# EDITORIAL

## CONFLATING ANSWERS: TO AND FROM DESIGN QUESTIONS

The design argument can be logically divided into two components: the argument TO design and the argument FROM design. The modern Intelligent Design (ID) argument is an argument *to* design about which confusion is commonly caused by jumping to the logically related *from* design side of the argument: If there is an Intelligent Designer, who is it? Opponents of ID frequently attempt to short-circuit the whole argument by conflating ID with arguments *from* design. To spice up these rejoinders, specific answers may be offered as in a recent AFP news article[1] which quotes an opponent of ID, Barbara Forrest, as saying "It [ID] is at its bottom a Christian religious movement." Some Christian apologists may be tempted to think the same thing, but to do this betrays a misunderstanding of ID.

Clearly, ID does not answer or even address questions about who God is, it only addresses the "*to design*" side of the design argument. On the one hand, there is the question of whether nature, or some part of nature, is the result of an intelligent cause. On the other hand there is the question of what kind of creator could make natural things like the living organisms? Different philosophical positions attempt to answer the second "*from design*" question before the "*to design*" first question. They then attempt to impose their premature answer on the evidence in nature. For example, it might be claimed that the almighty God, who only does good, kind and perfect things, is Creator of all we see; thus everything we see is perfectly good. This view is reflected in much of the natural philosophy of Victorian times and is one of the things that Darwin rightly rejected. Darwin was not alone; for example Voltaire lampooned this kind of "Pangloss" thinking in *Candide*.

Darwin chose to embrace an alternative view generally referred to as materialism. While he himself may not have fully subscribed to this philosophical position, the modern Darwinian synthesis is frequently equated with this train of thought. Materialism is a philosophy that claims the material world is, by definition, all that exists. Thus, the only mechanism available to produce things in nature is nature itself. The belief that natural causes explain everything in nature is commonly called naturalism. Neither materialism nor its logically conjoined twin naturalism are new ideas. Many ancient examples of these philosophies exist. For example, long before the birth of Christ, Cicero, who advocated naturalism, wrote:

> *For he who taught us all the rest has also taught us that the world was made by nature, without needing an artificer to construct it, and that the act of creation, which according to you cannot be performed without divine skill, is so easy, that nature will create, is creating, and has created worlds without number. You on the contrary cannot see how nature can achieve all this without the aide of some intelligence....*[2]

Like many theologies — and yes materialism functions as a theology — materialism answers the "from design" question prematurely before looking at the data. Then the answer is imposed on the "to design" question. This may lead to confident statements about where nature, and particularly the living things in nature, came from, but these answers are not well founded in the study of nature itself.

Materialism and theologies/philosophies that answer the "*from design*" question first ultimately must resort to heroic measures to circumvent what the data most reasonably seem to show. For example, a certain parasitic wasp was cited by Darwin as evidence that nature is not the product of a beneficent God[3]; and it seems reasonable to agree with him. On the other hand, the neo-Darwinian claim that something like amoebas turned into wasps seems unbelievable. When one looks at molecular mechanisms within wasp cells, the claim that they resulted from purely natural causes seems equally untenable.

This is where Intelligent Design provides a useful contribution. Instead of trying to answer the metaphysical question first, ID asks: Is nature best explained in terms of natural or intelligent causes? This allows examination of the evidence without first imposing a "*from design*" answer on it. In some cases, it may be reasonable to say that things most likely resulted from natural causes. For example, in the absence of other evidence, it is logical to conclude that rains falls in part as a result of gravity, a natural law, and thus results from natural causes.

ID is not controversial because it suggests some natural phenomena may result from natural causes. Controversy erupts because in some rigorously defined cases, ID allows those not already committed to materialism to infer an intelligent cause for at least some of the molecular machines found in cells and also the information encoded in DNA. Thus ID in a limited set of cases suggests nature is not exclusively the result of natural causes. By directly contradicting naturalism, ID calls into question materialist philosophy. ID argues strongly *to design* not because it starts out with the presupposition that nature is intelligently designed, but because this is in fact what nature appears to be.

Other than suggesting the existence of at least one intelligent designer, arguing *to design* does not tell us much about the Intelligent Designer. The "*from design*" argument is ultimately a more complex and nuanced question than the "*to design*" argument. Perhaps this is why answering it first with straightforward appearing philosophical claims before looking at the evidence is so tempting. Arguing in the absence of evidence greatly simplifies things. In reality, limited to the study of nature, learning much about the character of the Intelligent Designer can be confounding. On the one hand, there is evidence of incredible engineering at the molecular level and at higher levels — the designer must be a brilliant engineer. Nature is red in tooth and claw — the designer must be cruel. But there is much benevolence in the ways creatures interact — the designer must be kind. Some things, like human lower backs, are prone to failure — the designer must be incompetent. Gaining a single coherent picture of the Intelligent Designer from nature is problematic.

Arguing *to* design ultimately opens a Pandora's box of puzzles. However, just because the answer to a question leads to further questions does not mean that the original answer is untrue. An example from the world of art illustrates this. The fact that Leonardo DaVinci painted the Mona Lisa with an enigmatic smile on her face opens up questions about why he painted her that way and how he did it. But questions don't mean that he didn't paint the Mona Lisa. In seeking answers to questions raised by DaVinci's masterpiece, it seems reasonable to search out answers looking further afield than the painting itself. In this case history books, other paintings and geometry classes may all be useful additional sources of information about Leonardo and his paintings.

In reasoning *from* design in nature to the existence of an Intelligent Designer it also seems logical to ask many questions. But nature does not provide all the answers in simple easy-to-understand packages. Answering the question scientists ask about nature requires incredible effort, frequently over the course of a lifetime. Even after all this effort, too often the result is failure. Whether all the answers to questions about nature will ever be in hand is doubtful and thus a complete understanding of the Creator of nature based on nature alone seems beyond the reach of science. Even given a complete understanding of what nature is, the character of the Creator is unlikely to be fully evident. However, just as one would look beyond the Mona Lisa to find answers about its creator, one is well served to look beyond nature alone for answers to the questions it raises.

Aside from nature itself, there are plenty of books that claim to provide information about the Creator. These range from "Life Itself" by Francis Crick and Leslie Orgel[4] — in which they suggest that life was sent from outer space — to the Bible and it is ultimately the Bible that, with careful study, yields the most reasonable answers to those questions raised by the observation that much of nature, and particularly life, appears to be the product of Intelligent Design. That is not to pretend that there are not areas of tension between our current understanding of nature — science — and our current understanding of the Bible — theology. Many unanswered questions remain, but this is no reason to reject answers that are currently clear. Rather, this tension should be motivation to keep looking and studying. Life would be boring if one had all the answers in hand and they were all simple!

Timothy G. Standish

## ENDNOTES

1. Agence France-Presse. March 6, 2005. http://story.news.yahoo.com/news?tmpl=story&cid=1540&e=12&u=/afp/usssciencereligion.
2. Marcus Tullius Cicero c *De Natura Deorum.* http://www.epicurus.net/en/deorum.html.
3. Darwin CR. Letter to Asa Gray, May 22, 1860, reprinted in: Darwin F, editor.1888. *The life and letters of Charles Darwin*. Facsimile reprint 2001. Honolulu: University Press of the Pacific, p 105.
4. Crick FHC, Orgel L. 1981. *Life Itself*. NY: Simon & Schuster.

# REACTIONS

*Readers are invited to comment on the articles in our journal. Please address contributions to: ORIGINS, Geoscience Research Institute, 11060 Campus St., Loma Linda, California 92350 USA.*

## Re: Gibson: Chicken Soup, Self-Organization and the Origin of Life: A Test (ORIGINS 56:3-5).

I read with interest your editorial, "Chicken Soup, Self-organization and the Origin of Life: a Test." In this exercise you deal with the concept of life and death and molecules in a whimsical manner. This is the consequence of your not defining the difference between life and death on the biochemical level.

You seem to be saying that if molecules had the capacity to come together spontaneously to form a living entity once, then such should happen again and again. In the picture you paint it is the "coming together" of molecules that makes life happen. But the biochemical basis of life is not structural so much as a dynamic non-equilibrium steady state.

In previously published material[1] I describe the case of the *E. coli* cell that was just killed by a drop of toluene. This dead cell still has all of its proteins, nucleic acids, etc., in their perfect organizational state (in "irreducible complexity", if you will, ala Behe) — the only thing wrong with this cell is that it is also irreducibly dead! Why? Because the breach of the cell's cytoplasmic membrane resulted in a loss ATP synthesis and all chemical reactions went to equilibrium. That is what death on the cellular level is about.

I describe further how the life of such cell can be restored. Simply reset the non-equilibrium statuses of all reactions. This can be achieved by simultaneously providing the starting materials of all biochemical pathways and preventing the end products from accumulating.

We can have molecules self-assemble until we are blue in the face. Life will never happen no matter how complex and impressive our biological agglomerates are. These biological complexes serve only as the frame, the infra-structure which partitions living matter into compartments, enabling concentration gradients, etc.

George Javor
Loma Linda, California

## ENDNOTES

1. Javor GT. 1998. Life: an evidence for creation. Origins 25:5-48.

## Re: Hasel: Recent Developments in Near Eastern Chronology and Radiocarbon Dating (ORIGINS 56:6-31).

The dilemma between C-14 dating and historically based chronology is resolved by a correlation of C-14 ages with the Biblical time scale.[1] A mathematical conversion based on a date for the Flood indicates C-14 ages around the beginning of the third millennium BC are probably about 400 years greater than corresponding real-time ages. Accordingly, C-14 ages favor the younger placement of historical chronology, as treated by Dr. Hasel.

R. H. Brown
Loma Linda, California

## ENDNOTES

1. Brown RH. 1990. Correlation of C-14 age with the Biblical time scale. Origins 17:56-65.

# ARTICLE

## VISUALIZING BARAMINIC DISTANCES USING CLASSICAL MULTIDIMENSIONAL SCALING

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### WHAT THIS ARTICLE IS ABOUT

*Baraminology methodology continues to mature, and in this article, the multivariate technique of classical multidimensional scaling is introduced to baraminology. The technique is applied to three datasets previously analyzed in baraminology studies, a Heliantheae/Helenieae (Asteraceae) dataset, a fossil equid dataset, and a grass (Poaceae) dataset. The results indicate that classical multidimensional scaling can confirm and illuminate previous baraminological studies, thereby strengthening identifications of baraminic units.*

Although Frank Marsh introduced the term *baramin* in 1941, the concept and its application to creation biosystematics was not developed further until its revision as baraminology in the 1990s. By releasing creation biosystematics from its dependence on interspecific hybridization, baraminology explicitly allowed and encouraged the development of novel baraminology techniques. In 1992, Wise published the first baraminological study on turtles explicitly aimed at detecting discontinuity (Wise 1992). In 1998, Robinson and Cavanaugh introduced a technique based on the baraminic distance, a simple measure of organismal similarity. They applied the technique to catarrhine primates (1998b) and felids (1998a). More recently, Cavanaugh developed the multidimensional projection technique Analysis of Patterns (ANOPA), which has been utilized in several baraminological and systematic studies (Cavanaugh & Sternberg 2002; Cavanaugh & Wood 2002; Cavanaugh et al. 2003; Wood & Cavanaugh 2001; Wood & Cavanaugh 2003).

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Baraminic distance and ANOPA both utilize coded sets of characteristics that describe taxa of interest, such as could be used in a cladistic analysis. Baraminic distances are the number of characters in which two taxa differ, expressed as a fraction of the total characters analyzed. Baraminic distances between taxa can then be correlated by linear regression, yielding both a correlation coefficient and a probability. Significant positive correlation indicates taxa which are very close in character space, while significant negative correlation indicates taxa very far apart. Robinson and Cavanaugh (1998b) proposed that significant positive correlation indicates taxic continuity and significant negative correlation indicates taxic discontinuity.

