

## ESSENTIALISM AND THE HUMAN KIND, OR EXPERIMENTS IN CHARACTER WEIGHTING

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### ABSTRACT

Essentialist thinking, while not nearly as important or formal as Ernst Mayr depicted it, may undergird some creationist assessments of hominin fossils. Since essentialism cannot be falsified, it can only be used as a guiding principle for selecting character sets for further evaluation, which is a form of character weighting. Here, essentialist reasoning is used to design character sets that ought to distinguish human from nonhuman taxa in the fossil record. The first such set, consisting of fifteen bipedalism-related characteristics, fails to recognize *Au. africanus* as nonhuman. The second group of character sets derived from a larger set of craniodental characters also fails to reliably distinguish human from nonhuman fossils. The same craniodental character subsets, when subjected to distance correlation and cluster analysis, also produce spurious results by putting humans and obvious nonhumans together in the same clusters. These results indicate that the ideal of essentialism is a poor guide to distinguishing human from nonhuman.

### KEYWORDS

hominins, human origins, paleoanthropology, baraminology, essentialism

### INTRODUCTION

Ernst Mayr famously contrasted Darwinian evolution with a position he called typology or essentialism (e.g. Mayr 1969). According to Mayr, the essentialist defined a species by the possession of certain immutable and essential traits, the presence of which were both necessary and sufficient to identify an individual as a member of that species. Any species' essential traits are possessed only by that species and no others. According to Mayr, this approach to understanding species came to us from the work of Plato and his notion of the *eidos*, an unchanging form of which the material world was a changeable instantiation. Mayr contrasted essentialism with "population thinking," which he attributed to Darwin. Population thinking merely recognized that certain populations presently share traits in common but that the population could change in the future. For Mayr, the defining characteristic of a species was simply the ability to interbreed, which he acknowledged would change over time as new species emerged.

Mayr's view of essentialism and its connection to Platonic thinking is now recognized to be an oversimplified fabrication (Kitcher 1987; Winsor 2006). The history of pre-Darwinian biology only occasionally conforms to the essentialist way of thinking, and species change and transmutation were speculations before Darwin ever thought of the idea. Even essentialism's connection to Plato is questionable (Powers 2013). Perhaps most surprising of all, Mayr's correspondence shows that he was aware that at least one of his colleagues personally objected to Mayr's essentialist caricature, but Mayr ignored that objection (Winsor 2006). The fully developed "essentialist" view of biology is a myth.

Despite a greater understanding of the history of philosophy and biology today, we may still discover echoes of what appear to be Mayrian essentialist thinking in creationist biology, especially as it

applies to the identification of the human kind. For example, one encounters frequent claims that walking upright on the hindlimbs (obligate bipedalism) is a trait of humans not shared by any apes. Biddle (2016) states it simply, "Only humans stand and walk entirely on two feet." Similarly, creationists generate lists of traits that are ostensibly possessed only by humans and not by apes (e.g., see Menton 2005; Biddle 2016). Even the demand for character weighting in baraminology seems to echo essentialist thinking with its notion that some characters are more important than others for defining created kinds (see Williams 2004; O'Micks 2016).

When we consider the creation account in Genesis, one can easily see why an essentialist approach to humanity would be appealing. In Genesis, we see a repeated stress of humanity as distinct from the animal creation. Animals are made after their kinds, but humans are made in the image of God. Humans are given dominion over the animal creation, and Adam's inspection of the animals revealed no suitable counterpart. Some form of essentialism must therefore be true, because the Bible appears to reveal an essential and important difference between humans and animals. Should we therefore approach identifying humanity as a problem of identifying the essential characteristics that define human beings? To put it another way, is essentialism character-based?

Responding to any claim of character-based essentialism poses little difficulty: one simply asks why those traits ought to be considered essential for defining humanity, as one could do for an essentialist approach to any created kind. Is there any philosophical or theological justification within creationism to approach the identification of kinds in this manner? Is that justification sound and compelling? More generally, character-based essentialism is always vulnerable to future discoveries. The mere empirical observation that one category possesses traits not found in any other category does not require the metaphysical conclusion that such traits are essential and can never

change or be found in members of some other category. Because this vulnerability cannot be overcome, some creationists have argued for a different approach altogether.

In contrast to strict applications of character-based essentialism, the refined baramin proposal placed created kinds in the context of an area of “biological character space,” a limited set of character combinations that would allow the researcher to recognize the underlying unity of the kind (Wood et al. 2003). Using this approach, baraminology can proceed empirically without appeal to unchanging, discrete characteristics that define a baramin. This approach mimics the “population thinking” of Mayr’s approach to species, in the sense of de-emphasizing particular characteristics and emphasizing “populations” or clusters of species that share an underlying similarity that is different from other such clusters. This cluster-based approach to created kinds demonstrates that one need not be committed to evolutionary thinking to see the deficiencies of character-based essentialism, nor does population thinking entail a commitment to macroevolution.

Even though the refined baramin concept allows for the rejection of character-based essentialism, the authors of that concept made no explicit judgment on the validity of the essentialist approach. Further, objections to character-based essentialism are largely epistemological, based on the inherent uncertainty of any putative list of essential characters. Thus, the ontological question remains even in deference to the refined baramin concept: Could created kinds, especially the human kind, be characterized by some set of essential characteristics which together as a system define each baramin? Indeed, one could argue that the concepts of biological character space and potentiality regions are actually a more sophisticated and flexible form of essentialism. We might refer to this approach as a systems-based essentialism, where the essential features of any created kind are found in a full suite or system of a large number of discrete characters, which together constitute a functional system that is essential to that created kind. As a system, we might observe that the discrete characteristics are redundant (and potentially modular), thus the system can form from different combinations of the characteristics. In this way, none of the discrete characters are truly essential, but the system they form is. Consequently, we could continue to affirm an essentialist approach (especially as we attempt to distinguish human from nonhuman), while we might simultaneously be skeptical of character-based essentialism, especially of the practical application of character-based essentialism.

Thus, we should seriously consider the pragmatic value of the essentialist approach to created kinds, especially in the identification of humans in the fossil record. Should we try to distinguish humans from nonhumans by a simple list of traits that distinguish extant humans and apes? More succinctly, when presented with a new “ape-man” fossil, could its status as human or ape be established quickly based on a small number of essential characters? If so, character-based essentialism would be empirically justified, but if not, a systems-based approach, such as using the refined baramin concept in statistical baraminology, would be preferable.

In favor of the character-based essentialist approach, we can easily list a large number of differences between humans and apes. With more careful examination, we can compose a list of characteristics

that distinguish human from chimpanzee skeletons. Such features include the larger endocranial volume, the mental eminence, relatively smaller canines, a forward positioned foramen magnum, laterally facing glenoid fossa, relatively shorter forearms, relatively shorter metacarpals and manual phalanges, opposable thumb, lumbar lordosis, five lumbar vertebrae, a bowl-shaped pelvis, a deep patellar groove on the distal femur, bicondylar angle  $>4^\circ$ , and an adducted hallux.

Again, this list of characters brings to mind the persistent problem of essentialism mentioned above. How do we know these characteristics are the essential human characteristics? Surely being human does not reduce to a bowl-shaped pelvis or a laterally facing glenoid fossa? When thinking of the “essence” of humanity, one might think of our vast intellectual superiority, our unrivaled artistic creativity, or our spiritual relationship with God. Yet these attributes are more obviously “systems” and not easily detected in a skeleton, much less in partial and fragmentary skeletal remains. We are therefore reduced by necessity to using skeletal characteristics that may or may not diagnose our humanity.

That said, since we cannot be sure any list of skeletal characteristics consists of truly essential characteristics, the best we can do in testing character-based essentialism is to evaluate whether any particular character is valuable in distinguishing human from nonhuman. This strategy raises a second problem: In order to adequately test character-based essentialism, we would need to know which skeletons are human and which are not. Since that is the very question at hand, how can character-based essentialism ever be fully tested even if it might be true? We cannot know what characteristics are essential, and we have no reference set of taxa upon which we could test our putative essential characteristics.

Still, we may tentatively evaluate specific essentialist approaches using taxa that young-age creationists generally agree on. For example, bipedalism is commonly asserted to be an essential characteristic of humans, and we could test its essentiality by evaluating characteristics functionally associated with bipedalism in *Australopithecus africanus*, a taxon that all creationists agree is not human. Similarly, we could evaluate any list of human essential characteristics by its ability to identify Neandertals as human or *Australopithecus africanus* as nonhuman. Here we would again rely on the unanimous agreement of young-age creationists that Neandertals were human and *Au. africanus* were not. In this way, we can evaluate whether specific accounts of essential characteristics are successful in recovering the correct classification of taxa that we strongly believe belong to either the human or nonhuman category.

Another potential evaluation of the character-based essentialist approach would be to look for agreement between different essentialist methodologies. For example, we might construct different lists of purported essential characteristics and look for agreement or disagreement in the resulting classification. Alternatively, we might use different classification methods with the same set of purported essential characteristics and look for agreement in the classifications. Finally, we might compare classifications using essentialist-derived characteristics to our best estimates of the human kind based on previous baraminology research. None of these would be sufficient to fully test character-based essentialism (which is unfalsifiable), but

consistency of results could embolden us to pursue more research using essentialist-style methodology.

The procedures here described are not properly tests of character-based essentialism itself but rather tests of specific character weightings derived from an essentialist approach. Here, I evaluate character-based essentialism in three ways using seven different character weightings. First, I constructed a list of skeletal characteristics associated with bipedalism in extant humans and scored their presence or absence in *Au. africanus* and the Little Foot skeleton (*Au. africanus sensu lato* or *Au. prometheus*), two taxa that all creationists agree are not human and should not exhibit human-specific characteristics. Second, I use a larger list of craniodental characteristics to identify putatively essential characteristics for six different samples of taxa. I then use these characteristics to test for consistency and success in distinguishing human from nonhuman, based on cases that all creationists agree on. Finally, I use the same subsets of characteristics in distance-based clustering. Again, I look for consistency among the character samples as well as consistency with previous evaluations of the human kind in order to assess the utility of a character-based essentialist approach to identifying the human kind.

## METHODS

As an initial test of essentialism, I compiled a list of fifteen skeletal characters associated with bipedalism in human beings (Table 1), based on the published literature and personal examination of skeletal casts of a human, a chimpanzee, and a gorilla. The human skeleton cast is in the collection of Core Academy of Science, and access to the chimpanzee and gorilla skeletons was provided by Southern Adventist University. Each character was coded such that the presence of the character is consistent with bipedalism. Using photographs, 3D scans, and published descriptions, I scored each of these

**Table 1.** Characteristics associated with bipedalism in living human beings (*Homo sapiens*).

1. Anterior position of the foramen magnum
2. Lumbar lordosis or lumbar vertebral wedging
3. Bowl shaped pelvis or iliac flaring
4. Bicondylar angle  $>4^\circ$
5. Proximal articular surface of tibia in line with tibial shaft
6. Articulation of medial cuneiform and first metatarsal flat and inflexible
7. Distal articular surface of first metatarsal rounded in medial view and extended superomedially over metatarsal shaft
8. Adducted hallux
9. Superior surface of second metatarsal flat and not convex
10. Medial and lateral condyles of distal femur same size
11. Deep patellar groove of distal femur
12. Tibia-talar joint relatively perpendicular to tibial shaft
13. Superior surface of proximal pedal phalanges flat and not convex
14. Fifth metatarsals exhibit lateral torsion
15. Semicircular canal shape human-like (most similar to extant humans as judged by shape coordinate PCA)

characters for their presence in *Australopithecus africanus* and in the Little Foot skeleton, taxa that all creationists accept as nonhuman.

For a second test, I used a previously published set of 391 craniodental characters scored for 24 hominid taxa (Wood 2020). The taxa include eleven members of *Homo*, five *Australopithecus*, three *Paranthropus*, *Ardipithecus*, *Sahelanthropus*, *Kenyanthropus*, and the outgroups gorilla and chimpanzee. *Homo erectus* is treated separately as African and Asian forms, and the Dmanisi fossils are included as a single taxon, Georgian *H. erectus*. I used the recoded characters such that the character state zero always codes an absent character state.

Using these characters, I defined six subsets. The first subset consists of characters where the state in *Homo sapiens* is different from the state in chimpanzee and the state in gorilla. I call these the *sapiens* only (SO) characters. The second subset consists of characters found in extant apes only (EAO), where the character state in chimpanzee is the same as gorilla but different from *H. sapiens*. The third subset expands the set of apes to include *Au. afarensis* and *Au. africanus*, such that all four ape taxa have the same state that differs from the state seen in *H. sapiens*. I call these the four ape (FA) characters. For the fourth subset, I define a “Lubenow Core” (LC) set of humans to include *H. sapiens*, Neandertals, and African and Asian *H. erectus*. This subset corresponds to the taxa that Marvin Lubenow accepted as human in his book *Bones of Contention* (Lubenow 2004). The LC characters have the same state in all four human taxa and differ from the state in gorilla and chimpanzee.

