A COURSE EVOLVES

The first step in a survey of natural history…should be the acquisition of some familiarity with the system of names and the system of classification, with the word equipment used by naturalists.

-Marston Bates (1950)

I have taught a course on the diversity of life almost every year that I have had university teaching appointments. Even as a graduate student I taught or assisted in such courses. Through that period, the appreciation for the diversity of life within the biology curriculum has waxed and waned. Moreover, the subject itself has undergone considerable change from 1970 to the present. At first, all of life was divided into plants (Botany) and animals (Zoology). This dichotomy seemed natural and went all the way back to the time of Aristotle (384-322 BCE). Such was my training in college and graduate school. The first courses that I taught on biological diversity as a new professor was called Plant Diversity and covered all living things that were not considered animals. Someone else taught zoology. Then, the five-kingdom system finally took hold and the course evolved into something called Plants, Protists, and Fungi, which was similar to Plant Diversity but incorporated the animal-like protists into a standard survey of botany. Finally, after the animal kingdom had been eliminated from the other introductory courses, the course became Systematic Biology and embraced all living things with emphases on biodiversity and phylogenetic relationships. Throughout all iterations of the surveys, evolution had been the focus.

The evolution of the survey courses pretty much reflects the three common theoretical schools of classification that had developed since the Modern Synthesis. They were:

1. Evolutionary Taxonomy
2. Numerical Taxonomy
3. Phylogenetic Taxonomy

The three schools produce taxonomic hierarchies that resemble each other, and are fundamentally the same in some of their assumptions, particularly that all things have evolved from a common ancestor and that the classification reflects their degree of kinship. Nevertheless, the followers of the three schools have had some bitter fights from during the past 35 years.

Ernst Mayr (1904-; Germany & USA; see Figure 1), an architect of the evolutionary taxonomy school said that classification has always had two functions: a practical and a scientific one. The practical function of taxonomy always has been a way to organize life, a kind of giant roadmap of all living things. The scientific purpose, at least since Darwin, has been to reflect the degree to which they are related to each other. Similarly,
the tension between the classification systems is the tension between the practical and the scientific.

FIGURE 1. Ernst Mayr, a founder and continuing apologist for modern Evolutionary Taxonomy.

MODERN TAXONOMIC SYSTEMS

*If a classification system is based strictly and exclusively on the monophyly of the included taxa, it is a genealogical ordering system.*

- Ernst Mayr (1997)

Classical classification systems before Darwin also had a similar tension between the practical and the general, but a general function that was not based on evolutionary relationships. In a world in which life did not evolve, the classification system assumed that species were invariant or could undergo some minor changes. Either way, the general object of classification was to find the character or characters that defined the essence of the group. That was how Carolus Linnaeus (1707-1778; Sweden) defined the format of the taxonomic system that we still use today. However, his fundamental philosophy could not have been more different from the taxonomists of today. He defined the taxonomic hierarchy with the understanding that life did not change. Thus, the differences and similarities between taxa were the consequences of the similarities and differences between their essences.

Darwin recognized that the Linnaean taxonomic hierarchy and the particular relationships between species would have been the consequence of descent with modification, the principle of evolution (see Figure 2). Thus, he used classification as evidence for evolution, and it figured prominently in *The Origin*. Following Darwin’s lead, taxonomists began to use the essentialistic classifications to infer evolutionary relationships. Also, classification systems could be altered according to new evolutionary inferences. That became the goal of evolutionary taxonomy.

In the early days of evolutionary taxonomy, though, the purpose of systematics (= taxonomy) had been to define classification systems based on evolutionary lines

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4 You can find much more about Linnaeus and the initiation of his system in the essay called *Kingdoms in Paths of Science*.

5 The equivalence of the terms is only approximate. Systematics includes the diversity of all living things and the evolutionary relationships that bind them. Historically, taxonomy has been a component of systematics, and includes: identification, classification (how things are ordered into a hierarchy), and nomenclature (how things are named) according to Winston (1999).
(phylogeny) defined by fossils and by other disciplines like comparative anatomy. This led to a near fruitless search for “missing links”. The discipline matured in the late 19th and early 20th Centuries to recognize the population, not the species, as the unit of evolution. Thus, the use of statistics became appropriate in the study of evolutionary relationships leading to classifications.

FIGURE 2. Redrawn from an early illustration by Darwin showing the tree-like pattern produced by lineages derived by descent with modification from a common ancestor (black circle).