Analysis of Patterns, in contrast, treats characters as separate spatial dimensions, with each taxon represented as a point in $n$-dimensional space, where $n$ is the number of characters. ANOPA calculations then project the $n$-dimensional taxic pattern onto three dimensions, much in the same way that light projects shadows of three-dimensional objects onto two-dimensional surfaces. The three-dimensional taxic pattern of subtribe Flaveriinae is a trajectory structure, implying that the taxa belong to the same baramin (Wood & Cavanaugh 2003). The 3D ANOPA analysis of results on a dataset of fossil equids matches closely the inferred phylogeny of family Equidae and correlates with the stratigraphic appearance of the taxa (Cavanaugh et al. 2003), strongly implying that the equids belong to a single baramin.

Statistical baraminology methods have the potential to overcome limitations of other creationist systematics techniques. Marsh's hybridization-based method (Marsh 1947), although adopted and applied by German creationists (Scherer 1993), cannot be applied to asexual or fossil organisms or to organisms that are not known to hybridize (Scherer 1998). In contrast, statistical baraminology methods have been successfully applied to fossil equids as noted above (Cavanaugh et al. 2003). Further, studies of groups with few known hybrids, such as the felids, have been conducted (Robinson & Cavanaugh 1998a) and are currently underway. As a result of these developments, creationists can apply their own systematics methods to the full diversity of life for the first time in history.

Statistical baraminology methods also have their drawbacks. For example, Robinson and Cavanaugh (1998b) found significant, positive baraminic distance correlation between humans and primates when using molecular data. This violated their proposal that significant positive correlation indicated taxic continuity. Wood (2002) found a similar phenomenon when analyzing morphological and molecular datasets of the grasses. Significant negative correlation could be detected only with the morphological dataset but not with the molecular dataset of the same taxa. Wood interpreted his results and those of Robinson and Cavanaugh to indicate that discontinuity and continuity should be detected holistically, without an overrepresentation of a single type of characters (e.g., molecular).

Even with morphological character sets, ambiguous patterns of negative and positive correlation have been found. Cavanaugh et al.'s (2003) analysis of a fossil equid dataset revealed positive correlation that linked *Hyracotherium* to *Equus* through two other taxa (*Hyracotherium* is positively correlated with *Mesohippus*, which is positively correlated with *Parahippus*, which is positively correlated with *Equus*). *Hyracotherium* and *Equus* share significant negative correlation when compared directly. Cavanaugh et al. reasoned that contradictory correlation patterns (such as two taxa that could be positively and negatively correlated) could arise from a group of taxa that adopted an unusual shape, such as a line, in biological character space.

One approach to explain anomalous results of statistical baraminology methods is to utilize different methods on the same set of taxa. As Wood and Murray (2003) have argued, a plurality of methods applied to a single group should converge on the same baraminic identification and therefore provide consilient support for the baraminic membership. In practice, many modern baraminological studies have relied on multiple methods (Cavanaugh et al. 2003; Robinson 1997; Wood & Cavanaugh 2001), most notably ANOPA and baraminic distance correlation.

Because of the importance of methodological diversity, the development of novel baraminological methods should be encouraged. In this article, I apply the standard technique of classical multidimensional scaling (also called principle coordinate analysis) as a statistical baraminology method. Multidimensional scaling converts distance data for a given set of points into a set of *k*-dimensional coordinates, where *k* is a predetermined dimensionality. When applied to baraminic distances, a three-dimensional set of points representing the taxa can be generated and visualized using 3D viewing software. By revealing three-dimensional patterns, multidimensional scaling resembles 3D ANOPA. Whereas

ANOPA calculates 3D patterns directly from character data, multidimensional scaling requires baraminic distances to summarize character data. As a result, multidimensional scaling can serve as an independent verification of 3D ANOPA patterns, while also providing a novel means of visualizing baraminic distances.

## METHODS

A full presentation and explanation of multidimensional scaling is beyond the scope of this paper. For a detailed discussion, see Cox and Cox (1994). Briefly, given a set of $n$ objects, between each pair ($r$, $s$) of which is a measurement of dissimilarity $\delta_{rs}$, multidimensional scaling seeks a $k$-dimensional set of points, each of which corresponds to one of the $n$ objects and between which the distance in Euclidean space $d_{rs}$ is very close to the dissimilarity $\delta_{rs}$. Classical scaling begins with Euclidean distances as dissimilarities and recovers a set of points for which $d_{rs} = \delta_{rs}$.

To calculate $k$-dimensional coordinates given a matrix **D** of dissimilarities $\mathrm{d}_{rs}$ using classical scaling, calculate a matrix **A**, such that $a_{rs} = -0.5\delta_{rs}^{2}$. Doubly center **A**, giving **B**, where $b_{rs} = a_{rs} - a_{r.} - a_{.s} + a_{..}$, and $a_{r.} = \frac{1}{n}\sum_{s} a_{rs}$ ,$a_{.s} = \frac{1}{n}\sum_{r} a_{rs}$ , $a_{..} = \frac{1}{n}\sum_{r}\sum_{s} a_{rs}$ . Calculate eigenvalues and eigenvectors of **B**. The matrix **X** of $k$-dimensional coordinates is then calculated as $\mathbf{X} = \mathbf{V}_k \mathbf{L}_k^{1/2}$, where $\mathbf{V}_k$ is a matrix of the first $k$ eigenvectors and $\mathbf{L}_k^{1/2}$ is a diagonal matrix of the square roots of the first $k$ eigenvalues. When **D** is a matrix of Euclidean distances, the $k$-dimensional coordinates correspond exactly to the first $k$ principal components.

As mentioned above, to convert $\delta_{rs}$ to $d_{rs}$ such that $\delta_{rs} = d_{rs}$, the matrix of dissimilarities **D** must be Euclidean, with $d_{rr} = 0$ for all $1 \le r \le n$. Whereas Euclidean distances are used in Analysis of Patterns, baraminic distances are by definition not Euclidean, but they could be metric, are symmetric, and $d_{rr} = 0$ for all $1 \le r \le n$. Because the baraminic distance is defined as the number of different character states divided by the number of known character states, all states in which either taxa being compared have an unknown state are eliminated from the calculation. Thus in any given matrix, the denominator for the baraminic distance varies according to the number of known character states.

As a result, the resulting matrix of baraminic distances must be tested to determine if it is metric (see below).

Although baraminic distances do not fulfill the strict requirements of classical scaling, they can be converted to a metric matrix by addition of a constant $c$, where $c \leq$ the maximum $\delta_{rs}$. Even with a non-Euclidean, non-metric **D** however, Cox and Cox (1994) note that some statisticians "argue that classical scaling is still appropriate as an exploratory data technique for dimension reduction" (p 28). Following these suggestions, I have applied classical multidimensional scaling to uncorrected (non-Euclidean, non-metric) baraminic distance matrices and to baraminic distances corrected by the addition of the maximum baraminic distance for the given matrix (resulting in a metric matrix).

One might argue that to use classical multidimensional scaling in baraminology, a Euclidean measure of dissimilarity could be introduced, thus justifying the use of classical scaling and resulting in the equality $\delta_{rs} = d_{rs}$. For this paper, I prefer to utilize the previously defined baraminic distances for two reasons. First, as noted above, baraminic distance has already been defined and utilized in numerous baraminology studies. Whereas introduction of a Euclidean distance would be more appropriate to the technique, utilization of classical scaling on baraminic distances maintains continuity with the existing literature. Second, because Euclidean distances were already used in calculation of three-dimensional ANOPA structures, I sought an alternative, non-Euclidean measure of dissimilarity in order to evaluate 3D ANOPA results.

Because baraminic distance matrices are not Euclidean and not necessarily metric, scaled distances only approximate the baraminic distances (i.e., $\delta_{rs} \simeq d_{rs}$), and there is a potential for generating scaled distances that poorly represent the baraminic distances. Consequently, I use two different measures of "goodness of fit" between the scaled distances and the baraminic distances. The first is a "stress" measure suggested by Venables & Ripley (1997, p 385), which strongly resembles Kruskal's stress function for nonmetric scaling (Cox & Cox 1994, p 44-50), where distances and disparities are replaced with dissimilarities and distances respectively. Thus "stress" is here defined as

$$S = \sqrt{\frac{\sum_{r,s} (\delta_{rs} - d_{rs})^2}{\sum_{r,s} \delta_{rs}^{\ 2}}}$$

Smaller stress values indicate a better match between scaled distances and baraminic distances. For the second measure of fit, I calculate a linear correlation between the scaled distances and baraminic distances, as suggested in Ramsay (1982). If they match well, the correlation coefficient and slope should be near one, and the intercept should be near zero.

Baraminic distances were calculated using the BDIST software, as previously described (Wood 2002). For all baraminic distance calculations described in this paper, the relevance cutoff was set at 0.95. All multidimensional scaling calculations were done using the cmdscale function in S-Plus version 4.0 (Insightful Corp.). Datasets utilized in this study were as follows:

1. The Heliantheae and Helenieae (Asteraceae) dataset compiled by Karis (1993) and used in a previous ANOPA and baraminic distance study of tribe Heliantheae *sensu lato* (Cavanaugh & Wood 2002). The dataset consists of 141 morphological characters scored for 98 taxa.
2. The equid dataset compiled by Evander (1989) and used in a previous ANOPA and baraminic distance analysis of fossil horses (Cavanaugh et al. 2003). The dataset consists of 33 cranial and postcranial characters scored for 19 species.
3. The morphological portion of the Poaceae dataset compiled by the Grass Phylogeny Working Group (http://www.virtualherbarium.org/grass/gpwg/) and utilized in a previous baraminic distance study (Wood 2002). The dataset consists of 53 characters scored for 66 genera.

Determination whether a matrix is Euclidean was accomplished using the is.matrix function from the ADE-4 multivariate analysis package (Thioulouse et al. 1997), which implements a test originally devised by Gower and Legendre (1986). The is.matrix code was originally written in R (http://www.r-project.org) and was adapted for S-Plus version 4.0 for this study. Determination whether a matrix is metric was accomplished by applying the three characteristics of a metric matrix from Cox and Cox (1994, p 9): (1) $\delta_r = 0$ for all $1 \leq r \leq n$, (2) $\delta_{rs} = \delta_{sr}$ for all $1 \leq r, s \leq n$, and (3) $\delta_{rs} \leq \delta_{rt} + \delta_{ts}$ for all $1 \leq r,s,t \leq n$.

All 3D multidimensional scaling results were converted to Kinemages for display using Mage (http://kinemage.biochem.duke.edu/software/software1.html). Kinemages were then deposited in the ANOPA repository at the Baraminology Study Group website (http://www.bryancore.org/bsg/).

