Comparison of morphology-based and genomics-based baraminology methods

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New genomics-based statistical approaches have helped us in baraminology research. There is currently much genomic data available in the public databases suitable for baraminology studies. This paper discusses the strengths and weaknesses of both morphology-based and genomics-based methods. It is hoped that the use of both types of methods will complement one another in future baraminology research. With more than one line of evidence, baramin membership can be determined with more confidence. This also allows us to classify a greater number of species, since if one type of data (i.e. morphological) is unavailable, another data type (such as genomic data) may still be available for analysis.

Baraminology is the study of created kinds, as presented in the book of Genesis. Genesis 1, verses 11, 12, 21, 24, and 25 describe how organisms, plants, and animals were created to multiply according to their kind. Baraminology aims to group species into created kinds, which were each created separately from one another during Creation Week. Created kinds are also known as baramins, which comes from the Hebrew words for 'create' and 'kind'. Species within one kind may be capable of breeding with one another, but between created kinds no interbreeding is possible. A holobaramin is equal to the complete species membership of a created kind.

Methodological baraminology has been in existence for several decades, but it has recently come to a new point of development. Before now, the morphology-based baraminic distance (BDIST) method has been widely used and it has been generally successful in the prediction of holobaramins.[1,2] Recently a new genomics-based algorithm has been developed to predict holobaramins, which may be used to complement the existing morphology-based algorithm.[3,4] Thus, multiple lines of evidence can now be used in helping to determine baramin membership. In this paper, we assess the strengths and weaknesses of these two methods in defining baramin membership. Using either one or the other, according to data availability, also helps increase the number of species which can be subjected to baraminology studies. Table 1 shows a summary of advantages and disadvantages of both kinds of algorithms.

Morphology-based methodology: BDIST

The BDIST method has been used widely in the creation science community in the last 15 years. BDIST is a quantitative method of comparing both living and fossil specimens based on phenetics (i.e. observable traits). The software calculates the pairwise correlation and baraminic distance of the species under examination based on the character data set used as input and outputs these values into a matrix. It then maps out a statistical graph of how these creatures relate to one another on a baraminic distance correlation matrix. Optimally, species within a given baramin are highly similar (higher correlation, lower distance) to one another and dissimilar to species from another baramin (lower correlation, higher distance). Three-dimensional coordinates can also help depict species relationships in three dimensions.

The method has generally been useful, but it has received its fair share of criticisms.[5] In the creation science community, we are aware of the differences between those who would lump species together into a single holobaramin, thereby reducing the number of holobaramins at Creation Week, versus those who split up holobaramins, thereby increasing their number.[6]

BDIST tends to lump species into a smaller number of baramins than there seem to actually be. This was seen in a study of cephalopods where the BDIST method predicted only three baramins out of 104 species, whereas mitochondrial genome alignments predicted up to seven.[7] A recent analysis of dinosaur species using BDIST brought down the number of predicted dinosaur kinds from 50 to just eight.[5] Furthermore, the BDIST method incorrectly classified both *Homo habilis* and *Australopithecus sediba* as members of the human holobaramin,[8] despite the fact that these two species are merely commixtures of human and apelike extinct primate bones.[9] The method also misclassifies small-sized humans into a different holobaramin to the human holobaram.[10] Therefore, a caveat should be added to the method. It should be used exclusively on only healthy, adult members of a given species. Juveniles and deformed individuals and skeletal remains that represent assemblages of individuals should be avoided.

One of the strengths of multivariate analytical approaches such as BDIST is that it allows us to compare and quantify hundreds of phenetic measurements. But statistical output

depends heavily on the input data. For example, in a recent paper using a multivariate approach, Doran *et al.*, concluded that "some Jurassic and Cretaceous avians grouped with dinosaurs", grouping *Archaeopteryx* and *Wellnhoferia* within *Deinonychosauria*.[11] In their 'Feathered dinosaurs reconsidered' article, McLain *et al.*[12] likewise used a multivariate analysis method and concluded that there are "multiple holobaramins of feathered dinosaurs" and that the "old dichotomy of bird versus dinosaur is unhelpful and incorrect". They go on to say: "Birds could rightly be viewed as a specialized type of dinosaur without implying birds evolved from dinosaurs."[12] The first part of the McLain *et al.* paper surveyed the literature on feathered dinosaurs and concluded that many dinosaurs did indeed have feathers. The second part involved an extended multivariate analysis. The conclusion was that "many species of dinosaurs were indisputably feathered. The available fossils have moved us permanently beyond questioning whether some dinosaurs were feathered and onward to interpreting the implications of feathered dinosaurs."[12]

