

Symmetry in Evolution

by

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Diagrams by Christopher Engle

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ABSTRACT / INTRODUCTION

In this paper, evidence is presented that multicelled plants and animals are organized in accordance with a strict typological hierarchy consisting of a nested structure of monophyletic taxons (i.e., clades). It is further shown that, if this strict monophyletic hierarchy is to be regarded to be the result of an evolutionary process, then it must be the case that (in general) evolution has proceeded in such a way that each more-generic taxon has split *symmetrically* into two more-specific taxons: By *symmetrically* I mean that each more-generic taxon has ceased to exist *as an independent entity* after the split, instead continuing to exist only in the generic features of the two more-specific taxons into which it has become divided..

It is next demonstrated that there is *no* formulation of the evolutionary theory of *neo-Darwinism* that can account for this fact of symmetry in evolution, but that Robert F. DeHaan's theory of *macrodevelopment* (suitably expanded using concepts from nonlinear science) *can* explain evolutionary symmetry.

Finally the Stewart/Cohen formulation of the principle of evolutionary symmetry is presented and is then expanded to include cases of "temporary" imbalance in nested evolutionary bifurcations. The resulting *law of macrodevelopmental symmetry* is shown to provide for a far-more-elegant explanation of protein molecular-sequencing data than neo-Darwinism's clumsy and intricate "molecular clocks" hypothesis.

(Portions of this paper have been adapted from my book *Far From Equilibrium*, which can be found at www.laurelhighlandsmedia.com,¹ as well as from portions of the paper "Teleology and Information in Biology", which I presented at the first e-symposium of the International Society for Complexity, Information, and Design (ISCID) on October 3, 2002.²)

STRICT TYPOLOGICAL HIERARCHY IN EVOLUTION

Virtually all multi-cellular biological organisms, both past and present, can be scientifically, objectively classified according to a strict typological hierarchy. This is strong evidence that biological evolution generally proceeded by means of a process of *symmetrical* splits in which each *more-generic* “ancestor” taxon was entirely replaced by two *more-specific* “descendent” taxa. (Each such more-generic “ancestor” taxon *may* have had more-specific features, over and above its generic characteristics, but these more-specific features were not passed on to its “descendents”. Also, the two “descendent” taxa need not be at the next-lower *named* level in the hierarchy because there are always far more levels in the hierarchy than can be conveniently named.)

Typological hierarchies can themselves be classified into two types: those in which the boundaries between the taxa are indistinct and/or arbitrary (i.e., partially *subjective*), and those in which the boundaries between the taxa are clear and *objective*. (However, which hierarchical levels we actually give *names* to and what we *name* the individual taxa is, of course, arbitrary even in objective hierarchies.)

The *biological* taxonomic hierarchy is of the latter *objective* type, and the taxa within it are all *monophyletic* groups. A *monophyletic* group (i.e., a *clade*) consists of an “ancestor” taxon together with *all* taxa which are either immediate or more-distant “descendents” of that taxon. Figure 1, which can be found on the following page, depicts a simple nested hierarchy of monophyletic taxa. In addition to the more-specific “leaf” taxa at the top (Amphibians, Reptiles, and Mammals), we see a more-generic taxon which we have called Amniotes (i.e., animals which produce watertight eggs) and a still-more-generic taxon which we have called Tetrapods (i.e., four-limbed creatures).

The numbers beside each node of the hierarchy in Figure 1 (such as 1, 1.2, 1.2.2, etc.) may be thought of as biological “version numbers”: The first digit in the number represents a set of characteristics (or traits) at the most-generic level, the second digit (after the first period) represents a set of traits at the next-most-generic level, and so on down to the most-specific level, which is represented by the last digit. (A plus sign after the number means that this “ancestor” taxon *may* have had additional specific traits which were not passed on to its “descendents”.)

Notice in Figure 1 that a hierarchy of monophyletic taxa is a hierarchy in which each nested group is clearly defined and separated, which is exactly what we find in nature with respect to virtually all multi-celled animals and plants. Notice also that, in a sense, the root “ancestor” of every monophyletic taxon “dies” when it splits into its two immediate “descendent” taxa, continuing to survive only in the generic aspects of its “descendents”. That is why we may say that monophyletic splits are *symmetrical* splits. (This is reflected in the Venn diagram at the bottom of Figure 1 by showing the names *Amniotes* and *Tetrapods* in *italics*.)

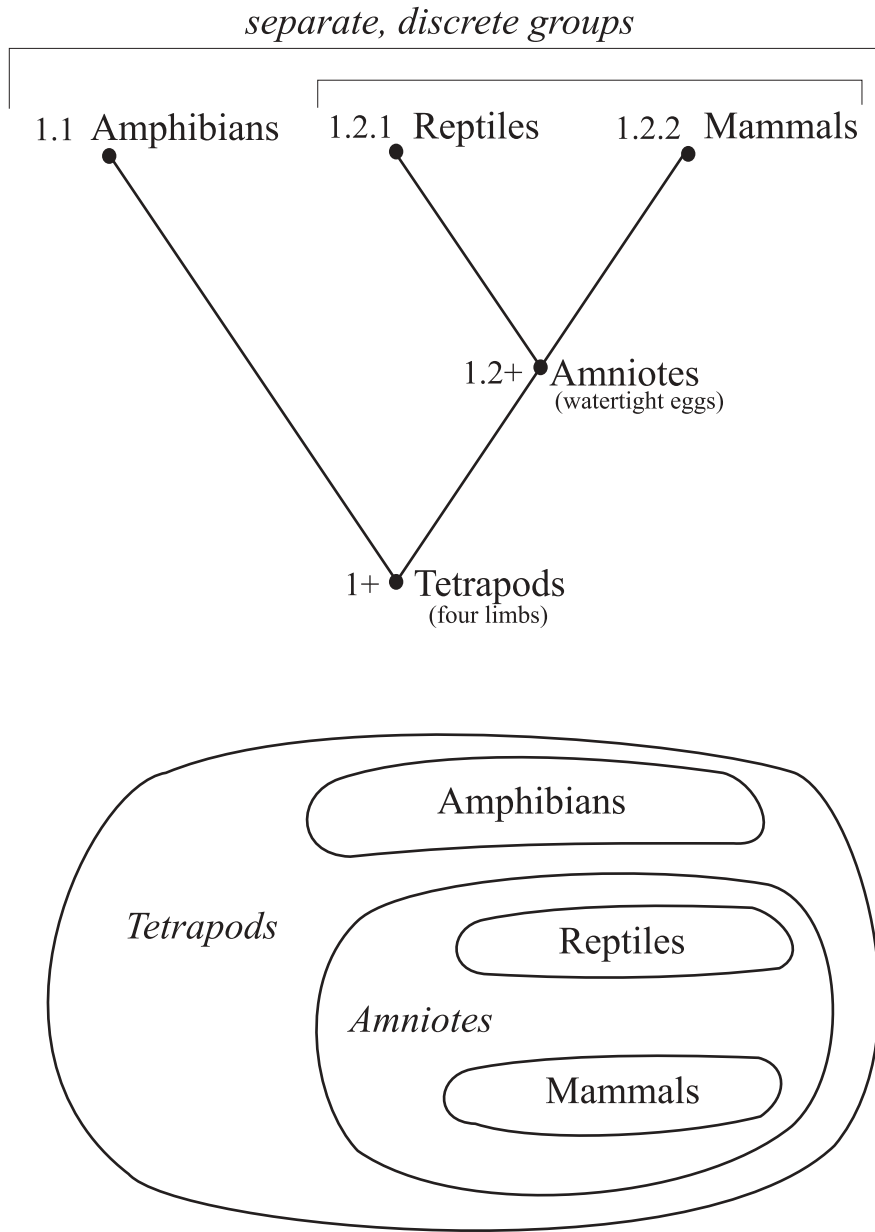


Figure 1 (*Monophyletic* hierarchy = CORRECT hierarchy)

Finally, note that, in the foregoing paragraphs, the word “taxon” means both “the root ancestor taxon” and “the group consisting of the root ancestor taxon plus all of its descendent taxa”. (In the case of *monophyletic* taxa there is no real conflict between these two complementary meanings.)

The most-modern and by-far most-dominant contemporary biological system of classification is *cladistics*. Cladistics uses *monophyletic* taxa exclusively, because that way

of classifying multi-celled biological organisms fits the biological facts best. By contrast, the basic problem with older biological classification systems, such as so-called *evolutionary systematics* and the *Linnean system* (kingdom, phylum, class, order, family, genus, and species), is that they sometimes use *paraphyletic* taxa in addition to monophyletic taxa.

A *paraphyletic* taxon (like a monophyletic taxon) consists of a group of “descendent” taxa, together with all of their common “ancestors”, down to a root “ancestor” taxon. However, *unlike* the monophyletic taxon, in the *paraphyletic* taxon not all descendents of this root “ancestor” taxon are included in the group. Consequently a *paraphyletic* taxon tends to suggest that the group of descendents was initially formed by “splitting off” from the root “ancestor” taxon, which itself continues to exist much as it did before the split. That is why we may regard the splits in a hierarchy of *paraphyletic* taxa to be *asymmetrical* splits.

Figure 2, drawn on the following page, shows a *paraphyletic* version of the monophyletic hierarchy depicted in Figure 1. It is important to note that Figure 2 is now known to be *incorrect*. However, Figure 2 *does* correspond to the textbook orthodoxy we were taught in school – namely, that the reptiles “split off” from the amphibians and that, later, the mammals “split off” from the reptiles.

Just as in Figure 1, the numbers in Figure 2 represent biological “version numbers”: The number 1 represents Amphibians, 1.1 represents Reptiles, and 1.1.1 represents Mammals. In Figure 2 the Mammals are a paraphyletic taxon because they are shown as descending from the Reptiles, who are themselves not part of the Mammal taxon group. Similarly, the *amniotes* (Reptiles plus Mammals) form a paraphyletic taxon because they are shown as descending from the Amphibians, who are not themselves part of the *amniotes* group. In other words, Figure 2 depicts the *amniotes* (actually, the Reptiles) as “splitting off” from the Amphibians: Later, the Mammals, in turn, are depicted as “splitting off” from the Reptiles.

The names *amniotes* and *tetrapods* do not appear in Figure 2 because, while both of these names could be regarded as naming paraphyletic taxa, no actual “ancestor” taxon corresponds to either of them in Figure 2. This is because the name of a *paraphyletic* taxon can only name the group, since there is really no corresponding actual, separate, unique “ancestor” taxon at the root of a paraphyletic taxon.

