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AUSTRALOPITHECUS SEDIBA, STATISTICAL BARAMINOLOGY, AND CHALLENGES TO IDENTIFYING THE HUMAN HOLOBARAMIN

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ABSTRACT

The recent discovery and description of *Australopithecus sediba* proved controversial among creationists after Wood (2010) broke with the majority and proclaimed it human based on an analysis of craniodental characters using statistical baraminology. Since creationists often judge postcranial characters more significant than craniodental characters, a re-analysis of the hominin holobaramin was undertaken using 78 postcranial characters published by Berger, *et al*. (2010) and 25 characters of the hand published by Kivell, *et al*. (2011). These character sets, along with subsets of the original craniodental characters evaluated by Wood (2010) were used to calculate baraminic distance correlations (BDC) and multidimensional scaling (MDS). The inconclusive results raise questions about the value of using correlation and clustering methods to identify holobaramins.

INTRODUCTION

In the creation/evolution debate, few issues inspire more passion than the subject of human origins. Even outside the confines of young-age creationism, evangelicals are wrestling with the theological importance of a historical Adam (Venema, 2010; Collins, 2011; Enns, 2012). Within young-age creationism, there is unanimous affirmation of the historicity of Adam and Eve as the true progenitors of all humans that ever lived. More contentious is the question of what counts as "human" among numerous fragmentary remains that are claimed to be intermediate between humans and apes by evolutionary anthropologists.

To date, paleoanthropologists have named 28 different hominin species (Foley, 2005; Berger, *et al*., 2010; Curnoe, 2010), but the significance of many of these fossils is regularly debated (*e.g.*, Curnoe, 2010; Brown, 2012; Van Arsdale & Wolpoff, 2012). Creationists have taken comfort in these ongoing controversies, since controversies give ample opportunity to question the interpretation of hominin fossils using the opinions of professional anthropologists. More recently, however, anthropologists are beginning to embrace the uncertainty about many hominin fossils as evidence that there is no sharp dividing line between human and non-human (*e.g.*, Cartmill, 2012).

While creationists continue to maintain that a dividing line between human and non-human exists, they do not agree where that line should be drawn. Creationists generally agree that

anatomically modern humans, archaic *Homo sapiens*, and Neandertals are human descendants of Adam and Eve (Wood, 2010). Beyond that, the majority (but not all) of creationists agree that *H. erectus* is also human. Opinion is divided on *H. rudolfensis*, with early opinions recognizing it as human (e.g., Cuozzo, 1977) and later writers classifying it with the australopiths (e.g., Mehlert 1999). *H. habilis* is generally not accepted as human or is considered a mix of human and non-human remains. For a full review of creationist opinions on hominid classification, see Wood (2010).

Recently, Wood (2010) applied statistical baraminology techniques to the identification of the human holobaramin ("created kind"). These techniques rely on inferring "distances" between species using discrete character data, such as those character sets assembled for a cladistic analysis. Distances are analyzed for patterns of clustered species, which are then interpreted as created kinds or holobaramins.

In striking contrast to the creationist consensus (Brandt, 2010; Line, 2010; Menton, *et al*., 2010), Wood's circumscription of the human holobaramin contained not only Neandertals and *erectus* but at least eight species, including the controversial *H. rudolfensis*, *H. habilis*, and *Australopithecus sediba*. In a later paper, Wood (2011) identified the newly described *Homo gautengensis* as a ninth human species (Table 1).

Wood (2010) acknowledged a number of outstanding problems in his original analysis, but his inclusion of *Australopithecus sediba* in the human holobaramin drew criticism from fellow creationists (Menton, *et al*. 2010). Critics focused on two main issues, character selection and methodology. On the subject of character selection, critics highlighted cranial and postcranial characteristics of the *A. sediba* fossils that significantly differed from modern humans as the basis for their judgment that *A. sediba* was neither human nor any sort of human ancestor (Menton, *et al*. 2010).

Research published since 2010 could expand the list of characteristics that significantly differ between *A. sediba* and modern *H. sapiens*. For example, the hand (Kivell, *et al*., 2011), foot (Zipfel, *et al*., 2011), pelvis (Kibii, *et al*., 2011), and cranial endocast (Carlson, *et al*., 2011) of *A. sediba* share important features in common with apes or australopiths. *A. sediba* is thought to be at least facultatively arboreal because of its long arms, strong flexor apparatus in the hand, mobile subtalar joint and robust medial malleolus in the foot, and wood and bark phytoliths in the dental calculus (Henry, *et al*., 2012). Such facultative arboreality/bipedality has been used by creationists in the past as evidence of an australopith ecology that is distinct from that of humans (Hartwig-Scherer, 1998). Furthermore, since Wood's (2010) baraminological analysis of hominids is based entirely on craniodental data in contrast to the "holistic" emphasis of baraminology, it is quite possible that an analysis of postcranial data would support the removal of *A. sediba* from the human holobaramin.

Some methodological objections have been addressed by clarifying the goals of statistical baraminology. In response to his critics, Wood emphasized testing the "discontinuity hypothesis" as a goal of baraminology. Wood (2011) described the discontinuity hypothesis as a belief that

> ... God created organisms in the categories that we call baramins, within which

> considerable diversification and speciation can take place but between which there are significant dissimilarities ... called discontinuity.

Since this discontinuity hypothesis is not a direct teaching of Scripture, it can be tested and even rejected, and statistical baraminology is just one attempt to test the hypothesis. Thus, according to Wood (2011), the detection of discontinuity between "humans" and (most) australopiths was more important than disputes over the precise membership of the human holobaramin.