This was the nature of systematics through much of the 20th Century. In this way Evolutionary Taxonomy seemed to be the legitimate heir of Classical Taxonomy. Unfortunately, such systems required specialists who seemed to apply arbitrary criteria for determining definitions of particular families, genera, etc. For example, within the insects, the orders and level of difference between orders seemed consistent, but an insect order could not be compared to a mammalian order. Could taxonomic hierarchies be created such that ordinal-level differences were consistent? This was not a problem for those who used biological classification for practical purposes, but it was very unsatisfactory for a few who insisted that biological classification reflect the branching tree of evolutionary descent with modification.

The introduction of the computer allowed for the development of statistical comparisons between many characters with multiple character states. If so, then comparisons between taxa could be made using a large matrix of taxa and characters such that the matrix was filled with observable character states. The characters were not ordered nor were they weighted. This would allow for a pristine, classification, untainted by preconceptions. The dream was to make taxonomy free and independent of theory, and, thereby, objective.

Peter H. A. Sneath (UK), who had employed such methods in the classification of bacteria in the 1950’s joined Robert R. Sokal (USA; see Figure 3), a biological statistician. Together, they founded this school with the publication of Principles of Numerical Taxonomy in 1963. That term was used interchangeably with Phenetics, a reference to the comparisons of phenotypes. The numerical methods mainly employed similarity indices between taxa based on their respective character states. The resulting
hierarchy of similarities would produce a tree-like diagram, a diagram reflecting their biological classification and their evolutionary relationships.

Numerical taxonomy produced a renaissance in systematics. The obvious power of having an objective means of classifying organisms was very appealing. Also, because it was theory-free, it could be used to explore evolution without the logical fallacy of circular reasoning.

Unfortunately, the promise of phenetics has not been fulfilled. Such pure objectivity is illusory because within science, all operations are theory-laden. Other difficulties include the treatment of characters. Within numerical taxonomy, all characters are equal, and, therefore, biased toward unimportant easily-observed ones.

FIGURE 3. Robert Sokal, a founder of the Numerical Taxonomy school.

FIGURE 4. Willi Hennig, founder of phylogenetic taxonomy.
Willi Hennig (1913-1976, Germany; see Figure 4) was an entomologist who was not satisfied with classification systems. He recognized that the classification produced by evolutionary taxonomy was subjective, and its methods could neither be codified nor repeated. On the other hand, classification produced by numerical taxonomy was arbitrary and based on the characters chosen. Hennig proposed that numerical-like methods be adopted. However, some rules needed to be assumed. First, character states should be identified as primitive (plesiomorphic) and derived (apomorphic). That taxa share primitive characters (symplesiomorphic) is uninformative. Only shared derived characters (synapomorph) are informative about their evolutionary histories, and, therefore, their systematic relationships. Also, because many trees can be derived from a single character X taxon matrix, the tree with the fewest number of changes (most parsimonious) would be the best according to Occam’s Razor. The proper statistical test, then would be a test of parsimony.

The attraction of phylogenetic taxonomy was that its methods were repeatable algorithms and that it used phylogenetic inference as its guiding principle. It was not, and made no pretense to be, theory-independent. Hennig presented this philosophy in 1966 in a book called *Phylogenetic Systematics*. His followers were few at first but grew within the Numerical Taxonomy community. The coexistence between the two philosophies, however, broke out into an acrimonious philosophical civil war.

**THE SYSTEMATICS WARS**

*We old survivors of the systematics wars sit around nursing our post-traumatic stress disorder and telling our war stories to the few who will listen.* -Joseph Felsenstein (2001)

The systematics wars between the three schools began in the 1970’s. The evolutionary taxonomists were concerned with variable rates of evolution and taxonomic evidence that considered such problems. Thus, they argued that a strict algorithmic approach to taxonomy would ignore one of the most important aspects of evolution and speciation. Nevertheless, evolutionary taxonomists were being nudged out of favor. Mayr, one of the principle critics of the new taxonomic schools called the phylogenetic taxonomists cladists in reference to the branch (clade) and the systematic importance given to clades. It was intended as a derogatory remark, but the phylogenetic taxonomists began to wear that as a badge of honor.

Sokal attempted to demonstrate that parsimony, one of the fundamental tenets of phylogenetic taxonomy, was inappropriate and that clusters of similar taxa should define a classification system. Through the 1970’s the differences between the pheneticists and the cladists grew increasingly rancorous until a full break came at the 1979 meeting of the Numerical Taxonomy meetings at Harvard. Following that meeting, an all out bitter fight ensued where cladists attempted to take over systematics by controlling its journals and societies.