## RESULTS

**Heliantheae/Helenieae**. The Heliantheae/Helenieae dataset consists of 98 representative taxa from four different Asteraceae tribes, Heliantheae (64 taxa), Helenieae (29 taxa), Eupatorieae (four taxa), and Senecioneae (one taxon). The 141 characters are entirely morphological. Calculation of character relevance revealed two characters below the 0.95 cutoff, resulting in 139 characters used for calculation of baraminic distances by BDIST. The maximum calculated distance is 0.616, observed between *Critonia* and *Silphium*. The baraminic distance matrix is metric but not Euclidean, and the baraminic distance matrix corrected by addition of the maximum distance 0.616 is both metric and Euclidean. After classical scaling to three dimensions, stress for the uncorrected

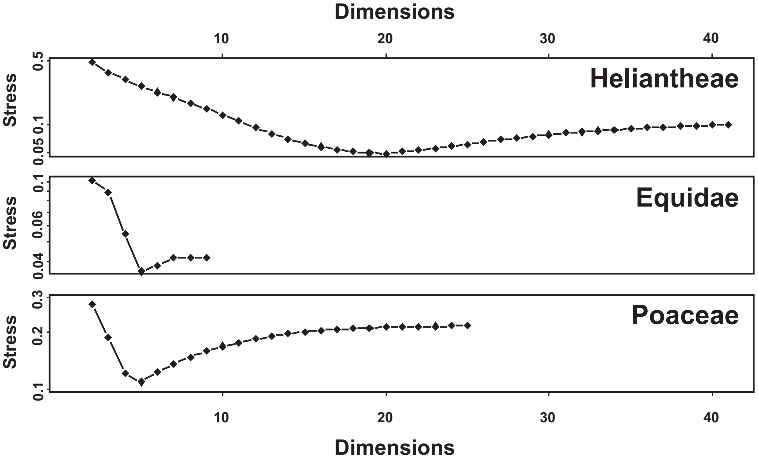


**Figure 1. Stress of *n*-dimensional classical scaling on uncorrected baraminic distance matrices (see text) plotted as a function of the number of dimensions (*n*), beginning with *n* = 2. Note that the maximum number of dimensions is determined by the number of positive eigenvalues of the distance matrix D.**

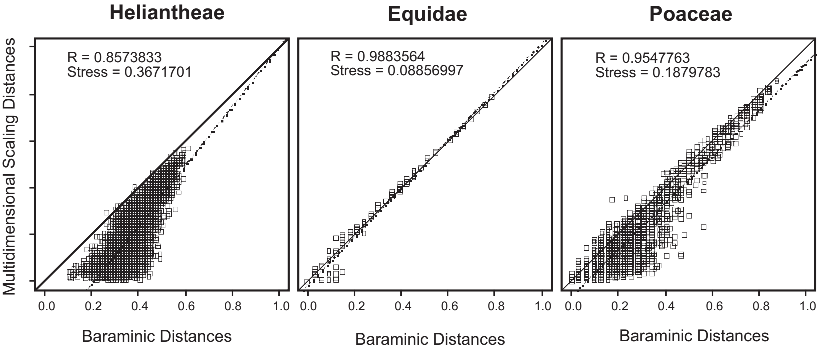


**Figure 2. Uncorrected baraminic distances plotted against Euclidean distances calculated from 3D calculated scaling results. For each dataset, the ideal of distance equality ($d_{rs} = \delta_{rs}$ for all *r*, *s*) is shown as a solid line. Least-squares regression lines for the actual distance data are shown as dashed lines with the correlation coefficient (R) given. The stresses of 3D classical scaling are also shown.**

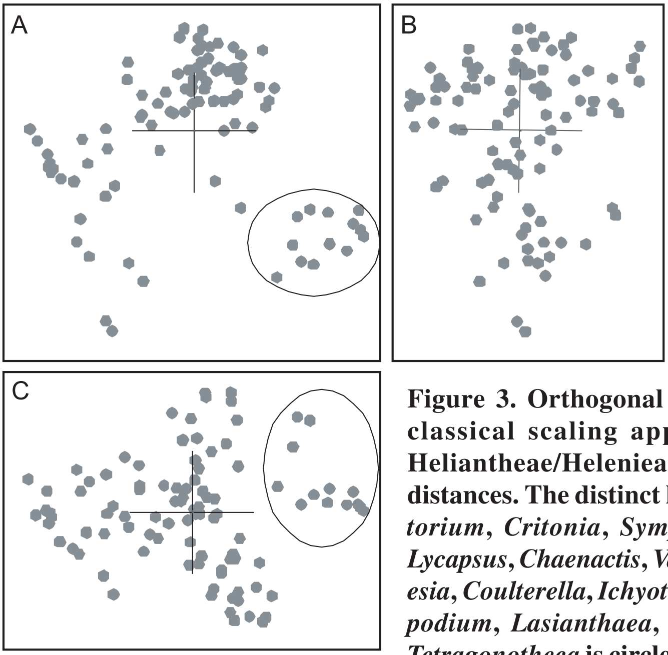


**Figure 3. Orthogonal views of 3D classical scaling applied to the Heliantheae/Helenieae baraminic distances. The distinct lobe of *Eupatorium*, *Critonia*, *Symphyopappus*, *Lycapsus*, *Chaenactis*, *Varilla*, *Dimeresia*, *Coulterella*, *Ichyothere*, *Melampodium*, *Lasianthaea*, *Fitchia*, and *Tetragonotheca* is circled in panels A and C.**

and corrected distances differed substantially: 0.3671701 and 0.58255 respectively. Similarly, correlation coefficient for the uncorrected distances was 0.8573833, and only slightly lower for the corrected distances, 0.8411189. Because of the significant difference in stress, I will here describe only the classical scaling of the uncorrected baraminic distances.

The stress for a series of scaling dimensions (2-41) is shown in Figure 1. The minimum stress for the Heliantheae/Helenieae dataset is 0.04875861 at 20 dimensions; the 0.3671701 stress for three dimensions indicates a structure that is highly distorted, as would be expected for reducing the dimensionality of a 20D structure to 3D. Nevertheless, the correlation between the Heliantheae/Helenieae baraminic distances and the distances inferred from the scaled points is very high (0.8573833), although the slope (1.25) and intercept (-0.22) differ markedly from 1 and 0 respectively (Figure 2). Despite the high stress, the distance correlation indicates that some meaningful patterns can be inferred from the 3D scaled structure, although the scaled distances are nearly without exception lower than the corresponding baraminic distance. Consequently, we should expect a structure more compact in 3D than it would be in 20D.

An orthogonal view of the 3D scaling results for the Heliantheae/Helenieae dataset is shown in Figure 3. The structure is noticeably partitioned into four lobe-like structures with poorly defined boundaries, consisting of at least ten taxa each. Only one lobe, consisting of *Eupatorium*, *Critonia*, *Symphyopappus*, *Lycapsus*, *Chaenactis*, *Varilla*, *Dimeresia*, *Coulterella*, *Ichyothere*, *Melampodium*, *Lasianthaea*, *Fitchia*, and *Tetragonotheca*, is well-separated from the other taxa. The remaining lobes comprise the remaining taxa but are too poorly bounded to provide a definitive membership list of each lobe.

**Equidae**. The Equidae dataset consists of 21 dental characters, five cranial characters, and seven postcranial characters scored for 19 taxa, including representatives from each of the three equid subfamilies. No characters scored below 0.95 relevance, and consequently none were eliminated from baraminic distance calculations. The maximum distance 0.788 is observed between two pairs of taxa (*Hyracotherium*, *Neohipparion*) and (*Hyracotherium*, *Pseudhipparion*). The baraminic distance matrix is neither Euclidean nor metric, but a matrix corrected by addition of the 0.788 to each baraminic distance is

Euclidean. After classical scaling to three dimensions, stress for the uncorrected and corrected distance matrices was 0.0886 and 0.4184 respectively. The linear correlation coefficients between the calculated distances and scaled distances were 0.9884 and 0.9699 respectively. Thus, as with the Heliantheae/ Helenieae dataset, classical scaling produces a structure with significantly lower stress for the uncorrected baraminic distance matrix. Consequently, I will use only the uncorrected baraminic distances for the remaining calculations.

Stress values calculated for classical scaling to dimensions 2-9 are shown in Figure 1. Unlike Heliantheae/Helenieae, the Equidae dataset has a minimum of 0.0354 at only five dimensions, which implies that the three-dimensional structure with a stress of 0.0886 is likely to be a reasonable representation of the five-dimensional structure. The close correspondence between the baraminic distances and scaled distances can be seen in a scatterplot (Figure 2). Not only is the linear correlation high (0.9884), but the slope (1.04) and intercept (-0.02) of the least-squares regression line are very close to 1 and 0 respectively.

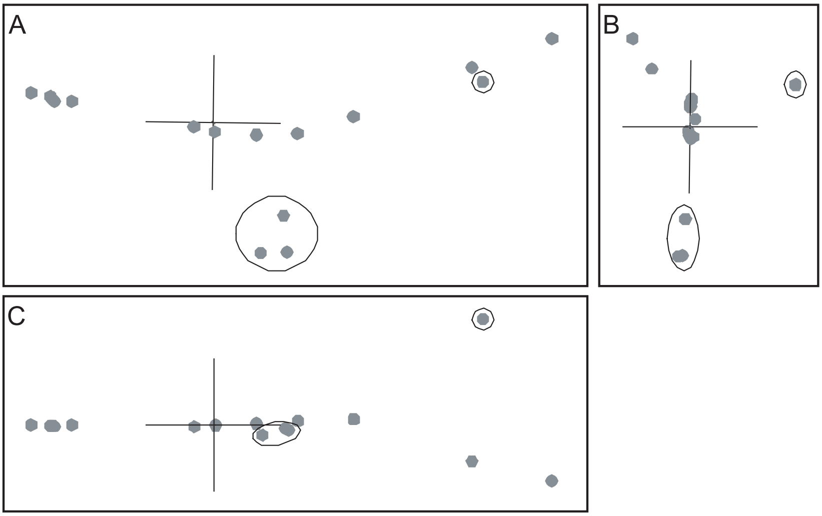


**Figure 4. Orthogonal views of 3D classical scaling applied to the Equidae baraminic distances. The two side-branches from the main axis (*Epihippus* and *Hypohippus-Anchitherium-Megahippus*) are circled.**

Orthogonal views of the 3D scaled structure reveal a very linear shape with two side-branches (Figure 4). One end of the linear structure (the right-most taxa in Figure 4) consists of the subfamily Hyracotheriinae: *Hyracotherium*, *Orohippus*, and *Epihippus*. The other end is a very densely packed cluster that includes eight genera: *Equus*, *Dinohippus*, *Hipparion*, *Neohipparion*, *Pseudhipparion*, *Protohippus*, and *Merychippus*. The remaining genera, *Parahippus*, *Archaeohippus*, *Kalobatippus*, *Miohippus*, and *Mesohippus*, are evenly-spaced between the two extremes of the linear structure. One side-branch consists of three genera, *Hypohippus*, *Anchitherium*, and *Megahippus*. The second side-branch is the single genus *Epihippus*. The side-branch consisting of *Hypohippus*, *Anchitherium*, and *Megahippus* is closest to *Kalobatippus* and *Miohippus*; whereas *Epihippus* is closest to *Orohippus*.

**Poaceae**. The Poaceae dataset is a subset of the Grass Phylogeny Working Group dataset consisting of 53 morphological characters. The taxa represent 62 grass genera from 36 tribes and four outgroup genera: *Baloskion*, *Elegia*, *Flagellaria*, and *Joinvillea*. Eleven of the grass tribes in the dataset are represented by more than one genus. Only 32 characters exceeded the relevance cutoff of 0.95 and were used to calculate baraminic distances. As with the Heliantheae/Helenieae and Equidae, I attempted classical scaling on the baraminic distance matrix and a matrix of distances plus the maximum distance calculated [0.875 between two pairs of genera: (*Baloskion*, *Centropodia*) and (*Elegia*, *Centropodia*)]. For uncorrected baraminic distances classically scaled to three dimensions, the stress was 0.1880 and the correlation between baraminic distances and scaled distances was 0.9548. Stress and correlation values for the corrected baraminic distance matrix were 0.5501 and 0.9298 respectively. Once again, despite the corrected baraminic distance matrix being Euclidean, the non-Euclidean, non-metric uncorrected baraminic distance matrix exhibits much less stress than the corrected distances. I will use the uncorrected distances for the remaining calculations.