While space does not allow for a more comprehensive rebuttal of every example listed in McLain *et al.*'s 42-page paper, we are convinced that most of the examples listed in the first half of their paper as 'feathered dinosaurs' are either examples where dermal collagen was misidentified as true feathers or examples of true feathered birds that have been misclassified as dinosaurs.[13,14] Most of the examples presented as true 'feathered dinosaurs' have already been adequately refuted in the scientific literature.[15–17] The error of conflating dermal collagen with that of true feathers is especially significant, since the second half of the paper involved a multivariate analysis related to the first part of their paper. Since the first part of the paper mistakenly conflates bird feathers with dinosaur dermal collagen, it is not surprising that the second half ends up conflating birds as a type of dinosaur. Wrong data in, wrong data out.

As stated earlier, one of the limitations of BDIST is that it tends to lump too many unrelated species into a single holobaramin. Part of the reason why this is the case has to do with the method itself. In the article 'How to think (not what to think)', Carter illustrates a helpful paradigm for interpreting evidence.[18] Using a Venn diagram with two overlapping circles (see figure 1 in Carter[18]), he illustrates how evidence often falls in what he calls Zone II. This area contains evidence that is consistent with two contrary views. Evidence that falls in Zone II cannot be used as evidence for or against two contrary positions.

How does this paradigm apply to our use of BDIST and other multivariate methods? BDIST indiscriminately evaluates a wide range of phenetic measurements. In this sense, BDIST is, methodologically speaking, a form of 'hyper-phenetics'. Applied to the study of baraminology, Zone I and Zone III represent diagnostic traits that are unique to two different creatures (i.e. autapomorphy), and Zone

Table 1. Comparison of advantages and disadvantages of morphology-based and genomics-based baraminology methods

Morphology-based methods (BDIST)	Genomics-based methods
Advantages	
Solid, descriptive statistical framework	Not sensitive to convergent morphology
Intuitive concept	Widely available data
Descriptive visualization	Intuitive concept
	Descriptive visualization
	Can be used to study micro-organisms
Disadvantages	
Sometimes data is incomplete (i.e. only craniodental characters, missing values)	Missing proteins, low-coverage genome
May lump species	Sensitive to species selection
Convergent morphology may confound algorithm	Sensitive to what counts as a protein sequence
Sensitive to both small and large number of species	Mitochondrial data not representative of whole genome
Must analyze all of one age group (i.e. adults/juveniles)	
Used primarily in multicellular organisms	

II refers to traits that are shared by both creatures but are not unique to either one. Traits that are unique to specific holobaramins are necessarily going to be rarer than traits that are non-diagnostic and shared between organisms. In other words, if we compare a whole series of traits between two organisms without regard to whether those traits are unique, we are likely to end up with a situation where two different organisms are grouped close together on a continuum. The more shared characteristics we include in the analysis, the closer the two creatures will cluster as one. In this sense, the more shared traits (from Zone II) we include in the analysis, the less accurate the analysis becomes—resulting in the tendency to over-lump different organisms into one single holobaramin. But if current BDIST approaches almost always include Zone II characteristics in their analysis, how reliable are they? As we have already mentioned, when compared with the more precise method of genomic-based algorithms, BDIST has consistently failed because it has a tendency to over-cluster different holobaramins as one.