What were they fighting about? Well, consider seven theoretical taxa (A, B, C, D, E, F, G). In this case, we will consider only two characters (I, II). The two dimensional distances between the taxa based on their characters and differences between their character states are given in Figure 5, which is a solution to a character-taxon matrix. A dendrogram based on their proximity or similarity is given in Figure 6. Taxa A, B and C form a cluster in which they differ by a taxonomic distance of 2. Taxa F and G form a
similar cluster. Taxa D and E are more alike and are separated only by a taxonomic distance of 1.

![Figure 5](image)

**FIGURE 5.** A diagram of distance between taxa A-F based on the states of two characters.

![Figure 6](image)

**FIGURE 6.** A dendrogram (tree-diagram) generated by the distances between taxa in Figure 5.

A cladistic analysis of the same set of taxa and characters likewise is based on a matrix of taxa and characters (see Figure 7). The solution to this matrix, however, is based on parsimony and a diagram that requires the fewest number of changes in character states from the base of the tree or cladogram (see Figure 8) to the ends with the taxa. In this case, the character I has 3 states and character II has 5 states. The cladogram...
is identical to the dendrogram of Figure 6; however, the difference in philosophy becomes clear when considering how the states of the characters change from the base of the tree to the taxa in question.

**FIGURE 7.** A Character X Taxon matrix for taxa A-G and characters I and II. Character I has three states (0, 1, 2) and character II has five states (0, 1, 2, 3, 4).

<table>
<thead>
<tr>
<th>TAXA</th>
<th>CHARACTER I</th>
<th>CHARACTER II</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>B</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>C</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>D</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>E</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>F</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>G</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

**FIGURE 8.** A cladogram that illustrates three clades or monophyletic lines. Each internode is labeled according to the characters and their states.

The primitive states of both characters in this example are 0 and 0. Note that as you work your way up the cladogram, taxon F retains both primitive states. Its sister taxon, G, exhibits the primitive state for character I, but character II has changed from 0 to 1. This monophyletic branch is called a clade. The clade that terminates in taxa D and F shows changes in both characters from the base of the tree. However, the two taxa cannot be differentiated based only on the two characters. Clade A-C is defined by character I,
state 2, but character 2 varies among all thee of them. Thus, the cladogram also charts the
evolution of characters within each clade. Note that in this example, there are no
reversals in characters, that is, the states never reverse to an earlier form from the base to
the terminal taxa.

These are very simple examples, but they illustrate the fundamental differences
between the phenetics and cladistics. Now, imagine a matrix with 100 or more
characters, each with more than one expressed character state. The number of solutions
to such a large matrix could be greater than the number of atoms in the universe. This is
true for both algorithmic methods, but more so for cladistic methods. Have they just
traded the complexity of biodiversity for the mathematical complexity of linear algebra?
Not really because the principle of parsimony and other statistical methods allow for the
determination of the best solutions.

Phenetics, because it made no pretense at constructing phylogenies, did not consider
fossils to be important and saw the construction of trees with fossil species as absurd.
The use of fossils in determining evolution and fundamental relationships has a long
history in the Darwinian era. They play a major role in the classification systems of the
evolutionary taxonomists. Cladists, because they were interested in constructing
classification systems that reflected phylogenies, also began to consider fossils and their
importance in determining primitive character states, etc. Even cladists armed with fossil
evidence did not assume that the cladogram was a phylogeny, but they assumed that a
phylogeny could be constructed from a cladogram.

Consider the question of the relationship between birds and dinosaurs. This had been
considered for some time. Thomas Henry Huxley was the first Darwinian scientist to
propose the connection between the two types of animals. The discovery of
Archaeopteryx, a clear intermediate between birds and dinosaurs in 1861 seemed to
underscore the connection. However, evolutionary taxonomists considered the
relationship to be superficial. They assumed that birds had emerged from a dinosaurian
line (or pre-dinosaurian line), but radiated into a group with class-status in the
vertebrates. Cladists interpreted the evidence differently.

Suppose a very simple cladogram of four taxa and two characters: number of walking
legs and presence of teeth (see Figure 9). The Iguana, a lizard, represents the primitive
state for both characters: it walks on four legs and has teeth. From that form emerged a
line, the dinosaurs, that had two walking legs. Brachiosaurus, a huge sauropod, returned
to the 4-legged position. This represented a reversal in the clade. However, this reversal
was borne out by fossil evidence. The other dinosaur, Velociraptor, was in a clade that
included birds.