Notice also in Figure 2 that a hierarchy of paraphyletic taxa ultimately produces a smooth gradation of organisms at the current, contemporary “leaf” level. (This is represented by the horizontal series of version numbers 1, 1.1, and 1.1.1 at the top of Figure 2.) In other words, no clear, distinct hierarchy is visible at the current, contemporary level. Consequently, where we draw the divisions between current biological organisms that are regarded as having arisen from a *paraphyletic* hierarchy is, to a large degree, *subjective* and *arbitrary*. Because of this, notice, in particular, that the Reptiles in Figure 2 are a

transitional taxon existing *between* Amphibians and Mammals. (But note, again, that Figure 2 is now known to be *incorrect*.)

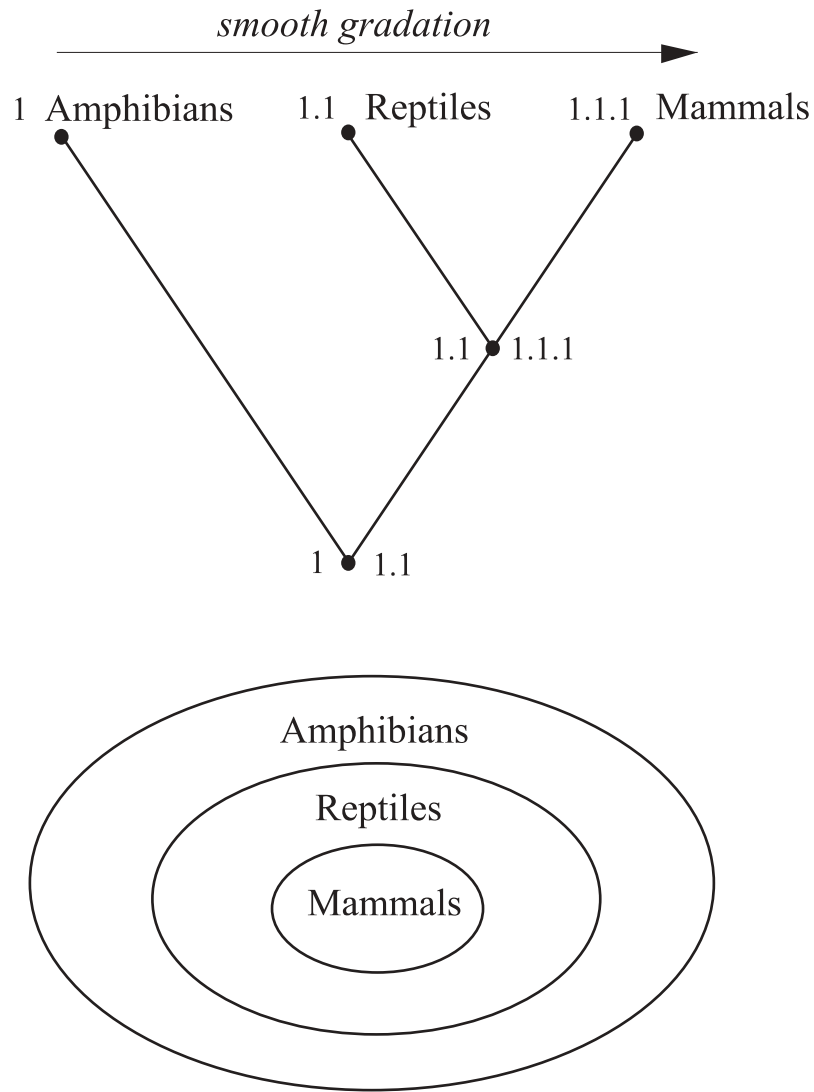


Figure 2 (*paraphyletic* hierarchy = INCORRECT hierarchy)

A final way in which biological organisms can be grouped together is in a *polyphyletic* group. A *polyphyletic* group of organisms (unlike the monophyletic and paraphyletic groups) *cannot* be traced back to a common “ancestor”. Rather, a *polyphyletic* group of organisms is grouped together (in part, at least) on the basis of *analogous* traits, rather than *homologous* traits. *Analogous* traits are those which have evolved separately along lines of *parallel* evolution (also called *convergent* evolution). By contrast *homologous*

traits are those which have evolved “vertically” up the evolutionary tree, such that they can be used as the basis for evolutionary classification. *No* systems of biological classification (neither the Linnean, the “evolutionary”, or the cladistic) permit the use of *polyphyletic* taxa. (Probable examples of *polyphyletic* groupings include: the class of all flying vertebrates, the class of all warm-blooded animals, and the class of all swimming amniotes.)

Nevertheless, determining *which* biological traits are *analogous* and *which* biological traits are, on the contrary, *homologous* is often not easy! To make this determination as objective as possible, biological taxonomists (i.e., *cladists*) try to consider many separate traits, treating them statistically via computer analysis in order to avoid having any subjective preferences for “pet” traits. The cladists then select from the many possible monophyletic trees (*cladograms*) according to the criteria of parsimony and simplicity, together with a consideration of the fossil evidence. (At least they *should* consider the fossil evidence; they are sometimes remiss in that respect!) The American Museum of Natural History summarizes well the situation of contemporary cladistics:

Although cladistics provides us with the best current method of determining evolutionary relationships, it is not perfect. Contradictions among advanced features often suggest alternative evolutionary trees. In such cases, the cladogram consistent with the most features is chosen for the time being. True evolutionary relationships can never be definitively established, either by examining fossils or studying DNA. But we can get closer and closer to the actual sequence of evolution by testing hypotheses about relationships with as many features as possible.³

In spite of these uncertainties concerning the precise results of cladistic classification, cladists *are* sure that evolution proceeded according to the process suggested by cladistic *monophyletic* evolutionary relationships (*symmetrical* splitting, Figure 1) rather than the process suggested by *paraphyletic* relationships (*asymmetrical* “splitting off”, Figure 2). How can they be so sure?

Evidence for Exclusively Monophyletic Evolutionary Relationships

In the first place, closer examination of both living multi-celled biological organisms and the fossils of their extinct ancestors began to cast doubt on previously-assumed neat transitional evolutionary series, such as the series of amphibians-to-reptiles-to-mammals: Such a series would tend to suggest that reptiles should be *transitional* (i.e., “half-way”) between amphibians and mammals in their morphological characteristics (as is implied by Figure 2), whereas closer examination revealed that both reptiles and mammals are instead morphologically *equidistant* from amphibians (as is implied by Figure 1). As Michael Denton has written:

[I]t has always been traditionally considered that the morphology of the vertebrate heart and aortic arches in fish, lungfish, amphibians, reptiles, and mammals form a clear series. However, the sequence is very much a broken one, and it is doubtful to what extent it really gives evidence of being a sequence. Take one section of the traditional sequence: amphibian → reptile → mammal. There are many detailed aspects of the comparative anatomy which do not support it, for example, the aortic

arches. The major vessel leaving the left ventricle in a reptile, which is the major vessel carrying aerated blood from the heart, is formed from the fourth right aortic arch, while in a mammal it is derived from the left aortic arch. Instead of arranging them in a sequence amphibian → reptile → mammal, we might just as easily arrange them circumferentially, with reptile and mammal equidistant from amphibians. . . .

But if there is some hint of a sequence in the case of the aortic arches, it is hopeless trying to arrange vertebrate egg cells, and the pattern of cell division in the earliest stages of embryology up to the formation of the blastula and beyond, into any sort of convincing sequence. In some ways, mammalian eggs are closer in their initial pattern of development to those of a frog [i.e., an amphibian] than to any reptile.⁴

Of course, classifying multi-celled biological organisms *morphologically* is non-quantitative, difficult, and often controversial: The “clincher” came when scientists began to *quantitatively* compare the differences between the sequences of amino acids in proteins that are common to many different species of multi-celled biological organisms. Michael Denton explains:

In the late 1950s it was found that the sequence of a particular protein, say, hemoglobin, was not fixed but varied considerably from species to species. The amino acid sequence of a protein from two different organisms can be readily compared by aligning the two sequences and counting the number of positions where the chains differ. . . [T]he differences between two proteins can be quantified exactly, and the results of these measurements can provide an entirely novel approach to measuring the differences between species. . .

It became increasingly apparent as more and more sequences accumulated that the differences between organisms at a molecular level corresponded to a large extent with their differences at a morphological level; and that all the classes traditionally identified by morphological criteria could also be detected by comparing their protein sequences. . .

However, as more protein sequences began to accumulate during the 1960s, it [also] became increasingly apparent that the molecules were not going to provide any evidence of sequential arrangements in nature, but were rather going to reaffirm . . . that the system of nature conforms fundamentally to a highly ordered hierarchic scheme. . . Moreover, the divisions turned out to be more mathematically perfect than even the most die-hard typologists would have predicted.⁵

Michael Denton provides detailed and conclusive proof of this in his chapter titled “A Biochemical Echo of Typology” from his brilliant book *Evolution: A Theory in Crisis*.⁶ For example, Denton cites information from the *Dayhoff Atlas of Protein Structure and Function* which shows clearly that the percent sequence divergence between the protein cytochrome C₂ in the bacterium *Rhodospirillum rubrum* and the corresponding cytochromes in *all* eukaryotic multi-celled organisms varies narrowly between 64% and 69%. (For example: humans 65%, rabbits 64%, ducks 64%, rattlesnakes 65%, bullfrogs 65%, tuna 65%, fruit flies 65%, and sunflowers 69%.) In other words, *all* contemporary eukaryotic multi-celled animals are typologically *equidistant* from the lowly bacteria, with no paraphyletic “transitional forms” bridging this gap! As Denton remarks:

Considering the enormous variation of eukaryotic species . . . and considering that eukaryotic cytochromes vary among themselves by up to about 45%, this must be considered one of the most astonishing findings of modern science.⁷

Furthermore, this clean, nested, monophyletic hierarchical pattern continues as we examine the more-specific taxonomic levels. For example, a comparison between the protein cytochrome C of the silk moth (an *insect*) and the corresponding cytochromes of the *vertebrates* reveals a relatively narrow variation of between 25% and 30% (horse 27%, pigeon 25%, turtle 26%, carp 25%, and lampreys 30%), which is strong evidence that there are no “transitional taxa” between insects and vertebrates.⁸ Or, again, the percentage difference between the cytochrome C in a carp (a *fish*) and the cytochrome C in the *tetrapods* varies quite narrowly between 13% and 14%: For the horse and the rabbit (both mammals) the variance is 13%, for the turtle (a reptile) it is also 13%, and for the bullfrog (an amphibian) the variance remains 13%. This, in turn, is strong evidence that amphibians are *not* “transitional” between fishes and reptiles (nor are reptiles “transitional” between amphibians and mammals), and that the statements of neo-Darwinian textbook orthodoxy saying that “the amphibians *split off* from the fishes, the reptiles *split off* from the amphibians, and (finally) the mammals *split off* from the reptiles” are highly unlikely to be true!⁹

If we choose a different protein, for example, hemoglobin rather than cytochrome C, then the difference between the carp (a *fish*) and the *tetrapods* varies closely *around 50%* for hemoglobin, rather than *around 13%-14%* for cytochrome C. Nevertheless, the tetrapods all remain *equidistant* from the carp, whether we measure them using hemoglobin, cytochrome C, or some other protein!