Despite this clarification, significant questions about current statistical baraminology methods remain. For example, "uncertain" statistical baraminology studies are common in baraminology literature (e.g., Wood, 2005; Wood, 2008a). For example, analysis of a group of rhinocerotid and outgroup taxa found only a single, diffuse cloud of taxa with no clustering (Wood, 2008a). Likewise, Senter (2011) argued that application of baraminic distance correlation (BDC) to dinosaur taxa demonstrates the evolution of birds from non-avian theropods. Further, Wood's (2012) evaluation of 512 discrete character matrices using BDC did not reveal discontinuity among the taxa any more frequently than expected by chance.

It is unclear precisely how to resolve these methodological problems. In the case of BDC, "distances" between taxa are inferred from a set of discrete characters, and the distances are then used to calculate correlations between all possible taxon pairs in the sample. If two taxa are very similar, they should be similarly distant to all possible third taxa, resulting in positive correlation. If two taxa are very different, they should be inversely distant to all possible third taxa, resulting in negative correlation. That is, given a taxon pair, taxa that are close to one of the pair should be distant from the other, and vice versa. One obvious drawback is that characters can be selected to emphasize either similarities or differences between any taxa, and therefore any pattern of taxon correlation can be obtained. Additionally, samples of very few taxa are not likely to exhibit significant correlation even if clusters are present, and samples of very many taxa could reveal correlations between many baramins, thus preventing the detection of discontinuity around just one baramin.

Given these problems, Wood (2011, 2012) recommended adopting a methodologically diverse approach to baraminology, incorporating multiple methods and lines of evidence, as in Wise's (1992) original discontinuity matrix. For statistical baraminology, different character and taxon samples can provide corroborating or contradictory evidence of discontinuity. With respect to identification of the human holobaramin, Wood's (2010) initial study used related character sets all consisting of craniodental data. That study could be improved by addition of characters from postcranial remains, thus making the character sample more "holistic." In doing so, however, the taxon sample size will be reduced, since postcranial characters are known 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.

In this study, I use postcranial characteristics of *A. sediba* published by Berger, *et al*. (2010) and Kivell, *et al*. (2011) to re-evaluate the baraminic status of *A. sediba*. I use standard BDC and multidimensional scaling (MDS) techniques, as in Wood's (2010) original study. The primary question at hand is whether additional characters will confirm or contradict Wood's circumscription of the human holobaramin. A secondary question is whether or not current

statistical baraminology methods are even able to resolve the human holobaramin with the fragmentary fossil evidence currently available. If the analysis of the postcranial data reveals a clear clustering pattern, then the first question should be resolved: Is *Australopithecus sediba* part of the human holobaramin? If there is no clear clustering pattern, then the secondary question becomes more important: What attributes of the characters, methods, or some combination of both prevent us from resolving the membership of the human holobaramin?

METHODS

To calculate BDC and multidimensional scaling (MDS), I used BDISTMDS 2.0 (Wood, 2008b). All BDC results included 100 bootstrap pseudoreplicates. Two separate postcranial character sets were selected for analysis: Berger, *et al*.'s (2010) 78 postcranial characteristics and Kivell, *et al*.'s (2011) 25 hand characteristics.

The 78 postcranial characters listed in Berger, *et al*.'s (2010) Table S2 included descriptions of only six taxa: *A. afarensis*, *A. africanus*, *A. sediba*, *H. habilis*, *Homo* sp. indeterminate, and *H. erectus*. Discrete coding was created from the character descriptions of Berger, *et al*. as shown in Table 2. Since baraminic distance is calculated from match/mismatch counts, the character states were not polarized. As in the previous study (Wood, 2010), I used a character relevance cutoff of 0.75, which resulted in 52 postcranial characters retained to calculate baraminic distances.

Kivell, *et al*.'s (2011) Table S16 described 25 characteristics of the hand commonly associated with precision gripping in humans. They scored these chracteristics for 14 taxa: *H. sapiens*, *H. neanderthalensis*, *H. antecessor*, *H. erectus*, *H. floresiensis*, *A. africanus*, *A. afarensis*, *A. sediba*, *A. anamensis*, *Ardipithecus ramidus*, *Orrorin*, *Pan*, Swartkrans (possibly *A. robustus*), and OH 7 (*H. habilis*). Taxic relevance for this character set ranged from 0.12 (*H. erectus*) to 1 (*H. sapiens*). To maximize the number of characters used in baraminic distance calculations, I eliminated taxa with taxic relevance less than 0.4 (*H. antecessor*, *A. anamensis*, *Orrorin*, and *H. erectus*) from the dataset. For the reduced dataset of 10 taxa, 15 characters were used to calculate baraminic distance, based on a character relevance cutoff of 0.75.

For comparison, the original craniodental characteristics used by Wood (2010) were also re-evaluated in taxonomic subsets that correspond exactly to the taxonomic samples of Berger, *et al*. (2010) and Kivell, *et al*. (2011). The craniodental characters were then combined with the postcranial characters to create three composite datasets, one consisting of craniodental and postcranial characters of Berger, *et al*. (2010), one consisting of craniodental characters of Berger, *et al*. (2010) and hand characters of Kivell, *et al*. (2011), and one consisting of craniodental and postcranial characters of Berger, *et al*. (2010) and hand characters of Kivell, *et al*. (2011).

To create the composite character sets, I added the 69 craniodental characters used in Wood's (2010) analysis to Berger, *et al*.'s (2010) postcranial characters, which necessitated removing the *Homo* sp. indeteterminate taxon from the postcranial set, since it was not included in the craniodental character set. The resulting composite set consisted of 147 characters scored for five taxa (*A. afarensis*, *A. africanus*, *A. sediba*, *H. habilis*, and *H. erectus*). After filtering using a character relevance cutoff of 0.75, 140 characters were used to calculate baraminic distances.