As with the Equidae dataset, the Poaceae baraminic distances showed a minimum stress value of 0.1099 with a five-dimensional classical scaling (Figure 1). The correlation between the baraminic distances and scaled distances is high (0.9548), but the least-squares regression line deviates slightly from the diagonal. The slope of the

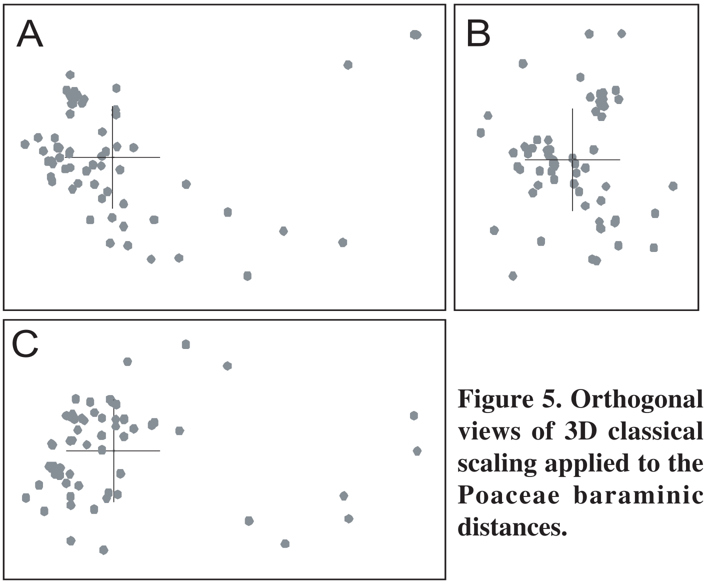
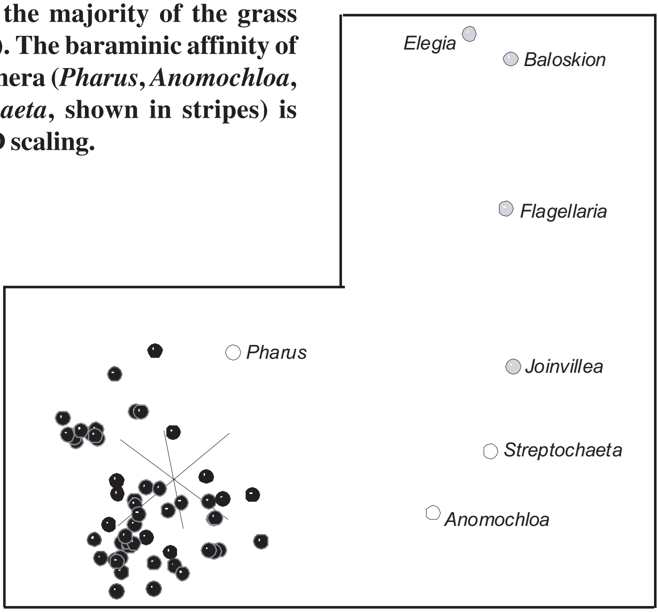


**Figure 5. Orthogonal views of 3D classical scaling applied to the Poaceae baraminic distances.**

**Figure 6. Proposed discontinuity surrounding the majority of grass genera is revealed in 3D classical scaling of the Poaceae baraminic distances. The outgroup (grey) genera *Elegia*, *Baloskion*, *Flagellaria*, and *Joinvillea* are distinct from the majority of the grass genera (black). The baraminic affinity of three grass genera (*Pharus*, *Anomochloa*, and *Streptochaeta*, shown in stripes) is clarified by 3D scaling.**



regression line is 1.00 and the intercept is -0.03. As can be seen in the scatterplot (Figure 2), the scaled distances tend to underestimate slightly the baraminic distances, as seen in the Heliantheae/Helenieae dataset. Unlike the Heliantheae/Helenieae distances, however, the high correlation and low stress indicates a good fit between the 3D scaled distances and the baraminic distances.

Orthogonal plots of the 3D scaling results reveals a generally compact central structure with several taxa located at some distance from the central structure (Figure 5). The deviants are the outgroup taxa *Elegia*, *Baloskion*, *Flagelleria*, and *Joinvillea*, together with *Streptochaeta* and *Anomochloa* (Figure 6). Of the eleven grass tribes represented by more than a single genus, all clustered closer to each other than the average scaled distance between grass taxa of 0.2012 (Table 1). The most disperse tribe is Arundineae with an average intra-tribal scaled distance of 0.1189. The most compact tribe is Stipeae, with an average intra-tribal scaled distance of 0.0334. Despite these low

**TABLE 1**

| Tribe | Genera | Distance ($d$) or mean distance ($<d>$) |
|---|---|---|
| Arundineae | *Arundo*, *Gynerium*, *Molinia*, *Phragmites*, *Thysanolaena* | $<d> = 0.1189$ |
| Olyreae | *Buergersiochloa*, *Lithachne*, *Olyra*, *Pariana*, *Eremitis* | $<d> = 0.1040$ |
| Oryzeae | *Leersia*, *Oryza* | $d = 0.1031$ |
| Chloridoid assemblage | *Distichlis*, *Eragrostis*, *Spartina*, *Sporobolus*, *Uniola*, *Zoysia* | $<d> = 0.1028$ |
| Centotheceae | *Chasmanthium*, *Zeugites* | $d = 0.0919$ |
| Aristideae | *Aristida*, *Stipagrostis* | $d = 0.0906$ |
| Bambuseae | *Chusquea*, *Pseudosasa* | $d = 0.0824$ |
| Danthonieae | *Centropodia*, *Danthonia*, *Merxmuellera*, *Austrodanthonia*, *Karroochloa* | $<d> = 0.0804$ |
| Meliceae | *Glyceria*, *Melica* | $d = 0.0600$ |
| Paniceae | *Panicum*, *Pennisetum* | $d = 0.0394$ |
| Stipeae | *Nassella*, *Piptatherum*, *Stipa* | $<d> = 0.0334$ |

intra-tribal scaled distances, there is a lack of noticeable clustering within the grass structure. Most tribes are consequently intermingled with members of other tribes.

## DISCUSSION

Although multidimensional scaling has been applied only rarely to biological problems outside of ecology (e.g., Kenkel & Orlóci 1986), the non-phylogenetic, descriptive nature of modern baraminology (Wood & Murray 2003), and particularly of the refined baramin concept (Wood et al. 2003), provide an ideal opportunity to apply classical scaling to biosystematics. My results here indicate that multidimensional scaling can be successfully applied to matrices consisting of baraminic distances

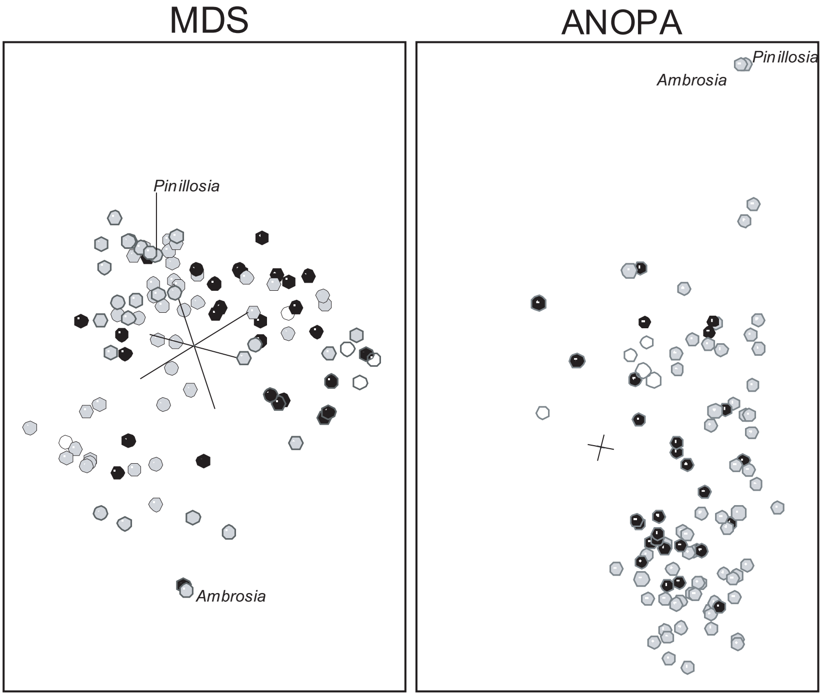


**Figure 7. Three-dimensional classical scaling of baraminic distances (left) and 3D ANOPA (right) for the Heliantheae/Helenieae dataset are shown. Heliantheae (grey), Helenieae (black), Eupatoriaceae (horizontal stripes), and Senecioneae (diagonal stripes) are distinguished.**

as defined by Robinson and Cavanaugh (1998b). The results of classical 3D scaling on three datasets previously utilized in baraminology studies reveal patterns that are both consistent with previous conclusions and also further illuminate the patterns in biological character space.

**Heliantheae/Helenieae, Equidae, and Poaceae.** When the scaled points for the Heliantheae/Helenieae dataset are compared to the 3D ANOPA results (Cavanaugh & Wood 2002), the 3D scaled points are recognizably different (Figure 7). In the ANOPA results, taxa of the tribe Eupatorieae are clustered together, whereas in the 3D scaled points, the four Eupatorieae taxa are separated into two groups, with *Lourteigia* separated from the other three, *Eupatorium*, *Critonia*, and *Symphyopappus*. Similarly, though visibly indistinguishable in the 3D ANOPA results, *Ambrosia* and *Pinillosia* are separated by a Euclidean distance of 0.4892 in the 3D scaling results. In contrast, Cavanaugh and Wood recognized ten distinguishable groups that do not correspond to any obvious groups in the 3D scaled points. For example, though united in the well-defined lobe in the 3D scaled points, *Coulterella*, *Ichthyothere*, *Critonia*, *Tetragonotheca*, and *Chaenactis* were all classified in different groups in Cavanaugh and Wood's 3D ANOPA results. Finally, although distinct from the main group of taxa in the 3D ANOPA structure, Senecioneae is much more intermingled with the other taxa in the 3D scaled results (Figure 7). In spite of the differences, 3D ANOPA and 3D scaling both agree that taxa from tribes Heliantheae, Helenieae, and Eupatorieae are intermingled.

In the 3D scaled results, the well-separated lobe consisting of thirteen taxa described above is probably not discontinuous from the other Heliantheae and Helenieae taxa for at least two reasons. First, *Varilla* is a close relative of subtribe Flaveriinae *sensu stricto* and has been assigned to the same monobaramin as *Flaveria* (Wood & Cavanaugh 2001; Wood & Cavanaugh 2003). Although *Flaveria* is included in this study, it is not part of the distinguishable lobe in question. Thus, the apparent separation is bridged by continuity from a different study using a different dataset. Second, the lobe contains taxa from tribes Heliantheae, Helenieae, and Eupatorieae, indicating that conventional taxonomy has not recognized a strong difference that would require separate classification of the taxa in question. Classifications based on easily recognized differences can be indicators of underlying discontinuity. The absence of an agreed-upon division of Heliantheae and Helenieae taxa imply that discontinuity is absent. Thus, despite recognizable lobes, there does not appear to be discontinuity between any group of taxa in the Heliantheae/Helenieae dataset. Instead, the taxa appear to be a single group with several subgroups.

Both of these major conclusions are identical to the conclusions of Cavanaugh and Wood (2002). The intermingling of taxa is prominent in both the 3D ANOPA and 3D classical scaling. Cavanaugh and Wood attribute the debates over classification of Heliantheae and Helenieae to this intermingling of taxa. Furthermore, as noted above, Cavanaugh and Wood distinguish at least 10 subpopulations within the 3D ANOPA results. Although these subpopulations are different from the lobes apparent in the 3D scaling results, subpopulations exist in both 3D

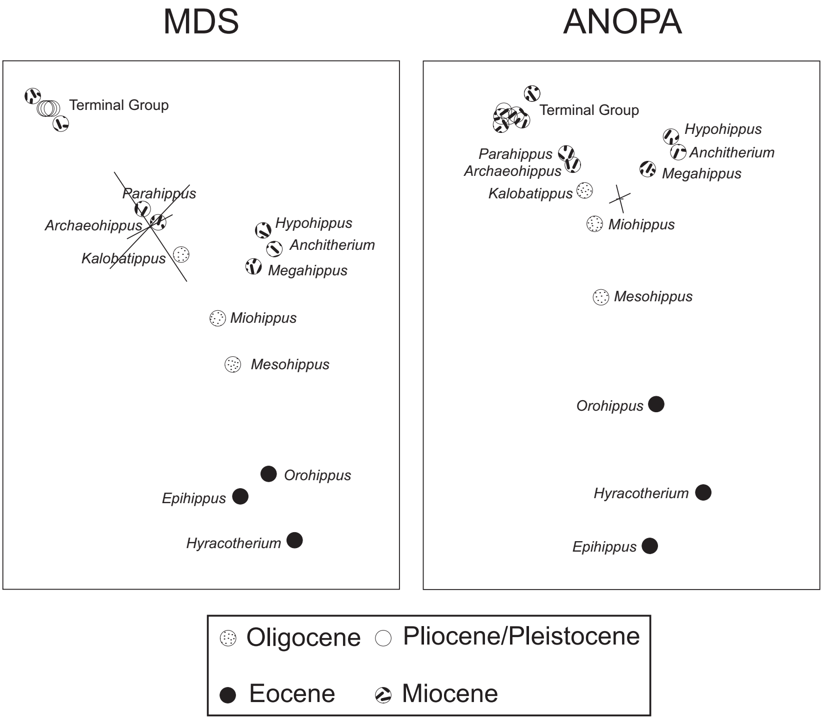


**Figure 8. Three-dimensional classical scaling of baraminic distances (left) and 3D ANOPA (right) for the Equidae dataset are shown. Stratigraphic first occurrence of each taxon is indicated.**

ANOPA and 3D scaling. The variation of the membership of these sub-groupings may be attributable to the attempt to visualize twenty dimensions in only three. Distances will necessarily be distorted in the attempt.