Michael Denton continues:

[The tetrapods] can themselves be divided into two basic classes, by virtue of their molecular similarities. One class contains the amphibians, and the other the reptiles & mammals. Again the subdivision corresponds to that based on classical morphological grounds, but whichever species are taken for comparative purposes, the distance between amphibian species on the one hand and mammalian & reptilian species on the other is always the same. No amphibian species is midway between other amphibians and the reptiles & the mammals. Similarly, no reptilian or mammalian species is closer to amphibians than any of the others. . .

The classification system that is derived from these comparative molecular studies is a highly-ordered non-overlapping system composed entirely of groups within groups, of classes which are inclusive or exclusive of other classes. There is a total absence of partially inclusive or intermediate classes, and therefore none of the groups traditionally cited by [neo-Darwinian] biologists as intermediate gives even the slightest hint of a supposedly transitional character.¹⁰

Denton goes on to show that the molecular evidence supports the appropriateness of a similarly strict monophyletic hierarchy in the classification of the primates (monkeys, gibbons, apes, and man). Furthermore, subsequent work comparing the sequences of *nucleotides* in *RNA* for various species (rather than the sequences of *amino acids* in *proteins*) has given the same kind of results as those that we have described above.¹¹

Ultimately, therefore, it is the *molecular* evidence which has “clinched” the case for a cladistic, monophyletic classification of multi-celled biological organisms (corresponding to the *symmetric* splitting shown in Figure 1), as opposed to the older classification

systems (such as the “evolutionary” and the Linnean), which erroneously included paraphyletic groups in their hierarchies. (These erroneous paraphyletic groups correspond to the *asymmetrical* “splitting off” shown in Figure 2.)

Another complementary way of viewing this cladistic, monophyletic “tree” of taxa is to recognize that it has a self-similar *fractal* structure. In other words, as we magnify our view of this genealogical “tree”, it continues to “look the same” at increasing levels of magnification. M.E.J. Newman and R.G. Palmer explain:

As long ago as 1922, it was noted that if one takes the taxonomic hierarchy of current organisms, counts the number of species n_s in each genus, and makes a histogram of the number of genera n_g for each value of n_s , then the resulting graph has a form which closely follows a power law (Willis 1922, Williams 1944):

$$n_g \text{ [is proportional to]} n_s^{-B}$$

[B, or beta, is a constant that varies for differing groups of organisms: For flowering plants it equals 1.5 ± 0.1 .]

Recently, Burlando (1990, 1993) has extended these results to higher taxa, showing that the number of genera per family, families per order, and so forth, also follow power laws, suggesting that the taxonomic tree has a *fractal* structure.¹²

Perhaps the most-important conclusion we can draw from this fact of the biological universality of monophyletic, fractal structure is that biological evolution must have proceeded historically from the *generic* to the *specific*, as is clearly shown in Figure 1. In other words, Figure 1 clearly reveals that the most-generic (least-specific) *tetrapods* appeared prior to the intermediate-generic (intermediate-specific) *amniotes*, which (in turn) appeared prior to the least-generic (most-specific) *amphibians*, *reptiles*, and *mammals*. This fact is confirmed not only by inferences from molecular biology and cladistics, but also by the fossil evidence: For it is now generally conceded that there is overwhelming fossil evidence that the generic body plans of *all* multi-celled biological organisms (i.e., the phylum-level taxa) appeared relatively quickly during the Cambrian era, with the more-specific taxa following later on in the approximate order of their specificity. In other words, the fossil evidence shows that the more-specific the taxon, the later it appeared in evolutionary history. (This is not to deny, of course, that what we are calling *more-generic* “ancestors” *may* have had *more-specific* features that were irrevocably lost to their “descendents” as a result of the evolutionary process.)

As the great geneticist Richard Goldschmidt wrote (commenting on the fact that a phylum contains classes, a class contains orders, and so on with increasing specificity):

Can this mean anything but that the type of the phylum was evolved first and later separated into the types of classes, then into orders, and so on down the line? This natural, naïve interpretation of the existing hierarchy of forms actually agrees with the historical facts furnished in paleontology. The phyla existing today can be followed furthest back into remote geological time. Classes are a little younger, still younger are the orders, and so on until we come to the recent species which appear only in the latest geological epochs. Thus logic as well as historical

fact tell us that the big categories exist first, and that in time they split in the form of the genealogical tree into lower and still lower categories.¹³

In contrast to the *correct* monophyletic tree shown in Figure 1, there is *no* clear historical movement from the generic to the specific in the *incorrect* paraphyletic tree shown in Figure 2: While, superficially, it may appear from Figure 2 that reptiles are “more generic” than mammals, and that amphibians are, in turn, “still more generic” than reptiles, neo-Darwinists would be the first to admit that these *apparent* differences in specificity between amphibians, reptiles, and mammals are purely subjective and arbitrary, depending on which traits of these multi-celled biological organisms we choose to look at.

Finally, we should note that the reason we have confined this discussion of taxonomy and cladistics to *multi-celled* biological organisms is that the taxonomy of *one-celled* organisms is far more complex than that of multi-celled organisms, due to the frequency of such phenomena as *horizontal gene transfers* and *endosymbiosis* in the one-celled realm. For this reason, it has recently been suggested that the “tree of life” is quite tangled at its one-celled base, and that consequently we may *never* be able to trace life back to a single archetypical cell.¹⁴

THE NEO-DARWINIAN EXPLANATION

Neo-Darwinism is (of course) the currently dominant, essentially *linear* theory of biological evolution. Neo-Darwinism builds on Charles Darwin's theory of evolution, as found especially in his famous book *On the Origin of the Species* (1st edition, 1859), but refines Darwin's theory through the use of the results of statistical *population genetics*, a field of study which was established by the Austrian monk and abbot Gregor Mendel (whose results became generally known only after 1900).

The basic principles of neo-Darwinism are often stated approximately as follows:

1. Microscopic, *purely random* changes (such as mutations and copying errors) occur within the genetic code (*genotype*) of biological organisms, resulting in macroscopic variations in the physical characteristics (*phenotype*) of the individuals within the population of any given species. The vast majority of these purely random microscopic changes are harmful, but a very few are helpful in promoting the survival of the individual and therefore of the species of which that individual is a member.
2. Nature selects phenotypes by means of an essentially *deterministic* macroscopic process called *natural selection* (analogous to the artificial selection practiced by human breeders of plants and animals) according to the principle of the *survival of the fittest*: Those individuals of the species having phenotypes *favorable* to survival tend to produce offspring which carry the corresponding genotype on to the next generation. By contrast those individuals of the species having *unfavorable* phenotypes tend to die off before they can reproduce themselves. (This process of *natural selection* is often said to proceed by *trial-and-error*.)
3. By means of the above two basic principles, all of the various species (together with biological phyla, classes, families, etc.) comprising the biosphere have been created and transformed gradually, minutely, step-by-step throughout the earth's long history.

Now, a major problem with this formulation of neo-Darwinism lies in point 2. For it is evident that concepts such as *natural selection*, *survival of the fittest*, and *trial-and-error*, as stated, are really *teleological* concepts, rather than scientific concepts: Nature is being *personified* as a *conscious being* who *chooses* (i.e., *selects*) by *trial-and-error* which individuals of the species are to survive in accordance with a *goal* (i.e., *survival of the fittest*). We therefore need to recast neo-Darwinism into a scientific "bracket out the subject" formulation (rather than a "bracket out the object" teleological formulation) in order to consider it to be a truly scientific theory.

Fortunately the neo-Darwinists themselves have re-interpreted point 2 scientifically, as follows:

2. Different phenotypes among the individuals who comprise a species have statistically different rates of reproduction and statistically different rates of mortality. Phenotypes which have the *highest* rates of reproduction and/or the *lowest* rates of mortality tend to predominate within the species and pass their corresponding genotypes on to the next generation. Moreover, random microscopic changes to the genotype (as specified in point 1) constantly result in new macroscopic phenotypes which are then subjected to these same essentially deterministic processes of *differential reproduction* and *differential mortality*.

Notice in particular that in neo-Darwinism the element of objective, absolute chance is confined entirely to the *microscopic* world of the genotype, while determinism essentially rules in the *macroscopic* world of the phenotype in the form of the “iron law” of differential reproduction and differential mortality (“survival of the fittest”). In this respect neo-Darwinism somewhat resembles quantum theory, which is characterized by objective randomness at the sub-microscopic level encapsulated within the *linear*, deterministic Schrodinger wave function at the macroscopic level. Another similarity between the two theories is that neo-Darwinism and quantum theory both rely heavily on the mathematics of statistics in their formulation.

Of course neo-Darwinists are not entirely unaware that the mathematics which describes differential reproduction versus differential mortality can result in nonlinearities (for example, the famous *logistic equation* and the nonlinear *Lotka-Volterra predator-prey equations*). Nevertheless, neo-Darwinists almost always regard any elements of chance which happen to arise at the *macroscopic* level due to such nonlinearities to be “merely subjective”, an attitude which enables them to continue to view the macroscopic processes of differential reproduction and differential mortality as being *essentially* linear and deterministic. (As an exception to this generalization, the maverick neo-Darwinist Stephen Jay Gould *does* regard macroscopic absolute chance to objectively exist, but only *chaotically*, i.e., *not* within any teleologically meaningful context of external and internal conditional equifinality.)