I created a second composite dataset by combining the 25 hand characters of Kivell, *et al*. (2011) with the 69 craniodental characters of Berger, *et al*. (2010). The composite dataset consisted of six taxa (*H. sapiens*, *H. habilis*, *A. afarensis*, *A. africanus*, *A. sediba*, and *Pan*) and 94 characters. After filtering for character relevance at a cutoff of 0.75, 60 characters were used to calculate baraminic distances, including 20 hand characters.

A third composite dataset consisted of the hand characters of Kivell, *et al*. (2011) and the craniodental and postcranial characters of Berger, *et al*. (2010). In this dataset, I combined *H. sapiens* and *H. erectus* into a composite taxon (using the hand and cranial characters of *H. sapiens* and the postcranial characters of *H. erectus*), and I omitted *Pan*. The resulting five taxon dataset contained 172 characters, 157 of which were used to calculate baraminic distances after filtering for a character relevance of 0.75.

RESULTS

Using just the postcranial characters of Berger, *et al*. (2010), only two taxon pairs shared significant, positive BDC: *Homo* sp./*H. erectus* and *A. afarensis*/*A. africanus* (Figure 1). Significant, negative BDC was observed between two taxon pairs: *Homo* sp./*A. afarensis* and *H. erectus*/*A. afarensis*. All correlations had bootstrap values <90%, and *A. sediba* was not positively or negatively correlated with any other taxa. MDS reveals an irregular tetrahedron with *Homo* sp./*H. erectus*, *A. afarensis*/*A. africanus*, *A. sediba*, and *H. habilis* at the vertices (3D stress 0.045) (Figure 1).

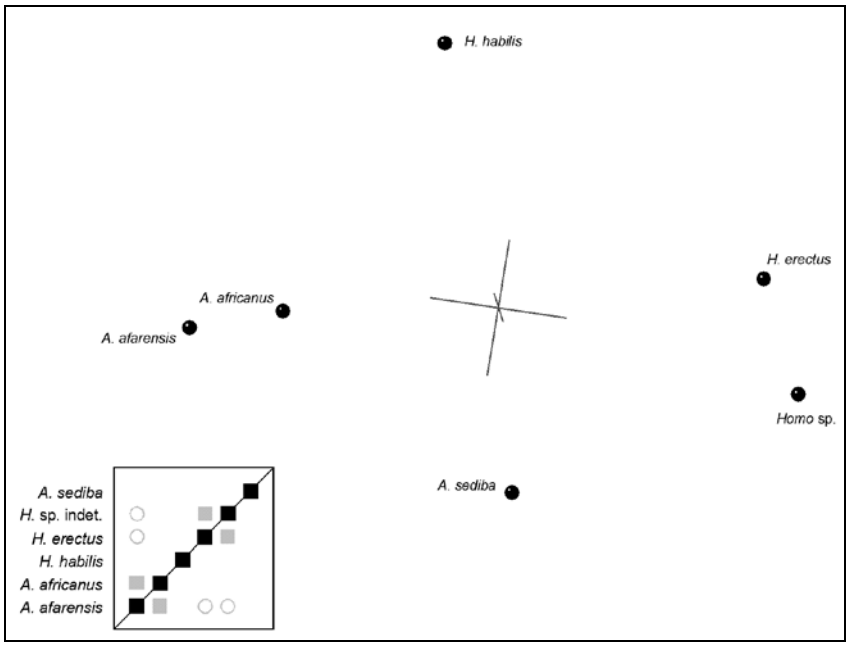

Figure 1. Three dimensional MDS and BDC results for Berger, *et al*.'s (2010) postcranial characters. Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

For the composite dataset of craniodental and postcranial characters, only *H. erectus* and *A. afarensis* showed significant, negative BDC, but the bootstrap value was 62% (Figure 2). No taxa were positively correlated. The MDS results revealed a crude arc, with taxa arranged in the following order: *A. afarensis*, *A. africanus*, *A. sediba*, and *H. erectus* (3D stress 0.025) (Figure 2). *H. habilis* lies within the arc. Using just the cranial characters for these same five taxa (no characters eliminated), the BDC results showed negative correlation between *A. sediba* and *A. afarensis* and between *H. erectus* and *A. afarensis* (bootstrap values <90%) (Figure 3). No positive BDC was observed. The MDS results (3D stress 0.083) were consistent with Wood's (2010) original analysis. *A. sediba* clustered with both *Homo* species (mean baraminic distance 0.386), and *A. africanus* and *A. afarensis* were separated from the *Homo/A. sediba* cluster (mean baraminic distance 0.555).

