From Cladograms to Classifications: The Road to DePhylocode

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I'd like to begin with a bit of personal history, since that seems to be the easiest way to get into the subject. Back in the middle ages, or at least the middling decades of the last century, when I was a grad student studying spiders in the green pastures of Harvard University, our catechism was supplied by Ernst Mayr and his "New Systematics" (or, as I prefer to call it, the "Non Systematics"). In retrospect, I should have known that something was amiss from day one. There I was, unpacking my stuff into the tiny cubicle I was assigned on the fourth floor of the Museum of Comparative Zoology, when a distinguished-looking gentleman strolled in, and asked a few questions about who I was, what I was interested in, what my thesis was going to be about, and the like. I was scheduled to take an evolution course that first semester, which was to be team-taught by Ernst Mayr, erstwhile malacologist Steve Gould, and lepidopterist John Burns. The assigned textbook, of course, was to be Mayr's "Animal Species and Evolution," so I had a copy of it out on my desk. My visitor pointed to the book and said "Oh, I see you've got a copy of the bible." That seemed like a very strange comment, indeed; hailing, as I did, from the fundamentalist bible-belt of the Appalachian mountains, I wasn't exactly used to hearing evolutionary texts referred to as biblical, in any sense! So I just shrugged the comment off, and went on with the conversation. After a while, my guest stood up, shook hands, said "Oh, by the way, I'm Ernst Mayr," and strode out. Be that as it may, I was soon properly indoctrinated. Species, I was told, are real, and what every right-thinking organismic biologist should focus on, to the exclusion of all else, because groups of species -- higher taxa -- are not real, but merely human and artificial constructs. Now, I have to say that I never found that position to be very sensible. I could look around at my major professor, for example, an arachnologist by the name of Herb Levi. His mentor had been the long- time spider curator at the American Museum, a true seat-of-the-pants taxonomist named Willis Gertsch. By this time, however, on at least a few occasions, Levi had published a revision of a group, and Gertsch had felt compelled to write a rebuttal. Levi was then having to publish papers attempting to explain why some of his species were, at least according to Gertsch and other highly respected colleagues, just artificial assemblages of several different and easily distinguished species that weren't even necessarily each other's closest relatives. Yet, despite all these disputes about species, none of these eminent systematists seemed to have any difficulty whatever in agreeing on at least some higher taxa, such as spiders. Indeed, spiders seemed, then and now, to be the quintessential example of a natural, or real group, so real that I thought it was utterly impossible for anyone to make a mistake about whether a given organism is or is not a spider. Now, I do have to stop and be honest here; what I actually thought was utterly impossible was for anyone other than a paleontologist to make that mistake. As usual, of course, I was wrong on that count, too. A few years back I had to co-author a paper on Brucharachne, the spider that wasn't -- a spider, that is. In 1925, as it transpires, one of the worst taxonomists South America ever produced, the immortal Candido Firmino de Mello- Leitao, actually described a whole new family of spiders, based on what turned out to be a single male mite (Krantz and Platnick, 1995). But I bring all this history up mostly to point out that we have now made our way fully to the opposite pole on the rather fundamental issue of taxa and their reality, with papers appearing in the journal Systematic Biology about so-called "phylogenetic taxonomy" and bidding "a farewell to species." In other words, some of our colleagues are now arguing exactly the opposite point of view from the "non systematics" I was taught as a grad student; they are arguing that higher taxa are real but species, somehow, are not. At least one author, Fred Pleijel, adopts "a view where species simply are