Let us take for example the question of how dinosaurs and birds relate to one another. If in the Venn diagram in
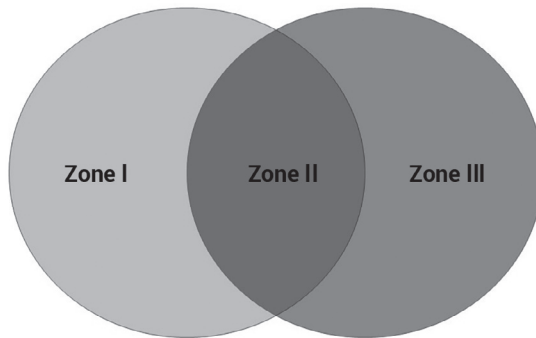
Overlapping Predictive Realms

Figure 1. Unique diagnostic traits for two creatures that are grouped under Zone I and Zone III respectively, while traits shared between two different organisms are classified under Zone II.
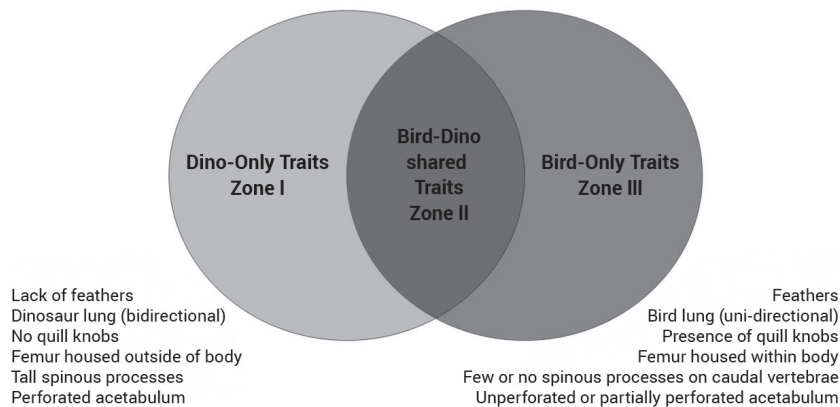

Lack of feathers
Dinosaur lung (bidirectional)
No quill knobs
Femur housed outside of body
Tall spinous processes
Perforated acetabulum

Feathers
Bird lung (uni-directional)
Presence of quill knobs
Femur housed within body
Few or no spinous processes on caudal vertebrae
Unperforated or partially perforated acetabulum

Figure 2. Using birds and dinosaurs as an example, unique diagnostic traits for dinosaurs are grouped under Zone I, while unique diagnostic traits for birds are grouped under Zone III. All traits shared between both creatures are grouped under Zone II and are excluded from BDIST analysis.

figure 1, we place dinosaurs in the left circle, and birds in the right circle, Zone I would represent traits that are unique to dinosaurs, while Zone III would represent traits unique to birds. Zone II would represent non-unique traits that are shared by both organisms.

If we compare birds and dinosaurs, as the number of shared traits is increased, birds and dinosaurs cluster closer and closer together. This problem can be avoided if we deliberately exclude Zone II characteristics from our analysis, and only compare Zone I and Zone III characteristics. So, for example (in figure 2), we list several unique characteristics of either dinosaurs and birds (Zone I and Zone III).[17]

By limiting BDIST to only unique Zone I and Zone III characteristics, we can avoid artificially conflating two potentially different holobaramins as one. And if in the scenario above, birds are indeed dinosaurs, excluding Zone II characteristics would actually allow us to identity this even more readily than if we include zone II characteristics in our analysis. For example, if birds are indeed dinosaurs, we should be able to find consistent examples where a creature exhibits a mixture of both dinosaur-only and bird-only traits.

So, we should be able to find examples of a bird that has flight feathers (Zone III) as well as a completely perforated acetabulum (Zone I). The completely perforated acetabulum is a diagnostic trait unique to dinosaurs, and flight feathers are, as far as we can tell, unique to birds. While some have argued otherwise, the evidence does not support the conclusion that there are dinosaurs with pennaceous feathers. Future analysis of BDIST can be improved by deliberately identifying Zone II characteristics and by excluding these characteristics from our study. In other words, the exclusion of Zone II characteristics actually allows us to both identify instances where traditional BDIST has over-clustered creatures together and identify instances where we have artificially separated one holobaramin into two different clusters.