I created two additional character subsets to act as controls. First, I selected characters that were the same in all three *Paranthropus* species but different in *Homo sapiens*. These *Paranthropus*-only (PO) characters provide an alternative ape group by which to evaluate a different set of putatively essential characteristics. For the second control set, I selected characters that differed between *Homo sapiens* and Neandertals (HN characters), as a test of characteristics that would be unique to modern *Homo sapiens*.

For all of these character subsets, polymorphic characters were not included in the putatively essential character subset. Since essentialism requires that all members of the same taxon have the same character state, polymorphisms by definition cannot be essential.

For each subset, I recorded how many of the characters agreed with the human (LC, SO, HN) or ape (EAO, FA, PO) characters for all remaining taxa. The raw number of character differences were then converted to percent differences to generate a simple matching distance. With this distance I then created a unidimensional scale that included all taxa. For the LC, SO, and HN characters, a distance of zero corresponded to the human taxa or taxon, and a distance of one corresponded to the apes (LC or SO) or Neandertal (HN). For the remaining taxa the distances from the human taxa placed each taxon at a specific location on the scale. Gaps between adjacent taxa on this scale could then be calculated. This procedure was then repeated for the EAO, FA, and PA characters, where zero distance corresponded to the ape taxa and the distance of one corresponded to the human taxa.

Statistical significance of the gap sizes between adjacent taxa was then estimated from simulations. Random positions from zero to

one were selected from a uniform distribution corresponding to the number of taxa in each character subset minus the number of reference taxa used to define the character subset (17 for LC, 19 for FA, 20 for PO, 21 each for SO and EAO, and 22 for HN). Gap distances between adjacent points (including 0 and 1) were calculated, and the procedure was replicated one thousand times. The resulting gap distances conformed to a Weibull distribution, and the statistical significance of any gap size could then be estimated using the pweibull function in R.

Each character subset was then subjected to standard cluster analysis using simple matching and Jaccard distances. Distance correlation, medoid partitioning, and fuzzy analysis were all calculated using BARCLAY (<https://coresci.org/barclay>). Any additional calculations were done in R.

## RESULTS

**Bipedalism characteristics.** Fifteen skeletal characteristics associated with bipedalism were selected from empirical comparisons and the published literature (Table 1). Fossils referred to *Au. africanus* exhibited twelve of the fifteen characteristics, with one more probable based on the anatomy of the proximal first metatarsal (Table 2). Since *Au. africanus* fossils are frequently found disarticulated and therefore might represent more than one taxon (as argued by Clarke 2013), the fifteen bipedalism characters were also scored on the Little Foot skeleton, StW 573. Most of Little Foot was found articulated in a small area and hence represents a single skeleton (Clarke 2019). Little Foot exhibited nine of the bipedalism characters out of ten that could be diagnosed from photographs and published descriptions (Table 2). If bipedalism is an essential characteristic of human beings, these bipedalism characters fail to distinguish human from taxa that are decidedly not human.

**Craniodental characters.** A published set of 391 craniodental characters were scored for 24 taxa. The overall completeness of the character matrix is 52.8%. Character relevance ranges from 8.3% to

100%. Taxic relevance ranges from 9.5% (*Kenyanthropus*) to 92.8% (African *H. erectus*). A simple majority of taxa (13) have more than 60% of their character states known. The incompleteness of the matrix therefore limits its utility for wide samples of putatively essential character states. For example, only ten characters are scored for all eleven members of genus *Homo*, and none of the character states are identical in all eleven taxa. With the smaller sample of five *Australopithecus* species, 28 characters are scored for all five members of the genus, with only nine characters (1, 21, 58, 78, 79, 244, 249, 262, and 266) exactly the same for all australopiths. These nine characters fail to meet the definition of essential characters, however, since all nine character states are shared by at least one member of genus *Homo*. Smaller samples of taxa will therefore be necessary to explore character states that meet the requirement of being shared by the ingroup but not shared by the outgroup.

The first character set from a restricted taxon sample is the simplest and most intuitive: characters for which the states found in *Homo sapiens* differ from the states found in chimpanzee and gorilla (*sapiens*-only or SO characters). I found 104 SO characters (Table 3). The remaining 21 taxa shared between 81 (African *H. erectus*) and 4 (*Homo antecessor*) of these character states found in *Homo sapiens* (Table 4). Neandertals—a taxon widely accepted as fully human by creationists—exhibited only 60 of these character states out of the 69 that were known for Neandertals. In fact, none of the characters with known states for all taxa have a unique, autapomorphic state in *Homo sapiens*. Therefore, we find no characters that meet the requirement of essential characters for *Homo sapiens* only.

By taking the number of character states that differ from the SO character states, we can calculate a simple matching distance that represents the percent difference between a taxon's character states and the SO character states. These distances can be arranged on a linear scale, and we can examine that scale for any notable gaps that might indicate a discontinuity between human and nonhuman taxa. This procedure dispenses with the strict essentialist approach and treats

**Table 2.** Character scoring and documentation of bipedalism characters in *Au. africanus* and StW 573

Character Number	<i>Au. africanus</i>	StW 57
1.	Present, STS 5 (Ahern 2005)	Present (Clarke and Kuman 2019)
2.	Present, STS 14	Not yet described
3.	Present, STS 14	Present (based on photographs in Clarke 2019)
4.	Present, STS 34	Present (Heaton et al. 2019)
5.	Present, StW 514	Present (Heaton et al. 2019)
6.	Present, StW 595	Present (McHenry and Jones 2006)
7.	Present, StW 595	Unknown, distal surface damaged
8.	Probable, StW595	Present (DeSilva et al. 2019)
9.	Present, StW 89	Unknown, fossil not recovered
10.	Present, TM 1513, STS 34	Absent (Heaton et al. 2019)
11.	Present, TM 1513, STS 34	Present (Heaton et al. 2019)
12.	Present, StW 363	Present (DeSilva et al. 2019)
13.	Absent, StW 355	Unknown or not yet described
14.	Present, StW 114/115	Unknown, distal end damaged
15.	Absent (Beaudet et al. 2019)	Present (Beaudet et al. 2019)

**Table 3.** Character subset definitions and characters, numbered according to Wood (2020).

Subset SO (found in *Homo sapiens* but differ in chimps and gorillas): 2, 6, 11, 20, 32, 35, 39, 42, 44, 45, 48, 51, 55, 58, 63, 64, 66, 68, 69, 70, 73, 75, 83, 88, 89, 106, 107, 113, 116, 117, 119, 134, 136, 137, 138, 139, 141, 142, 143, 144, 150, 153, 157, 159, 170, 178, 184, 185, 187, 188, 191, 198, 200, 204, 205, 206, 207, 208, 212, 219, 228, 229, 232, 234, 235, 236, 237, 238, 239, 242, 244, 245, 249, 252, 253, 257, 263, 265, 266, 267, 270, 272, 274, 275, 283, 284, 285, 288, 291, 296, 299, 323, 324, 325, 330, 331, 333, 334, 340, 341, 347, 351, 356, 360

Subset LC (found in *H. sapiens*, Neandertal, African and Asian *H. erectus* but differ in chimps and gorillas): 45, 66, 69, 113, 134, 136, 139, 143, 153, 157, 159, 191, 204, 205, 207, 208, 252, 257, 263, 265, 266, 270, 272, 274, 275, 283, 285, 288, 296, 299, 330, 334, 360

Subset EAO (found in chimps and gorillas but differ in *H. sapiens*): 1, 2, 6, 11, 20, 32, 35, 39, 42, 44, 45, 48, 55, 58, 63, 64, 66, 68, 69, 70, 73, 75, 113, 116, 117, 119, 134, 136, 137, 138, 139, 141, 143, 144, 150, 153, 157, 159, 170, 178, 184, 185, 187, 188, 198, 200, 204, 205, 206, 207, 208, 212, 213, 219, 228, 229, 232, 234, 235, 236, 237, 239, 242, 244, 245, 252, 253, 257, 265, 266, 267, 270, 272, 274, 283, 284, 285, 288, 291, 296, 299, 323, 324, 325, 330, 331, 333, 334, 339, 340, 341, 349, 351, 356, 360

Subset FA (found in gorilla, chimp, *Au. afarensis*, and *Au. africanus* but differ in *H. sapiens*): 1, 2, 11, 44, 58, 75, 134, 139, 159, 178, 184, 245, 257, 267, 272, 291, 330, 331, 333, 339, 340, 356

Subset PO (found in all three *Paranthropus* species but not in *Homo sapiens*): 1, 6, 11, 14, 21, 22, 42, 45, 51, 55, 63, 64, 65, 66, 67, 71, 72, 75, 82, 86, 87, 89, 93, 96, 97, 102, 105, 106, 108, 109, 134, 142, 162, 185, 191, 204, 211, 213, 244, 253, 277, 284, 288, 291, 293, 295, 299, 320, 325, 331, 340, 347, 355, 356

Subset HN (found in *Homo sapiens* but not in Neandertal): 6, 8, 32, 34, 42, 46, 78, 82, 116, 131, 137, 167, 179, 199, 222, 223, 231, 232, 249, 260, 286, 289, 291, 302, 311, 352, 373, 374, 384, 391

the SO characters as a weighted subset of the full character matrix. For the SO characters, simulations show that gaps between the adjacent taxa follow a Weibull distribution with a shape parameter of 1 and a scale parameter of 0.04. The gaps between the taxa therefore exhibit only one length that is greater than expected by chance ( $p < 0.05$ ). The significantly long gap between the extant apes and *Ar. ramidus* is 0.179 ( $p = 0.0114$ ) (Figure 1). Thus, the significantly long gap partitions the taxa into two “groups,” consisting of the extant apes in one and everything else in the other. The SO characters therefore do not demonstrate a significant gap between *Homo sapiens* and the most similar taxon to *Homo sapiens*.

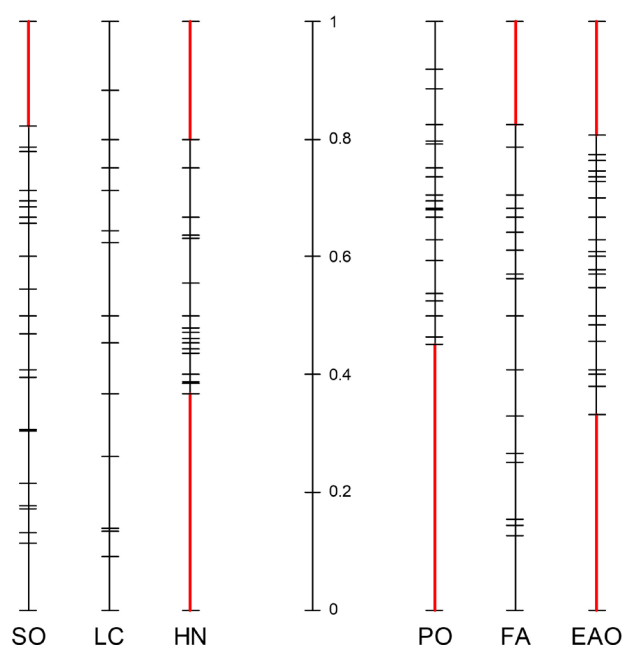
Expanding the sample of human taxa to include those recognized by Lubenow as human (the “Lubenow core” humans, LC) results in a sample of 33 characters that have identical states in *H. sapiens*, Neandertals, and African and Asian *H. erectus* but with different

states in chimpanzee and gorilla (Table 3). Of the remaining 18 taxa, *Homo antecessor* has no character states recorded for these characters. The other 17 taxa shared between 33 (*H. heidelbergensis*) and 1 (*Kenyanthropus*) of the human character states (Table 4). *Par. robustus* shared 19 of the LC character states, and *Au. africanus* shared 18 of the LC character states. Every LC character state is shared by at least one fossil hominin not in the LC. Therefore, the LC character states fail the strict definition of essential characters. Examining the linear distances and gaps between adjacent taxa reveals no significantly long gaps (Figure 1); thus, even the distance-based approach fails to clearly distinguish human from nonhuman taxa.

Instead of basing our “essential” character states on humans, we might approach this from the opposite perspective by defining essential ape character states that differ in known humans. The first such set is based on extant apes only (EAO), namely character states that are the same in chimpanzee and gorilla but different in *Homo sapiens*. I found 95 EAO characters (Table 3). The remaining taxa shared between 4 (*H. antecessor*) and 49 (*Au. africanus*) of the EAO character states (Table 4). Neandertals shared 15 of the EAO character states, despite being widely accepted as human by creationists. The linear array of simple matching distances revealed two significantly long gaps, between the extant apes and *Ardipithecus* (gap length 0.333,  $p = 6.11 \times 10^{-4}$ ) and between *H. heidelbergensis* and *H. sapiens* (gap length 0.194,  $p = 0.0134$ ) (Weibull shape parameter 1, Weibull scale parameter 0.04) (Figure 1). Hence, the EAO characters do not distinguish fossil taxa accepted as human by creationists (e.g. Neandertals) from fossil taxa accepted as ape by creationists (e.g. *Ardipithecus*).