denied any role in taxonomy and where only monophyletic groups are recognized by formal Latin names" and he says he applies "uninomials for all names, because this treatment does not recognize any species entities and applies the same nomenclature for all taxa" (Pleijel, 1999: 756). As you might guess, I personally consider both of these polar positions to be preposterous, wrong-headed, and insidious. Let's proceed by getting rid of the obvious. I assume we all recognize that species, and groups of species, are first of all hypotheses, and in that sense only, represent artificial constructs of the human mind. But I assume we all recognize that it is possible, at least in theory, for one of those hypotheses to be an accurate statement about the real world. Who knows, on a good day, maybe even more than one of our hypotheses might be accurate! Throughout the centuries since Clerck (and here you have to forgive me, for spider systematics, in its typically precocious fashion -- and with all due respect to our august surroundings -- starts with Clerck in 1757, rather than that late-comer Linnaeus, in 1758), most systematists have avowedly been seeking natural classifications, by which they meant classifications that consist of species, and groups of them, that actually exist in the real world. And I would suggest that this is an entirely appropriate goal. After all, how do we know that anything, such as the chair you're snoozing in, actually exists? The answer, of course, is that we can keep bumping into it -- lots of different sources of evidence agree. So lets look at a putatively natural group like spiders, and ask whether we have evidence that it is real. Spiders have at least two characters that are completely universal within the group, and completely unknown outside the group. The most obvious character is the abdominal spinerets through which silk is emitted. But there is another unique character, namely that adult males have modified structures on the tips of their pedipalps that are used to transfer sperm to the females during copulation. In a male spider, there is no anatomical connection between the gonads and the intromittent organ; the male spider has to deposit a drop of sperm from his abdomen, and then dip his palps into the sperm to charge them for mating. To date, systematists have described some 1.75 million species, and of those, some 37,600 species are currently considered valid members of the Order Araneae, the spiders. If we pick abdominal spinnerets as a character, that feature allows us to group 37,600 species, and no others, as spiders. If we then group together those species with male pedipalps modified for sperm transfer, we are once again grouping together a mere 37,600 out of 1.75 million species. For those of you interested in statistics, imagine that you were asked to draw 37,600 species from a pool of 1.75 million, and then to repeat that procedure. What would be the probability of picking exactly the same set of 37,600 species, the second time, by chance alone? In fact, that probability is so infinitesimally small that in this case no real statistician would need Joe Felsenstein's preferred three characters to conclude that spiders, as a group, are one of the best corroborated hypotheses around. So I suggest that at least some of the groups in our current classifications are real, natural, or monophyletic -- choose whichever adjective you prefer, since the choice actually makes no difference whatever to anything important. No one would claim that all our groups are real, but I would hope that we can all agree that basically we would like our classifications to consist entirely of groups like spiders -- groups based on the congruence of different sources of evidence. The same is true, of course, for species, but that is actually a somewhat tougher tune to carry, simply because there is such a diversity of species concepts. The amount of literature devoted to species concepts is astonishingly large, and all I can do here is to outline my own prejudices, so that you have a basis for evaluating my conclusions, and how they relate to the reality of species as well as groups. For, unlike the Non Systematists and their modern mirror images, I contend that both species and groups of them are, or at least can be, real. There is a book produced by Columbia University Press, edited by Quentin Wheeler and Rudolph Meier (2000), called "Species Concepts and Phylogenetic Theory: A Debate," which I usually recommend as a good place to get oriented to this chunk of the literature. The book represents a debate among five different species concepts, with the papers organized into three sections. In the first section, proponents of each concept get a chapter to outline their views. In the second section, each of the proponents gets a chapter to indicate what they think is wrong with each of

the competing presentations, and in the third section, each of the proponents gets a chapter to respond to the criticisms made of their views. That book provides us with at least a start on a taxonomy of species concepts. Some workers have enumerated several dozens of different species concepts, but most of those are just trivial variants of others, and the classification in the Wheeler and Meier book will amply serve my purposes. Here is the layout:

Proponent's name	Unique identifier	Proponent(s)	Species Real?
Biological	Interbreeding	Mayr	Yes
Hennigian	Internode	Meier & Willmann	Yes
Phylogenetic I	Diagnosable	Wheeler & Platnick	Yes
Phylogenetic II	Autapomorphic	Mishler & Theriot	???
Evolutionary	Historical Roles	Wiley & Mayden	Yes

