. The dinosaur connection has prompted some ornithologists to rethink the origins of such important bird characteristics as flight and parental care. Similarly, cladistics has enabled biologists to explore the interrelationships of other groups of organisms, and some of the implications of this work have been downright provocative.

Cladistics tries to identify '*branching points*' where novel characteristics first appear, regarding these evolutionary events as indicative of how and when new groups arise. Thus, for a cladist, identifying branching points is the same thing as tracing genealogy. Proponents claim that, since cladistics relies on observed characteristics independent of any overriding evolutionary theory (which is subject to change), this systematic method is more objective than traditional evolutionary approaches. Critics suggest that cladists classify characters, not organisms, and that they ignore important consequences of evolutionary history (such as a change in the timing of developmental events, which sometimes results in the appearance new species). Even within the cladistics community, there is much contention over which characters are derived as opposed to ancestral and the polarity (direction) of evolutionary change over time.

Each systematist uses somewhat different - sometimes idiosyncratic - characters in his or her cladistic analyses. Essentially any feature that can (in theory, at least) be modified through the processes of evolution is 'fair game'. Some systematists use skeletal or dental features, some soft tissue characters like muscle blocks, blood vessel or nerve pathways; others use biochemical pathways or molecular genetics, and still others include behavioral characters. Character selection seems to be a rather subjective process. In choosing characters most systematists tend to favor their own area of specialty and weigh the significance of these characters more heavily than others.