Expanding the set of apes to include australopiths that all creationists accept as nonhuman, namely *Au. afarensis* and *Au. africanus*, results in a set of 22 character states that are identical in all four ape taxa but differ in *Homo sapiens* (four ape, FA characters, Table 3). Between 2 (*Kenyanthropus* and *H. antecessor*) and 13 (*Par. boisei*) of the FA character states are shared with the remaining taxa. Neandertals shared five of the FA character states. The linear array of simple matching distances revealed one gap of significant length: between *H. heidelbergensis* and *H. sapiens* (gap length 0.176,  $p = 0.0183$ , Weibull shape parameter 1, Weibull scale parameter 0.044). The resultant partition separates *Homo sapiens* from all other taxa (Figure 1), instead of including the human Neandertals with *Homo sapiens*.

As a further exploration of this technique, two additional character subsets were created as controls. The first set contains character states identical in all three species of *Paranthropus* (*Par. boisei*, *Par. robustus*, *Par. aethiopicus*) but different in *Homo sapiens*. This set of 54 *Paranthropus*-only (PO) character states were chosen as a second ape group that might distinguish human from ape, since all creationists agree that *Paranthropus* are not human. The number of PO character states shared with the remaining taxa ranged from 2 (*H. antecessor*) to 29 (*Au. africanus*) (Table 4). Neandertals shared 4 of these PO character states. The linear array of simple matching distances revealed only one significantly long gap length between *Paranthropus* and *Sahelanthropus* (gap length 0.451,  $p = 4.44 \times 10^{-5}$ , Weibull shape parameter 1, Weibull scale parameter 0.045). Thus, the character states only partition *Paranthropus* from everything else and are not useful for distinguishing humans from apes (Figure 1).



**Figure 1.** Linear representation of shared fractions of character states by each subset as indicated. All scales place putative “humans” at the bottom and putative “nonhumans” at the top. Significant gaps are shown in red. For more information on the calculation of statistical significance, see the Methods.

For the second control character subset, I identified 30 characters for which the *Homo sapiens* state differs from the state in Neandertal (HN characters). These characters were selected as a means of evaluating the results of separately partitioning taxa that belong in the same group. The remaining taxa shared between 1 (*Ardipithecus*, *Kenyanthropus*, *Sahelanthropus*, *Au. garhi*, and *Au. anamensis*) and 19 (Asian *H. erectus*) of the HN character states. As with the PO character states, the linear array of simple matching distances revealed one significantly long gap between *Homo sapiens* and Asian *H. erectus* (gap length 0.367,  $p=1.04 \times 10^{-7}$ , Weibull shape parameter 1, Weibull scale parameter 0.04). A second significantly long gap of 0.2 occurs between Neandertal and *Sahelanthropus* and between Neandertal and *Au. anamensis*, both of which share only one of five HN characters scored for those taxa. The gap length of 0.2 has a p value of 0.00674 (Weibull shape parameter 1, Weibull scale parameter 0.04). Unsurprisingly, this procedure again merely partitioned *Homo sapiens* from all other taxa and Neandertals from all other taxa (Figure 1).

Overall, this procedure of defining “essential” characters fails to define sets of characters that can be used to correctly classify taxa not included in the original character partitioning. All subsets tested here either show ape-specific character states in putatively human taxa like Neandertals or show human-specific character states in putatively nonhuman taxa like *Au. africanus*. Even if we approach these character subsets by looking for a threshold percentage of shared character states that might be used to separate putatively human from putatively nonhuman taxa, no such threshold has been found. A comparison of partitions derived from the simple matching distances reveals little consistency. Instead, these character subsets excel at defining only the taxa used in making the subset (SO, LC,

EAO, PO, and HN), and where they do not, the partitions mix humans and nonhumans in the same partition (FA). Examining a single dimension of simple matching distances does not partition taxa sensibly, but could the subsets be used in true cluster analysis to group human and nonhuman taxa?

**Cluster analysis.** Instead of treating these character subsets as essential characters that diagnose taxa merely by their presence or absence, we might instead think of them as heavily weighted character subsets that could be used in cluster analysis. Effectively, the character subset maximizes the distance between the ingroup and the outgroup used to select the characters for the subset. Secondly, it also minimizes the distance between the members of the ingroup by requiring that they all have identical character states. Cluster analysis can be done using the standard methods of distance correlation, medoid partitioning, and fuzzy analysis. Since this character matrix has already been coded so that the state 0 exclusively represents the absence of a character, Jaccard distances can be evaluated in addition to simple matching distances. For all of these cluster analyses, no characters were omitted for low relevance, and all characters were used for distance calculations.

Distance correlation results for the SO character subset using simple matching distances are shown in Figure 2. Three clusters are apparent. First, *Homo floresiensis* stands as a singleton with no significant, positive correlation with any other taxa. The second cluster contains a set of apes: *Sahelanthropus*, *Au. garhi*, *Au. anamensis*, chimpanzee, *Au. afarensis*, *Ardipithecus*, gorilla, *Kenyanthropus*, and *Au. africanus*. The remaining species of *Homo* belong to the third cluster, along with *Au. sediba* and all three species of *Paranthropus*. Two-cluster medoid partitioning and fuzzy analysis place members of *Homo*, including *Homo sapiens*, in the same cluster as members of *Paranthropus* (Figure 2). Three-cluster medoid partitioning places members of *Homo* together with *Au. sediba*, *Par. robustus*, and *Par. boisei* in a single cluster, but three-cluster fuzzy analysis places *Par. robustus* and *Par. boisei* in a separate cluster. Medoid partitioning (two- and three-cluster) places *H. floresiensis* in the same cluster with *H. sapiens*, but fuzzy analysis places *H. floresiensis* in the same cluster with *Au. africanus* for both two and three cluster partitions. The average silhouette width for all partitions is relatively low, with the highest average 0.37 seen for the two-cluster fuzzy analysis hard partition. Distance correlation has the worst average silhouette width at 0.22. Visual inspection of three-dimensional MDS reveals no obvious clustering, which explains the discordant cluster analysis results (Figure 3).

Using Jaccard distances on the same SO character subset reveals a similar pattern of positive and negative correlation, but the resulting partition is quite different (Figure 4). *Homo floresiensis* shares significant, positive correlation with *Kenyanthropus*, placing it in a cluster of apes, and the three *Paranthropus* taxa are separated into their own cluster. The resulting partition has an average silhouette width of 0.39, which is slightly higher than the average silhouette width of 0.35 from the two-cluster partition of the fuzzy analysis and medoid partitioning. In the two-cluster medoid partition, *Par. robustus*, *Par. boisei*, *Kenyanthropus*, and *H. floresiensis* are placed in a cluster with *H. sapiens*. The three-cluster medoid partition separates all *Paranthropus* species into a single cluster by themselves

**Table 4.** Character distributions for all subsets.

	SO <sup>1</sup> <i>n</i> = 104	LC <sup>1</sup> <i>n</i> = 33	EAO <sup>2</sup> <i>n</i> = 95	FA <sup>2</sup> <i>n</i> = 22	PO <sup>2</sup> <i>n</i> = 54	HN <sup>1</sup> <i>n</i> = 30
African <i>H. erectus</i>	81 / 98	NA	23 / 91	7 / 22	11 / 53	14 / 28
Asian <i>H. erectus</i>	65 / 79	NA	25 / 75	6 / 18	10 / 40	19 / 30
Neandertal	60 / 69	NA	15 / 66	5 / 17	4 / 35	NA
<i>H. heidelbergensis</i>	63 / 71	33 / 33	13 / 67	3 / 17	3 / 37	15 / 30
<i>H. habilis</i>	68 / 98	30 / 33	27 / 90	7 / 21	11 / 54	13 / 23
<i>H. rudolfensis</i>	53 / 76	25 / 29	19 / 70	7 / 18	15 / 49	9 / 17
<i>H. floresiensis</i>	11 / 32	3 / 8	18 / 30	11 / 13	8 / 25	5 / 9
<i>H. naledi</i>	44 / 56	26 / 30	14 / 53	3 / 14	10 / 34	6 / 11
Georgian <i>H. erectus</i>	26 / 43	16 / 16	16 / 41	5 / 14	13 / 32	8 / 22
<i>H. antecessor</i>	4 / 8	NA	4 / 8	2 / 4	2 / 6	7 / 13
<i>Au. afarensis</i>	24 / 79	11 / 31	45 / 76	NA	28 / 51	7 / 19
<i>Au. africanus</i>	39 / 98	18 / 33	49 / 90	NA	29 / 54	12 / 23
<i>Au. anamensis</i>	8 / 36	4 / 16	16 / 31	6 / 7	13 / 26	1 / 5
<i>Au. garhi</i>	6 / 21	2 / 7	8 / 19	3 / 4	5 / 19	1 / 3
<i>Au. sediba</i>	29 / 49	17 / 23	17 / 46	7 / 16	13 / 41	6 / 10
<i>Par. boisei</i>	44 / 97	18 / 33	36 / 90	13 / 22	NA	11 / 18
<i>Par. aethiopicus</i>	22 / 70	11 / 22	29 / 64	11 / 15	NA	3 / 12
<i>Par. robustus</i>	44 / 83	19 / 30	18 / 76	9 / 21	NA	8 / 13
<i>Kenyanthropus</i>	5 / 15	1 / 4	6 / 14	2 / 3	5 / 15	1 / 3
<i>Sahelanthropus</i>	6 / 28	2 / 10	13 / 21	3 / 3	10 / 21	1 / 5
<i>Ardipithecus</i>	7 / 39	2 / 17	22 / 33	7 / 8	4 / 23	1 / 3

<sup>1</sup>For each taxon, the recorded fraction is the number of character states that match that of the human taxa divided by the number of character states known for that taxon. Distances are calculated as one minus the fraction shown.

<sup>2</sup>For each taxon, the recorded fraction is the number of character states that match that of the ape taxa divided by the number of character states known for that taxon. Distances are calculated as one minus the fraction shown.

but mixes members of *Homo* and *Australopithecus* in another cluster. The hard partition from the two-cluster fuzzy analysis places all members of *Homo*, *Au. sediba*, and *Par. robustus* in a single cluster. Three-cluster fuzzy analysis places *Au. africanus* and *H. floresiensis* in the *Paranthropus* cluster with a notably lower average silhouette width of 0.33. As with the simple matching distances, visual inspection of the three-dimensional MDS results reveals no obvious clustering (Figure 5).

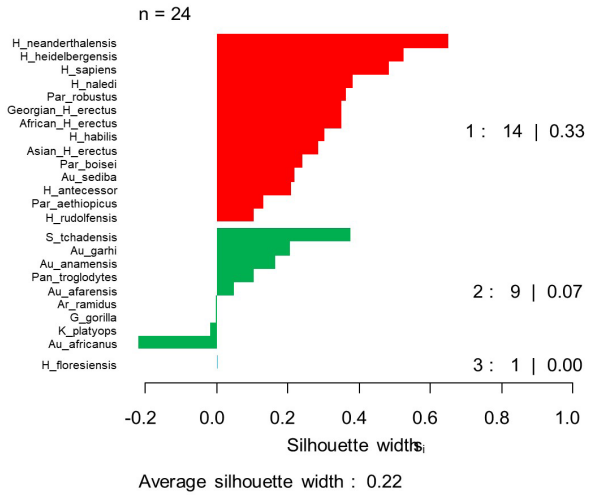
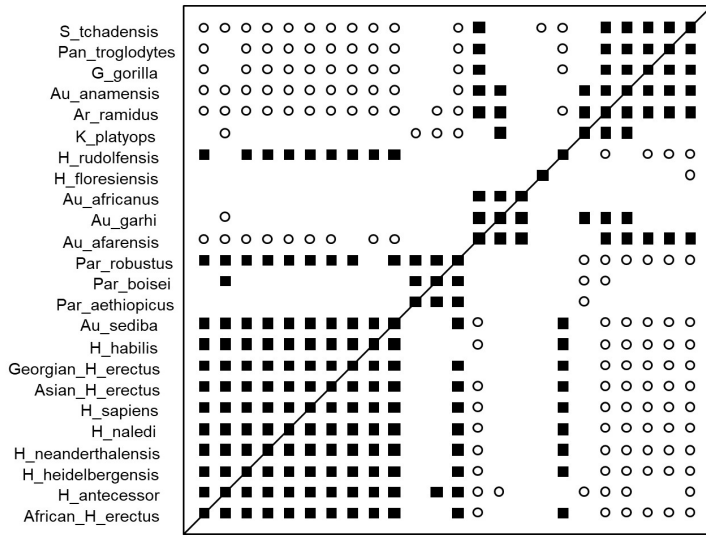
For the LC subset of characters, distance correlation using simple matching distances partitioned the taxa into three clusters (Figure 6). Once again, *H. floresiensis* shared no significant, positive correlation with any other taxa. With additional instances of significant, positive correlation, the *Paranthropus* species are more decisively included in the cluster with *Homo sapiens*, *Au. sediba*, and the remaining *Homo* taxa, along with *Au. africanus*. The remaining non-*Homo* taxa form the third cluster. Despite the better support afforded by additional instances of significant, positive distance correlation, the resultant clustering has a poor average silhouette width of 0.26. Two-cluster partitions from medoid partitioning and fuzzy analysis both place *Paranthropus* taxa in the same cluster with *Homo sapiens*, and *Homo floresiensis* is placed in the other cluster by both methods. Despite the difference, both two-cluster partitions have average silhouette

widths of at least 0.5. Three-cluster medoid partitioning has a cluster consisting of all three *Paranthropus* taxa with *Au. afarensis* and *Au. africanus*, and *H. floresiensis* is placed in a cluster with *Ardipithecus*, chimpanzee, and gorilla. Three-cluster fuzzy analysis resembles the three-cluster medoid partition, except *H. floresiensis* and *Au. sediba* are placed in the *Paranthropus* cluster. Again, visual inspection of the three-dimensional MDS reveals no obvious clustering (Figure 7).