First is the so-called biological species concept. Of course, this concept is actually no more or less biological than any of its competitors, so I call it the interbreeding concept. It dates back to the 1930's and views actual or potential interbreeding as the touchstone of species. Originally propounded by the vertebrate zoologists of the Non Systematics movement, this concept never won much favor with botanists, and since it doesn't apply at all to asexually reproducing organisms, it is unquestionably unfit as a general concept for systematics. And, of course, we now recognize that within any particular monophyletic group, retention of the ability to interbreed is a plesiomorphic character, and hence not a phylogenetically acceptable basis for classification. The Hennigian concept, dating back to the 1960's, is a definite improvement, viewing species as internodes -- those units set off by successive speciation events (or in some cases a speciation event plus a later extinction event). This takes care of the interbreeding as plesiomorphy problem. According to this view, however, ancestral or stem species cannot survive speciation events; they cease to exist even if one of their descendant species happens to be identical in all known characteristics. Any such actual example would clearly represent a case of theory triumphing over data, hardly an elegant solution to anything. The real phylogenetic species concept, dating back to the late 1970's, regards species as the smallest diagnosable samples of self- perpetuating organisms. It differs from another concept sometimes also called phylogenetic, the autapomorphic species concept, in differentiating between species and higher taxa, in that regard. Putative higher taxa, under the real phylogenetic species concept, must be evidenced by autapomorphic characters, but species are not required to have an autapomorphy, merely a unique combination of characters. In other words, species must be diagnosable, not necessarily autapomorphic. You might think that the difference between diagnosable and autapomorphic is insignificant, but consider one conceivable mode of speciation, in which a tiny peripheral population of a widespread species becomes isolated and eventually speciates. The peripheral isolate presumably has to develop at least one autapomorphy, in order to be recognized as different from the original species. If it is possible for that to happen without the widespread population also acquiring a new autapomorphy, then the "mother" population cannot remain a species under the autapomorphic species concept, because it no longer has any apomorphies not also shared by the peripheral species. Personally, I would argue that if the species we systematists hypothesize are to be useful to other evolutionary biologists, and most particularly to those biologists investigating speciation mechanisms, then they must be agnostic with regard to modes of speciation -- they cannot rule out some potential modes of speciation, such as peripheral budding, simply by theoretical fiat. Hence, to me, the autapomorphic species concept is simply unacceptable. Finally, there is the so-called evolutionary species concept, which dates back to Simpson rather than Mayr. Here again, it is no more or less evolutionary than any other concept,