The cladistic interpretation of Figure 8 is that all taxonomic units (e.g. species,
genera, families, etc.) must be monophyletic. So, if the dinosaurs were reptiles (like
lizards) then the whole cladogram would represent reptiles and subgroups of reptiles.
Although dinosaurs as reptiles might be palatable, birds as reptiles is not. The alternative
is that modern reptiles like lizards are separate from the dinosaurs and birds, which
together should make up a class Dinosauria, of which Aves would be a subclass. The
alternative of allowing birds and dinosaurs to be separate groups would destroy the
monophyletic (making them paraphyletic) aspect of the groups and is not allowed in the
rules of cladistics.

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6 By this phrase, I mean after the publication of The Origin.
Interpretation by Evolutionary Taxonomists

**FIGURE 8.** A simple cladogram of four taxa: *Iguana, Brachiosaurus, Velociraptor*, and *Pigeon* separated on the basis of two characters: number of walking legs and presence of teeth. The upper cladogram groups the taxa in the classical, evolutionary taxonomy mode while the lower one interpret the taxa by the rules of phylogenetic taxonomy.
In cladistic terms, the *Iguana* is an outgroup genus. That is, it is related to, but not part of the organisms in question. Placing an outgroup in the cladogram causes the states of the characters to become polarized, and more likely produce a tree that reflects phylogeny. The resulting inferred phylogeny, then, is used to produce a classification.

The particular rules for converting cladograms to classifications brought about the ire of the evolutionary taxonomists. Although they agreed that the goal of classification should be to reflect evolutionary relationships, they (particularly Ernst Mayr and George Gaylord Simpson, 1902-1984, USA) said that the *a priori* assumptions made for the connection between evolution and classification in a cladistic analysis did not recognize the reality of evolution. In the view of the evolutionary taxonomists, some groups emerged from a line and then went through a rapid radiation that made them a separate group. The evolutionary taxonomist would have interpreted Figure 8 as the emergence of the birds (as a separate class) from a reptilian ancestor. The phenetecists would have rejected the analysis all together because they did not allow the incorporation of fossil or extinct groups. Besides, phenetic classifications were assumed to be artificial anyway.

All was not calm within the ranks of the cladists, though. Prior to the open warfare between cladistics and phenetics, a quiet revolution began to brew within the camp of the Phylogenetic Taxonomists. A group of cladists began to apply even more draconian methods than Hennig had. In essence, they believed that if all *a priori* evolutionary assumptions were purged, then the cladistic analyses generated could be used to test evolutionary hypotheses without the problem of circular reasoning. Members of the movement called themselves transformed cladists.

The cladists, transformed or not, rapidly won the systematics civil war. By the end of the 1980’s cladistic analyses were quite common in the systematics literature. By the 1990’s almost all publications dealing with systematics were based on cladistic analyses.

**MOLECULAR TREES**

*Evolution at different amino acid and nucleotide sites is easily comparable: one change at one site is equivalent to one change at another. This is a huge advantage when we are weighing up conflicting evidence.*

- Mark Ridley (2004)

Classification systems had all been based on morphological characters. However, the drawback of morphology (this includes anatomy, physiology, and development) is the relative paucity of homologous characters that span large groups. Also, the importance of morphological characters varies. The use of macromolecules, particularly biopolymers, like proteins and nucleic acids, however, provides a very large number of characters that are about equal in importance. For example, consider the insulin molecule, the first biopolymer to be sequenced. It has 51 amino acids linked in a particular order. Thus, insulin could be used as 51 different characters, each with 20 potential amino acids (thus, 20 characters states). Insulin is not universal, however, and it could not be used to distinguish humans from chimps.

Consider something even more universal, like nucleic acids (DNA and RNA). These are found in the nucleus, the mitochondria, the chloroplasts, and the cytoplasm. Comparable strands of nucleic acids could yield 100’s to 1000’s of characters, each with four character states (the four bases). With current molecular sequencing methods and instrumentation, such comparisons can be made with suitable speed. Such analyses have revolutionized our understanding of life.
At first glance it would seem that chromosomal DNA would provide the key to the fundamental relationships of all life. The problem, though, is that all organisms compared have to the same gene. They could be used to compare closely related organisms, but they could not be used to make a universal tree. Also, although such sequences might provide many characters (nucleotides), each one has only four possible character states. Short sequences might give results that appear to indicate homology. Useful sequences, therefore, must have hundreds or thousands of nucleotides. So, even though Transfer RNA is universal, the sequences are too small to be reliable and reflect changes of a long history. Ribosomal genes and RNA, however, are universal, highly conserved, and large enough to bear the changes from its history. In theory, ribosomal sequences should be adequate to elucidate the universal tree of life.