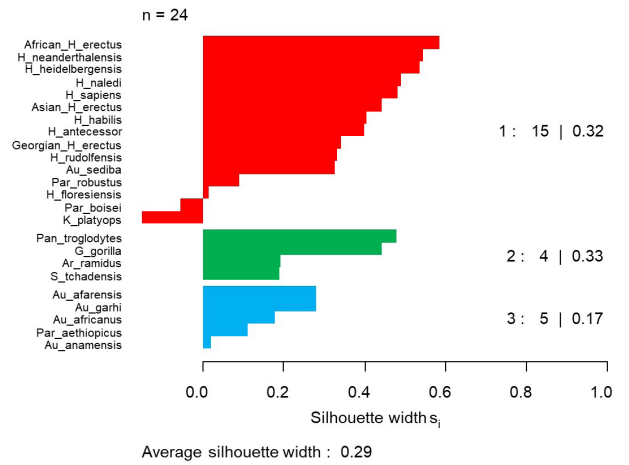
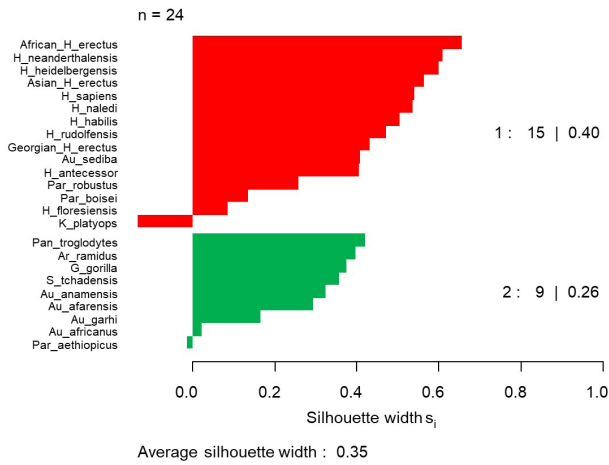
Clustering (Figure 8) and three-dimensional MDS (Figure 9) using Jaccard distances for the LC characters were nearly identical to the results from the simple matching distances. The major difference is seen in the three-cluster medoid partition, where using Jaccard distances results in moving gorilla into the *Paranthropus* cluster.

For the EAO subset of characters, distance correlation using simple matching distances reveals two clusters (Figure 10). Again we find *Paranthropus*, *Homo*, and *Au. sediba* combined in a single cluster with *H. floresiensis* placed in a cluster with gorilla and chimpanzee. Two-cluster medoid partitioning closely resembles these clusters but places *Au. africanus* and *Au. garhi* in the cluster with *Homo sapiens*. The hard partition from two-cluster fuzzy analysis places *Par. boisei* and *Par. robustus* in the cluster with *Homo sapiens* and *Par. aethiopicus* in the cluster with gorilla and chimpanzee. Average silhouette widths do not single out any of the two-cluster arrangements as obvi-

Distance Correlation



Medoid Partition



Fuzzy Analysis

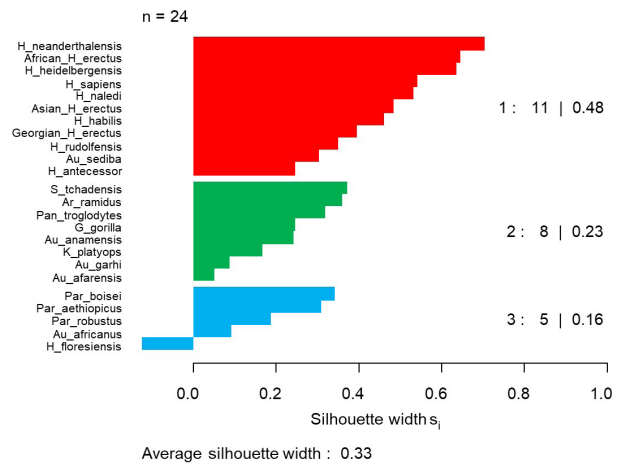
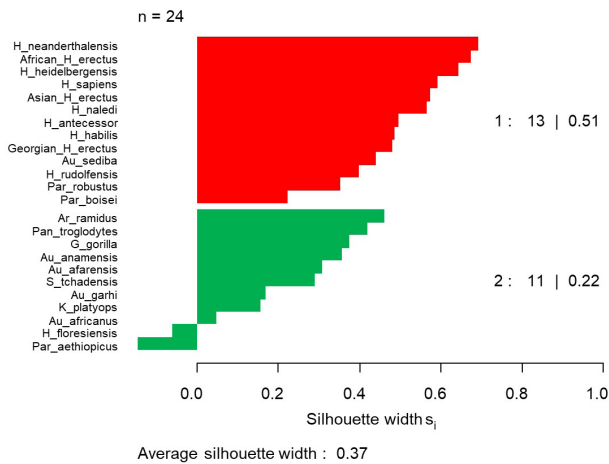


Figure 2. Clustering for simple matching distances using the SO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

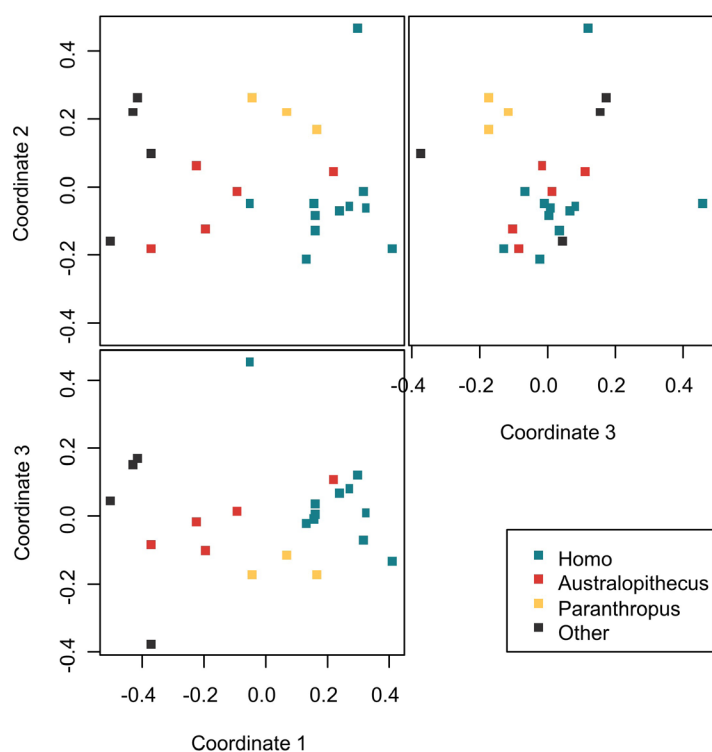
ously better than the others (0.4 for distance correlation, 0.38 for medoid partitioning, and 0.39 for fuzzy analysis). The three-cluster results for both medoid partitioning and fuzzy analysis have nearly identical silhouette widths than the two-cluster results (0.38 for medoid partitioning, 0.37 for fuzzy analysis). In both of the three-cluster partitions, all three *Paranthropus* species are separated into their own cluster with members of *Australopithecus*. As with previous character subsets, three-dimensional MDS again does not reveal any obvious clusters (Figure 11).

Distance correlation using Jaccard distances and the EAO characters separates *Paranthropus* into their own cluster, leaving *Homo* species and *Au. sediba* in a cluster and *H. floresiensis* in a cluster with gorilla and chimpanzee (Figure 12). Three-cluster medoid partition closely resembles the distance correlation, except *Au. africanus* and *Au. garhi* are moved into the cluster with *H. sapiens*. This move results in a drop in the average silhouette width from 0.42 for the distance correlation to 0.36 for the medoid partition. Three-cluster fuzzy analysis moves *Au. africanus* and *Au. garhi* along with *Au. sediba* into the *Paranthropus* cluster for an even lower average silhouette width of 0.34. The two-cluster medoid partition places all *Paranthropus* taxa, *Au. africanus*, and *Au. garhi* in the human cluster, for an average silhouette width of only 0.36. In contrast, the hard partition from the two-cluster fuzzy analysis places *Au. garhi*, *Au. africanus*, *H. floresiensis*, and *Par. aethiopicus* in the cluster with chimpanzee and gorilla but keeps *Par. robustus* and *Par. boisei* in the cluster with *Homo sapiens*. Visual inspection of three-dimensional MDS again reveals no obvious clusters (Figure 13).

Distance correlation using simple matching distances from the FA

characters reveals two clusters (Figure 14). *Homo sapiens* is placed in a cluster with other members of *Homo* and *Au. sediba*. The rest of the australopiths and *Homo floresiensis* are placed in a cluster with gorilla, chimpanzee, and the *Paranthropus* species. The two-cluster medoid partition and fuzzy analysis exactly match the partition from the distance correlation, except in moving *Par. robustus* into the same cluster with *Homo sapiens*. The average silhouette width is the same for fuzzy analysis and medoid partitioning (0.52). The three-cluster medoid partition appears to be the best partition of all with an average silhouette width of 0.57. In this partition, *Paranthropus* are separated into their own cluster, *H. floresiensis* is placed in a cluster with chimpanzee and gorilla, and the remaining *Homo* taxa and *Au. sediba* appear the third cluster. The three-cluster fuzzy analysis is worse with an average silhouette width of 0.51, resulting from the shift of *Homo habilis* from the *Homo sapiens* cluster to the *Paranthropus* cluster. Again, the three-dimensional MDS reveals a diffuse cloud of taxa with no obvious clustering (Figure 15).

Distance correlation with FA characters and Jaccard distances reveals an identical clustering as seen with the simple matching distances (Figure 16). With Jaccard distances, the two-cluster medoid partitioning exactly matches the distance correlation partition. The hard partition from two-cluster fuzzy analysis differs by placing *Par. robustus* and *Par. boisei* in the same cluster with *Homo sapiens*. The average silhouette widths reveal a very slight preference for the fuzzy analysis partition (0.54) vs. the medoid partition (0.52). The three-cluster medoid partition using the Jaccard distances was identical to the three cluster medoid partition using the simple matching distances, with a matching average silhouette width of 0.57. Again, the three-cluster fuzzy analysis is worst of all with an average silhouette width of 0.38. Three-dimensional MDS again reveals a diffuse set of taxa with no obvious clustering (Figure 17).