and I call it the historical roles concept. Proponents like Wiley say that an evolutionary species is "an entity composed of organisms that maintains its identity from other such entities through time and over space, and which has its own independent evolutionary fate and historical tendencies." Since I don't know how to determine the evolutionary fate or historical tendencies of any of my spider species, I don't have much use for this mysticism. Interestingly, though, at least four of the five concepts seem to view species as real, just as real as higher taxa. Peculiarly, it is the one concept that treats species and higher taxa identically that has spawned some latter-day relunctance to view species as real! Bizarre, isn't it? I realize that not all the proponents of the autapomorphic species concept take this approach to its logical conclusion, but it is only under this concept that views like Pleijel's could even surface. Of course, for me, that's just another reason to consider the autapomorphic species concept guilty, as charged. But that still leaves us with the question of how best to reflect real taxa in our classifications. Back in the early days of the cladistics wars, it was fashionable in some circles to see classification as a serious problem for phylogeneticists. The problem, of course, was imaginary. As we all now recognize, cladistic analysis gave us the tools to discover that some groups, such as spiders, are natural, or putatively monophyletic, and that other groups, such an invertebrates or reptiles, are not. Cladists, of course, argued that only monophyletic groups should be included in classifications, and their opponents argued that this creates an overly complex system with too many groups being named. That, of course, was merely a canard. No monographer is, or ever was, forced to name any groups that they don't (or didn't) find it useful to name. All that phylogenetics requires is that no groups be named that are hypothesized to be non-monophyletic. For example, I recently published a monograph of the spider family Lamponidae (Platnick, 2000), in which I recognized three subfamilies, each of which is monophyletic according to the cladistic analysis carried out in the monograph. It is true that one of those subfamilies represents the sister group of the other two, but I chose not to apply a formal name to the latter group. If someone else wishes to, that's fine, but my classification is fully phylogenetic, as it includes only putatively monophyletic groups. There are even conventions proposed, such as phyletic sequencing, where the order in which taxa are listed in a formal classification provides information about the branching pattern, without requiring additional names. There are other conventions proposed, such as plesions, that can help cope with the problems encountered in trying to include fossil fragments in formalclassifications as well. But the basic point is simple: the Linnaean hierarchy is inherently pre-adapted to presenting cladistic information, for the hierarchy can mirror a cladogram in as much, or as little, detail as one would like. There are even conventions proposed for generating lots of categorical ranks for such purposes, for those favoring maximal amounts of detail. And if you don't like extra named ranks, you can always use a system like that recently suggested by Papavero, Llorente-Bousquets, and Abe (2001), in which you just add a suffix, like -1 or +2, to an existing group name to indicate that you're talking about a group one or two nodes above or below the named one. It is very strange, therefore, that some systematists have begun to argue that we need to abandon the Linnaean hierarchy entirely. You can often recognize these folks easily enough; they're the ones wandering around in t-shirts that read "Phyla Schmyla" (which is apparently a lapsus or mere printer's error; the shirts were actually supposed to have read "Yale Schmale"). And, of course, these are the same folks now promoting the so-called Phylocode (Cantino and de Queiroz, 2000) as the cure to all our woes. It seems that there are at least two motivations behind this movement, which I'm ashamed to say was originated by two herpetologists from the U.S., Kevin De Queiroz and Jacques Gauthier. One motivation, seemingly, is just to find some way to salvage non- monophyletic groups like Reptilia and Dinosauria, so that herpetologists are not inconvenienced by increased understanding of amniote interrelationships. But the real motivation, and I'll quote from De Queiroz & Gauthier (1990: 320), is that: "if the Darwinian Revolution is ever to occur in biological taxonomy ... then the role of the principle of descent must change ... from an after-the-fact interpretation to a central tenet from which the principles and methods oftaxonomy are deduced. ... Previously, taxa were

considered to be defined by characters and only interpreted after-the-fact as products of evolution." In the benighted view of these authors, most if not all previous systematists have been ignorant or misled essentialists or typologists who have been so stupid as to use character-based definitions or diagnoses of taxa. Now one thing I've learned from 30 years of watching biologists is that whenever you find one systematist calling another one an essentialist or a typologist, you can be 100% sure that the name-caller is purely, simply, and entirely, wrong, and is just creating a smokescreen to cover his or her tracks. In this case, there are a lot of tracks to cover, and they rank about as high on the SIP scale as any I've encountered; the SIP scale, incidentally, measures the levels of sanctimony, inflation, and pomposity. Rest assured, these authors truly believe that their proposals have already created (and here again I quote), a "new era in biological taxonomy" (de Queiroz & Gauthier, 1990: 312). That's one brave new world I'd choose to slide from! The complaints of these workers about the non-evolutionary basis of the existing system are entirely specious and unconvincing exercises in metaphysics, and are not worthy of serious attention. Let's look instead at what they suggest is an improved system, which they argue will do a better job of promoting explicitness, universality, and stability of names, as now encapsulated in the draft Phylocode. To accomplish this goal, they wish to define the names of taxa in terms of common ancestry, rather than characters. My colleagues Kevin Nixon and Jim Carpenter (2000) have therefore referred to this view as the node-pointing or NP system. Now that's a highly unfortunate choice of terms, since NP is a fine pair of initials that doesn't deserve to be sullied in such fashion; even my wife's initials are NP, which I guess makes us an NP-complete family. I'll call it the NB (or node-based) system instead, since that is the phrase actually used by de Queiroz and Gauthier themselves, and "N.B." has all the appropriate connotations. Those authors and their fans have repeatedly (i.e., de Queiroz and Gauthier, 1990, 1992, 1994, and ad nauseum ever since) illustrated:

Three classes of phylogenetic definitions

(a) A node-based definition is used to define the name of a clade stemming from the most recent common ancestor of two specified organisms, species or clades (e.g. Aves = the clade stemming from the most recent common ancestor of Struthio camelus and Passer domesticus).