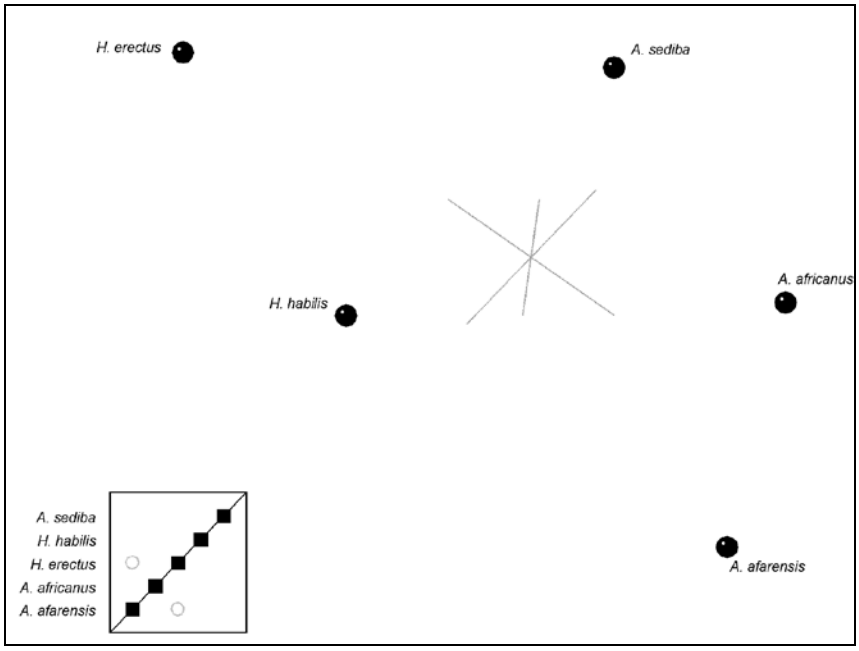

Figure 2. Three dimensional MDS and BDC results for a composite dataset of Berger, *et al*.'s (2010) postcranial characters and the craniodental characters used by Wood (2010). Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

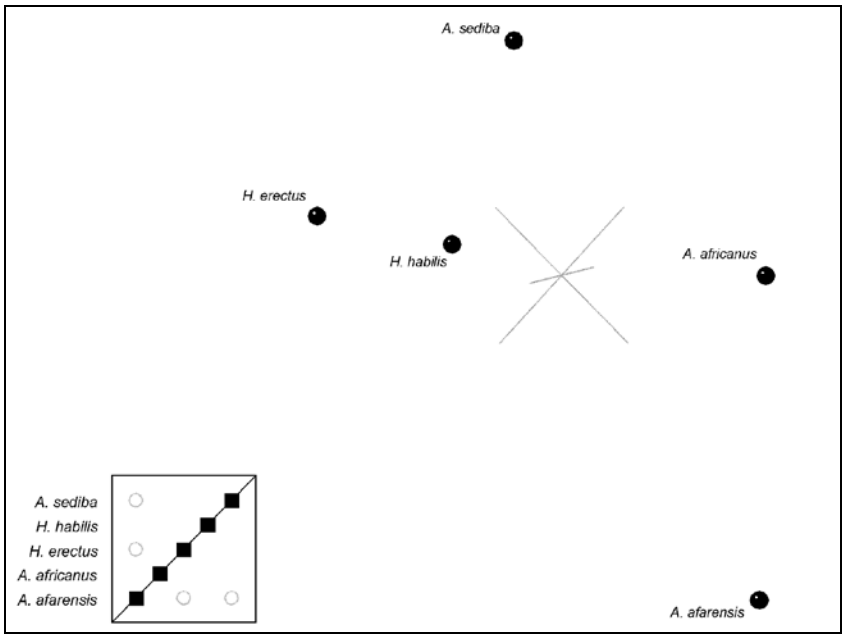

Figure 3. Three dimensional MDS and BDC results for the craniodental characters used by Wood (2010) and the taxon sampling used in Figure 2. Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

For the hand characteristics listed by Kivell, *et al*. (2011), very little positive BDC is observed. *H. sapiens* and *H. neanderthalensis* share significant, positive BDC with 100% bootstrap support, but this result is trivial since they have a baraminic distance of zero (Figure 4). *Pan* is positively correlated with *Ardipithecus*, *A. afarensis*, and OH 7 (*H. habilis*), but none of these correlations have bootstrap support greater than 67%. Significant, negative BDC is observed between the *H. sapiens*/*H. neanderthalensis* cluster and the cluster composed of *Ardipithecus*, *Pan*, *A. afarensis*, and OH 7, but only the negative BDC between *Pan* and *H. sapiens*/*H. neanderthalensis* had a bootstrap value >90%. *A. sediba*, along with the rest of the taxa in the dataset, showed neither significant positive nor negative BDC with any other taxa. MDS reveals a diffuse cloud of taxa with little clustering (3D stress 0.125) (Figure 4).

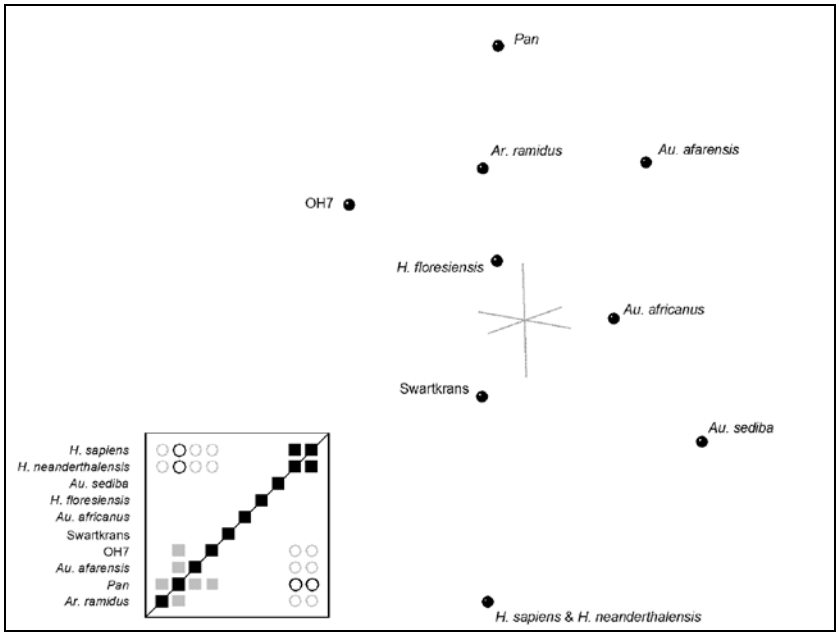

Figure 4. Three dimensional MDS and BDC results for Kivell, *et al*.'s (2011) hand characters. Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