For example, a new character matrix filtering method based on filtering out low-entropy characters filtered out Zone II characters from the data matrices used in the baraminology analysis of cephalopods[7] using data from studies by Lindgren *et al.*[19] and Sutton *et al.*[20]. A low-entropy value for characters means that character values for all species in the data set are very much uniform. After re-running the BDIST method on the filtered data set, and selecting highly correlated species pairs with a 95% bootstrap value, the Decapod group was split up into three groups: Oegopsina, Myopsina, and Sepiida+Sepiolida+Spirulida (see figure 3).

The precision of BDIST also suffers if there are only a few species available for comparison, or if only an incomplete data set is available.[21] For example, the method has been used on many data sets for which we only have craniodental characters, but this does not provide a holistic view of the baraminic relationships between species based on their entire morphology.

In a first analysis of hominin craniodental characters, Wood concluded that *A. sediba* was part of the human holobaramin.[8] His position changed somewhat after using the BDIST method to analyze not just craniodental characters, but also post-cranial characters,[22] as well as hand characters.[23] Wood found that with added post-cranial characters (present for six species), significant discontinuity was only demonstrated between *Australopithecus afarensis* and *Homo sapiens/erectus*.[24] Whereas *A. sediba* did not show

any significant continuity with the human holobaramin any more, it did not show discontinuity with this holobaramin. These are exactly the results which one would expect, since *A. sediba* has been classified as a basket taxon,[9] containing characters of both human and apelike extinct primates, causing it to cluster away from both holobaramins.

As Wood correctly noted, "samples of very few taxa are not likely to exhibit significant correlation even if clusters are present".[24] Wood had to reduce the number of species in his analysis which included post-cranial data. He claimed that due to post-cranial characters being available for only a few hominins, "This tradeoff between character sample size and taxon sample size may inhibit rather than enhance the detection of taxon clusters." The ideal case would be if we had craniodental and post-cranial characters for all desired species. We may have to accept the limit that such characters may never be available, unless found in fossils by further paleontological excavations. Here data quality and availability are key issues to be balanced.

Furthermore, the BDIST method also has the potential of misclassifying many species into the same baramin, just because they resemble each other phenotypically. In contrast with the more accurate approach of using genomics-based algorithms, BDIST does not account for homoplasy. By eliminating zone II traits, we are at the same time also eliminating homoplastic traits, allowing the method to be more accurate. However, in an analysis of cephalopod species by O'Micks, the method does correctly classify *Argonauta nodosa* as an octopod rather than a species of the nautiloid kind.[7]

Baraminology researchers using this method should be wary of the underlying assumptions that evolutionists have when assembling their data sets (i.e. when *H. habilis* and *A. sediba* were misclassified as real taxa). To bring us back to the illustration used earlier: if creationists would have excluded Zone II traits from the analysis and only performed a BDIST on unique traits of humans and australopithecines, (since *H. habilis* contained both unique traits of humans and australopithecines) it would have been apparent to the creationist researcher that he is dealing with a basket taxon, since the Bible makes it plain that humans belong to their own separate holobaramin, which is separate from all animal species. This means that humans were created separately from the apes. Thus, a mix of Zone I and Zone III traits in *H. habilis* would be indicative that it is a basket taxon and not a real individual. Furthermore, when selecting characteristics for analysis, only non-fragmentary and non-ambiguous characters should be considered. In other words, those characters should only be chosen based on clear diagnostic traits that are unique to a holobaramin.