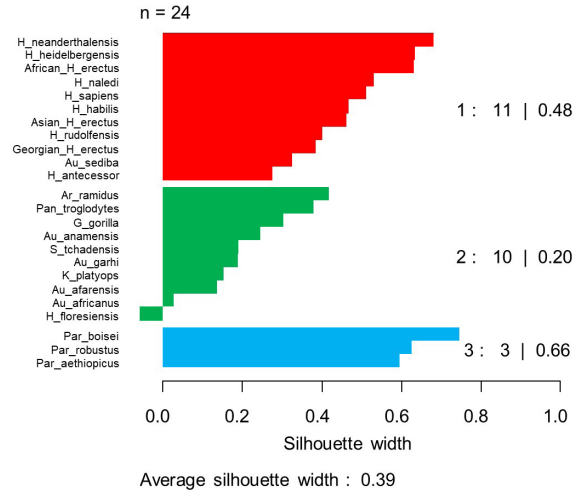
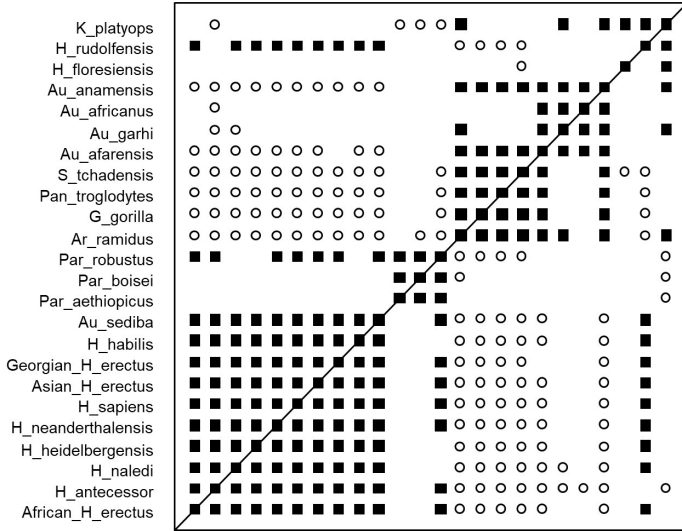


**Figure 3.** Orthogonal views of the 3D MDS results for the simple matching distances using the SO character subset.

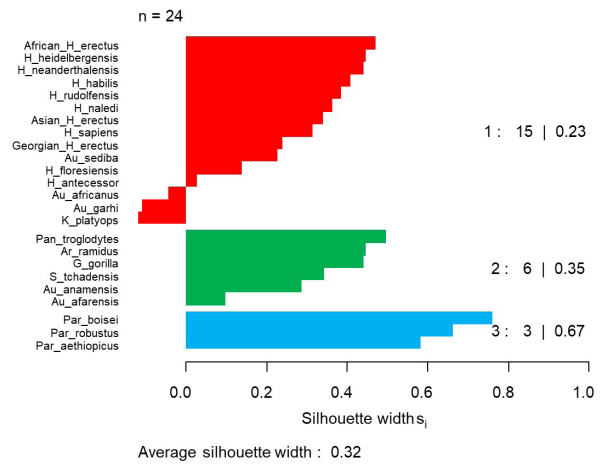
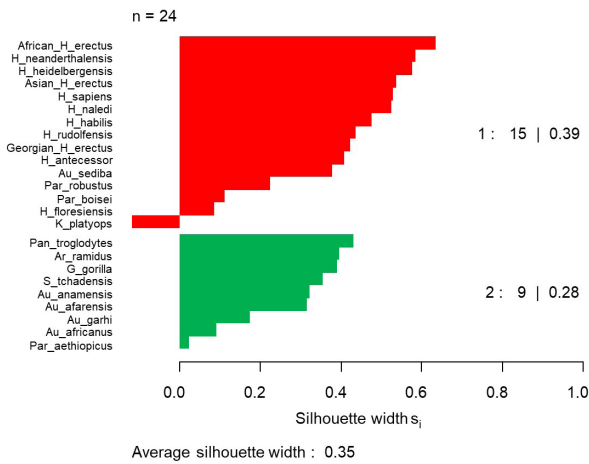
Distance correlation for the control set of PO characters using simple matching distances reveals three clusters with an average silhouette width of 0.44 (Figure 18). Unsurprisingly, the three *Paranthropus* species form one cluster, with a second cluster containing all eleven members of *Homo* and *Au. sediba*. Three-cluster medoid partitioning moves *Kenyanthropus* into the *Homo* cluster. The hard partition from the three-cluster fuzzy analysis moves *H. floresiensis* into the cluster with chimpanzee and gorilla. The average silhouette width of 0.44 for the distance correlation and 0.45 for the three-cluster fuzzy analysis were comparable, but the average silhouette width for the three-cluster medoid partition was lower at 0.41. Two-cluster medoid partition and fuzzy analysis were both lower than their three-cluster counterparts with average silhouette widths of 0.3 and 0.38 respectively. Three-dimensional MDS does show a moderate separation of *Paranthropus* from the other taxa but otherwise poor clustering (Figure 19).

Distance correlation for the PO characters using Jaccard distances closely resembled the simple matching partition, except for the placement of *H. floresiensis* in the cluster with gorilla and chimpanzee (Figure 20). All partitions from fuzzy analysis and medoid partitioning were identical to the corresponding partitions generated using simple matching distances. Three-dimensional MDS of the Jaccard distances also closely resembles that of the simple matching distances, with a slight offset of *Paranthropus* (Figure 21).

Distance Correlation



Medoid Partition



Fuzzy Analysis

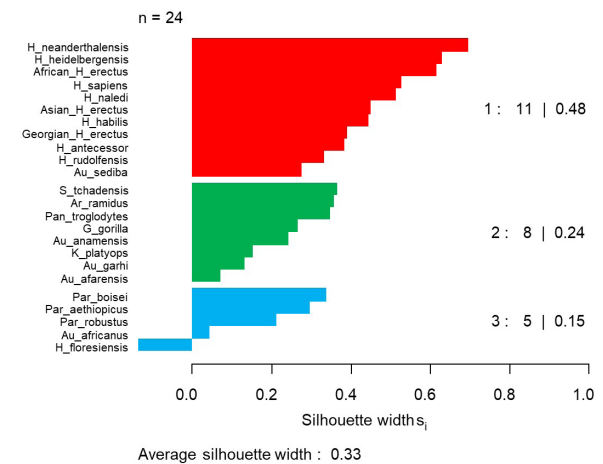
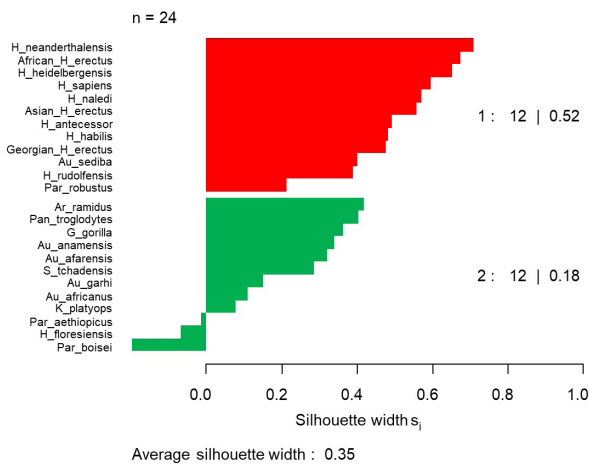


Figure 4. Clustering for Jaccard distances using the SO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

Clustering with the HN subset of characters was easily the worst of all character subsets for both simple matching and Jaccard distances. Distance correlation with simple matching distances revealed four poorly-defined clusters with an average silhouette width of -0.01 (Figure 22). *Homo sapiens* clusters with chimpanzee and gorilla. Neandertals cluster with *Par. aethiopicus*, *Par. boisei*, *Sahelanthropus*, and *Au. africanus*. Medoid partitioning, while better than the distance correlation clusters, still produced poor results. Two-cluster medoid partition had an average silhouette width of 0.15, and three-cluster medoid partition had an average silhouette width of 0.26. In both partitions, *H. sapiens* clustered with *Au. afarensis* and two *Paranthropus* species. Fuzzy analysis produced a two-cluster hard partition with an average silhouette width of 0.25 and a three-cluster partition with an average silhouette width of 0.26. In both fuzzy partitions, *H. sapiens* clusters with *Par. boisei*. Three-dimensional MDS of these simple matching distances revealed no obvious clusters (Figure 23).

Clustering using Jaccard distances from the HN characters was not notably different from the clustering based on simple matching distances (Figure 24). Distance correlation again revealed a four-cluster partition with an average silhouette width of 0.02, and the cluster partition of taxa was identical to that derived from simple matching distance correlation. Medoid partitioning and fuzzy analysis were again quite poor with no average silhouette width exceeding 0.25. Three-dimensional MDS of these simple matching distances revealed no obvious clusters (Figure 25).

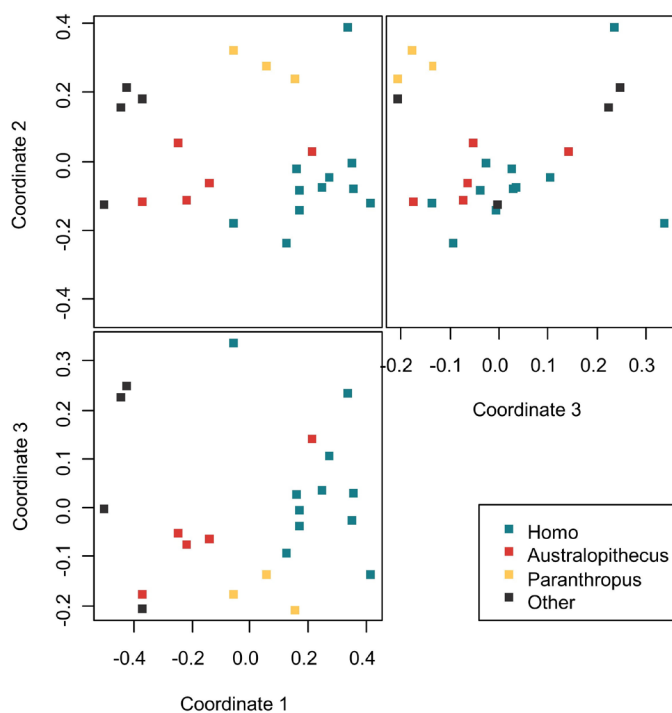
A summary of all sixty cluster partitions is shown in Figure 26. Leaving aside the spurious results of the HN character subset, we

see that despite repeated observation of odd clusterings (e.g., *Homo sapiens* with *Paranthropus*), we do find a core of taxa that tend to cluster with *Homo sapiens*. These taxa include Neandertals, *H. heidelbergensis*, African *H. erectus*, Georgian *H. erectus*, and *H. naledi*, all of which cluster with *Homo sapiens* exclusively using all character subsets except the HN characters. In addition, Asian *H. erectus*, *H. habilis*, *H. rudolfensis*, and *H. antecessor* nearly always cluster with *Homo sapiens*. Of the fifty cluster analyses involving the SO, LC, EAO, FA, and PO character subsets, *Au. sediba* clusters with *H. sapiens* 46 times. In contrast, *H. floresiensis* clusters with *Homo sapiens* only eight times, four times using the SO character subset, once using the LC subset, and three times using the PO subset.

Among the more clearly ape-like taxa, only *Ardipithecus* and *Au. anamensis* cluster apart from *H. sapiens* using every clustering method and character subset except the HN characters. Every other ape-like taxon occurs rarely in a cluster with *Homo sapiens*, with the surprising exception of the *Paranthropus* species. *Par. robustus* clusters with *Homo sapiens* in twenty of the fifty clusterings (not counting the HN character subset). *Par. boisei* and *Par. aethiopicus* cluster with *Homo sapiens* seventeen and eight times respectively, but never apart from *Par. robustus*. Of the fifty non-HN taxon partitions, *Homo sapiens* clusters with a nonhuman ape (i.e., *Au. afarensis*, *Au. africanus*, *Au. garhi*, *Paranthropus*, *Kenyanthropus*, or *Ardipithecus*) 26 times (52%). We must remember, of course, that these sixty clusterings are not of equal quality, but the frequency with which nonhuman apes occur in the same cluster as *Homo sapiens* gives us reason to be cautious and skeptical of these character sets.

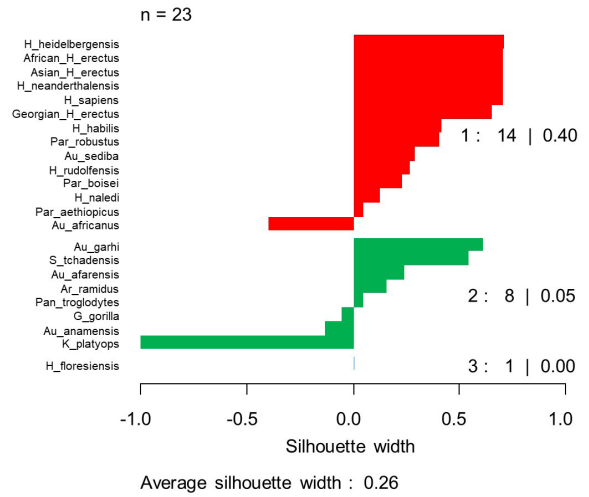
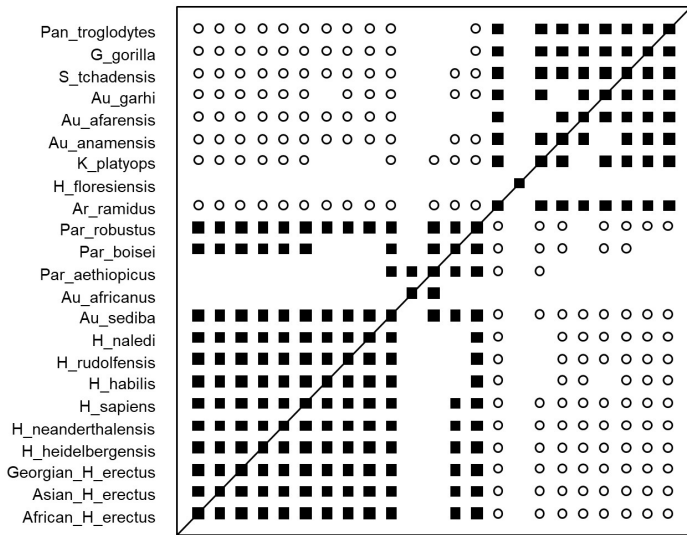
## DISCUSSION