For the Equidae dataset, the 3D classical scaling results exhibit a striking correspondence to the 3D ANOPA results of Cavanaugh et al. (2003) (Figure 8). In both the taxa appear in a Y-shaped linear configuration. In both the major side-branch consists of *Hypohippus*, *Anchitherium*, and *Megahippus*, and it branches near *Miohippus* and *Kalobatippus*. In both *Epihippus* deviates from the main linear structure. In both the genera on the main linear structure appear in the same order: *Hyracotherium*, *Orohippus*, *Miohippus*, *Kalobatippus*, *Archaeohippus*, *Parahippus* and the terminal group of eight. An obvious difference is that the scaling results appear to be more linear than the ANOPA results (Figure 8).

Although the Poaceae dataset was not previously subjected to 3D ANOPA, it was analyzed using the baraminic distance correlation method (Wood 2002). The distance correlation results indicated a high frequency of significant, positive correlation between 59 of the 62 grass genera. Two grass genera, *Streptochaeta* and *Anomochloa* were negatively correlated to 48 and 27 grass genera respectively but were positively correlated to 4 and 2 of the outgroup genera respectively. *Pharus* was positively correlated to the outgroup genus *Joinvillea* and negatively correlated to two of the grass genera. *Pharus* was positively correlated to only 16 other grass genera. From the 3D scaling results (Figure 6), the reason for these patterns is apparent. The four outgroup taxa *Elegia*, *Baloskion*, *Flagellaria*, and *Joinvillea* form a curvilinear structure at a noticeable distance from the main cluster of grass genera. *Streptochaeta* and *Anomochloa* appear to be part of the same curvilinear outgroup structure. *Pharus* is a definite outlier of the main grass cluster but is poorly associated with the curvilinear outgroup structure.

What may be concluded about the baraminological classification of these three groups from the classical scaling results? The scaling results confirm previous baraminological conclusions. The Heliantheae, Helenieae, Eupatorieae, and probably Senecioneae belong to a single monobaramin, with no clear evidence of discontinuity in the Karis (1993) dataset. The Equidae are a single monobaramin that forms a biological trajectory (Wood & Cavanaugh 2003) that correlates well with the stratigraphic first occurrence of the taxa. The 3D scaling results for the Equidae are nearly identical with the 3D ANOPA results. The Poaceae dataset reveals a holobaramin encompassing 60 of the 62 grass taxa, exhibiting discontinuity with *Streptochaeta*, *Anomochloa*, *Joinvillea*, *Flagellaria*, *Baloskion*, and *Elegia*. Future baraminological studies of these groups should seek alternative datasets to confirm the results here reported.

**Multivariate Methods in Baraminology.** The refined baramin concept depicts taxa as points in a multidimensional biological character space. As a result, baraminology studies using the refined baramin concept are ideally suited for multivariate analysis. Previous baraminology studies have utilized two multivariate methods, Analysis of Patterns (Cavanaugh & Wood 2002; Cavanaugh et al. 2003; Wood & Cavanaugh 2001) and principal component analysis (García-Pozuelo-Ramos 2002). In this report, I introduced a third multivariate technique, classical multidimensional scaling. Each of these techniques has advantages and disadvantages, but as I have already demonstrated, using more than one multivariate technique provides not only a complementary perspective on the same dataset but also a confirmation and clarification of previous results.

As noted above, ANOPA is a pattern projection technique that creates a three-dimensional depiction of multidimensional data. In the case of baraminology, the dimensions of the multidimensional data are characters, and the resulting pattern can reveal clustering patterns among the taxa. Often the shapes adopted by the clusters are complex (Cavanaugh & Sternberg 2002; Cavanaugh & Wood 2002), but occasionally the patterns closely resemble phylogenetic hypotheses (Wood & Cavanaugh 2003). Because 3D ANOPA is a projection of points, distortion is expected for datasets of high dimensionality.

Classical scaling can provide an independent test of the clustering patterns revealed in 3D ANOPA. As seen in this report, classical scaling essentially confirmed the clustering of the fossil equids, but the clustering of the Heliantheae and Helenieae dataset was distinctly different. In 3D ANOPA, the taxa adopted an elongated structure, but in 3D classical scaling the taxa were much more compact. Even though these patterns differed, the stress of classical scaling over a range of dimensions revealed a possible reason for the differences. Whereas the minimal stress for the equid dataset was observed at five dimensions, the minimal stress for the Heliantheae/Helenieae dataset was observed at twenty dimensions. Thus, reduction of dimensionality in the equid dataset would be expected to produce few distortions of taxic positions, whereas reduction of dimensionality in the Heliantheae/Helenieae dataset should produce far more distortions and alternative topologies of similar high distortion.

Wood's (2002) baraminic distance correlation analysis of the Poaceae dataset revealed some ambiguities with regard to the classification of three genera: *Pharus*, *Streptochaeta*, and *Anomochloa*. Although both *Anomochloa* and *Streptochaeta* are classified as grasses, they exhibited negative correlation with other grasses and positive correlation with non-grass taxa. The third ambiguous grass genus *Pharus* exhibited very little significant correlation, either positive or negative. The classical 3D scaling in this report reveals that *Pharus* appears to be an outlying member of the grass holobaramin, but *Streptochaeta* and *Anomochloa* do appear to cluster with the outgroup genera and are probably not members of the grass holobaramin. Thus, Wood's (2002) omission of *Streptochaeta* and *Anomochloa* from the grass holobaramin is confirmed, and the ambiguous classification of *Pharus* is clarified.

Based on the successful application of classical scaling seen in this report, I recommend that baraminologists seek additional multivariate and clustering techniques to apply in baraminological research. Although a common technique, principal component analysis has been used only once in a study of canid variation (García-Pozuelo-Ramos 2002). Although discriminant analysis and fuzzy analysis are used in biological research, they have not been applied in baraminology. Considering the fruitful results of this present study, baraminologists should seek to use other statistical techniques and thereby to broaden the statistical basis of baraminology and to strengthen baraminic hypotheses.

## ACKNOWLEDGEMENTS

Thanks to Phil Lestmann and Bob Simpson (Bryan College) for their advice and guidance.

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# ANNOTATIONS FROM THE LITERATURE

## BIODIVERSITY: CONSERVING TROPICAL FOREST BIRDS REQUIRES LARGE REFUGES

Ferraz G, Russell GJ, Stouffer PC, Bierregaard RO, Pimm SL, Lovejoy TE. 2003. Rates of species loss from Amazonian forest fragments. Proceedings of the National Academy of Sciences (USA) 100:14069-14073.

**Summary**. Species of birds vary in the size of habitat necessary to sustain a viable population. One of the major questions in conservation is the size of refuge required to protect the biodiversity of a region. The effects of habitat fragmentation were studied in the central Amazon region of Brazil. Diversity of understory birds was surveyed over a period of 13 years in forest fragments of about 1, 10, and 100 hectares (1 hectare is approximately 2.5 acres). Results showed that about half the species disappeared from the 10-hectare fragments in less than 15 years. This is not enough time to put conservation measures into place to preserve diversity. Comparison with experience in the Kakamega Forest of Africa suggests that even 10,000-hectare reserves may lose half their understory species in about 100 years.

**Comment**. Habitat fragmentation is probably the most serious threat to biodiversity. Refuges must be large enough to preserve a viable, self-sustaining population. Creationists should support responsible efforts to be good stewards of the biodiversity God has created.

## BIODIVERSITY: CORAL CONVERGENCE CONFOUNDS TAXONOMY

Fukami H, Budd AF, Paulay G, Solé-Cava A, Chen CA, Iwao K, Knowlton N. 2004. Conventional taxonomy obscures deep divergence between Pacific and Atlantic corals. Nature 427:832-835.

**Summary**. Reef-building corals are found in both the Pacific and Atlantic Oceans, with the Atlantic corals generally considered to belong to lineages from the Pacific. Two families, “Faviidae” and “Mussidae” are prominent in both regions. DNA sequences show that some of the Atlantic "Faviidae" are more closely related to the Atlantic "Mussidae" than to the Pacific "Faviidae." Of the 27 genera of Atlantic reef-building corals, nine genera belong to a previously undetected lineage endemic to the Atlantic. These results indicate a previously unrecognized high degree of endemism in the Atlantic corals, a high degree of morphological convergence among these corals, and a need to re-evaluate the systematics of corals using molecular methods.

**Comment**. These results show the need for caution in drawing conclusions from phylogenies constructed solely on morphological data. This has important implications in conservation and biodiversity studies, in that similar groups from different regions may actually represent different clades. The implications for paleontological studies are even more serious, since relationships of fossils are generally based on morphological data that are incomplete at best.

## BIOGEOGRAPHY: DISPERAL DOMINANT IN THE SOUTHERN HEMISPHERE

Sanmartin I, Ronquist F. 2004. Southern Hemisphere biogeography inferred by event-based models: plant versus animal patterns. Systematic Biology 53:216-243.

**Summary**. Vicariance is the splitting of a population by development of a barrier within its range. Vicariance has been the dominant explanation for biotic distributions in the southern hemisphere. In this study, 54 animal phylogenies and 19 plant phylogenies were compared with the sequence of continental separation, to see if the two patterns coincide. Results showed that plant phylogenies did not correlate well with the sequence of continental separation, while animal phylogenies did. This indicates that long-distance dispersal has been more important for plants than for animals. Only two of the plant groups do not seem to require long-distance dispersal. Ten insect groups, two other invertebrate groups, and three groups of fish do not require dispersal. Dispersal seems important for the ratite birds, but not for the marsupials. Several groups show closest relationships between Australia and South America, which can be explained by Antarctica forming a bridge between the two continents.

**Comment**. These results indicate the importance of long-distance dispersal in explaining distributions in the southern continents, even for groups restricted to the southern hemisphere. Most of the data are consistent with predictions of creation biogeographic theory, since plants, fish and invertebrates are not mentioned as taken into the ark, but the marsupials present an interesting opportunity for further investigation.

## BIOGEOGRAPHY: DISPERSAL MORE IMPORTANT THAN CONTINENTAL VICARIANCE AMONG PLANTS

Munoz J, Felicisimo AM, Cabezas F, Burgaz AR, Martinez I. 2004. Wind as a long-distance dispersal vehicle in the Southern Hemisphere. Science 304:1144-1147.

**Summary**. The southern continents are separated by oceans, yet frequently have similar plants. This could be due to vicariance — separation of a once-connected population when the continents broke away from each other. An alternate explanation is dispersal — immigration from one continent to the other across the ocean. Long-distance dispersal is a difficult hypothesis to test, so biogeographers have tended to focus their attention on vicariance explanations. This paper reports the results of a study of floristic similarities among 27 southern land masses, including several subantarctic islands. Four taxonomic groups were studied: mosses, liverworts, lichens, and pteridophytes (ferns and their allies). Floristic similarities among land masses were tested for correlation against distance to the nearest land mass, versus "wind connectivity." "Wind connectivity" incorporates both wind speed and direction. Results showed that "wind connectivity" is more important than geographic proximity in explaining floristic similarity. This suggests that long-distance dispersal by wind is an important factor in explaining the distribution of these groups of plants.

**Comment**. Although vicariance explanations may be easier to test, the desire to provide "scientific" explanations has led many biogeographers to neglect explanations including dispersal. Yet this and other studies have shown that dispersal is often much more important than vicariance in explaining present distributions. Just because a method is thought to be "scientific" does not insure that is will be more accurate.