Genomics-based algorithms

The genomics revolution has caused quite a bit of controversy, invalidating and qualifying multiple older morphometric studies. Yet, genomics-based algorithms
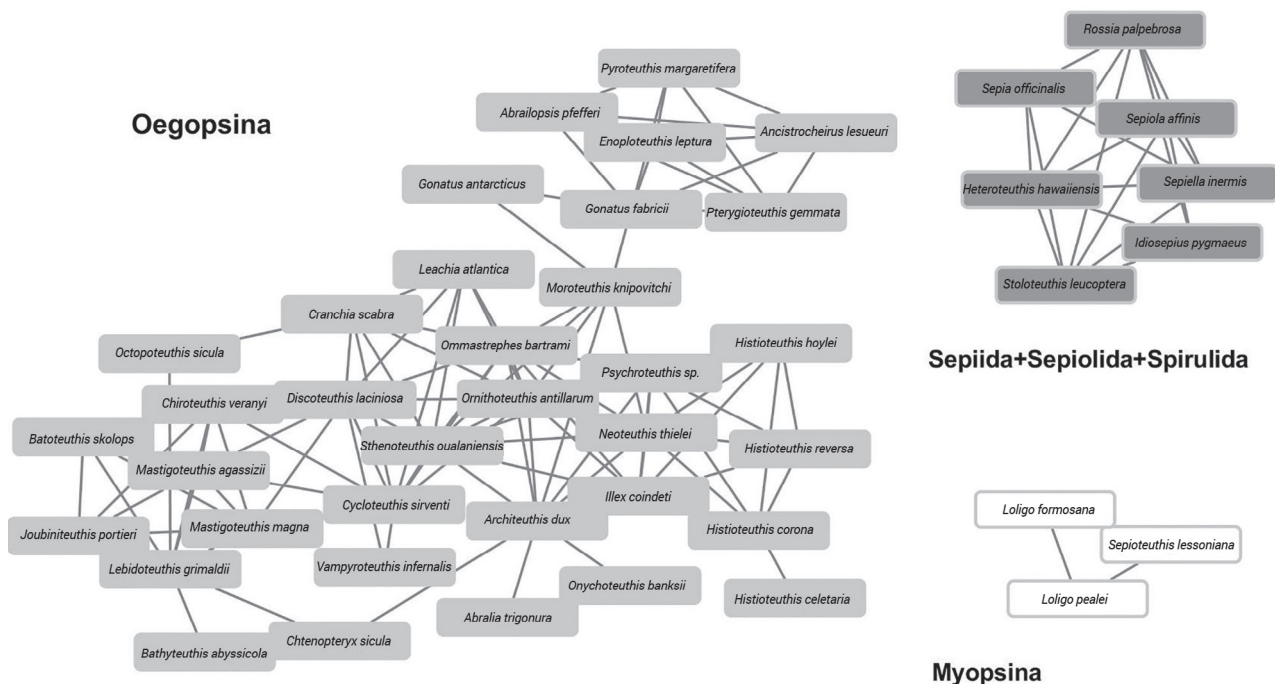

Figure 3. Depiction of baraminic relationships between different decapod species after entropy filtering of the Lindgren *et al.*[19] and Sutton *et al.*[20] data sets. After the original data sets were filtered to increase character entropy, BDIST was re-run on the resultant character matrix. Those species are linked together which have at least a 95% bootstrap value in at least one of the BDIST results.

should always be given preference over morphology-based algorithms, for several reasons. First, the genotype determines the phenotype, meaning that genetic factors are ultimately responsible for determining the morphology of a given species. Second, morphologically similar organisms may be genetically different, and vice-versa—genetically similar organisms may be different morphologically. For example, the kingsnake and the coral snake look very similar externally, but are quite dissimilar internally. As a further illustration, if morphology-based techniques *alone* would have been used in the analysis of cephalopods, the octopod species *Argonauta nodosa could* have been classified as a nautiloid on (rough) morphological grounds, yet genetically it is an octopod (and was correctly classified as such by genetics-based algorithms).[7] Third, with the break-up of the archebaranome (that is, the genome of the archebaramin which was created during Creation Week), new species arise via vertical descent. In other words, the genomes of all species within a created kind can be derived from the original archebaranome. Because these methods study the genome, any kind of organism may be studied, irrespective of its morphology. Even individuals with hardly any morphological remains can be included (e.g. Denisovans).

Early on, a number of mitochondrial studies were used to aid in morphology-based baraminology studies, for example to help determine the number of turtle baramins[25] or to measure the diversity of the cat, dog, and horse baramins.[26] Mitochondrial comparison is useful because gene order is the same across a great number of species, and gene paralogy and diploidy do not complicate the picture, as in the case of the nuclear genome. Furthermore, it is much easier to sequence the mitochondrial genome, and it is usually available for species for which the nuclear genome is not yet available.