Essentialism may be scientifically or philosophically unverifiable, but it still remains a very likely true description of God's created kinds, especially the human kind. Here, I've explored a much simpler and more tractable question: Can we adopt a naïve, character-based essentialist approach to distinguishing humans from nonhumans by using very simple lists of character traits? The lure of character-based essentialism would seem to be simplicity: a quick and easy test for placing God's creatures into well-defined categories. Here, character sets derived from essentialist assumptions generally fail to distinguish human from nonhuman. The fifteen bipedalism characters listed here certainly do not distinguish human from nonhuman. The character subsets derived from the larger sample of 391 craniodental characteristics likewise fail uniformly to delimit a sensible human cluster. SO characters, defined as character states in living humans that differ from those in chimpanzee and gorilla, would seem to be the safest set of characteristics that could be reliably said to define human beings, but they exclude Neandertals, which creationists widely accept as being human. Expanding the set of "humans" reduces the number of character states they share that differ from those of extant apes. The Lubenow Core (*H. sapiens*, Neandertals, and African and Asian *H. erectus*) share only 33 characteristics not found in living apes, compared to 104 found in living humans only but not in living apes. Every one of the LC character states are shared by at least one fossil hominin that creationists agree are not human. Similar results were seen when trying to define character states essential to living apes (EAO characters)

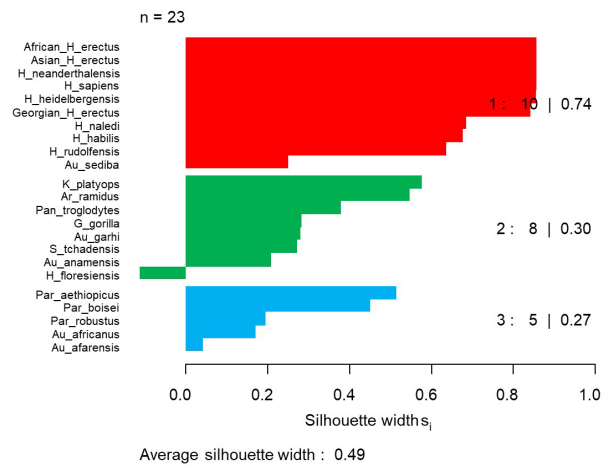
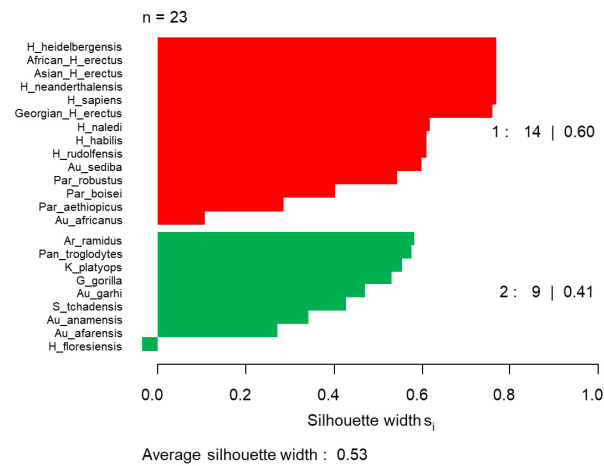


**Figure 5.** Orthogonal views of the 3D MDS results for the Jaccard distances using the SO character subset.

### Distance Correlation



### Medoid Partition



### Fuzzy Analysis

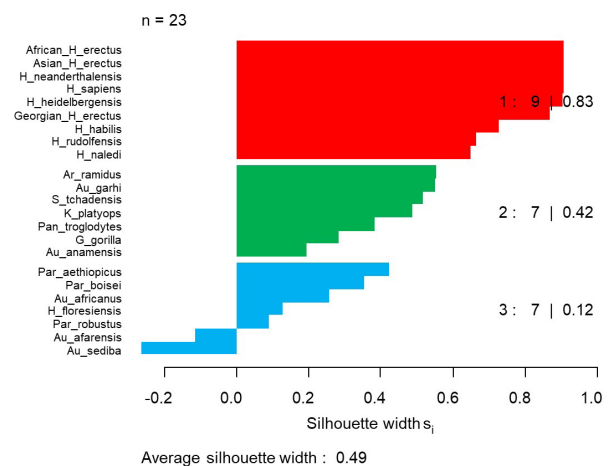
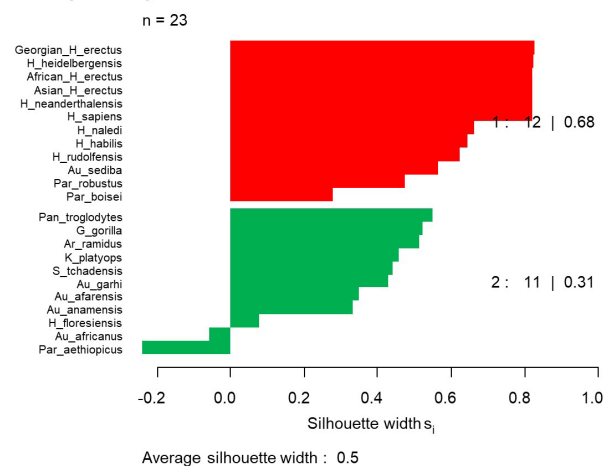


Figure 6. Clustering for simple matching distances using the LC character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

or a mix of living and fossil apes (FA characters). The procedure implemented here for defining a set of essential characteristics that can be used to include and exclude taxa from the category “human” does not produce reliable results. The character states are found in nonhuman fossil taxa, or the character states fail to include even the most obviously human fossil forms (Neandertals).

Evaluating these essentialism-derived character subsets with clustering methods produce more interesting results. The consistency with which *Homo sapiens* clusters with other human taxa such as Neandertals and *H. erectus* seems reassuring, but different clustering methods frequently produce alternative clusterings of relatively equal quality using the same subset of characters and distance metrics, as judged by average silhouette width. Similarly, clustering of relatively high average silhouette width often place obviously nonhuman taxa (particularly *Paranthropus robustus*) in the same cluster as *Homo sapiens*. None of the character subsets is immune to these problems.

Although these results seem to be entirely negative, there are important conclusions from this work that can inform baraminology studies. First, we can see that even though all character samples are not of equal quality, there is a remarkable consistency to the taxon clustering from these character subsets (except for the deliberately nonsensical HN characters). Even as we must be cautious due to the poor quality of the clustering and the frequency with which nonhuman and human taxa occur in the same cluster, it remains notable that certain taxa always or frequently cluster together. In the larger world of statistical baraminology, we sometimes have little choice but to use character matrices containing relatively few characters, but these results suggest that even that small sample may reveal something of

value in the clustering patterns even when the cluster assignment for every taxon might not be reliable.

Finally, the HN character subset reminds us that wildly inconsistent clusterings with poor average silhouette widths should not be trusted, and a different character set should be sought. The exceptionally poor results with these characters also support the basic humanity of Neandertals. Most young-age creationist scholars agree that Neandertals are human (Ross et al., in review), but some old earth creationists claim that Neandertals are not human (e.g., Rana and Ross 2015). If that were correct, I would expect that characters that distinguish *H. sapiens* from Neandertals would be the best at classifying apes and humans, but that is definitely not the case.

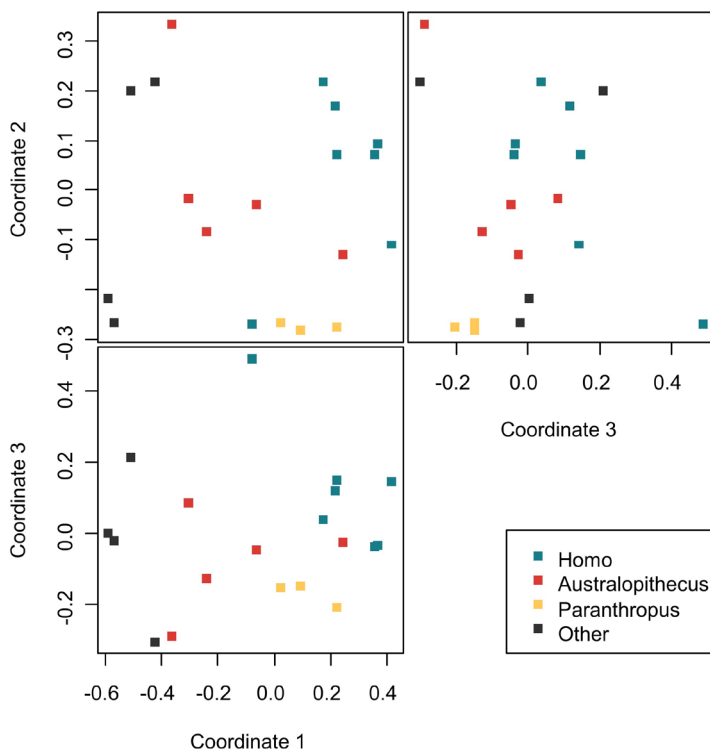
It must be emphasized again that these results are not properly a test or falsification of character-based essentialism, since we have no reason to believe that any of these characters here tested would or should be essential. Instead, the character subsets evaluated here can be seen as a form of character weighting, where “important” characters were selected using essentialist thinking. In that respect, this procedure has been found wanting. These character subsets repeatedly fail to distinguish human from nonhuman in a reliable fashion, which is an expectation of essentialism. If we are to identify truly essential character traits, we must begin with a more deliberate approach to identifying the sorts of traits that reasonably might be essential to humans. Such an approach must consider theological and biological issues in targeting the most likely essential traits. We must also consider the possibility that the theological essentialism described in Scripture is a systems-based essentialism and will not reduce to specific sets of discrete characteristics. What we can see clearly in this study is that naïve, character-based essentialism, with its quick and easy selection of “essential” traits, is unreliable.

## ACKNOWLEDGEMENTS

This work was sponsored in part by a grant from the Genesis Fund and by donations to Core Academy of Science. I am also grateful to Lucinda Hill and Southern Adventist University for providing access to the cast skeletons of chimpanzee and gorilla in their collection.

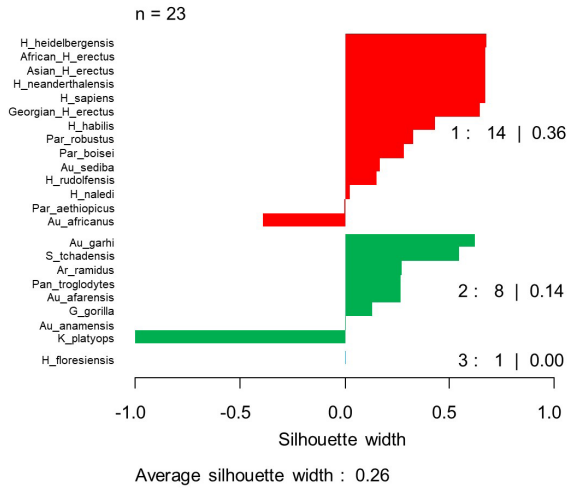
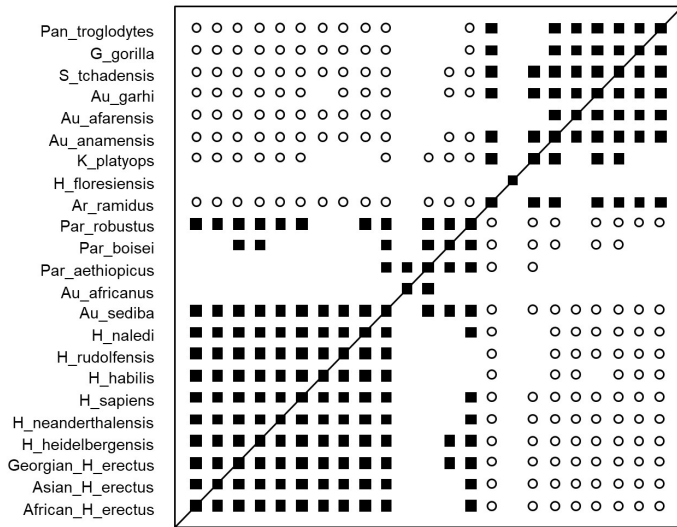
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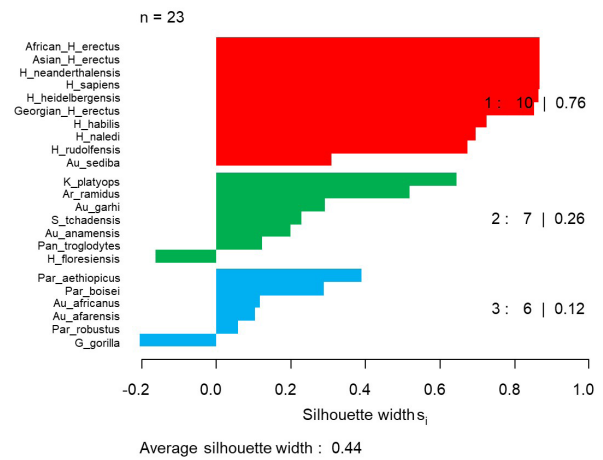
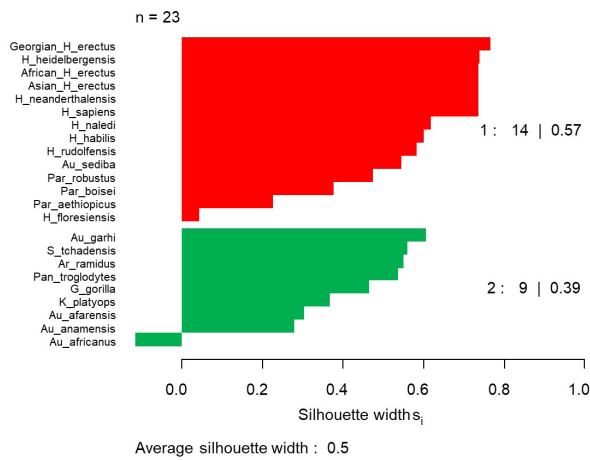