In the 1960’s the Neutral Theory of molecular evolution appeared, expounded mainly by Motoo Kimura (1924-1994, Japan). This view held that genomes mutate at a particular rate. Thus, the number of differences in a genome provided a kind of molecular clock that timed the separation of species. This became the fundamental principle that guided molecular phylogenetics. Thus, when molecular methods began to be used in cladistic analyses, phylogenetic analyses began to proliferate, and, in some cases, provide many unexpected answers. One of the first based on rRNA was that life consists of three domains, two of which are bacterial.

**FIGURE 9.** This cladogram is from an example in MacClade 4.0. It shows 12 taxa of primates with Lemur as the outgroup. It shows 4 clades that have been derived by comparing 900 nucleotides from mitochondrial DNA.
The molecular sequences have come back to tell us more about ourselves. Consider Figure 9. This is a cladogram of 12 primate taxa and 900 characters (nucleotide positions from mitochondrial DNA). The outgroup is a Lemur (far left). According to the rules of cladistics, the Tarsier (far right) is one clade (clade 1). Saimiri is clade 2. Four different tailless monkeys in the genus *Macaca* make up clade 3. Clade 4 includes the great apes and *Homo sapiens*. However, by the rules of cladistics, we have to be part of the group that includes the great apes, or should I say, the other great apes? This particular cladogram has branches that vary in length according to the number of changes in the branch. The macaques (monkeys within the same genus) show about the same variability as the apes above *Hylaobates* (gibbon). Another curious outcome is that any node can swivel without changing the tree length. If the Pan-Homo clade were to swivel, *Homo* (our genus) would be clearly within the great apes. This is not great surprise. Even Linnaeus placed chimpanzees within our own genus. Since then, the evolutionary taxonomists removed us to our own family, the Hominidae, and left the other apes in the family Pongidae. The cladists would have us united again.

**CLASSIFICATION REVISITED**

*The first step of science is to know one thing from another. This knowledge consists of their specific distinctions; but in order that it may be fixed and permanent distinct names must be given to different things, and those names must be recorded and remembered.*

- Carolus Linnaeus from Smith (1821)

The classification of birds, reptiles, and our genus points to a major rift between the positions of cladists-pheneticists and classical taxonomists (more in the vein of evolutionary taxonomy). The Numerical Taxonomists were more extreme than all other groups in recognizing that the taxonomic system is artificial, and, therefore, the terminal taxa would not even be called species, but referred to as Operational Taxonomic Units (OTU).

Both Phenetics and Cladistics, because they are inherently hierarchical, would seem to lend themselves well to the Linnaean classification hierarchy. The nodes of the cladogram (or dendrogram) could be given Linnaean taxonomic status. However, even with the current system, there are only 8 major categories if the domain is included as the highest taxon\(^7\). Then given multiplications of the main taxa with prefixes like sub-, super-, or infra, up to 20-24 taxonomic levels could be designated in any full hierarchy. However most dendrograms or cladograms with many taxa could have many nodes from the root to the terminal taxon. For that reason, some of the more rabid cladists, insist that the Linnaean system be swept away entirely. In its place would be a series of numbers that indicate the position of a terminal taxon and the nodes that lead to it. Such a system might sound fine in theory, but it abandons the practical need for classification as a retrieval system. Furthermore, the “true and final” cladogram on which the cladistic classification would be built is far, far away, both in time and complexity. Right now, fewer than 2 million species have been described. There may be as many as 10-100 million species. How many nodes would be required to separate them?

Another more subtle, but important point is that the need for a practical system is to support those who do not know the groups well. Colin Tudge suggested that most of those who work with particular types of organisms tend to think in terms of the species or

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\(^7\) The hierarchy would be: Domain, Kingdom, Phylum (sometimes Division in Botany), Class, Order, Family, Genus, Species.
genera. For them, the higher taxa have little meaning. I can say that this applies to me. I work with diatoms and dinoflagellates, both of which have higher taxa that I know only generally. However, I know the common freshwater species well.

So far, classical classification prevails. The cladistic modification likely will not be used in a major way any time soon. So, in a way, even the cladists lost this war.