Genomics-based methods, such as the Gene Content Method (GCM) could potentially harness the vast quantities of genomic data in public databases, such as NCBI, the UCSC Genome Browser, UniProt, and others. For example, bacterial genomes can be sequenced in a matter of hours, based on the latest technologies. Whole genome sequences have been created for an estimated 50 bacterial and 11 archaeal *phyla*, amounting to more than 14,000 total species by 2014.[27] Since it deals with gene content, not the specific nucleotide sequence, GCM depends on the availability of annotated genomic data. Even if the whole proteome of a species is unknown, dozens of gene/protein prediction algorithms exist, such as Augustus, GeneMark, and others which can predict protein sequences for them. Furthermore, databases such as the Pathosystems Resource Integration Center (PATRIC) already contain data for orthologous gene content in dozens of bacterial species.[28] In addition, databases such as MetaRef contain data on the core- and pan-genomes of numerous bacterial species.[29]

It would also be highly interesting to analyze the genome of archebaramins. The whole genome sequences of

Neanderthal and Denisovan have already been determined.[30] Such analyses could shed light on intrabaraminic relationships and could possibly resolve certain issues regarding the baraminic status of certain species, such as the recently discovered *Homo naledi*, which is held in creationist circles to be either an ape, human, or a mixture of the two. [9,31,32] Fossils may be interpreted in many different ways, but genome sequences are less subjective and more easily quantifiable.

Despite the seeming utility of genomics-based algorithms, they do suffer from some drawbacks. First, the mitochondrial genome represents only 0.01% of the entire human genome. Thus, certain conclusions about the entire human genome in general cannot be made by analyzing the mtDNA alone. Second, genomics-based methods are sensitive to the type of data used, whether it be an incomplete proteome or a genome sequence with low-coverage (i.e. lower-quality) data. A related problem is where to draw the boundary of protein sequence homology, which is necessary to determine protein homologues between two species, which is used as input for the Gene Content Similarity Method, a recently developed genomics-based baraminology method.[4] The twilight zone is a protein sequence similarity limit above which common functionality can be inferred between two protein sequences. This is because sequence determines structure, which in turn determines function.[33] Finally, whether or not non-genic elements such as pseudogenes or non-coding RNAs should be used is still an open question. These methods are also sensitive as to the number of species, and what kinds of species are selected for study. For example, if species are selected from a wide range of taxonomic categories (such as species from different phyla), the algorithm will discover clusters of species, no matter what. Therefore, it is advisable to select many species for study which appear to be within the same lower taxonomic category (family or order).

Summary and outlook

In conclusion, morphology-based methods may have their drawbacks, so it may be time to rethink and redevelop such algorithms. However, they are still useful. Overall, the BDIST method uses an intuitive concept and a descriptive mode of visualization, as does the genomics-based GCM method. BDIST is complementary to genomics-based algorithms, and while it is useful under the right circumstances, it should only be relied upon if genomic data is not available. Moving forward, special care must be given to separating possible ambiguous (Zone II) and diagnostic (Zone I and III) characters from one another in future baraminology studies. This should be done as a part of our creationist presuppositions in order to avoid over-lumping species into smaller numbers of clusters with large species membership as opposed to many clusters with small membership.

With the gigantic amount of genomic data that is currently available, genomics-based baraminology methods seem to be a useful tool, which can be put to much use. Much of the available genomic data has yet to be tapped for use in baraminology. As an idea for future genomics-based baraminology methods, it would also be useful to measure the correlation between the k-mer/motif content, instead of the protein content, of the genomes of different species to measure similarity. Such a method is currently being developed.

In sum, current baraminology algorithms and methods of any kind are finite and imperfect, reminding us that God's perfect truth never changes. We must strive to improve our methods so as to be able to "think God's thoughts after Him" (Johannes Kepler, 1571–1630).

Materials and Methods

Figure 3 was created using Cytoscape version 3.6.1.

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