## GEOLOGY: BIFS, A CONFUSING STATE OF AFFAIRS

Dauphas N, van Zuilen M, Wadhwa M, Davis AM, Marty B, Janney P. 2004. Clues from Fe isotope variations on the origin of Early Archean BIFs from Greenland. Science 306:2077-2080.

**Summary.** Precambrian banded iron formations (BIFs) are enigmatic structures of uncertain origin. Current theories propose 1) abiotic photo-oxidation of ferrous Fe to ferric Fe, 2) direct oxidation by anaerobic bacteria or 3) mediated oxidation by aerobic bacteria. The identification of bio-signatures has been difficult due to the overprinting of the original characteristics of the Archean rocks by high grade metamorphism. This paper correlates the Fe enrichment of the BIFs in SW Greenland with the titanium content of the deposits to ascertain the source of the Fe as either igneous or sedimentary. The alteration of basalt (the probable igneous source) results in a loss of Fe relative to Ti; whereas, precipitation and sedimentation associated with hydrothermal vents results in enriched Fe relative to Ti. Support for the latter model is presented by this paper.

**Comment.** The formation of the BIFs is currently debated and the theory for biotic oxidation of ferrous to ferric Fe is based largely on the proposed age of the deposits and the theoretical concept of an anoxic environment for the origin of the amino acid building blocks necessary for the origin of life. The authors of this paper recognize that the fractionation of the Fe isotopes cannot be used to unequivocally identify biotic activity. More research is needed to determine the essential characteristics that might identify fractionation by abiotic photo-oxidation. (EK)

## GEOLOGY: END-CRETACEOUS MASS EXTINCTION DOWNSIZED?

Belcher CM, Collinson ME, Sweet AR, Hildebrand AR, Scott AC. 2004. New constraints on the thermal energy released from the K-T impactor: evidence from multi-method charcoal analysis. Abstract 81-9. Geological Society of America Program with Abstracts 36(5):204.

**Summary**. The K-T impactor has been postulated to have delivered sufficient energy to the biosphere to cause spontaneous, near-global wild fires. This would produce large quantities of charcoal in K-T boundary sediments. A study of K-T boundary sediments from Saskatchewan to Colorado revealed abundant non-charred plant remains, and an amount of charcoal only one-ninth the amount found in Cretaceous sediments. This indicates the impact did not deliver as much energy to North America as has been proposed.

**Comment**. Some calculations have suggested a global inferno at the K/T boundary, making it difficult to understand how any terrestrial life could have survived. The evidence reported here suggests a much smaller energy release by the impact. This may explain the inferred survival of some terrestrial organisms across the boundary, but it still leaves unexplained why certain groups disappear from the fossil record at that point, while other groups continue. It also points out a gap in our understanding of the energetics of such impacts.

## GEOLOGY: END-CRETACEOUS IMPACT PRECEDED THE END OF THE CRETACEOUS

Keller G, Adatte T, Stinnesbeck W, Rebolledo-Vieyra M, Fucugauchi JU, Kramar U, Stüben D. 2004. Chicxulub impact predates the K-T boundary mass extinction. Proceedings of the National Academy of Sciences (USA) 101:3753-3758.

**Summary**. A core taken from the Chicxulub impact structure shows a 50-cm layer of finely laminated sediments containing latest Cretaceous microfossils, is capped by a clay that represents the Cretaceous-Tertiary boundary. The 50-cm layer shows several intervals of bioturbation, indicating *in situ* deposition over a period of time. The microfossils (forams) are indicative of zone CF1, which spans the last 300,000 years of the Cretaceous. This shows that the impact site accumulated 50 cm of bioturbated sediments after the impact and before the Cretaceous-Tertiary boundary, and suggests that the mass extinction may have occurred in stages rather than triggered by a single event.

**Comment**. The relationship of mass extinctions to extraterrestrial impacts has always had some puzzling aspects. Why are the last dinosaurs found below, rather than in the impact horizon. Why did some groups disappear while others did not? This report makes matters more complicated: what is the actual causal relationship between a mass extinction and an impact that preceded it?

## GEOLOGY: END-PERMIAN MASS EXTINCTION AND ITS CAUSES

Becker L, Poreta RJ, Basu AR, Pope KO, Harrison TM, Nicholson C, Iasky R. 2004. Bedout: a possible end-Permian impact crater offshore of northwestern Australia. Science 304:1469-1476. Reactions: Science 306:609-612.

**Summary**. An uplifted area near the northwestern coast of Australia has been proposed as the site of a giant end-Permian extraterrestrial impact. The Bedout High is about 40-60 km in diameter and 3-4 km high. It is located along a passive continental margin, which indicates a cause other than tectonic activity. The authors propose that the uplifted area represents the central uplift of a large impact crater. They report a negative gravity anomaly, suggestive of an impact, but admit it is somewhat obscured by subsequent geologic activity. Minerals found at the site include maskelynite, silica glass and shocked plagioclase. Minerals with unique chemical compositions were also found. Each of these features is consistent with an impact. Argon/argon dating indicates an age equivalent to the Permian/Triassic boundary. The proposed impact might explain the presence of P/T boundary meteorites in Antarctica, shocked quartz in Australia and Antarctica, and extraterrestrial fullerenes in Asia. It might also be related to the Siberian flood basalts, and perhaps the end-Permian mass extinction.

This proposal has been severely criticized by other scientists. There seems to be fewer shocked minerals than expected from such a large impact. Surrounding regions lack evidence of impact ejecta or turbidites. The gravity anomaly is very weak, the altered rocks resemble volcanic breccias, the evidence of shocked minerals is weak, and the radioisotope age was not properly measured.

**Comment**. This is probably the most dramatic claim to date relating extraterrestrial impacts to the end-Permian fossil turnover (mass extinction). There is variation in the kinds of evidence seen at impact sites; one important variable is whether the impactor was an asteroid or a comet. The cause(s) of the end-Permian mass extinction are currently being debated. The major contenders include large-scale volcanism, release of methane hydrates from the ocean floor, and changes in sea level. New developments are to be expected.

Erwin DH, Bowring SA, Jin Y. 2002. End-Permian mass extinctions: a review. In: Koeberl C, MacLeod KG, editors. Catastrophic Events and Mass Extinctions: Impacts and Beyond. Geological Society of America Special Paper 356:363-383.

**Summary**. The cause of the P/T mass extinction remains unclear. Putative causes need to include explanations for anoxia in ocean sediments, reduced concentrations of carbon-13, occurrence during a sea-level transgression, increase of fungal spores, and relationship to the Siberian flood basalts. The available data are largely consistent with an extraterrestrial impact, climatic effects of the Siberian flood basalts, and perhaps a release of marine hydrates. A combination of these and other factors may have been the cause of the extinction.

**Comment**. The end-Permian fossil turnover ("mass extinction") is one of the most prominent features of the fossil record. It occurs globally and involves both marine and terrestrial organisms. About two-thirds of the genera fossilized in the upper Permian are absent from the overlying sediments. This dramatic feature of the fossil record begs for an explanation. Mass extinctions in general have not been explained satisfactorily, and remain a fertile topic for exploration.

Koeberl C, Farley KA, Peucker-Ehrenbrink B, Sephton MA. 2005. Geochemistry of the end-Permian extinction event in Austria and Italy: No evidence for an extraterrestrial component. Geology 32:1053-1056.

**Summary**. Extraterrestrial impacts are expected to leave a geochemical signature that includes enriched concentrations of iridium, helium-3, and osmium-188. Examination of sediments spanning the P/T boundary sections in Austria and Italy showed only a relatively small increase in iridium and osmium-188 concentrations, but no increase in helium-3. These results are not typical of sediments associated with extraterrestrial impacts, but are compatible with terrestrial anoxic sedimentation regimes. This suggests the end-Permian mass extinction was not the result of a giant extraterrestrial impact.

Racki G. 2003. End-Permian mass extinction: oceanographic consequences of double catastrophic volcanism. Lethaia 36:171-173.

**Summary**. This review favors the flood basalt hypothesis for the end-Permian mass extinctions. The Siberian flood basalts erupted at the end of the Permian, coincident with the end-Permian mass extinction. The massive basalt outpouring could have completely melted the northern glaciers and the permafrost. This would disrupt ocean circulation by reducing the latitudinal temperature gradient. Normally, deep water originates in the north and flows southward at depth, promoting mixing of waters. Cessation of this system would produce anoxia in deep water. Marine anoxia might explain the end-Permian collapse of chert production and the marine mass extinction. Runaway greenhouse effects due to gases released by the flood basalts could explain the terrestrial phase of the mass extinction event. A smaller mass extinction at the end of the Permian Guadelupian stage seems to be correlated with a smaller basalt outpouring in China, the Emeishan Traps. This two-staged flood basalt pattern is unique to the upper Permian, and appears to be a good candidate to explain the two mass extinctions.

Ryskin G. 2003. Methane-driven oceanic eruptions and mass extinctions. Geology 31:741-744.

**Summary**. The P/T boundary is marked by a large decrease in the C-13/C-12 ratio. This might have resulted from release of massive amounts of methane hydrates from the floor of the ocean. Methane can potentially dissolve in ocean water and accumulate to high concentrations in stagnant basins, where it may form a metastable complex with seawater. If such a system were disturbed, such as by an earthquake, methane bubbles could be shaken loose and rise to the surface, expanding quickly as they rise. This movement would further disturb the water column, reinforcing the release of methane. The result could be a violent eruption of methane, similar to the eruption of carbon dioxide in Lake Nyos in 1986. Methane is typically depleted in C-13, so the release of large volumes of methane could explain the reduction in the C-13/C-12 ratio at the P/T boundary. An area of ocean floor the size of the Black Sea could hold, at saturation, $10^{18}$ g of carbon, which is about half the total content of the terrestrial biomass. Oxidation of the methane could severely reduce the atmospheric oxygen level, killing much of the world's biota and producing a major mass extinction.

**Comment**. The release of large amounts of methane into the water column would be a catastrophic event that, although perhaps capable of causing a mass destruction of marine life, should produce a kill horizon of rather limited thickness. This does not appear to be a satisfactory explanation for the extinction pattern in Upper Permian sediments.

Ward PD, Botha J, Buick R, De Kock MO, Erwin DH, Garrison GH, Kirschvink JL, Smith R. 2005. Abrupt and gradual extinction among Late Permian land vertebrates in the Karoo Basin, South Africa. Science 207:709-714.

**Summary**. A total of 126 vertebrate skulls were collected from Permo-Triassic boundary sediments in the Karoo Basin of South Africa. Twenty-one taxa of reptiles and amphibians were identified. Four of thirteen Permian taxa have ranges extending into the Triassic. Three taxa disappear between 50 to 20 meters below the boundary, and six of the remaining ten taxa disappear within ten meters of the boundary. This shows a gradual extinction punctuated by a larger, abrupt extinction at the boundary. The extinction pattern differs from that at the K/T boundary, and is not what is expected from an extraterrestrial impact.

## GEOLOGY: MAYBE THE MEDITERRANEAN WAS NOT A DESERT?

Hardie LA, Lowenstein TK. 2004. Did the Mediterranean Sea dry out during the Miocene? A reassessment of the evaporite evidence from DSDP Legs 14 and 42 A cores. Journal of Sedimentary Research 74:453-461.

**Summary.** Hardie and Lowenstein maintain that the evidence that had been used to support the shallow water deposition of evaporites during repeated dessication of the Mediterranean Sea had been misinterpreted for more than 30 years by a number of researchers. In this paper, the authors systematically review the data used in the arguments for dessication and submit evidence for the deep water deposition of these same data, in particular, the "chicken-wire" anhydrite (anhydrite crystals forming a mosaic pattern in the sediments) and algal stromatolites.

**Comment.** The finer points regarding the repeated dessication of the Mediterranean Sea have been discussed through the past three decades with the majority of the scientists favoring the shallow water, dessication model. Recently scientists with expertise to address this issue garnered their evidence and arguments to review the data first-hand and present their case for an alternative view. Following the example of these authors, Christian researchers do not necessarily need to change their views though the opposing majority opinion may hold sway for decades; but rather we need to study the literature and data seeking insight into the issues. (EK)

## HUMAN PALEONTOLOGY

Brown P, Sutikna T, Morwood MJ, Soejono RP, Jatmiko, Saptomo EW, Due RA. 2004. A new small-bodied hominin from the Late Pleistocene of Flores, Indonesia. Nature 431:1055-1061.