Specifically with respect to the twin evolutionary facts of strict typological hierarchy and monophyletic fractal symmetry, it is important to note that *all* proposed neo-Darwinist evolutionary processes involve the *asymmetrical* “splitting off” of the newly-emergent taxon from the old taxon. For example, Darwin’s original theory of *phyletic gradualism* involves a continual asymmetrical “splitting off” of individuals into different phenotypes due to random mutations in their corresponding genotypes. “Natural selection” (i.e., differential reproduction and differential mortality) then determines which of these “split off” phenotypes will survive to become new varieties, species, and higher-level taxa. By contrast, in the *punctuated equilibrium* model of Eldredge and Gould, this “splitting off” process occurs much less frequently, but speciation according to punctuated equilibrium still requires a small population to be *geographically* “split off” from the main population of the ancestor species. Even Goldschmidt’s “hopeful monster” scenario requires an

individual to be “split off” from the main population of the ancestor species via a radical mutation or radical genetic reorganization of that individual. Yet we have seen that *all* of the evolutionary evidence supports the *symmetrical* “splitting” of taxa, as shown in Figure 1, rather than the *asymmetrical* “splitting off” of taxa depicted in Figure 2. In short, there is *no* evidence for the traditional neo-Darwinian story that amphibians “split off” from the fish, that reptiles then “split off” from the amphibians, and that, finally, the mammals “split off” from the reptiles! As Michael Denton puts it:

One of the most celebrated cases of [supposed] sequence is that of the vertebrate classes leading from the cyclostomes, through fish, amphibians, and reptiles to the mammals. While no [neo-Darwinian] has ever claimed that any of the living representatives of any vertebrate class is *directly* ancestral with respect to another vertebrate group, it is definitely *implied* that in terms of their general biology and overall morphology there are clear grounds for viewing the series as a natural phylogenetic sequence. .

[Y]et in terms of their biochemistry, none of the species deemed “intermediate”, “ancestral”, or “primitive” by generations of [neo-Darwinist] biologists, and alluded to as evidence of sequence in nature, shows any sign of their supposed intermediate status.¹⁵

For the same reason, there is also no scientific evidence for the philosophical *nominalism* of most neo-Darwinists. This nominalism is evident, for example, in the following statement from the noted neo-Darwinist Ernst Mayr:

[T]he assumptions of [neo-Darwinian] population thinking are diametrically opposed to those of the typologist. The populationist stresses the uniqueness of everything in the organic world. . . . All organisms and organic phenomena are composed of unique features and can be described collectively only in statistical terms. . . . [O]nly the individuals of which the populations are composed have reality.¹⁶

Yet we have seen, that, on the contrary, the hierarchical organization of multi-celled biological organisms into real, clearly-defined monophyletic “groups within groups” is simply a *scientific fact* which most neo-Darwinists adamantly refuse to recognize, essentially for dogmatic philosophical reasons.

What about the clear scientific evidence that more-generic taxa appeared *before* more-specific taxa during the history of life on earth? Neo-Darwinism can give no coherent explanation of this either, fundamentally because it is a *linear* scientific theory whose primary mechanism, “natural selection”, causes the statistical distribution of phenotypes to track *any* environmental change, whether that particular environmental change happens to favor organisms with *more* specificity or *less* specificity. Furthermore, according to “natural selection” any such change in the statistical distribution of phenotypes is easily *reversible* if environmental conditions change back to their former state.

Consider, for example, Darwin’s own discussion of the only diagram that appears in his famous book, *On the Origin of the Species*. Immediately prior to discussing this diagram, Darwin writes:

[I]n the general economy of any land, the more widely and perfectly the animals and plants are diversified for different habits of life, so will a greater number of individuals

be capable of there supporting themselves. A set of animals, with their organization but little diversified, could hardly compete with a set more perfectly diversified in structure. . .

. . . [W]e may, I think, assume that the modified descendants of any one species will succeed by so much the better as they become more diversified in structure . . .¹⁷

And a little later Darwin writes:

[A]s a general rule, the more diversified in structure the descendants from any one species can be rendered, the more places they will be able to seize on, and the more their modified progeny will be increased.¹⁸

These passages might suggest that Darwin believed that the evolution of taxa *from* the generic *to* the specific is favored by “natural selection”. Yet the full context of Darwin’s discussion of his diagram belies this:

Darwin’s diagram shows eleven species (which Darwin says are all members of *the same genus* “large in its own country”) marked *A* through *L* at the bottom of the diagram. A complex and diversified pattern of branches, forming a tree, extends up from species *A*, ultimately leading to eight species marked *a*¹⁴ through *m*¹⁴ as the “leaves” of this tree at the top of the diagram. A similar, but less “full” tree leads up from species *I* to six species marked *n*¹⁴ to *z*¹⁴, also at the top of the diagram. After a rather long and involved discussion, Darwin states:

[T]he six new species descended from (*I*), and the eight descended from (*A*), will have to be ranked as very distinct genera, or even as distinct sub-families.¹⁹

Now, the interesting thing is that if these two new groups of species are ranked as genera, then there has been *no* movement either from the generic to the specific *or* from the specific to the generic during the long course of evolution depicted in Darwin’s diagram! Rather, what has happened is that *one* genus containing eleven species has been replaced by *two* genera containing six and eight species, respectively, each such new genus being at the *same* level of specificity as the original genus. (In addition, species *F* continues in a straight line from the bottom up to the top of Darwin’s diagram, all of the original species *except* for *F* having become extinct).

On the other hand, if the two new groups of species at the top of Darwin’s diagram are ranked at the more-generic level of *sub-family*, then the historical movement of evolution depicted in the diagram is actually from the *specific* to the *generic* (since *one* genus turns into *two* sub-families)!

A few paragraphs later, Darwin further suggests that “[I]f, in our diagram, we suppose the amount of change represented by each successive group of diverging dotted lines to be very great”, then the two new groups of species “will form two distinct families, or even orders, according to the amount of divergent modification supposed to be represented in the diagram. And the two new families, or orders, will have descended from two species of the original genus.”²⁰

What Darwin is essentially proposing is that, as the varieties of biological organisms diversify via natural selection, they first give rise to species, then later group themselves into genera, still later into families, and (finally) into orders, so that the sequence of evolution historically proceeds from the *more-specific* taxa to the *more-generic* taxa. This in spite of the fact that the individual organisms *themselves* are all-the-while becoming increasingly diverse and specific! Quite apart from being a strange and confusing model, Darwin's proposal flatly contradicts what we now know to be the truth: namely, that the more-generic taxa appeared *before* the less-generic taxa during the long course of evolutionary history.²¹

Now, even though neo-Darwinists can't *explain* the scientific evidence represented by these two vital facts of evolution (i.e., strict monophyletic typological hierarchy, together with evolution's progression from the generic to the specific), they nevertheless understandably feel strongly obligated to *explain* these facts *away*. This *explaining-away* process began with Darwin himself in his book *On the Origin of the Species*:

Darwin was well aware that the theory of evolution which he was proposing (i.e., biological varieties and species "splitting off" from one another numerous times via the processes of random microscopic variation and macroscopic "natural selection") would necessarily create a smooth continuum of creatures such as that suggested in Figure 2 by the "version number" series 1, 1.1, 1.1.1 across the top of the figure. Why, then, (Darwin asked himself) is such a continuum not actually found in nature? The answer he suggested was that the *pattern of extinction* created by "natural selection" would be such as to cause "gaps" to occur in this continuous series. For example, if Reptiles were an *extinct* taxon (instead of a currently existing one), then the "version" number series at the top of Figure 2 would "jump" discontinuously from 1 to 1.1.1, rather than proceeding continuously from 1 to 1.1 to 1.1.1. Such a pattern of extinction might be expected to arise, Darwin theorized, if species became extinct *principally due to intense competition with closely-related species*, including competition with their immediate parent.

In discussing his own diagram in *On the Origin of the Species*, Darwin makes it clear that it is principally the *extinction* of virtually all of the species *B* through *H* (which intervene between species *A* and *I* at the bottom of his diagram) that creates the separation between the two genera (or sub-families, or families, or orders) at the top of his diagram. He writes:

The intermediate species, also (and this is a very important consideration), which connected the original species (A) and (I), have all become, excepting (F), extinct, and have left no descendants. Hence the six new species descended from (I), and the eight descended from (A) will have to be ranked as very distinct genera, or even as distinct sub-families.²²

Unfortunately, a very significant problem with Darwin's patterned-extinction hypothesis is that, while such extinctions might create an irregular *granularity* within the continuum of contemporary organisms (such that the contemporary biological "version numbers" might, for example, jump from 1 to 1.1.1 to 1.1.1.1.1 to 1.1.1.1.1.1.1.1.1, and so on), this

pattern would *still* not duplicate the clear, monophyletic “nested hierarchy” pattern that actually occurs in nature (for example, the monophyletic “version number” series from 1 to 1.2.1 to 1.2.2 that occurs at the top of Figure 1). Darwin’s patterned-extinction hypothesis therefore fails to “explain away” the formidable typological evidence against his theory.

Even more damaging, as neo-Darwinist paleontologist Niles Eldredge admits in his book *The Miner’s Canary*, paleontologists have found *no* evidence that Darwin’s proposed process for biological extinction (namely, the supposedly intense competition for survival between closely-related species) is of any importance – and such a process may not, in fact, occur at all!²³

The Molecular Clocks Hypothesis

There is another far-more-elaborate hypothesis with which the neo-Darwinists have tried to “explain away”, in particular, the overwhelming *biochemical* evidence against neo-Darwinism which we presented above. That hypothesis is the *molecular-clocks hypothesis*. According to the molecular-clocks hypothesis, the reason (for example) that the percentage difference between the cytochrome C in a carp (a fish) and the cytochrome C in all of the tetrapods varies quite narrowly between 13% and 14% is that the cytochrome C in all of the tetrapods has been subject to mutation at the same steady, minute, clock-like rate over the millions of years of geological time since the tetrapods “split off” from the fish. Furthermore, the reason the percentage difference between the hemoglobin in a carp (a fish) and the hemoglobin in all of the tetrapods varies narrowly around 50% (rather than 13% - 14%) is that the mutational “molecular clock” for hemoglobin ticks at a rate that is over three-times the rate of the “molecular clock” for cytochrome C (at least, with respect to the evolution of the tetrapods since they supposedly “split off” from the fish).

Applied to all of the many taxonomic groupings of multi-celled biological organisms and to all of the many families of proteins, this molecular-clocks hypothesis requires the existence of hundreds (and perhaps thousands) of separate molecular clocks, each keeping perfect, regular calendar time, yet each also ticking at a *different* constant rate that depends on *a*) the difference between the taxonomic groups being measured and *b*) the family of proteins being measured.

Now, according to neo-Darwinism, there are only two kinds of mutations which can gradually accumulate over time in a given protein of a given biological lineage: *neutral* mutations which are neither advantageous nor disadvantageous and which therefore accumulate via *genetic drift*, and (on the other hand) *advantageous* mutations which accumulate via “*natural selection*” (i.e., differential reproduction and differential mortality). By contrast, *disadvantageous* mutations can *never* accumulate, according to neo-Darwinism, because they are quickly weeded out by “natural selection”. That version of the molecular-clock hypothesis which says that the “ticks” of the molecular clocks are

neutral mutations is called the *neutralist* hypothesis, while that version of the molecular-clock hypothesis which says that these “ticks” are *advantageous* mutations is called the *selectionist* hypothesis.