[Of course, in the real world, you and I both realize that De Queiroz and Gauthier don't actually have any knowledge whatsoever about the most recent common ancestor of those two species; like us, they actually know only the characters that happen to optimize at the node of their preferred cladogram that happens to subtend those two taxa.]

(b) A stem-based definition is used to define the name of a clade of all species sharing a more recent common ancestor with one specific organism, species or clade than with another (e.g. Lepidosauromorpha = Lepidosauria and all species sharing a more recent common ancestor with Lepidosauria than with Archosauria).

(c) An apomorphy-based definition is used to define the name of a clade stemming from the first ancestor to evolve a specified character (e.g. Tetrapodomorpha = the clade stemming from the first vertebrate to evolve pentadactyl limbs). (de Queiroz and Gauthier, 1994: 29).

Of course, these are all old ideas, thoroughly discussed by Hennig and others in the context of fossil fragments, stem groups, crown groups, and the like. A favorite example of these authors is the lizard family Agamidae, and here again, I'll quote: "For example, the name 'Agamidae' might be defined as the clade stemming from the most-recent common ancestor of Agama and Leiolepis. Such a definition is thoroughly evolutionary in that the concept of common ancestry is fundamental to the meaning of the name" (de Queiroz and Gauthier, 1994: 29).

As if the definition could possibly be one wit less evolutionary if it concerned itself with the evidence from which those author's conclusions about common ancestry were drawn (after-the-fact)! The reason they like this example is that the Agamidae is another one of those groups, like Reptilia, that recent research suggests may be artificial. As their figure indicates, although these largely Old World lizards were formerly divided into two separate families, the Agamidae and Chamaeleonidae, some agamids may actually be closer to chameleons than to other agamids. To them, this is apparently a tragedy. An ordinary systematist would ask first, where on the cladogram the type genus of the Agamidae happens to fall, and would then choose a solution that conveys the phylogenetic information accurately while doing the least possible damage to existing concepts. Probably the easiest solution would be to restrict Agamidae to the group including Agama and supply a new family-group name for the remaining taxa previously misplaced in the Agamidae. Alternatively, all three clades could be lumped into a single family, a solution de Queiroz and Gauthier dislike because the name Chameleonidae happens to have priority over Agamidae. But de Queiroz and Gauthier are slippery as salamanders here, and elsewhere. Although they suggested that Agamidae might be defined as "the clade stemming from the most-recent commonancestor of [just two taxa] Agama and Leiolepis" they have also supplied a figure (and other examples) in which six and three, respectively, descendent taxa are used to point to nodes. Apparently, their view is that the more ambiguous our knowledge of relationships is, the more taxa should be used to point to a given node. As Nixon and Carpenter have shown, however, the choice of taxa can have major effects on the stability of the name involved. But ultimately, the question is what, exactly, it is that remains stable. In their lizard example, they suggest that:

"Under phylogenetic definitions, 'Chamaeleonidae" retains its association with the clade stemming from the most recent common ancestor of the species represented by filled circles, and 'Agamidae' retains its association with the clade stemming from the most recent common ancestor of the species represented by open circles, although the chamaeleonid species are now also thought to have descended from this ancestor. The manner in which the definitions are stated ensures that no names designate paraphyletic taxa, and neither splitting nor lumping occurs, but hierarchical relationships may be altered (e.g., Chamaeleonidae is now judged to be nested within Agamidae)."

As the last comment shows, what has actually been achieved, by abandoning Linnaean ranks and categories, as they advocate, is merely stability of spelling. Here is the Linnaean classification before the altered concepts of relationship:

Family Agamidae, containing taxa ABCDEF
Family Chamaeleonidae, containing taxa GHI

This Linnean classification accurately reflects the traditional view of the interrelationships of these taxa, under which taxa A, B, and C form the sister group of D, E, and F, with taxa G, H, and I representing the sister group of A-F together. What matters, here, however, is not that particular cladogram. What matters is that from the information in these two lines:

Family Agamidae, containing taxa ABCDEF
Family Chamaeleonidae, containing taxa GHI,

and that information alone, any systematist can deduce a whole series of three-taxon statements of relationship, all of which must be true if the classification is true: (AB)G, (AB)H, (AB)I, (AC)G, etc. -- if I've counted correctly, there are actually 63 such three-taxon statements that

follow from this classification. Such inferences are possible solely because of the use of Linnaean categories: the classification asserts that taxa A-F are not chamaeleonids, and that taxa G-I are not agamids, and it is precisely those prohibitions that allow the detailed hypotheses about relationships. As Popper (1959) has shown, it is also precisely by making prohibitions that hypotheses become testable and hence scientific. Contrast that with the de Queiroz and Gauthier solution, which looks like this:

[unranked group]Agamidae, containing taxa ABCDEFGHI
[unranked subgroup]Chamaeleonidae, containing taxa GHI

From this classification, one can deduce only 18 three-taxon statements: (GH)A, (GH)B, etc. They have indeed kept the spelling stable, but at the cost of reducing the information content of the classification by about 75%! And the name Agamidae, although still spelled the same, now refers to a different group (A-I rather than A- F). Imagine what would happen if, for example, it turned out that instead of being most closely related to crocodiles, birds are most closely related to chameleons. We would now have a node-based definition in which Agamidae would still persist as the spelling of a name, but would now refer to a group including both lizards and birds! It would be hard to imagine a case that would better fit Gene Gaffney's quip that stability equals ignorance.

According to de Queiroz and Gauthier, "a name should not designate different taxa [I guess they mean, unless the name is Agamidae], nor a taxon be designated by different names, at different times." By that standard, it is difficult to see any benefit whatever to node-based nomenclature. Of the two original group names, one now designates different taxa, and information content has been strangled. If instead we
opt for:

Agamidae, containing taxa ABC
DEFidae, containing DEF
Chamaeleonidae, containing GHI

(i.e., a conventional Linnaean classification, albeit one implying nothing more than a basal trichotomy among these three families), again one name now designates different taxa, but information content decreases only to 54 three-taxon statements, rather than 18.

If instead we opt for the more resolved, fully subordinated
classification:

Chamaeleonoidea, containing taxa ABCDEFGHI
Agamidae, containing taxa ABC
Chamaeleonidae, containging taxa DEFGHI
DEFinae, containing DEF
Chamaeleoninae, containing GHI

two names now designate different taxa (although one of them also remains accurate, with just a slight change in spelling) but information content zooms, to 81 implied three-taxon statements. In this
particular case, the phyletic sequencing option actually seems optimal, for if our earlier arrangement:

Agamidae, containing taxa ABC

DEFidae, containing taxa DEF
Chamaeleonidae, containing taxa GHI

is considered as sequenced, we can retrieve the full branching pattern, and hence all 81 implied three-taxon statements, while changing the meaning of only one name.If you are unhappy with implied three-taxon statements as a measure of information content, then try other measures; based on the comparisons by Mickevich and Platnick (1989), the results are unlikely to differ significantly. But consider for a moment what classification is all about. Is stability the primary goal of classification? Of course not! The primary goal of classification is and always has been maximal predictive power. Cladists have long argued that phylogenetic classifications are both the best summaries of the limited character information already available, and the best basis for making predictions about the much larger universe of as yet unstudied characters. Taxonomists are in the business of providing highly predictive classifications on the basis on extremely small amounts of data, and our track record of success, over the last two and a half centuries, is none too shabby. Every three-taxon statement that a classification implies represents a prediction that whatever future synapomorphies might be found, in any character system whatever, may fit the pattern (A & B as opposed to)C but will not fit the two conflicting patterns (A & C as opposed to)B or (B & C as opposed to)A. Again, scientific classifications prohibit things.