**Figure 7.** Orthogonal views of the 3D MDS results for the simple matching distances using the LC character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

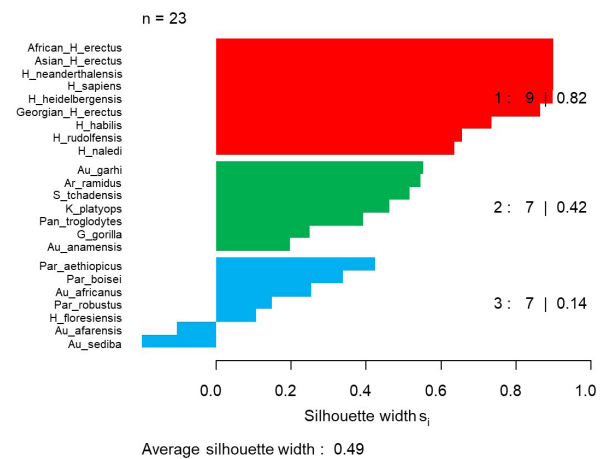
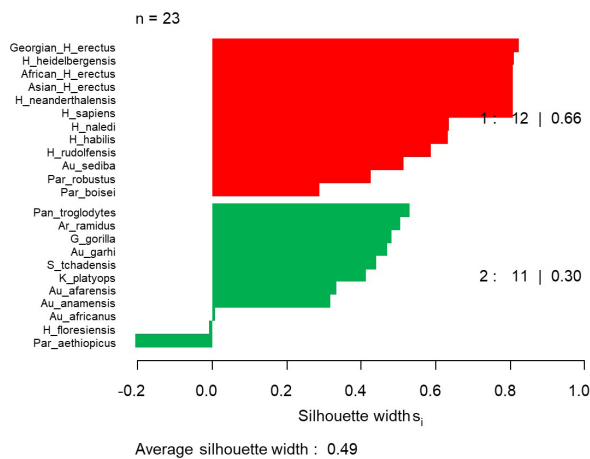


Figure 8. Clustering for Jaccard distances using the LC character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

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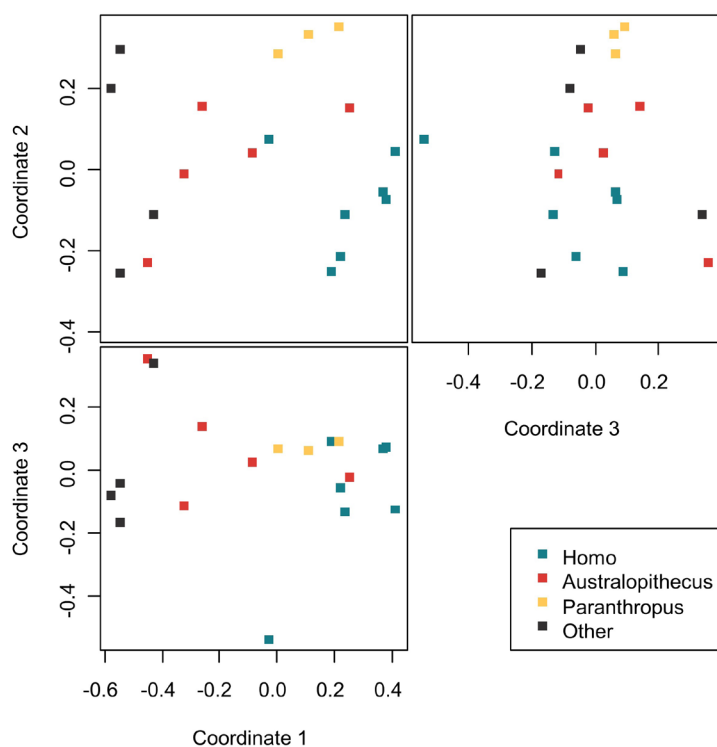
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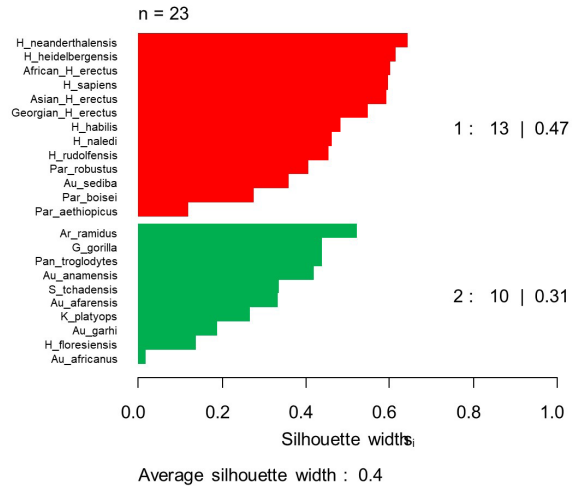
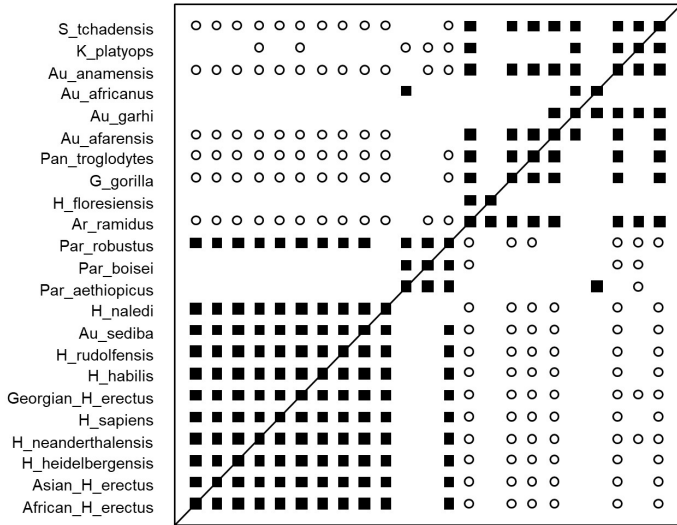
## THE AUTHOR

Todd Charles Wood is a researcher, teacher, and lecturer with twenty years’ experience working in young-age creationism. He is especially known for his studies of created kinds and fossil hominins. He is currently president of Core Academy of Science and resides in Dayton, Tennessee, home of the Scopes Trial.

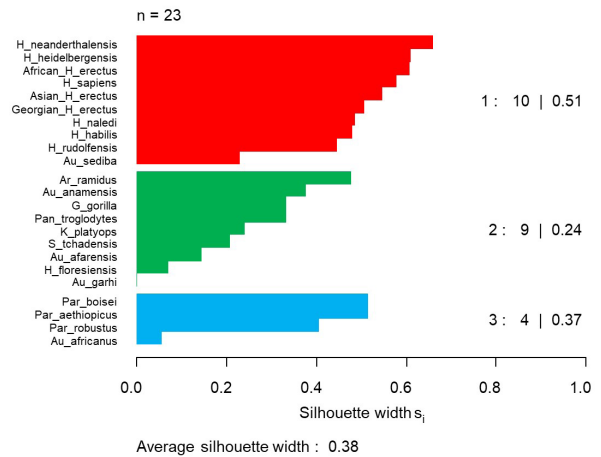
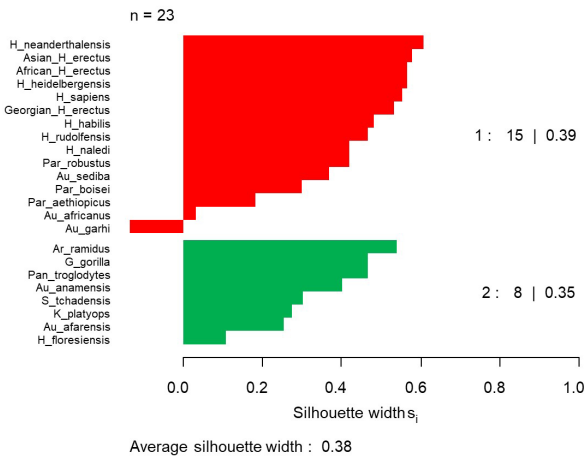


**Figure 9.** Orthogonal views of the 3D MDS results for the Jaccard distances using the LC character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

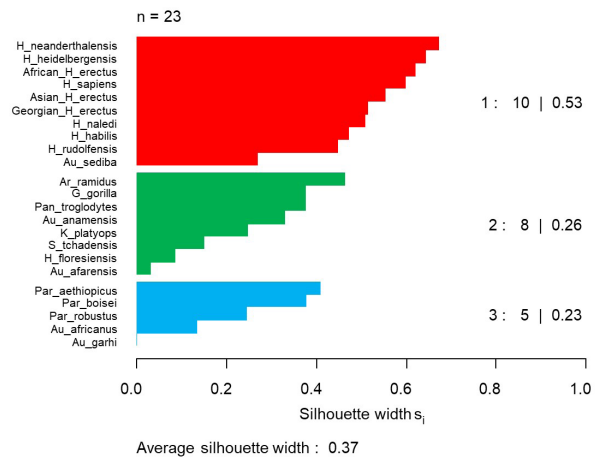
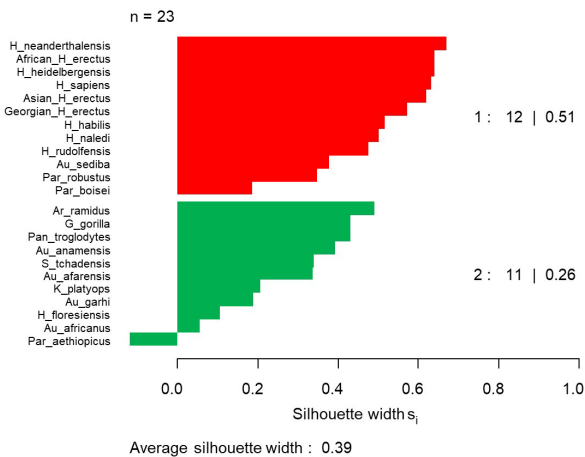


Figure 10. Clustering for simple matching distances using the EAO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