When the craniodental and hand characters are combined, significant, positive BDC was observed between *Pan* and *A. afarensis* but with only 58% bootstrap support (Figure 5). Significant, negative BDC was observed between *H. sapiens* and *Pan* and between *H. sapiens* and *A. afarensis*, each with bootstrap support >80%. *A. sediba* was neither positively nor negatively correlated with any other taxa. The 3D MDS results revealed another diffuse cloud with little clustering (3D stress 0.011) (Figure 5). Using just the cranial characters for these six taxa, baraminic distances were calculated from 40 characters after filtering at a character relevance cutoff of 0.75. Significant, positive BDC was observed between *H. habilis* and *A. sediba* with a bootstrap value of 75% and between *A. afarensis* and *Pan* with a bootstrap value of 76% (Figure 6). Significant, negative BDC with bootstrap values <75% was observed for comparisons of *Pan* with *H. sapiens*, *Pan* with *H. habilis*, and *Pan* with *A. sediba*. The only BDC with >90% bootstrap support was a negative correlation between *H. sapiens* and *A. afarensis* (98% bootstrap value). As in previous MDS analyses of these taxa, MDS results for the cranial characters revealed a cloud of taxa with little clustering (3D stress <0.05) (Figure 6).

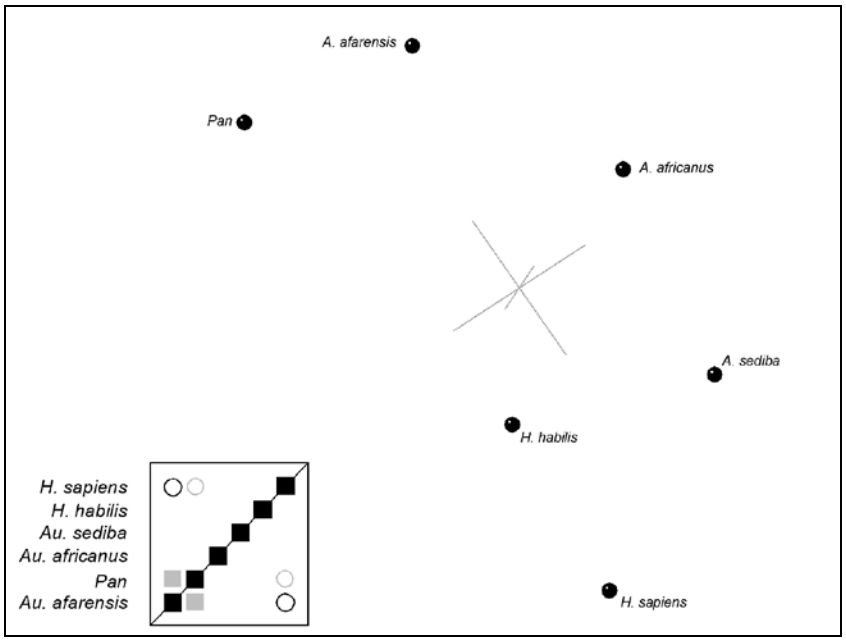

Figure 5. Three dimensional MDS and BDC results for a composite dataset of Kivell, *et al*.'s (2011) hand characters and the craniodental characters used by Wood (2010). Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

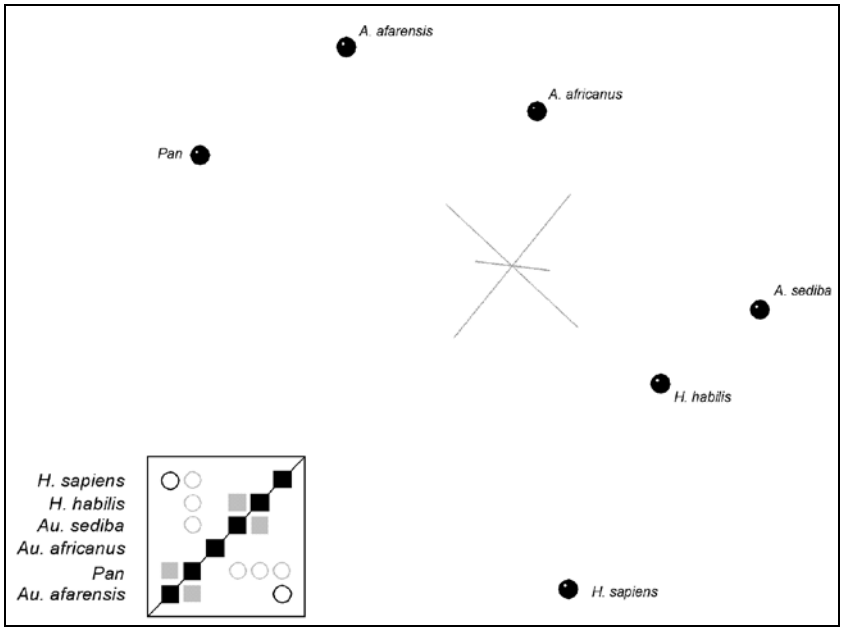

Figure 6. Three dimensional MDS and BDC results for the craniodental characters used by Wood (2010) and the taxon sampling used in Figure 5. Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

For the combined composite dataset containing the craniodental, postcranial, and hand

characters, the only correlation observed was significant, negative BDC between *A. afarensis* and the *H. erectus*/*H. sapiens* composite taxon, with a bootstrap value of 74% (Figure 7). As in previous analyses, the MDS results revealed little clustering (3D stress 0.036) (Figure 7).