In contrast, the NB system achieves stability in spelling only, and often at great expense in terms of sacrificed information content and predictive power. Ultimately, no NB system can possibly produce a more predictive classification than would a fully informative, completely subordinated, sequenced, or otherwise conventioned Linnaean hierarchy based on the same cladogram. In other words, there is no possible potential gain in predictive power to be achieved by switching to an NB system, and many possible potential losses of that power. In short, it would indeed be rational to consider abandoning the Linnaean hierarchy, if by so doing we could achieve classifications with greater information content and increased predictive power. In my opinion, however, abandoning the Linnaean hierarchy in order to achieve stability in spelling accompanied by instability in meaning, frequently decreased information content, and frequently decreased predictive power is simply not rational. As a goal, stability in spelling seems dubious, at best; is this approach most stably spelled i-n-s-a-n-e, or merely i-n-a-n-e? Let me close with one final example, involving (of course) spiders. I was wandering around John Murphy's garden out in Hampton, and came across a nice jumping spider. Now, jumping spiders, the family Salticidae, are probably the easiest of all spider families to recognize. With their large anterior median eyes, their excellent vision, the often highly exuberant and ornamented morphology that males use in their elaborate courtship displays, and their prowess at jumping on prey several body-lengths away, salticids are quite distinctive. Probably the vertebrate analog would be best exemplified in Archie Carr's Subjective Key to the Fishes of Alachua County, Florida, in which the first couplet reads "Any damn fool knows a catfish." The botanical analog might be the mints, which may be the only plant family duffers like me can manage to recognize successfully, wherever we roam! A fair chunk of my time over the past 15 years has been spent on The World Spider Catalog (Platnick, 2001), which is now easily accesible via the aptly-named World Wide Web. The catalog provides a listing of all the currently valid spider species, all the other names that have ever been applied to them in the past, and all the citations to every important taxonomic treatment ever published on every one of those species. To my knowledge, the only thing like it currently available for any other sizable group of organisms is Bill Eschmyer's catalog of the fishes. If you visit the site, you'll find a summary table that shows, for each of the 109 currently recognized spider families, the numbers of currently valid genera and species, including, at the very end of the list, the salticids, with 4,834 species. Using the Linnaean hierarchy, when I identified the spider in John's garden as a salticid, I was asserting that John's spider is more closely related to any single species currently included within the Salticidae than it is to any single species that is

currently excluded from that family. In other words, if my identification, and the current classification, are both correct, then John's spider is more closely related to salticid species #1 than it is to any of the 32,752 spider species currently excluded from the Salticidae. It is also more closely related to salticid species #2 than it is to any non-salticid spider. So, assuming that the spider from John's garden belongs to one of the currently known 4,834 salticid species (and this being England, that's certainly a fair assumption), then my identification enables 4833 (other salticids) times 32,752 (non-salticids) three-taxon statements. So by placing the animal as a salticid, the current Linnaean hierarchy allows me to make 158,290,416 three-taxon statements about it, within spiders alone. If I were to expand the arena to include all arthropods, or all life, the number of implied three-taxon statements would, for all practical purposes, approach one-third of infinity -- the other two-thirds would be prohibited. That's none too shabby, for a single word -- Salticidae (admittedly, in a context provided -- solely -- by the Linnaean hierarchy, and the mutual exclusivity of equally ranked names it requires). Contrast that with an identical list of names that happen to end in "idae," and the numbers of genera and species they contain, but now under the assumption that the NB system is in use. Salticidae still refers to a group, that is still presumably monophyletic, but one can no longer infer anything about the status of the species included in other groups. Thus, for example, even the first family on that list, the Liphistiidae, could in fact, in the current classification, be just a subgroup of the Salticidae. The fact that both names end in "idae" -- in the NB system -- does not prevent either group from being a subgroup of the other. Now, in fact, calling John's spider a salticid does not allow me to make even a single three-taxon statement involving any other species. I can't say that it must be more closely related to another salticid than to a liphistiid, because Liphistiidae might in fact constitute the sister-taxon of John's species, for all I know (or, more accurately, for all the names in an NB system could ever let me know; unlike an NB systematist, I do actually know better than that!). So, let's see, we have John's salticid and either the Linnaean hierarchy, with 158 million predictions about spiders alone, or the NB system, with no useful predictions at all. The Linnaean system, with built-in exclusivity that forces classifications to prohibit things and thereby become scientific hypotheses, or the NB system, in which classifications prohibit nothing and names, by themselves, become mere propaganda, like the Phylocode itself. Gee, life is full of tough choices, isn't it?

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