Taking first the *neutralist* hypothesis, we observe that the rate of *genetic drift* over time is directly related to and determined by the *mutation rate*, which for higher organisms has been estimated to be around 10^{-6} per gene per generation.²⁴ Genetic drift is therefore expected to be much faster, in terms of *calendar* time, for organisms which reproduce quickly than for those which reproduce slowly. Michael Denton explains this problem for the *neutralist* hypothesis as follows:

A mouse may go through four to five generations in one year. The time taken by an elephant, a chimpanzee, or a man to reach maturity is about fourteen, seven, and ten years respectively. This means that at present the generation times of some mammalian species varies by a factor of nearly one hundred. Since the rodent order diverged from the primate, it is practically certain that the line leading to the mouse has undergone nearly one hundred times as many reproductive cycles as that leading to man. If mutation rates are approximately constant *per generation*, how then could [genetic] drift have generated equal [*calendar*] rates of genetic divergence in mice and men [relative, say, to the carp]? . . .

Only if the rate of mutation in homologous proteins in different organisms was, for some mysterious reason, adjusted so that it was constant with respect to absolute time would uniform rates of [genetic] drift occur.²⁵

As W.J. Ewens has put it:

I note the well-known fact that the neutral theory predicts a constant rate of substitution per generation, whereas we appear to observe more a constant rate per year. In some of the species for which protein sequence comparisons have been made, there is a difference of one or even two orders of magnitude in generation time. It surely gets us nowhere simply to assume that the mutation rate adjusts itself in species of different generation time so that constant rates per year will arise.²⁶

Michael Denton sums up the serious problems with the *neutralist* hypothesis as follows:

Unfortunately, all the evidence suggests that in different groups of organisms the mutation rate per unit of absolute time is vastly different, and this effectively excludes [genetic] drift as a mechanism for the generation of uniform rates of evolution. On top of this there is the additional difficulty of envisaging how [genetic] drift could have occurred at different rates in different genes to account for the different rates of evolution in different families of homologous proteins.²⁷

One way in which both neutralists *and* selectionists try to explain the fact that the mutational “molecular clocks” of differing families of homologous proteins “tick” at vastly different rates is the *functional constraint* theory. According to this theory, some proteins (such as histone 4) have relatively few gene sites at which a mutation would *not* be disadvantageous, due to “functional constraints”: Consequently, there are very few gene sites available for either neutral *or* advantageous mutations, and that is why the “molecular clock” of histone 4 is supposed to “tick” relatively slowly. By contrast, other proteins

(such as the fibrinopeptides) are supposed to have far fewer “functional constraints”, which is why their “molecular clocks” are supposed to “tick” much more quickly. But, as Alan Wilson, an authority in this area, has pointed out:

. . . [W]e are not aware of direct experimental evidence showing rigorously that histone function is especially *sensitive* to amino acid substitution or that fibrinopeptide function is especially *insensitive* to amino acid substitution. Experimental studies would require that quantitative in vitro assays for the specific functions of histone 4 and fibrinopeptides be available. These have not been developed for histones, fibrinopeptides, or, indeed, most of the proteins whose evolutionary rates are listed.²⁸

Furthermore, Michael Behe reports in a 1990 peer-reviewed article that experiments with yeast have shown that large parts of the histone molecule may be deleted without significantly affecting the viability of the organism. Behe writes:

[The experimental] results pose a profound dilemma for the molecular clock hypothesis: although the theory needs the postulate of functional constraints to explain the different degrees of divergence in protein classes, how can one speak of ‘functional constraints’ in histones when large portions of H2A, H2B, and H4 are dispensable for yeast viability? And if functional constraints do not govern the accumulation of mutations in histones, how can they be invoked with any confidence for other proteins?²⁹

Michael Denton concludes:

Again, it is the sheer universality of the phenomenon – the necessity to believe that the functional constraints in *all* the members of a particular protein family, say *A*, in *all* diverse phylogenetic lines for *all* of hundreds of millions of years have remained precisely five times as stringent as those operating on the members of another protein family, say *B* – which fatally weakens the [functional constraints] theory.³⁰

But what of the neo-Darwinist *selectionist* hypothesis as an alternative to the neo-Darwinist *neutralist* hypothesis? (Recall that the *selectionist* hypothesis states that the mutational “ticks” of the “molecular clocks” are *advantageous* mutations rather than neutral mutations.) Again, Michael Denton:

But if neutral drift gets us nowhere, selectionist explanations fare no better. It is very difficult to understand why all the members of a particular family of proteins, such as the hemoglobins or the cytochromes, should have suffered the same number of *advantageous* mutations since their common divergence.³¹

The serious problems with the *selectionist* hypothesis basically fall into two categories:

First is the current existence of “living fossils” such as the lungfish and the opossum, which have remained morphologically the same for tens (or even hundreds) of millions of years, yet which (in terms of their proteins) are just as equidistant from their ancestors as are “sister” species which have arisen much more recently and therefore have had a much more diverse morphological history. As Denton remarks:

It is very difficult to understand why a protein [like hemoglobin] functioning in the basically unchanging physiological environment of the lungfish’s red [blood] cell should have undergone precisely the same number of beneficial mutations as a related protein evolving in a line subject to such global adaptational changes [as the lineage

leading to man]. While selection at the morphological and molecular level may be relatively unlinked, it is surely inconceivable that they could be *absolutely* unrelated.

. . .

Of course, the implausibility of selectionist explanations do not stop with the hemoglobins of a few living fossils. As in the case of uniform [genetic] drift, it is the sheer universality of the phenomenon – the necessity to believe that since their common divergence every single family of homologous proteins have suffered the same number of adaptive substitutions over the same period of time in *all* phylogenetic lines – which fatally weakens selectionist explanations.³²

The *second* category of serious problems with the *selectionist* hypothesis relates to protein sequences which (so far as is known) have no other function than as “spacer” sequences, yet which have the *same* percent divergence with respect to ancestor species as do protein sequences which clearly are highly functional (and therefore are supposedly strongly subject to “natural selection”). Denton gives this example:

A classic example of this are the two short amino acid sequences which are snipped out of the protein fibrinogen after it is activated during blood coagulation. These are known as fibrinopeptides *A* and *B*. As far as is known, neither of these two short peptides have any biological function, yet their percent sequence divergence in different mammalian groups conforms to the same ordered pattern as is found in all other proteins, i.e., the fibrinopeptides in all the members of any group are equally isolated from all the fibrinopeptide sequences found outside their group. . . .

. . . [S]electionist explanations [of this] . . . lead to absurd conclusions. Because the spacer sequences such as the fibrinopeptides exhibit the highest interspecies divergence of all proteins, if this is to be accounted for on purely selectionist grounds it is necessary to propose that they must have suffered adaptive changes very much more often than the hemoglobins or the cytochromes. In other words, they must have been under the intense scrutiny of natural selection. Not only must such sequences have suffered more adaptive changes than other proteins, but, in addition, these substitutions must have occurred regularly.³³

Michael Denton sums up the serious problems with the neo-Darwinian “molecular clocks” hypothesis (in both its neutralist *and* selectionist flavors) as follows:

The difficulties associated with attempting to explain how a family of homologous proteins could have evolved at constant rates has created chaos in [neo-Darwinian] thought. The [neo-Darwinian] community has divided into two camps – those still adhering to the selectionist position, and those rejecting it in favor of the neutralist. The devastating aspect of this controversy is that *neither* side can adequately account for the [supposed] constancy in the rate of molecular evolution, yet each side fatally weakens the other. The selectionists wound the neutralist position by pointing to the disparity in the rates of mutation per unit time, while the neutralists destroy the selectionist position by showing how ludicrous it is to believe that selection would have caused equal rates of divergence in “junk” proteins or along phylogenetic lines as dissimilar as those of man and carp. . . .

Despite the fact that [there is] *no* convincing explanation of how random [neo-Darwinian] processes could have resulted in such an ordered pattern of diversity [as is found in molecular protein sequences], the idea of uniform rates of evolution is presented in the literature as if it were an empirical discovery. The hold of the [neo-Darwinian] paradigm is so powerful that an idea which is more like a principle of

medieval astrology than a serious twentieth-century scientific theory has become a reality for [neo-Darwinian] biologists. . . .

What has been revealed as a result of the sequential comparisons of homologous proteins is an order as emphatic as that of the periodic table. Yet in the face of this extraordinary discovery the biological community seems content to offer explanations which are no more than apologetic tautologies.³⁴

Apropos Denton's reference to "medieval astrology", it is interesting to note that these neo-Darwinian "molecular clocks" are strongly reminiscent of the complex, nested epicycles which were multiplied in later Ptolemaic astronomy in order to be able to continue to place the earth firmly at the center of the solar system: These epicycles "worked" in the sense that they made the astronomical calculations come out "right", thus "saving" the Ptolemaic theory. But the epicycles were themselves so badly in need of explanation that the simpler Copernican theory placing the sun in the center of the solar system ultimately prevailed.³⁵

As a side note: How does *creationism* fare when confronted with this evolutionary fact of strict monophyletic hierarchy? Creationism is actually *partially* confirmed by it: For over a hundred years creationists have maintained that strict, monophyletic typological biological hierarchy is a scientific fact. And, over this same period, neo-Darwinists have mockingly inveighed against the sin of "essentialism" and have continually asserted that the apparent biological monophyletic hierarchy of "groups within groups" (shown in Figure 1) is merely a subjective, arbitrary illusion, and that instead the *paraphyletic*, smooth, continuous "splitting off" model depicted in Figure 2 is the correct one. It now turns out that on this point the creationists were right, and the neo-Darwinists were (and are) dead wrong.

However, the facts on this point do not *entirely* confirm creationism. For creationists regard the typological biological hierarchy as existing solely within the "mind of God" when He created all biological organisms "in the beginning". Yet, clearly, the fossil evidence shows phyla appearing before classes, classes appearing before orders, orders before families, families before genera, and genera before species over the course of millions of years. In other words, the fact that the more-generic taxa have appeared before the more-specific taxa throughout the long course of evolutionary history is just as contrary to creationism as it is contrary to neo-Darwinism: True, all of the *phyla* appeared together during a relatively short period of time (i.e., the Cambrian era), but this is not enough to prove the creationist hypothesis that *all* biological taxa were created during a short period of time "in the beginning".

Clearly a completely different theory of evolution is required to account for the ubiquity of strict monophyletic hierarchy among the multi-celled plants and animals of the biosphere. That theory is Robert F. DeHaan's theory of *macrodevelopment*, which we will present in the next section.