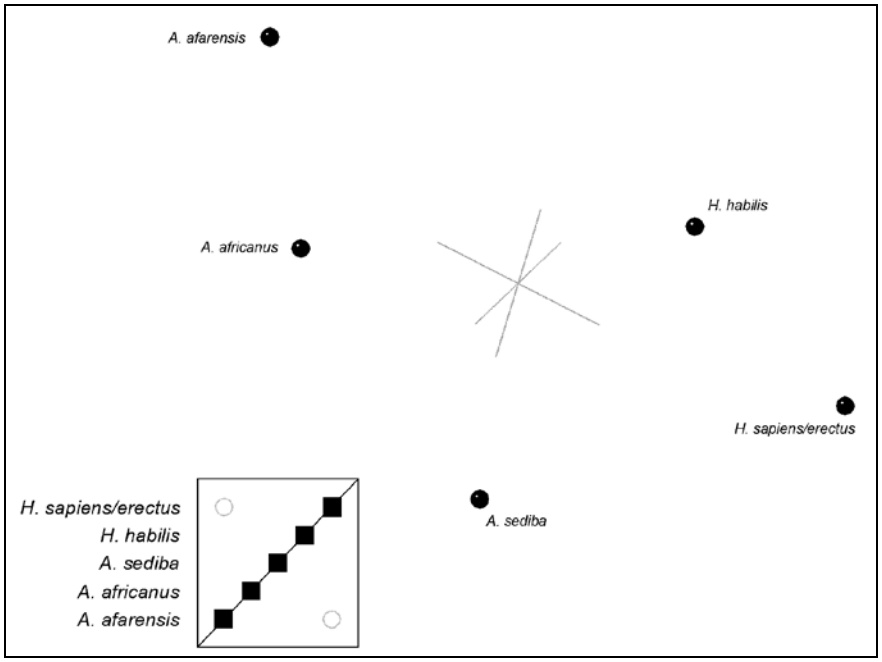

Figure 7. Three dimensional MDS and BDC results for a composite of Berger, *et al*.'s (2010) postcranial characters, Kivell, *et al*.'s (2011) hand characters, and the craniodental characters used by Wood (2010). Closed squares indicate significant, positive BDC, and open circles indicate significant, negative BDC. Black symbols indicate bootstrap values >90% in a sample of 100 pseudoreplicates. Gray symbols represent bootstrap values ≤90%.

DISCUSSION

If we could easily infer holobaramin membership from statistical baraminology studies, we would expect in this case to find corroboration or contradiction of Wood's (2010) circumscription of the human holobaramin, including *Australopithecus sediba*. Instead, we find that the present analysis reveals no clear clustering pattern, and thus cannot be used to verify or falsify Wood's original study. No analysis of the postcranial characters of Berger, *et al*. (2010) or Kivell, *et al*. (2011) revealed any strong affinity between *A. sediba* and *H. sapiens* or *H. erectus*. In fact, in all five BDC analyses of postcranial characters in the present study, *A. sediba* was neither positively nor negatively correlated with any other taxon.

Should the failure of the present analysis constitute evidence against including *A. sediba* in the human holobaramin? I think not, since failure to corroborate a previous result is not the same as falsifying that result. Furthermore, the present results seem to arise from the very small set of taxa used rather than for biological reasons. Since BDC uses a standard correlation coefficient, the fewer data points (taxa) available, the greater the correlation must be before it becomes statistically significant. Thus, it is entirely possible that BDC would be incapable of detecting weak clustering with very few taxa. This problem is especially apparent when we consider the

results for just the craniodental characters in this study. In each case where only craniodental characters were used with small taxon samples (Figures 3 and 6), the clustering seen in Wood's (2010) original analysis of the same characters is no longer detectable.

While these methodological problems must be acknowledged when interpreting the present results, we also must keep in mind that the same problems are present in the previous analysis of craniodental characters. In other words, since the clustering patterns are sensitive to the taxa and characters included in the sample, why should we accept a positive result (*i.e.*, the detection of a cluster) as having any biological meaning? Bootstrapping can provide one means of addressing this question by looking for recurring patterns of correlation in pseudoreplicates of characters (Wood, 2008b), and using different sets of characters can provide a similar advantage. Neither strategy, however, addresses the problem of taxon sample, and this problem must be addressed by future baraminology studies.

Turning back to basic anatomical and biological considerations, we still find reasons to doubt the humanity of *A. sediba*. Carlson, *et al*. (2011) report that the convolution pattern on the frontal lobes of *Australopithecus sediba* are typically australopith rather than characteristic of *Homo*. Similarly, Leakey, *et al*. (2001) suggested that *Homo rudolfensis* might better be placed within the genus *Kenyanthropus*, and Hartwig-Scherer (1998) excluded *H. habilis* from the human baramin based on postcranial characteristics. Recent analyses of *A. sediba*'s dental calculus indicates a diet that might have included tree bark (Henry, *et al*., 2012), which would be consistent with a semi-arboreal lifestyle like other australopiths and unlike fully bipedal humans.

Character choice and the fragmentary nature of key fossils also pose serious problems for interpreting the hominin fossil record. Traditionally, creationists and other antievolutionists have used the poor preservation of hominin fossils as a critique of evolutionary interpretations (e.g., Lubenow, 2004; Gauger, *et al*., 2012), but the same criticism applies to any creationist interpretation as well. Fragmentary fossils severely limit the number and type of characteristics that can be compared across a broad sample of taxa, and they also inhibit the seemingly simpler task of recognizing species. As the number of putative hominin species ballooned in recent years to at least 28 (26 listed in Foley [2005] plus *A. sediba* and *H. gautengensis*), skepticism about some of these species has also grown (Curnoe and Thorne, 2003; Bokma, *et al*., 2012; White, 2013). Quintyn (2009) even called for a "temporary cessation" of assigning new hominin species names. The announcement of the Red Deer Cave people (Curnoe, *et al*., 2012), the Denisovans (Krause, *et al*., 2010; Reich, *et al*., 2010), and new South African *Homo* fossils (Leakey, *et al*., 2012) without bestowing novel species names exemplifies this new, more cautious treatment of hominin discoveries.