**A TRUCE?**

So, we are waiting for the dust to settle down over these several decades, and we suspect that waiting for things to quiet down totally is as fruitless as spending hours each evening watching the sky for the next major meteor impact. The Editors of *Taxon* (2000)

The classification systems created by molecular phylogenetics remain classical Linnaean in form. However, because molecular instrumentation and the power of the computer have provided for an almost cottage industry in systematics, the proliferation of classifications produced by molecular phylogenetics often are dissimilar, and, therefore, not practical, either. This aspect of practicality will not go away. Classification must be useful and usable. The information must be easily transferable. All of these practical attributes of classification systems are particularly valuable at a time when the inventory and discovery of biodiversity is so important. Molecular phylogenetic systems alone lead to questionable relationships anyway. As Max Taylor (1999) declares, the solution must be to tie molecular attributes to morphological characters. Only in that way can phyletically sound classification systems be made useful.

A crisis in systematics developed in the latter 1990’s and culminated in the first years of the 21st Century. Single sequences had been very informative and had given much insight to the evolution of some organisms, but the method produced unacceptable relationships for groups in large hierarchical units. The eukaryotes, organisms with nuclei, seemed at first to conform to the five-kingdom system, four of which were eukaryotic. Then, some unexpected results appeared. The Fungi and Animals seemed to be sister groups (clades that branch from a common ancestor) and were lumped into a higher taxon called the Opisthokonts. However, more and more groups under phylogenetic scrutiny did not fit. Finally, in 1999 David Patterson declared that there are 60 to 120 groups that have no clear sister groups. Did that mean there could there be 60 eukaryotic kingdoms? Ribosomal RNA, mitochondrial and nuclear DNA sequences did not help. A possible solution had been proposed in 1992. If multiple datasets and trees were combined, the problems with any one or few datasets would be swamped. The analysis began to be used with hundreds of datasets after 2000. In 2001 Vincent Daubin, Manolo Gouy, and Guy Perriere of France performed such an analysis, called a supergroup analysis, for all prokaryotes and defined 11 coherent groups. Similar supertree analyses on eukaryotic groups revealed 5 supergroups, which, like the prokaryotes, contain about 11 kingdoms (see Figure 10). Not only did the supergroup analysis resolve the chaos of 60 sisterless groups into 5 supergroups, but also it found relationships between orphaned, seemingly disparate taxa in what is now called the Cerozoa. It confirms relationships between the red algae and the green plants, between the amoebozoa and the opisthokonts, and between the excavates and the dicristates. The resolution to the systematic chaos of the past 10 years seems to be at hand. Similarly, the general solution to the complete tree of life is within our grasp by the use of such

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8 I interpret these as 9 Eubacterial Kingdoms, and 2 Archaea Kingdoms.
powerful methods.

The systematics wars have died down to periodic skirmishes, but cladistics is the clear winner. Still, Phylogenetic Taxonomy is not a clean break from its rivals. Evolutionary Taxonomy is based on inferred phylogeny, but its methods are very subjective. Numerical Taxonomy is based on the similarities among groups, but not on a presumption of phylogenetic relationships. The methods of Numerical Taxonomy are algorithmic, and, therefore repeatable. Cladistics, in my opinion, takes the best of both schools: the phylogenetic basis of Evolutionary Taxonomy and the repeatable algorithmic methods of Numerical Taxonomy. Thus, the systematics wars brought about a revolution by replanting the tree of life and producing powerful methods to study it.

\[\text{FIGURE 10.} \quad \text{The results of a eukaryotic supergroup analysis published by Sandra Baldauf in 2003. Note that there are five independent clades from the unrooted tree.}\]

\textbf{Sources that I used to write the essay:}


QUESTIONS TO THINK ABOUT

1. What are the three schools of modern taxonomy? Who were their founders?

2. How do the three schools differ regarding to their fundamental bases or philosophies?

3. What are the two functions of classification?

4. What are the distinctions between pre-Darwinian and post-Darwinian (post Origin) taxonomy?

5. Why did I call the period between 1979 to the early 1990’s the Systematics Wars? In what way was it a civil war?

6. What would be an advantage of algorithmic methods for classification?

7. Distinguish between character, character state, apomorphy, plesiomorphy.

8. What is the neutral theory of molecular evolution?

9. Are we members of the Hominidae or the Pongidae?

10. Aside from the Systematics Wars, what was the crisis in phylogenetic taxonomy in the 1990’s? How was it resolved (at least so far)?

11. What is wrong with the five-kingdom system?