THE MACRODEVELOPMENTAL EXPLANATION

The nonlinear David which we have chosen to oppose the linear Goliath of neo-Darwinism is Robert F. DeHaan's theory of *macrodevelopment*, which he first presented in three articles in 1996 and 1997.³⁶ Note that our terminology differs somewhat from DeHaan's in that DeHaan uses the term "evolution" to essentially mean what we have called the *theory* of neo-Darwinism, while by contrast we are using the term "evolution" to denote the *fact* of transformation of life forms over millions of years. (In other words, for us, "evolution" is the general *fact* which the respective *theories* of neo-Darwinism and macrodevelopment are competing to explain.) Furthermore, DeHaan is willing to concede that neo-Darwinian mechanisms play a role in the evolution of *species* (as opposed to higher taxonomic categories such as phyla and families), whereas we will view neo-Darwinian mechanisms as effective *only* in creating and preserving *varieties within* species.

Here, then, are the basic principles of the evolutionary theory of *macrodevelopment*:

1. The evolution of life on earth over millions of years is essentially a *nonlinear* process which is analogous to the nonlinear process of individual embryonic development (*morphogenesis*). In other words, the irreversible nonlinear *macrodevelopment* of the biosphere over millions of years parallels in important ways the irreversible nonlinear *microdevelopment* of the individual biological organism over its lifetime (especially during its embryonic stage).
2. One important parallel between macrodevelopment and microdevelopment is the manner in which the overall *body plans* of biological organisms (corresponding to the *phylum* taxon-level) appeared rapidly during the Cambrian era and the correspondingly rapid manner in which the overall *body plan* of the individual is established during morphogenesis. (That is why Robert F. DeHaan calls Cambrian animals *stem animals*, analogous to the *stem cells* in the individual embryo.) DeHaan explains:

Both individuals and phyletic lineages begin with a general body plan. The body plan is among the first structures to appear in the individual embryological development. The earliest and defining feature of the Cambrian animals was their basic body plan.

Both individuals and phyletic lineages develop very rapidly at the start. Early development in the embryo is extremely rapid. In human beings all systems and morphological features are in place in slightly more than three months after conception. The formation of body plans in the Cambrian [era] occurred with extreme rapidity, geologically speaking, paralleling the very rapid formation of the body plan early in individual embryonic development and growth.³⁷

3. The parallels between macrodevelopment and microdevelopment are not confined to the embryonic stage, but extend to the entire span of the individual's life, from birth until death. Again, Robert F. DeHaan:

The entire life span of individual animals is a manifestation of development. All organisms start small and simple at conception, rise rapidly through

the prenatal and juvenile stages, grow large and complex, reach a rounded maximum on many variables in maturity, decline in old age, and eventually die. The rise and subsequent decline is an invariant characteristic of lifelong individual development.

There is also an unvarying succession of changes in ancestral lineages, starting with a few, small, insignificant animals, that increase in size, complexity, population density, and on many other dimensions; reach a rounded maximum, and then decline to fewer, smaller, less robust groups. This orderly sequence is isomorphic to development in the individual life span. . . .

In short, the overall shape of individual development and the general shape of ancestral lineages are remarkably similar. The only major difference between them is the time scale: enormous for the historical lineages, insignificantly short for the individual organisms. The resemblance between large-scale sequences of [ancestral] changes covering millions of years and the sequence of changes in [the] early embryonic and lifelong development of individual organisms is quite astounding. It cannot be a meaningless coincidence that so many phyletic patterns of change in the fossil record are found to resemble patterns of development found in individual organisms. These similarities are surely not trivial or merely coincidental. On the contrary, they point to a deep unity between the overarching historical processes, called macrodevelopment, and small-scale individual development. Patterns in the fossil record are sufficiently similar to [the] patterns in [the] development of individual organisms that those in the fossil record can provisionally be considered [to be] the results of development on a large historical scale.³⁸

4. The evolution of the biosphere has proceeded via a long historical series of nonlinear continuity-breaking bifurcations. In each of these bifurcations a *single* instance of a *more-generic* taxon (i.e., kingdom, phylum, class, order, family, genus, or species) has split into *two* instances of taxa at the *next most-specific* level. As a result of this split, the more-generic ancestral taxon continues to exist only in the form of the generic features of the two more-specific taxa into which it has split. That is why the splitting of taxa in accordance with the process of macrodevelopment is a process of *symmetrical* splitting in which the “ancestor” taxon ceases to independently exist. (By contrast, neo-Darwinism proposes that new taxa *split off* from previous taxa, leaving the older ancestral taxon to continue to independently exist and evolve. As we saw in the previous section, neo-Darwinian taxonomic splits are therefore inevitably *asymmetrical*, whether the version of neo-Darwinism is the phyletic gradualism of Charles Darwin, the punctuated equilibrium of Niles Eldredge and Stephen Jay Gould, or even the “hopeful monster” theory of Richard Goldschmidt.) Two important points:
 - When a more-generic taxon splits into two more-specific taxa, those more-specific taxa need not be at the next-most-specific *named* level. In other words, a phylum need not split into two classes, a class need not split into two orders, and so on. (This is because there are far too many taxonomic levels to be able to actually *name* them all.)

Nevertheless the *direction* of the splits is always from the *generic* to the *specific*.

- The more-generic animals and plants of the past were not necessarily “bland” than the animals and plants of today: Contemporarily they may have had all of the particularity of today’s animals and plants. However, the traits comprising that exact particularity were irrevocably lost to the future as a result of the taxon-splitting process.
5. Each taxonomic bifurcation within the biosphere was a holistic, taxon-wide phenomenon of nonlinear continuity-breaking that occurred within one (or a few) generations: It did *not* occur gradually, minutely, and mechanically, as neo-Darwinism proposes, but rather *suddenly* and *holistically*, like the sudden holistic reorganizations that occur periodically during the course of individual morphogenesis (or like the sudden organization of Benard cells in nonlinear thermodynamics).
 6. It is probably true that taxon-wide nonlinear bifurcations within the biosphere do not occur today. Nevertheless they were once a prominent feature of the biosphere’s past.
 7. Genetic evidence strongly supports the macrodevelopment hypothesis (especially when we exclude the individualistic “hopeful monster” hypothesis, essentially because it requires taxonomic “splitting off”). This genetic evidence includes: *polyploid speciation* events among contemporary plants; at least two major *tetraploid events* within the evolutionary history of vertebrates, one associated with the evolutionary emergence of jawless fish and the other associated with the evolutionary emergence of the four-limbed vertebrates, a.k.a. tetrapods (Susumu Ohno, 1970); the *structure of the differences between the DNA of closely-related species* (typically characterized by long, identical segments of DNA that are rearranged and/or “flipped” relative to one another, rather than differing primarily by point mutations, as neo-Darwinism would suggest); and, finally, John A. Davison’s evidence for the involvement of *semi-meiosis* in the “origin of the species”.³⁹
 8. Neo-Darwinian mechanisms, described in the previous section, only succeed in changing the statistical distribution of phenotypes *within* the species. This change in the statistical distribution of intra-species varieties occurs as a continuous process of adaptation to the environment. However, all such statistical changes are almost-instantly *reversible* if the environment reverts back to its former state. Therefore, calling such changes “microevolution” (as is often done) is a misnomer, since true biological evolution is essentially a nonlinear *immanently irreversible* process.
 9. Biological systems (including the biosphere as-a-whole) are highly complex, hierarchical, holistic, open, *organized* nonlinear systems, rather than being

either the macroscopically deterministic and microscopically random systems envisioned by orthodox neo-Darwinism *or* the *chaotic* nonlinear systems envisioned by the “heretical” neo-Darwinism of Stephen Jay Gould.

The above nine points express the essence of the theory of *macrodevelopment* as used in this paper. Points 1 through 3 are essentially the same as Robert F. DeHaan’s original theory of macrodevelopment, while points 4 through 9 represent expansions of DeHaan’s original theory with which DeHaan himself may or may not agree.

DeHaan is careful to distinguish his theory of *macrodevelopment* from a theory which superficially seems to be similar, namely, the so-called *biogenic law*, popularly expressed as “ontogeny recapitulates phylogeny”:

[Macrodevelopment] is not a warmed-over version of the so-called biogenic law, popularized by the slogan “ontogeny recapitulates phylogeny”. This outmoded “law of recapitulation”, formulated by Ernst Haeckel (1834-1919), held that there is a one-to-one correspondence between phylogeny and ontogeny; that each organism in its development from zygote to adult repeats its phyletic history in condensed form, i.e., climbs its own family tree, so to speak. Raff described the biogenic law more technically as follows: “All animals should recapitulate their phylogenies in an abbreviated form during development, and developmental stages should reveal those histories.”

[Macrodevelopment], however, is not concerned with trying to find replications of exact stages of phyletic transformation in the development of individual organisms; rather, it focuses on generalized processes and patterns that are universal across all lineages.⁴⁰

DeHaan also distinguishes his theory of *macrodevelopment* from an earlier theory called *orthogenesis*:

[Macrodevelopment] is distantly related to ideas that were held in the 1920s by several paleontologists. [Niles] Eldredge reported the situation as follows:

Paleontologists have had an abiding interest in long-term evolutionary trends that struck Cope and many others as linear or “rectilinear”. “Orthogenesis”, a term coined by Haacke (1893; fide Simpson 1944), describes a pattern of linear directional change in phylogeny, a pattern generally thought in pre-synthesis days to reflect internal evolutionary processes. This line of thinking, at least in paleontological circles, reached its culmination in the work of vertebrate paleontologist Henry Fairfield Osborn, whose theory of orthogenesis (later called “aristogenesis”) saw linear evolutionary change arising from within organisms themselves, a mechanism, moreover, taking precedence over natural selection if not supplanting it altogether.

The general theory of [macrodevelopment] is an advance over the earlier ideas of “orthogenesis” and “aristogenesis” because it (1) is a multidimensional concept; it identifies many different kinds of long-term trends that are parallel to individual development, and because it (2) relates the process to real causal genetic mechanisms.⁴¹

We may expand on DeHaan’s remarks by noting that from Eldredge’s description it appears that orthogenesis was viewed as being a *linear*, mechanical (albeit internal) process, whereas by contrast macrodevelopment is an inherently holistic *nonlinear* process.

In addition, we may distinguish the theory of macrodevelopment from the work being done on evolution by Stuart Kauffman and others at the Santa Fe Institute: Their work *does* contain a high awareness of the presence of nonlinearity in the biosphere. However, their work is also almost entirely confined to a statistical population-genetics approach, which has had the effect of enmeshing them in residual stochastic/deterministic neo-Darwinian assumptions.