Given this caution among paleoanthropologists identifying hominin species, should creationists likewise exercise caution in identifying the human holobaramin? It might be tempting to refrain from any judgments for fear of making too bold a proclamation that might turn out to be wrong when newer fossils are discovered. I suggest a more moderate approach of continued study of the available material with appropriately tentative conclusions.

At the moment, the clearest baraminological studies we have imply a very broad human holobaramin, containing fossil forms assigned to several different species (Wood, 2010).

Following the general creationist consensus, the statistical baraminology studies support including *Homo sapiens*, Neandertals, and *Homo erectus* in a single baramin. Statistical baraminology analysis of craniodental characteristics also supports placing *Homo rudolfensis*, *Homo habilis*, and *Australopithecus sediba* in the human holobaramin, but the present results should inspire additional studies of these contentious fossils before we make a firm conclusion about their baraminic status. With the information we have at present, hominin classifications based on extremely limited material are likely to remain controversial for creationists and evolutionists alike for the foreseeable future.

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Table 1. Human species according to Wood's (2010, 2011) baraminology research

1. *Homo sapiens*
2. *Homo neandertalensis*
3. *Homo heidelbergensis*
4. *Homo erectus*
5. *Homo ergaster*
6. *Homo habilis*
7. *Homo rudolfensis*
8. *Homo gautengensis*
9. *Australopithecus sediba*

Table 2. Character coding based on descriptions in Berger et al.'s (2010) Table S2.

Character	*A. afarensis*	*A. africanus*	*A. sediba*	*H. habilis*	*H.* sp. indeterminate	*H. erectus*
1. Body size (small, 0; large, 1)	0	0	0	0	1	1
2. Brachial index (72-90, 0)	0	?	0	0	?	0
3. Relative humeral length (long, 0; intermediate, 1; short, 2)	0	?	1	?	?	2
4. Humeral-to-femoral diaphyseal strength (0.3-0.4, 0; >0.4, 1)	?	?	0	1	?	0
5. Upper-to-lower limb joint size proportions (large, 0; small, 1)	0	0	0	?	?	1
6. Angle of acromial extremity to plane of clavicle shaft (anterosuperiorly inflected, 0; uninflected , 1)	?	0	0	1	?	0
7. Conoid tubercle (angular margin, 0; weak/absent, 1)	0	0	0	1	?	1
8. Clavical mid-lateral shaft cross-sectional shape (dorsoventrally elongated, 0; rounded, 1)	0	0	0	1	?	{01}
9. Scapular spine thickness (moderate, 0; thick, 1)	0	0	0	1	?	0
10. Scapula axillary border ventral pillar (strong, 0; moderate, 1)	0	0	0	?	?	1
11. Scapula axilloglenoid angle (114-116°, 0; >120°, 1)	0	0	0	?	?	1
12. Humerus midshaft cross section %CA (60-75, 0; >75, 1)	?	0	0	1	?	1
13. Humeral torsion (124-126°, 0; <110°, 1; 110-126°, 2)	0	0	1	?	?	2
14. Humerus projection of medial epicondyle (weak, 0; moderate, 1; strong, 2)	{01}	1	2	2	?	2

15. Humerus lateral epicondyle (moderate, proximal position, 0; pronounced, 1; moderate, distal position, 2)	0	1	1	1	?	2
16. Humerus brachioradialis crest (marked, 0; weak, 1)	{01}	0	0	?	?	1
17. Humerus septal aperture (present, 1; absent, 0)	1	0	1	1	?	0
18. Humerus supracapitular fossa (moderate, 0; deep, 1; well excavated, 2; shallow, 3)	0	0	{01}	2	?	3
19. Humerus olecranon fossa (large/deep, 0; narrow/deep, 1; narrow/shallow, 2)	0	1	0	0	?	2
20. Humerus capitular morphology (superoinferiorly elongated, 0; moderately superoinferiorly elongated, 1)	0	0	0	0	?	1
21. Humerus trochlear/capitular keel (marked, 0; moderate, 1)	0	0	0	0	?	1
22. Radius head diameter/neck length (0.38, 0; >0.5, 1; 0.49-0.5, 2)	0	1	2	2	?	?
23. Ulna orientation of trochlear notch (anterior to anteroproximal, 0; anteroproximal, 1; anterior, 2)	0	1	1	?	?	2
24. M. Flexor carpi ulnaris tubercle (weak-moderate, 0; pronounced, 1)	0	1	1	?	?	0
25. Ulnar trochlear keel (mild, 0; moderate, 1)	0	0	0	?	?	1
26. Orientation of plane of ulna radial notch (slight proximolateral, 0; lateral, 1)	0	0	0	?	?	1
27. M. flexor digitorum superficialis origin (crest, 0; tubercle, 1)	0	0	0	?	?	1
28. Ulnar supinator crest (weak, 0; moderate, 1; prominent, 2)	0	1	1	?	?	2
29. Ulnar mid-proximal diaphyseal shape (round, 0; laterally flattened triangle, 1; laterally flattened *D*, 2; anteriorly flattened triangle, 3)	0	1	2	?	?	3
30. Ulnar interosseous crest (moderate, 0; weak, 1; prominent, 2)	0	1	1	?	?	2
31. Acetabulocristal buttress (slight, 0; pronounced, 1)	0	0	1	?	1	1
32. Position of cristal tubercal on os coxa (anterior, 0; posterior, 1)	0	0	1	?	1	1
33. Ilac crest shape (shallow sigmoid, 0; moderate sigmoid, 1; deep sigmoid, 2)	0	0	1	?	2	2
34. Anterior inerior iliac spine shape (rectilinear, 0; sigmoid, 1)	0	0	1	?	1	1
35. Posterior os coxa fossa for M. gluteus medius (small, 0; moderately expanded, 1; expanded, 2)	0	1	1	?	2	2
36. Posterior iliac height (short, 0; intermediate, 1; tall, 2)	0	1	2	?	2	2
37. Os Coxa retroauricular area (short, 0; expanded, 1)	0	0	1	?	1	1
38. Tuberoacetabular sulcus (wide, 0; narrow, 1)	0	0	1	?	1	1
39. Relative tuberoacetabular sulcus width (>0.4, 0; <0.4, 1)	0	0	1	?	1	?