Morwood MM, Soejono RP, Roberts RG, Sutikna T, Turney CSM, Westaway KE, Rink WJ, Zhao J-x, van den Bergh GD, Due RA, Hobbs DR, Moore MW, Bird MI, Fifield LK. Archaeology and age of a new hominin from Flores in eastern Indonesia. Nature 431:1087-1091.

**Summary**. A skeleton of a very small fossil human has been found in a limestone cave on the Indonesian island of Flores, associated with bones of extinct pygmy elephants and large Komodo dragons. The human skeleton is of an adult female about 1 meter in height, with an estimated weight of around 20-25 kg, and a cranial capacity of about 380 $cm^3$. The brain size is smaller than a chimp, and as small as any known australopithecine. The skull has several features that link it to *Homo erectus* skulls. The new find has been given the name *Homo floresiensis*.

**Comment**. Populations isolated on islands often change in size. For example, fossil pygmy elephants are known from several islands, including Sicily and Malta, where they shrank from 4 meters to 1 meter in height in less than five thousand years. Flores is quite isolated, and is separated from both Asia and Australia by deep water. This individual may have belonged to a population of small humans that were isolated on Flores, showing that humans, as do other species, possess the capacity for rapid changes in morphology. The fossils apparently had human mental abilities in a brain as small as an australopithicine, reminding us that brain structure is more important than brain size in determining intelligence.

## PALEONTOLOGY: ARCHAEOPTERYX HAD A BIRD-BRAIN

Dominguez Alonso PA, Milner C, Katcham RA, Cookson MJ, Rowe TB. 2004. The avian nature of the brain and inner ear of *Archaeoptyeryx*. Nature 430:666-669.

**Summary**. The London specimen of *Archaeopteryx* was subjected to a computed tomography scan (CAT-scan). Three-dimensional reconstruction of the braincase indicates that *Archaeopteryx* had enlarged regions for seeing, hearing, and spatial perception. These features indicate that *Archaeopteryx* had a brain much more like modern birds than like reptiles.

**Comment**. These findings are consistent with expectations based on the presence of well-developed flight feathers and other bird-like features. Application of computer tomography scan is a welcome advance in understanding this enigmatic fossil.

## PALEONTOLOGY: SHELL MINERALOGY AND FOSSIL TRENDS

Kidwell SM. 2005. Shell composition has no net impact on large-scale evolutionary patterns in mollusks. Science 307:914-917.

**Summary**. Patterns and trends in the fossil record are based on preservation of fossils, generally of hard parts such as shells. But shells are made of different materials, and a bias favoring preservation of one material over another could distort the observed patterns. Shells made of calcite are generally better preserved than those made of aragonite. This study of shells of marine bivalve genera through the Phanerozoic compared stratigraphic ranges with shell composition. Results show no bias toward preferential preservation of calcitic shells over aragonitic. This implies that patterns observed in the fossil record are reliable, and not due to preservational bias.

**Comment**. These results strongly suggest that shell preservation is not unduly dependent on differences in shell composition. Thus, fossil patterns in bivalves may carry an important signal that could help us in understanding the processes leading to their preservation.

## PALEONTOLOGY: FIRST FOSSIL INSECT SHOWS ADVANCED FEATURES

Engel MS, Grimaldi DA. 2004. New light shed on the oldest insect. Nature 427:627-630.

**Summary**. Fossil insects first appear in Devonian sediments, in such places as the Rhynie Chert of Scotland. This is the report of a fragmentary insect fossil, *Rhyniognatha hirsti*, found in the Rhynie

Chert. The specimen is the oldest known fossil insect, but it is not the most primitive. *Rhyniognatha* has a mandibular structure found only in true insects, with details that resemble flying insects. This discovery implies that insects were present in the Silurian.

**Comment**. Creation theory predicts that insects were present throughout the time when Phanerozoic sediments were deposited. The discovery that the first fossil record of an insect is that of a relatively "advanced" insect is not surprising. It is, perhaps, more surprising that fossil insects seem to be missing from Upper Devonian and Lower Carboniferous sediments.

## PALEONTOLOGY: HUMMINGBIRDS IN EUROPE?

Mayr G. 2004. Old World fossil record of modern-type hummingbirds. Science 304:861-864.

**Summary**. Hummingbirds are a specialized group of birds presently restricted to the New World, and most speciose in the Neotropical region. The fossil record of hummingbirds is poor. A few fossils from Europe and Asia are thought to represent extinct types of hummingbirds or their close relatives, but none of them appears to be closely related to living hummingbirds. Two fossil hummingbirds have been found in Oligocene deposits in Germany. These fossils have the elongated beak and other features of modern hummingbirds, although they are not believed to belong to any living group of hummingbirds.

**Comment**. This discovery raises some interesting biogeographic questions. How could hummingbirds travel between Europe and the New World? In which area did they start? If a group is presently restricted to a geographic region, does this mean they probably originated in that region? If a group is restricted to two separate geographic regions, does this mean the two regions were once connected and later became separated? Examples such as this fossil hummingbird remind us of how precarious are our speculations regarding the history of life.

## PALEONTOLOGY: WHAT CAUSES CHANGES IN MAMMAL PALEOFAUNAS?

Prothero DR. 2004. Did impacts, volcanic eruptions, or climate change affect mammalian evolution? Palaeogeography, Palaeoclimatology, Palaeoecology 214:283-294.

**Summary**. A careful analysis of Cenozoic mammal diversity curves failed to show a strong correlation between high rates of mammal turnover and environmental events such as climate change, volcanic eruptions, or extraterrestrial impacts. Episodes of high faunal turnover were not correlated with any extrinsic cause. Factors causing high mammal turnover are still unknown.

**Comment**. The observed disconnect between large-magnitude environmental events and faunal changes in Cenozoic mammals is unexpected. The cause of the disconnect is not clear, but it would seem worthwhile to explore the effects of compressing the time scale over which the events are deemed to have occurred.

## PALEONTOLOGY: DINOSAUR-EATING MAMMALS

Hu Y, Jin M, Yuanqing W, Chuankui L. 2005. Large Mesozoic mammals fed on young dinosaurs. Nature 433:149-152.

**Summary**. A medium-sized triconodont mammal with dinosaur remains in its stomach area has been found in the Lower Cretaceous Yixian Formation of China. The mammal is the size of an opossum, while the baby *Psittacosaurus* dinosaur was five to six inches in length. (Adult *Psittacosaurus* reached the size of a sheep, and are common in the area.) An even larger fossil mammal, about the size of a badger, was also found in theYixian Formation. These fossil mammals challenge conventional thinking that Mesozoic mammals were small because they could not compete with dinosaurs.

**Comment**. Fossils from the Yixian Formation have spectacularly expanded our knowledge of the fossil record, and remind us of how much remains to be discovered.

## SPECIATION: ARE MINOR MORPHOLOGICAL DIFFERENCES DUE TO MOLECULAR REPEATS?

Fondon (III) JW, Garner HR. 2004. Molecular origins of rapid and continuous morphological evolution. Proceedings of the National Academy of Sciences (USA) 101:18058-18063.

**Summary**. Repeated DNA sequences associated with seventeen genes known to be active in development were analyzed in 92 breeds of dogs, and quantitatively compared with differences in skull and limb morphology. Results showed a close correlation between the number and purity of DNA repeats and morphological differences. The authors conclude that differencse in the number and length of repeat sequences can explain rapid, but topologically conservative, morphological changes seen in species.

**Comment.** This discovery may hold the key to understanding how species can change rapidly, producing morphological variations equivalent to those seen among members of a taxonomic family. A possibility worth exploring is whether repeat sequences cause differences in rates of division among cell lineages during development. This mechanism might explain post-flood diversification of lineages at a rate much faster than evolutionists have predicted.

# LITERATURE REVIEWS

*Readers are invited to submit reviews of current literature relating to origins. Please submit contributions to: ORIGINS, Geoscience Research Institute, 11060 Campus St., Loma Linda, California 92350 USA. The Institute does not distribute the publications reviewed; please contact the publisher directly.*

## TEACH THE CONTROVERSY

**Darwinism, Design, and Public Education**. Edited by John Angus Campbell and Stephen C. Meyer. 2003. E. Lansing, MI: Michigan State University Press. 634 p. Paper, $28.95.

*Reviewed by Henry Zuill, Norman, Arkansas*

The editors of *Darwinism, Design, and Public Education* (*DD & PE*) advocate presenting design along side evolution in public education curricula. Their plea is to “teach the controversy” so that science education will be more rigorous when taught with the give and take that is part and parcel of real science. They suggest evolution classes should not only teach perceived evidentiary strengths, but also evidentiary weaknesses. Evidence should take one to where it leads, and in the view of most of the contributors to *DD & PE*, that is to Intelligent Design (ID).

Thirty authors, representing an array of disciplines and perspectives, contributed to the 27 chapters, five appendices and glossary that make up *DD & PE*. Unashamedly biased toward ID, the editors have included a number of chapters that argue the opposite position, an unlikely concession if the tables were turned. To me, however, this adds to the value of the work. Juxtaposed as the two arguments are, the contrast between design and evolution is stark.

Given its size, *DD & PE* is not a quick read. I often found myself reflecting on what I had read, slowing my pace even more. Several contributors, including editor John Angus Campbell, are rhetoricians. It seems to be their nature to drive one to the dictionary. Many times I wished to return to something I had previously read, but found myself frustrated in being able to quickly do so. An index would be helpful.

*DD & PE* will be of value even to those not directly involved in determining educational policy. For example, while reading *DD & PE*, I wished I had had such a work available when I used to teach an Origins course. I would have done things differently and students would have been better informed. Science and science-education majors should both read and discuss this book.

American science educators make up the primary audience of *DD & PE*. In the US there are two hurdles that proponents of teaching ID in public schools must cross. One is constitutional, the other philosophical. The first is the argument that ID is a subtle intrusion of religion, violating the separation of church and state. The second is that ID is not scientific, or that it is not good science.

However one may define science, DeWolf, Meyer and DeForrest argue (p 78) that it is not possible to include evolution while excluding creation. When applied narrowly, the definition of science excludes both; when applied more liberally, both are embraced.

Is ID a subtle form of religion? ID proponents are careful to note that their work is entirely based on observations in nature without reference to biblical descriptions of creation. They are at pains to distance themselves from creationists whose work references scriptural accounts of the creation and the flood. This is an important point, especially for constitutional purposes. That ID has theological implications is not a substantial argument that teaching ID violates the First Amendment Establishment Clause. *DD & PE* notes that evolution also has religious implications. If students ask theological questions after a classroom consideration of ID, does that then make ID inherently religious? What about when students ask theological questions after studying evolution? *DD & PE* argues that the religious connection has to be more direct.

Most examples given for ID are molecular and cellular. Indeed, a significant portion of *DD & PE* is devoted to questions about the origin of life, with less attention to natural selection, as such. Pro-ID arguments appear stronger when set against fanciful ideas about a naturalistic origin of life. Given what we see and experience, ID appears to be the best explanation. I found myself wishing the design argument had been carried to higher organizational levels, even to ecology. However, the cellular–molecular foundation is strongest for ID.

Hypotheses for biochemical evolution have themselves evolved. Adapting to challenges brought against them, one scheme after another has been proposed to replace predecessors, but to little avail. Notwithstanding this, the jump from hypothesis to hyperbole is often rapid indeed. Sidestepping all previous challenges, a currently popular argument postulates “self organization.” This suggests that complex living things are an inevitable outcome of the physical nature of atoms. Examples given, such as crystal formation, naturally forming vortices such as tornadoes, and convection currents, fall far short in supporting the argument. In fact, the evidence seems weaker than ever. But what alternatives are available within a naturalistic world view? ID, on the other hand, continually accrues compelling data.