Much closer to the theory of macrodevelopment (and, indeed, important confirmation of it) is the *Stewart/Cohen hypothesis*, created by the famous mathematician Ian Stewart and his biologist collaborator Jack Cohen. It all started when Cohen asked Stewart about nonlinear “symmetry breaking” (which is another name for nonlinear macroscopic “continuity-breaking”). After Stewart replied, Cohen remarked: “Speciation - that’s symmetry breaking, isn’t it?” Ian Stewart explains what happened next:

First I thought he didn’t understand what I was talking about. Then I asked him what he meant. He said: If you’ve got one species, that’s a very symmetric situation, because all the animals are pretty much the same, but two species must be less symmetric.

We’ve written a few papers about this as a mathematical metaphor for speciation, modeling a species as identical organisms and worrying about the differences between individuals later on. These models turn out to include a general mathematical process, called *bifurcation*, where the state of the system changes quite dramatically, even though the system’s environment only changes a small amount.

The models produce some general predictions: the split happens very fast, on an evolutionary timescale, and the two new species ‘pull apart’ in opposite directions compared with the original. For instance, if the original species is a bird with a medium-sized beak, then the species splits into one with a big beak and one with a small. The average size of beak doesn’t change at all.

Until very recently, I’d have left that as a metaphor. . . [But now it] looks as if it’s going to go beyond metaphor and into science.⁴²

The theory of macrodevelopment has even (to some extent) been anticipated by the noted critic of neo-Darwinism and advocate of intelligent design, Phillip E. Johnson, who writes:

Certain features, like the existence of natural groups and common “junk DNA” sequences, support an inference that there was some sort of process of development [of species] from some common source. We may call that process “common ancestry”, but it does not necessarily follow that we are referring to the ordinary process of reproduction that we observe in today’s world, where ancestors give birth to descendants very much like themselves. Normal reproduction is not known to produce radically new organs or organisms, and if it did so it would have to proceed one tiny step at a time. In fact there is a great deal of evidence that innovative transformations must have involved organisms doing something “different from what they ordinarily do”.⁴³

But can this theory of macrodevelopment explain the pervasiveness of strict typological hierarchy throughout the biosphere, where neo-Darwinism failed to do so? In fact, Figure 1’s depiction of the *symmetrical* splitting of each more-generic “ancestor” taxon into two more-specific “descendent” taxa (with the more-generic “ancestor” taxon then ceasing to independently exist) is *exactly* what the theory of macrodevelopment predicts! Further-

more, the appearance of the more-generic taxa *before* the more-specific taxa throughout evolutionary history is clearly analogous to the development of the individual biological embryo, where the early group of generic “stem cells” soon differentiates via nonlinear continuity-breaking to form increasingly more-specific groups of cells and organs.

This close analogy between *evolutionary* macrodevelopment and *individual* embryonic development is especially clear in Brian Foley’s description of the morphogenesis of mammals:

[V]ery early on in [the individual embryonic] development [of mammals], the cells that develop from the zygote [i.e., the egg cell] differentiate into three types. One type will make the skin and nerves, one type will make muscles and bone, and the third will make organs and blood. A bit later, the three types further differentiate into individual organs and tissues.

Such a method of development is called *hierarchical*, meaning “different levels”. Thus we can’t have skin without first having the zygote form the three basic types of cells and then the skin/nerve type further splitting into skin and nerve types, and then the skin type splitting further into hair follicles and sweat glands and other skin parts.⁴⁴

What about the many serious problems surrounding the neo-Darwinian “molecular clocks” hypothesis? The theory of macrodevelopment deals with these problems in a manner precisely analogous to how the Copernican theory of astronomy dealt with the problem of Ptolemaic epicycles, i.e., by simply declaring that *there are no such things as molecular clocks!* Rather, the strict monophyletic hierarchical pattern of differences between homologous protein sequences within the biosphere was created as a byproduct of the same complex series of nonlinear continuity-breaking bifurcations that created the monophyletic biological taxon hierarchy itself. Since each such nonlinear bifurcation occurred quickly and holistically over the span of (at most) a few generations, macrodevelopment has no need to postulate the existence of hundreds (or thousands) of “molecular clocks” mysteriously ticking “slowly, minutely, gradually” at different linear calendar rates over millions of years!

The Law of Macrodevelopmental Symmetry

In order to successfully account for the evidence of homologous protein-sequence differences, the theory of macrodevelopment requires that the evolutionary, nonlinear continuity-breaking bifurcations within the biosphere must have obeyed the following law, which we shall propose as the *law of macrodevelopmental symmetry*:

- Any given instance of evolutionary macrodevelopmental bifurcation must have either:
 - a. Changed exactly the same amino-acid sites on a given homologous protein on *each* side of the split (i.e., the homologous protein for each of the two “descendent” taxa must have been changed at *exactly* the same amino-acid sites), *or*

- b. If the bifurcation *also* changed *additional* amino-acid sites on *one* side of the split, then subsequent bifurcations on the *other* side of the split tended to correct this imbalance by modifying those additional sites as well. (These subsequent bifurcations could *also* have modified any *previously* modified amino-acid sites, but could *never* have modified sites which were left untouched on *both* sides of previous bifurcations.)

Point *a* above corresponds to the *Stewart/Cohen hypothesis* mentioned earlier (i.e., that the traits of the two “descendent” taxons arising from a nonlinear continuity-breaking bifurcation will “average back” to the traits of the common “ancestor” taxon). However, point *b* goes beyond the Stewart/Cohen hypothesis to deal with the more-complicated case of nested bifurcations. (The fact that amino-acid sites which were completely untouched by previous bifurcations cannot be touched by subsequent bifurcations is closely related to the fact that a base of “generic” traits is passed unchanged from each “ancestor” taxon to *all* of its “descendent” taxa.)

Of course, any given instance of macrodevelopmental bifurcation can quickly affect *many* or even *all* of the relevant homologous proteins (via the DNA and RNA that templates these proteins), and it can affect each of those homologous proteins to a very different degree. (That’s why the difference between a carp and man with respect to hemoglobin is around 50%, while the difference between a carp and man with respect to cytochrome C is only around 13%-14%.)

Also, it is important to remember that macrodevelopmental bifurcations act not only suddenly, but also *holistically*, so that these rapid and various changes in homologous protein sequences are really only byproducts of a sudden, global, taxon-wide process. Furthermore, the *temporal* aspect of this holism is why subsequent nonlinear bifurcations seem to “know” that they can’t replace amino acids at sites that were left completely untouched by previous bifurcations.

To get an idea of how this *law of macrodevelopmental symmetry* works out in practice, consider Figure 3, on the next page.

The basic structure of Figure 3 is based on Figure 1, except that under each node of the diagram are the numbers 1-through-5. Each number represents one position in an imaginary protein that has five amino-acid sites. (Of course, real proteins have hundreds, or even thousands, of such amino-acid sites.) Under each number 1-through-5 is a letter (or short sequence of letters) representing the amino-acid at that position.

For example, under all of the numbers 1-through-5 at the Tetrapods node is the letter **O**, which stands for “Original” (meaning, the original amino-acids occupying these five positions, before any bifurcations occur).

Due to a nonlinear macrodevelopmental bifurcation, the Tetrapods “ancestor” taxon splits into the Amphibians “descendent” taxon on the left and the Amniotes “descendent” taxon on the right. As a result, *three* amino-acid sites (2, 4, and 5) under the Amphibians node

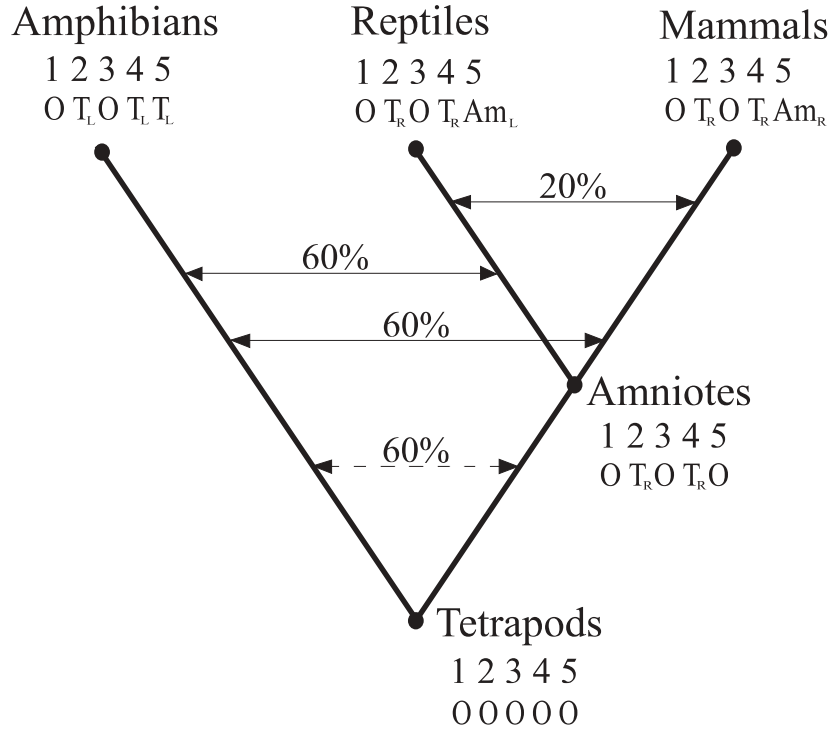


Figure 3

show an amino-acid substitution, symbolized by T_L (meaning “the left side of the Tetrapods split”), while *two* amino-acid sites (2 and 4) under the Amniotes node also show an amino-acid substitution, symbolized by T_R (meaning “the right side of the Tetrapods split”). The Tetrapods split, therefore, represents the kind of temporarily *unbalanced* split described in point *b* of the *law of macrodevelopmental symmetry*.

A subsequent nonlinear bifurcation of the Amniotes produces the Reptiles on the left and the Mammals on the right. As a result, both the Reptiles and the Mammals experience an amino-acid substitution at position 5. We call the Reptiles’ substitution at position 5 Am_L (meaning “the left side of the Amniotes split”), while the Mammals’ substitution at position 5 we call Am_R (meaning “the right side of the Amniotes split”). This Amniotes split therefore represents the kind of *balanced* split described in point *a* of the *law of macrodevelopmental symmetry*.