40. Relative auricular-acetabular distance (long, 0; intermediate, 1; short, 2)	0	0	1	?	2	2
41. Acetabulosacral buttress (moderate, 0; small, 1; pronounced, 2)	0	1	2	?	2	2
42. Minimum thickness of acetabulosacral buttress (<17, 0; >17, 1)	0	0	1	?	1	1
43. Retroauricular height (<40, 0; >40, 1)	0	0	1	?	1	1
44. Pubic symphyseal face (short, 0; tall, 1)	0	0	1	?	1	1
45. Relative femur neck length (0.95-1.442, 0)	0	0	0	?	0	0
46. Femoral neck-shaft angle (high, 0; low, 1; moderate, 2)	0	0	1	0	2	1
47. Femoral neck shape index (68.7-86.9, 0)	0	0	0	?	0	0
48. Femoral neck cross-sectional long axis (superoinferior, 0; anterosuperior to posteroinferior, 1)	0	0	1	0	1	1
49. Femur proximal diaphyseal cross-sectional shape (mediolaterally expanded, 0; mediolaterally buttressed, 1; circular, 2)	0	1	0	2	1	1
50. Femoral metric index (<71, 0; 71-74, 1; 79.6, 2; 100, 3)	0	1	2	3	1	1
51. Femoral midshaft-to-mid-proximal cross-section %CA (65-86, 0)	?	0	0	0	0	0
52. Femoral pilaster (absent, 0; present, 1; well-developed, 2; slight, 3)	1	2	0	2	0	3
53. Femoral linea aspera (weak, 0; prominent, 1)	0	0	0	1	1	1
54. Tibia popliteal (soleal) line (prominent, 0; moderate, 1; marked, 2)	0	0	1	2	2	2
55. Tibia proximal shaft curvature (slight, 0; absent, 1)	0	1	1	0	1	1
56. Tibia diaphyseal anterior border (round, 0; sharp, 1)	0	?	1	0	1	0
57. Tibia midshaft relative muscle attachment size (flexor digitorum longus = tibialis posterior, 0; tibialis posterior > flexor digitorum longus, 1; flexor digitorum longus > tibialis posterior, 2)	?	?	0	1	?	2
58. Tibia distal shaft curvature (absent, 0; slight, 1)	{01}	?	1	1	?	1
59. Morphology of tibia triangular attachment area for inferior interosseous ligament (poorly marked, superoinferiorly short, 0; well marked, elongate, 1; poorly marked, elongate, 2)	0	0	0	1	1	2
60. Distal tibiofibular articular facet on tibia (small, 0; L-shaped, 1; narrow rectangle, 2)	0	0	0	0	1	2
61. Tibia talar articular surface orientation (posteriorly tilted, 0; anteriorly tilted, 1; neutral, 2)	{01}	{12}	1	1	2	2
62. Fibular malleolar breadth (broad, 0; narrow, 1)	0	?	0	1	0	1
63. Distal tibiofibular articular facet on fibula (small, 0; rectangular, 1; oval, 2)	0	?	1	0	2	?

64. Fibula talar articular surface orientation (laterally sloping, 0; vertical, 1)	0	?	1	1	1	?
65. Talar trochlear surface (flat, 0; grooved, 1)	0	0	0	1	?	1
66. Talar trochlear medial and lateral radii of curvature (roughly equal, 0; elevated lateral margin, 1)	0	{01}	0	0	?	1
67. Talar medial malleolar surface (extends onto talar neck, 0; does not extend onto neck, 1)	0	0	1	0	?	1
68. Talar neck (short, twisted, 0; long, not twisted, 1)	0	0	0	0	?	1
69. Talar head/neck orientation angle (neutral, 0; valgus deviation, 1; varus deviation, 2)	0	0	0	1	?	2
70. Horizontal angle of talar neck (15-26°, 0; 28°, 1)	0	0	1	1	?	0
71. Angle of inclination of talar (<15°, 0; 30°, 1; 16°, 2)	0	0	1	0	?	2
72. Talar neck torsion angle (<30°, 0; >30°, 1)	0	0	0	1	?	1
73. Talar fibular facet/neck length index (>150, 0; <150, 1)	0	0	0	1	?	1
74. Talar head projection index (37, 0; 61, 1; 45, 2)	0	0	1	2	?	?
75. Talar trochlear breadth/length index (80-87, 0; 72, 1; 100, 2)	0	0	1	2	?	0
76. Talar trochlear breadth/fibular facet projection index (253-267, 0; 330-336, 1; 239, 2)	0	1	0	1	?	2
77. Calcaneal fossa on inferomedial surface for cuboid projection (absent, 0; present, 1)	?	?	0	1	?	?
78. Metatarsal diaphyses (gracile, 0; robust, 1)	0	0	0	1	?	0