A paragraph written by Steve Fuller (p 539) particularly caught my attention. It carries the argument to new heights:

> *If, however, we take seriously that nature is a unified object in the mind of the Creator, then it is entirely possible — and I believe more plausible — to suppose that the purpose of specific entities, be they cells or species, cannot be discerned until at least the main contours of the entire world-picture are in place. On this more holistic view of creation, any given cell or species taken in isolation may seem the product of contingency, exactly as Darwinists suppose. But while Darwinists conclude their inquiry at that point, holistic creationists argue that the appearance of contingency merely reflects the incompleteness of our knowledge of the divine plan.*

I like Fuller’s designation, “holistic creationist.” It conveys a suggestion of wholeness and completeness that fits well with ID. Moreover, it impacts how we think of ourselves.

For years, creationists have attempted to “prove” creation by disproving evolution, responding defensively to claims by evolutionists, and even reinterpreting their findings. Another approach involves short-changing the time necessary for evolution.Neither approach demands creation as an alternative.

ID, on the other hand, presents a positive alternative in which evolution is put on the defensive. Readers of *DD & PE* will get a tone of evolutionary bravado from authors opposing ID, which comes through as overdone. Are they whistling in the dark?

Evolution isn’t wrapped up yet by any means, but there is a new confidence in the design camp that cannot but auger of exciting days to come. And “teaching the controversy” well compliments the new spirit.

## INVESTIGATING THE DESIGNER

**The Case For A Creator: A Journalist Investigates Scientific Evidence That Points Toward God.** Lee Strobel. 2004. Grand Rapids, MI: Zondervan. 341 p. Cloth, $19.99.

*Reviewed by Werner Vyhmeister, Yucaipa, California*

Lee Strobel holds a Master of Studies in Law degree from Yale Law School and also a journalism degree from the University of Missouri. "His journey from atheism to faith has been documented in the Gold Medallion-winning books *The Case for Christ* and *The Case for Faith*" (p 341).

Using his experience in journalism and law, Strobel's approach in *The Case for a Creator* is "to cross-examine authorities in various scientific disciplines about the most current findings in their fields." He chose doctoral level professors "who refuse to limit themselves only to the politically correct world of naturalism or materialism…." Having listened to the arguments, Strobel stands, "in the shoes of the skeptic, reading all sides of each topic and posing the toughest objections that have been raised" (p 28).

Interviewing Jonathan Wells, Strobel begins by probing Darwinism (naturalism) in general as a theory, and some specific "proofs," including Darwin's "tree of life," Haeckel's embryos, *Archaeopteryx* as a missing link, the "legend of Java man" and a number of other significant icons of evolutionary theory (p 31-67). Then, in his interview with Stephen C. Meyer, Strobel learned that "there are insurmountable hurdles involving the origin of biological information that simply cannot be resolved by more research and effort" (p 278). These and other factors led him to his first general conclusion:

> *… if I were to embrace Darwinism… I would have to believe that: nothing produces everything, non-life produces life, randomness produces fine-tuning, chaos produces information, unconsciousness produces consciousness, non-reason produces reason....Simply put, the central pillars of evolutionary theory quickly rotted away when exposed to scrutiny (p 277).*

Strobel's probe continued with six different scientific disciplines "to see whether they point toward or away from the existence of an intelligent designer" (p 279).

On *Cosmology*, William Lane Craig emphasized the new credibility that the old cosmological argument has taken thanks to discoveries of the last fifty years: “First, whatever begins to exist has a cause. Second, the universe had a beginning. Therefore, the universe has a cause” (p 96-121).

On *Physics*, Robin Collins noted that one of the most striking discoveries of modern science is that the laws and constants of physics are indispensable to make the universe habitable for life. For instance, gravity is fine-tuned to one part in a hundred million billion billion billion billion billion. “One expert said there are more than thirty physical or cosmological parameters that require precise calibration in order to produce a universe that can sustain life” (p 280). The “God hypothesis” has significantly gained credibility.

On *Astronomy*, after interviewing Guillermo Gonzalez and Jay Wesley Richards, Strobel remarked that, like in physics, “Earth’s position in the universe and its intricately choreographed geological and chemical processes work together with exquisite efficiency to created a safe place for humans to live” (p 281).

On *Biochemistry*, Michael Behe explained that “irreducibly complex” molecular “systems are strong evidence of a purposeful, intentional design by an intelligent agent” (p 215). On the related question of *Biology* and its quest for the origin of life, Stephen C. Meyer explained that the naturalistic explanation is facing its greatest challenges today.

In the last chapter of this book, Strobel highlights the impact that this research had on himself: “As I reviewed the avalanche of information from my investigation, I found the evidence of an intelligent designer to be credible, cogent, and compelling” (p 283).

It is not difficult to agree with Strobel. Yet, a flaw is present in the chapter on “The Evidence of Consciousness.” Strobel is correct in stating that, according to numerous Biblical references, the whole human person is constituted by body and soul or spirit (p 250). Following the majority view of Roman Catholicism and Protestantism, Strobel believes that the existence of the soul (spirit) refutes the assertion of Darwinism that “the [physical] brain is solely responsible for consciousness” (p 252). He appears unaware of the fact that the Bible identifies the spirit as the divine spark of life that transforms the material body into a “living soul” (or living human being, Gen 2:7). The “living soul” dies when the spirit of life is withdrawn. The spirit (soul) by itself is not a separate thinking entity. Strobel's basic conclusion still points in the right direction: the human being is not just a material body. The body by itself is not only incapable of consciousness, but it is simply dead. Consciousness is an emergent property when the God-given spirit brings matter to life.

As a whole, *The Case for a Creator* summarizes well, for the non-specialist, the essential elements of the debate between naturalism and intelligent design during the last decade. The language can be understood by a high-school graduate who has taken the basic sciences courses.

# DOES FREE WILL EXIST?

**Agents Under Fire: Materialism and the Rationality of Science**. Angus Menuge. 2004. NY: Rowman and Littlefield. 220 p. Cloth, $37.50.

*Reviewed by Stephen Bauer, Southern Adventist University*

*Agents Under Fire* is a book written by a philosopher, for philosophers. The reading is heavy and dense, with highly intricate arguments. Angus Menuge, who teaches at Concordia University Wisconsin, clearly presupposes the reader has a basic knowledge of classic philosophers, especially Kant, Hume, and Plato. However, with the possible exception of Hume, Menuge usually gives just enough background for the reader lacking philosophical training to comprehend his arguments. The first seven chapters are dedicated to refuting evolutionary reductionism. The fourth chapter specifically defends Behe's biological irreducible complexity argument. The eighth and final chapter shifts in focus to discussing the relationship between religion and science.

Menuge seeks to refute naturalistic reductionism by exposing its inadequate understanding of human agency. His overall strategy is to extend Behe's argument of irreducible complexity into the psychological arena by arguing that human agency is an irreducibly complex phenomenon. He repeatedly asserts that Darwinians cannot adequately explain human agency within the confines of naturalistic reductionism. While doing this, Menuge is thorough almost to a fault, making accurate use of his diverse and copious sources, and is more than even handed in his treatment of opposing opinions. His argumentation is strong, yet not belittling.

Menuge borrows Daniel Dennet's metaphor of "Skyhooks and Cranes," to develop his initial argument against a naturalistic explanation of human agency. In Dennet's metaphor, cranes provide objective, empirically verifiable evidence for drawing conclusions, while skyhooks dangle without visible support. Thus, cranes are asserted to be scientific while skyhooks are not. Menuge, however, argues that skyhooks are not always negative. First, history shows they have helped advance true scientific knowledge. Second, some naturalistic cranes have become so convoluted in the attempt to avoid agency, that their explanatory power is inferior to some skyhooks. Finally, he convincingly shows that some proposed cranes are actually relocated skyhooks. Thus, he clearly shows that reductionist scientists rely on unprovable assumptions which influence the outcome of their work.

Menuge seeks to refute what he calls "Strong Agent Reductionism" (SAR). SAR denies any real agency, admitting only an appearance of agency. He cogently shows that if SAR is true, then scientific inquiry is impossible, for that task is based on experiments and analysis which are carefully designed and controlled. Thus SAR is incoherent and self-defeating. Additionally, he defends Plantinga's argument that we have no reason to trust our cognitive abilities if evolutionary reductionism is true.

Menuge also shows that reductionism sometimes presupposes what it denies. For example, reductionist scientists tend to deny the actual existence of a "self" such as is found in "folk psychology." The self is said to be just a collection of genetic and memetic impulses. Menuge, however, shows that something must process and organize these impulses in order to have meaning. He proposes that the concept of the unified self better explains this phenomenon than evolutionary reductionism. He also charges reductionists with unwittingly "smuggling" both the concepts of agency and teleology into the picture, while trying to deny both.

A key component of Menuge's argument is based on computer and information engineering. Computers can be programmed to "learn" by mathematical responses to stimuli — for example when a computer "learns" to play chess — without any inherent intelligence. Menuge asserts that this implies that the mechanistic-reaction model demonstrates a superior ability to adapt to stimuli in a survival enhancing way. But this enhanced survivability means that the reductionist view of nature cannot provide any adequate reason to explain why agency evolved, as it would not be needed for enhancing survival. Menuge further argues that it is impossible for non-agency to spawn agency, and that the only reasonable explanation of human agency is a prior agent who intended humans to have that capacity. Thus, a divine agent is the best explanation for human agency.

In the final chapter, Menuge discusses the relationship of Christianity to science. First, Menuge cogently argues that Darwinism is dogma, not science. He asserts that Darwinism is to science what medieval Scholasticism was to theology. He characterizes this Scholasticism as a "flawed attempt to extend knowledge by uncritically affirming the logical consequences of preconceived opinions" (p 194). Thus, "dogmatic Darwinism" is prone to uncritical deduction from accepted premises, making it susceptible to accepting frauds as facts, and to offer proofs of naturalistic reductionism that have already been refuted. (He gives 10 examples based on Jonathan Wells' book, *Icons of Evolution*[1].) Thus, Darwinism is essentially a secular religion, which like the medieval church, persecutes "heretics" who disagree with its dogmas.

Menuge then critiques Michael Ruse's book, *Can A Darwinian Be A Christian?*[2] While applauding Ruse's boldness in addressing the topic, he finds Ruse's work wanting. Ruse's concept of God is essentially the God of eighteenth-century deism. Such a God is incompatible with the concept of God held by traditional Christianity. Thus, Menuge concludes that, "[Scientific] Reductionism is not only incompatible with Christianity, but it is false" (p 208).

Menuge then proposes that the current relation of Christianity to Science is understood in terms of non-competing authorities over different domains as suggested by Stephen Jay Gould's Non-Overlapping Magisteria (NOMA).[3] He asserts that this approach has, by definition, made Christianity an inherently unequal, inferior partner in any discussion with science.[4] Menuge proposes that since Darwinian reductionism is not scientific but dogmatic, Science needs to forsake its propensity to dogmatism, and should dialogue with Christianity as an equal.

How effective is Menuge at demonstrating the inadequacies of Darwinian reductionism? His arguments are both potent and devastating. Philosopher and arch-defender of Darwinian naturalism Michael Ruse declares in the "Forward" to this book that he fundamentally disagrees with Menuge and continues, "for that reason I urge you to read his book. Partly because I think he is wrong, and I want him refuted. Partly because he makes a good case, and he is worth refuting" (p xii). This is noteworthy validation of the weight of arguments in *Agents Under Fire*. The significance of Menuge's work may not be fully grasped until years from now.

## ENDNOTES

1. Wells J. 2000. Icons of evolution: science or myth? Why much of what we teach about evolution is wrong. Washington, DC: Regnery.
2. Ruse M. 2001. Can a Darwinian be a Christian? The relationship between science and religion. NY: Cambridge University Press.
3. Gould SJ. 1999. Rocks of ages: science and religion in the fullness of life. NY: The Library of Contemporary Thought, Ballantine.
4. According to Tim Standish, Nancy Pearcy has recently made a similar point. See: Pearcey N. 2004. Total truth: liberating Christianity from it's cultural captivity. Wheaton, IL: Crossway.