Now, notice that the Amphibians and the Amniotes differ in three out of five positions (2, 4, and 5), resulting in a protein sequence difference of 3/5, or 60%. (This is represented by the broken dimension line labeled as 60%. The dimension line is broken because we can’t directly measure this variance today.) The Reptiles and the Mammals also each differ from

the Amphibians in three out of five positions (2, 4, and 5), again resulting in a protein sequence variation of 60%. (This is represented by the two solid dimension lines stretching from Amphibians to Reptiles and from Amphibians to Mammals, each respectively labeled as 60%.) Finally, the Reptiles and the Mammals differ from one another in only one position (position 5), resulting in a protein sequence variance of 1/5, or 20%, between Reptiles and Mammals. (This is represented by the solid dimension line stretching between the Reptiles and the Mammals that is labeled as 20%.) Note that this general theoretical pattern of protein variance closely matches what we actually find in nature, with the Reptiles and Mammals being equally distant from the Amphibians in their own clearly-defined monophyletic group.

Notice also that the subsequent Amniotes split modifies position 5, which is the additional position that was modified on the *left* side of the original Tetrapods split. The Amniotes split therefore rectifies the failure of position 5 to be initially modified on the *right* side of the Tetrapods split. (In other words, the Amniotes split acts to restore the macrodevelopmental symmetrical balance.)

Furthermore, if the **Am_L** substitution for the Reptiles had occurred at position 3 (a position unmodified by *either* side of the Tetrapods split), rather than at position 5, then the protein sequence variance between Amphibians and Reptiles would have been 80%, as opposed to a Amphibian/Mammal variance of 60%, thus violating the actual evidence of the pattern of protein-sequence variation which we find in nature. Even if the **Am_R** substitution for the Mammals had *also* been at site 3 rather than at site 5, thus again rendering the Reptiles and Mammals equidistant from the Amphibians (only with an equal variance of 80% rather than an equal variance of 60%), the variance between the Amphibians and the Amniotes (represented by the broken dimension line) would still remain at 60%. This would not, strictly speaking, violate the evidence of the pattern of protein sequence variation (since we can't *directly* measure the variance between the Amphibians and the Amniotes), but it *would* suggest that our current, most-recent situation is somehow unique and temporally privileged with respect to the past, and this does not seem at all likely.

(Note also that the fact that the Tetrapods split is *asymmetrical* in Figure 3 because it is unbalanced with respect to the number of amino-acid sites actually modified does *not* contradict the fact that the Tetrapods split is *symmetrical* in Figure 1, since all that is required for "symmetry" in Figure 1 is for the two "descendents" to be clearly different from the original Tetrapod "ancestor".)

We may therefore tentatively propose that the above *law of macrodevelopmental symmetry* expresses both the *necessary* and *sufficient* conditions for macrodevelopmental, nonlinear, continuity-breaking bifurcations to produce the pattern of homologous protein differences between taxa that we actually find in nature.

Evolutionary “Unfolding”

Now, we have seen that evolutionary macrodevelopment is evidently an “unfolding” process from the generic to the specific, just as is the case for individual embryonic development. Can we say anything else about this “unfolding” process?

Because there is some evidence that RNA (and hence, presumably, DNA) follow the same pattern of monophyletic hierarchical grouping as the homologous proteins, and because DNA, via messenger RNA, has been shown to provide a template for the creation of proteins, it might be proposed that this macrodevelopmental “unfolding” of the biosphere via nonlinear continuity-breaking bifurcations is *genetically programmed*. This is essentially what Robert F. DeHaan himself proposes:

According to the developmental perspective, the central [genetic] library was highly organized, with its information divided and subdivided into sections. Thus the phyletic germ line of each stem animal was differentiated and segregated into suites or modules of genetic programs along with their controlling regions. As a given phyletic germ line unfolded after the Cambrian explosion, it produced a lineage whose long journey through geologic time was shaped like a step-pyramid in Egypt, descending in step-wise fashion from the topmost stem animal into ever-lower, more-specific, and widening categories of lineage. That is, the control was hierarchical. The body plan of the stem animal at the top constrained the offspring in the next-lower category, the second-lower category controlled all those below it, etc. These progressively descending, more-specific steps are called taxonomic levels of lineage that help scientists classify animals and plants. The phyletic germ line continued to be differentiated and segregated and expressed in this fashion, descending ever more-specifically through classes, order, families, genera, clear down to species, at which point the last programs of the lineal germ line were completely played out. This [macrodevelopmental] process resulted in the multiplicity of species found in the present time, numbering by some estimates, from 5 million to 50 million, but which have not produced any new, higher-level organisms.

The above scenario suggests further that the phyletic germ line may have originated, perhaps as sets of highly-ordered genes, such as the Hox genes, tucked away in relatively simple, undifferentiated, Precambrian proto-animals.⁴⁵

While I do think that Robert F. DeHaan is *essentially* correct, I believe that he here overstresses the role of *genetic programming* in this process. Rather, it seems to me much more likely that the nonlinear continuity-breaking bifurcations of macrodevelopment were *holistic* processes in which *cell-level epigenetic factors* and *macroscopic factors* (perhaps including the “decisions” of biological taxa and individuals to respond to their environment in specific ways) significantly affected precisely how the biosphere has “unfolded”.

The major problem with DeHaan’s view as stated is that it appears to require that *all* of the information necessary to construct *all* of the biological organisms in the biosphere for *all* time were contained within the DNA of the first “relatively simple, undifferentiated, Precambrian proto-animals”. While it is, indeed, possible that this huge amount of information could arise out of the quantum depths of primitive DNA, or alternatively could arise as a result of the “unmasking” of existing DNA genes, it seems to me far more

likely that this huge amount of information at least partially arose as a result of multi-millions of “decisions” at all biological levels over millions of years being “fed back” holistically into DNA, epigenetic storage, and even into macroscopic biological storage (e.g., into macroscopic organs such as the brain).

This holistic viewpoint (a kind of “super-Lamarckism”!), as opposed to the pure-genetic-programming viewpoint, is suggested, for example, by the fact that genes and homologies don’t always coincide. As Gavin de Beer wrote in 1971: “Because homology implies community of descent from . . . a common ancestor, it might be thought that genetics would provide the key to the problem of homology. This is where the worst shock of all is encountered. . . [because] characters controlled by identical genes are not necessarily homologous . . . [and] homologous structures need not be controlled by identical genes.” De Beer concluded that “the inheritance of homologous structures from a common ancestor . . . cannot be ascribed to identity of genes.”⁴⁶

Other factors pointing to this kind of “super-Lamarckian” holism include: *a*) cases where different proteins are read off the *same* stretch of DNA by *frame-shifting* the reading, *b*) cases where the *alternative splicing* of messenger RNA causes the same DNA “gene” to “encode” for hundreds (or even thousands) of different proteins,⁴⁷ *c*) the fact that there are often far fewer genes than proteins, and *d*) the fact that homologous proteins are not, by themselves, “traits”, but only the building-blocks of “traits”.

These facts strongly suggest, as James Barham has pointed out, that:

genes are [only] one element within a complex physiological system consisting of countless, densely connected, massively coordinated, semiautonomous metabolic networks. Furthermore, they are a *passive* element in that system. Genes *do* little or nothing; it is proteins that manipulate DNA, not the other way around.⁴⁸

Even with respect to the development of the individual embryo, it is now widely recognized that epigenetic factors are of the utmost importance, and that the embryo itself holistically “decides” such important things as the sex of the organism and which other traits the organism will take from which parent. (In other words, even the development of the individual embryo is not entirely deterministically “programmed” by its genes.)

Nevertheless, we do not, in fact, really know the extent to which the nonlinear bifurcations that occurred during macrodevelopment were characterized merely by *spatial* continuity-breaking (and therefore would occur again in approximately the same way if the evolutionary “experiment” were to be repeated) and the extent to which these nonlinear bifurcations were, on the contrary, characterized also by *temporal* continuity-breaking (and consequently were significantly affected by the “decisions” made by biological organisms and taxons during the history of the biosphere). In the case of *individual* development, of course, we know that mere *spatial* continuity-breaking predominates, because the process of morphogenesis is so-nearly reliably repeatable. But in the case of the macrodevelopment of the biosphere we (unfortunately) have only one example to study!

It is also important to note that the *law of macrodevelopmental symmetry* (discussed in the previous section) may have seriously constrained the extent to which local decisions of organisms could have affected the course of evolution, since the many “temporary” imbalances in macrodevelopmental symmetry would have had to have been “remembered” and “corrected” by the biosphere over the course of millions of years.⁴⁹

If, in fact, evolutionary macrodevelopmental bifurcations were dominantly merely spatial, and if true typological speciation no longer occurs today (with the exception of small-scale polyploidal speciation among plants), and if Robert Broom and John A. Davison are correct in asserting that, among animals, not a single new genus has appeared in the last two million years and that the last genus to appear was *Homo* and the last species to appear was *Homo sapiens*,⁵⁰ then it may very well be the case that the emergence of mankind and human society was truly the *goal* towards which the macrodevelopment of the biosphere has been aiming all along (just as the fully-formed biological individual is the evident *goal* towards which the development of the embryo aims).

Such an understanding of the place of man in the biosphere would, of course, be diametrically opposite to the view of neo-Darwinism, according to which “man is the result of a purposeless and natural process that did not have him in mind.”⁵¹

Thus, as with all new, revolutionary paradigms in science, the theory of macrodevelopment opens up a whole new viewpoint with a whole new set of questions and concerns.⁵²

END NOTES

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- ⁶ Denton, pp. 274-307.
- ⁷ Denton, pp. 280-281.
- ⁸ Denton, p. 282.
- ⁹ Denton, p. 285.
- ¹⁰ Denton, pp. 285-286.
- ¹¹ Denton, pp. 287-288.
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- ¹³ Richard Goldschmidt, *The Material Basis of Evolution* (New Haven: Yale University Press, 1940), as cited by Gordon Rattray Taylor in *The Great Evolution Mystery* (London: Secker & Warburg, 1982), p. 162.
- ¹⁴ W. Ford Doolittle, “Uprooting the Tree of Life”, *Scientific American* (February 2000), pp. 90-95.
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- ¹⁸ *The Darwin Reader*, p. 100.
- ¹⁹ *The Darwin Reader*, p. 103.

²⁰ *The Darwin Reader*, p. 104.

²¹ Many others in the creationist movement and intelligent-design movement, such as Jonathan Wells and even Robert F. DeHaan, have made similar observations. (See, for example, Wells' chapter on "Darwin's Tree of Life" in his book *Icons of Evolution*, pp. 29-58.)

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²⁴ Denton, p. 297.

²⁵ Denton, pp. 297-8.

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²⁹ Michael Behe, "Histone deletion mutants challenge the molecular clock hypothesis", *Trends in Biochemical Science*, 15:374-376 (October 1990), p. 375.

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