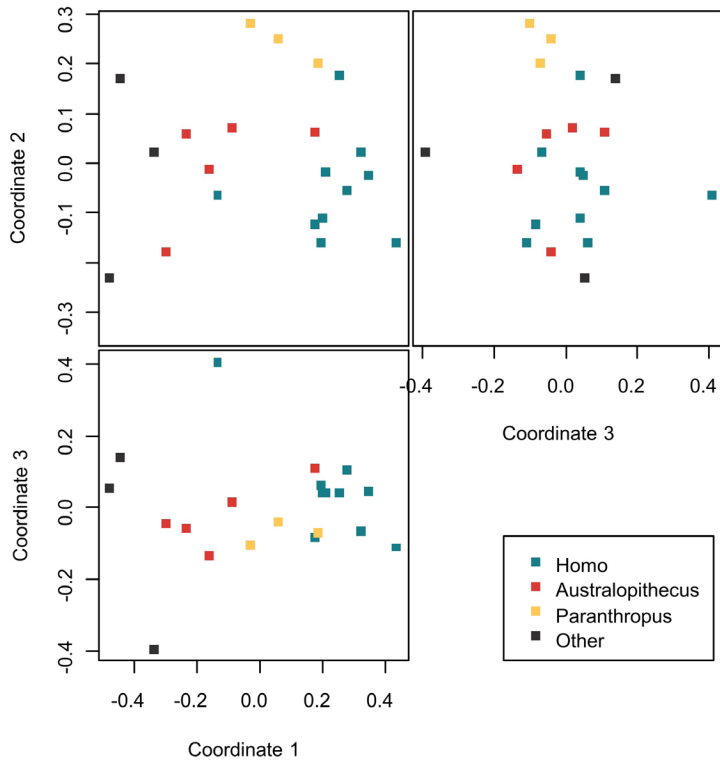
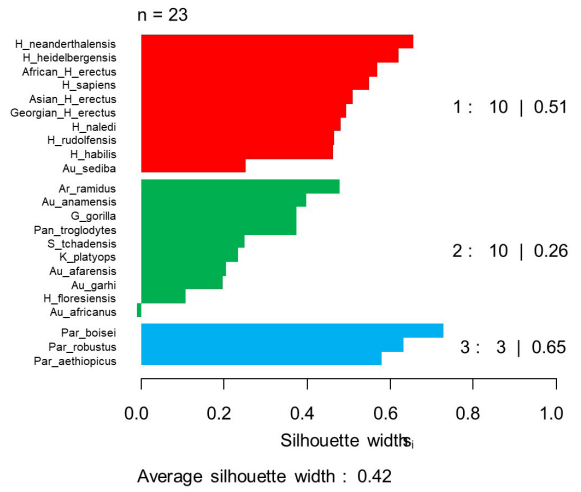
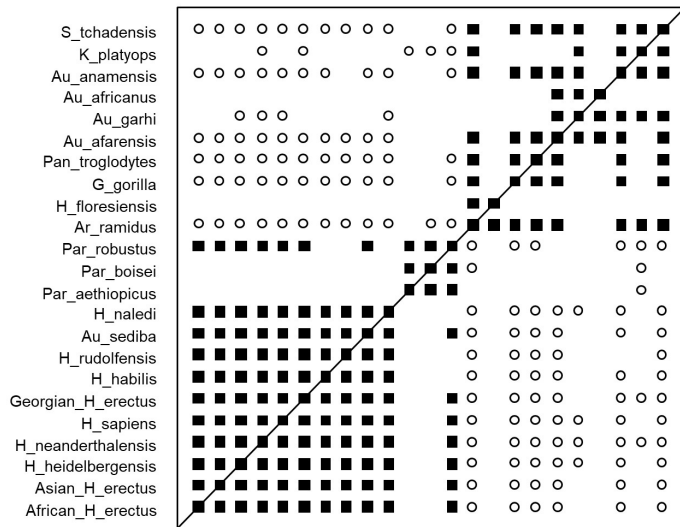
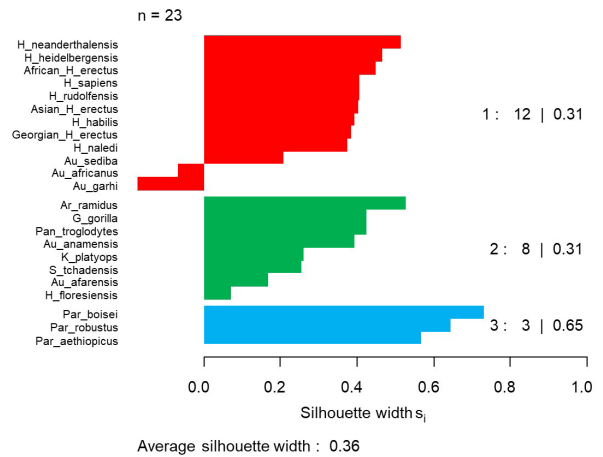
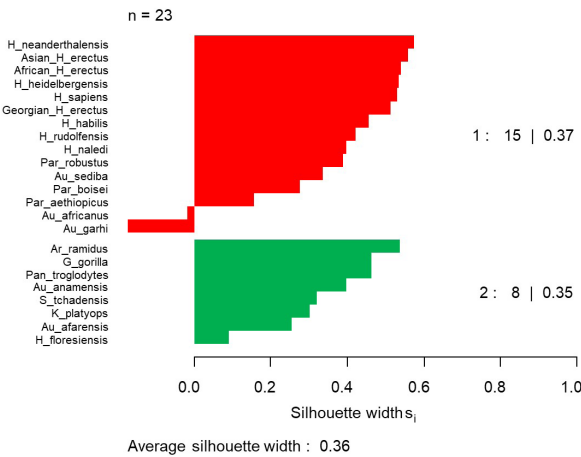


Figure 11. Orthogonal views of the 3D MDS results for the simple matching distances using the EAO character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

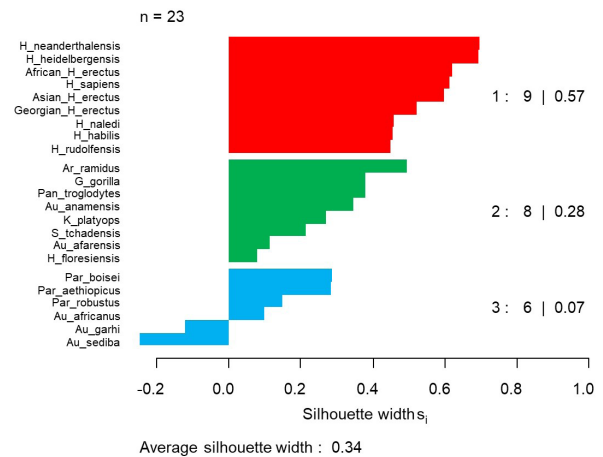
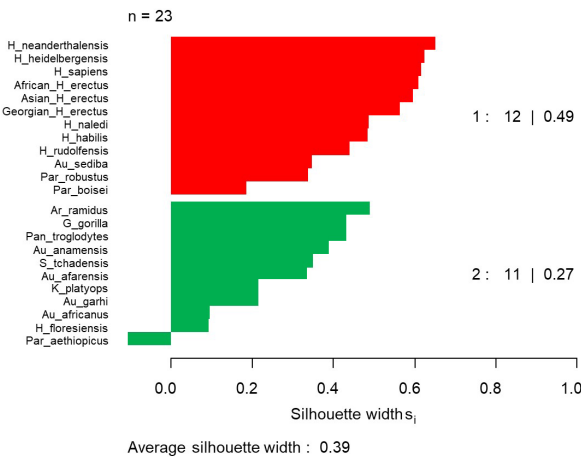
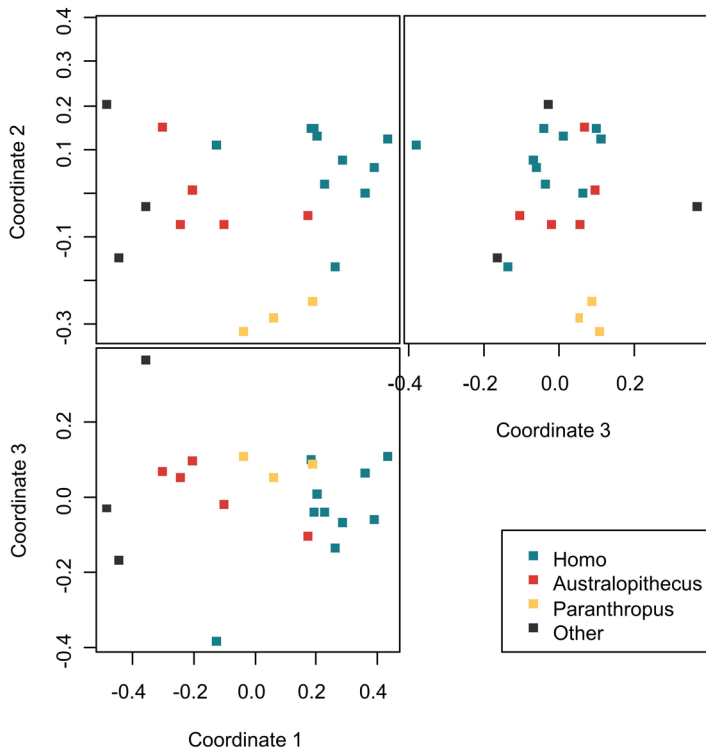
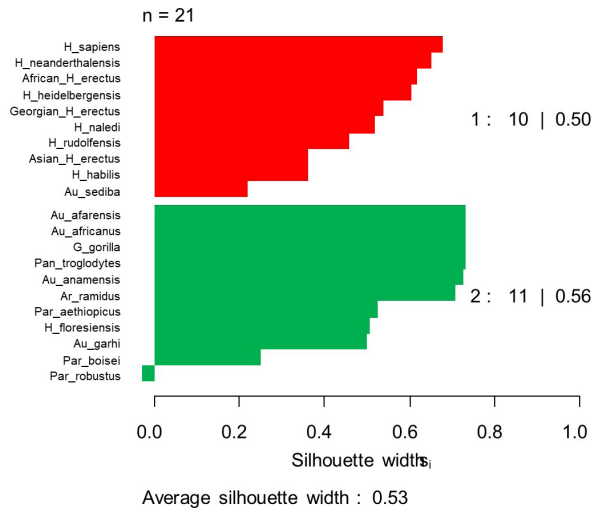
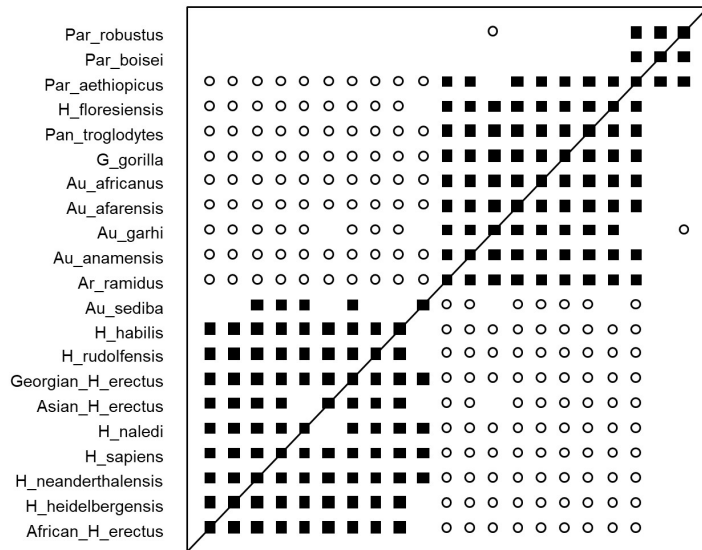


Figure 12. Clustering for Jaccard distances using the EAO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

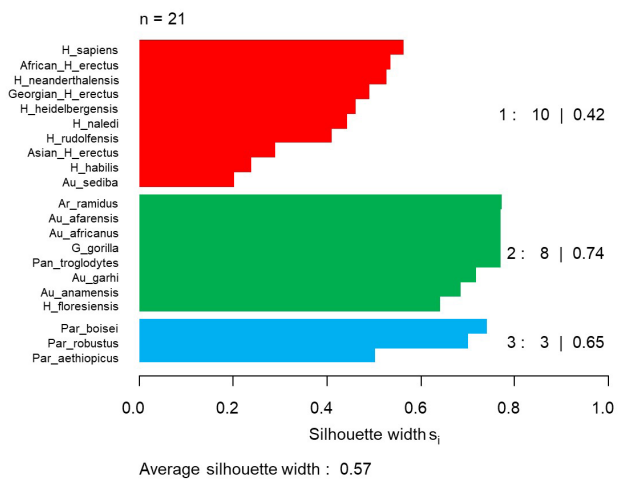
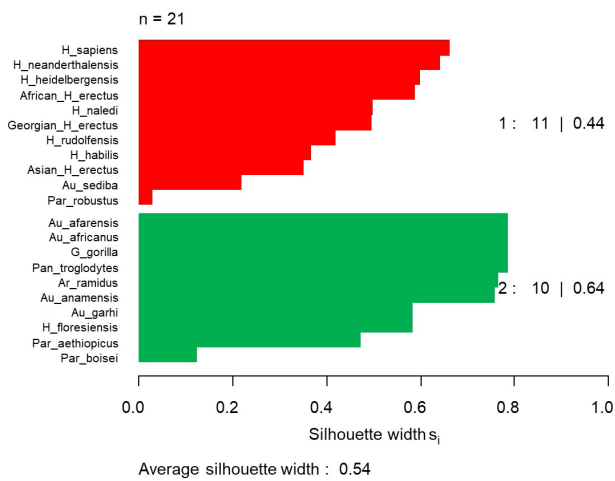


**Figure 13.** Orthogonal views of the 3D MDS results for the Jaccard distances using the EAO character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

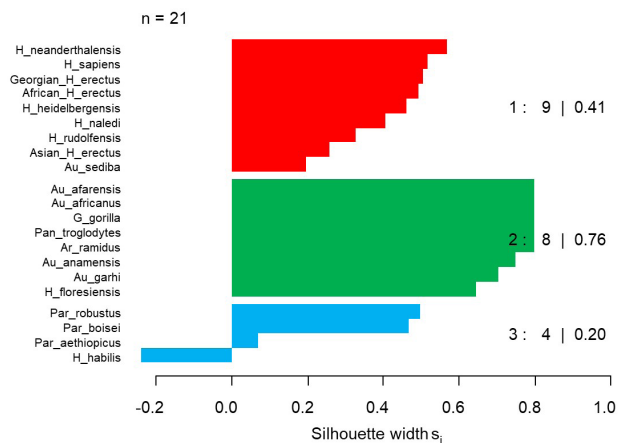
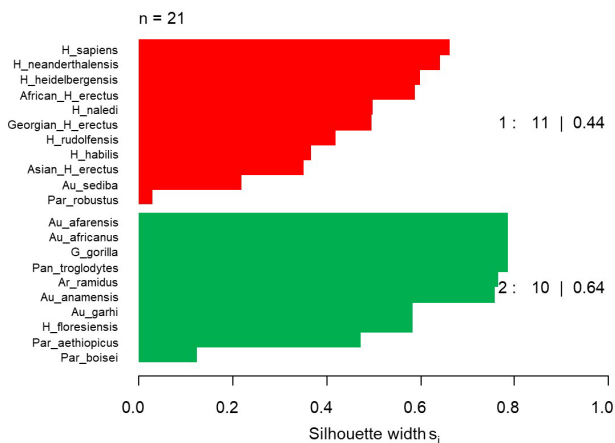
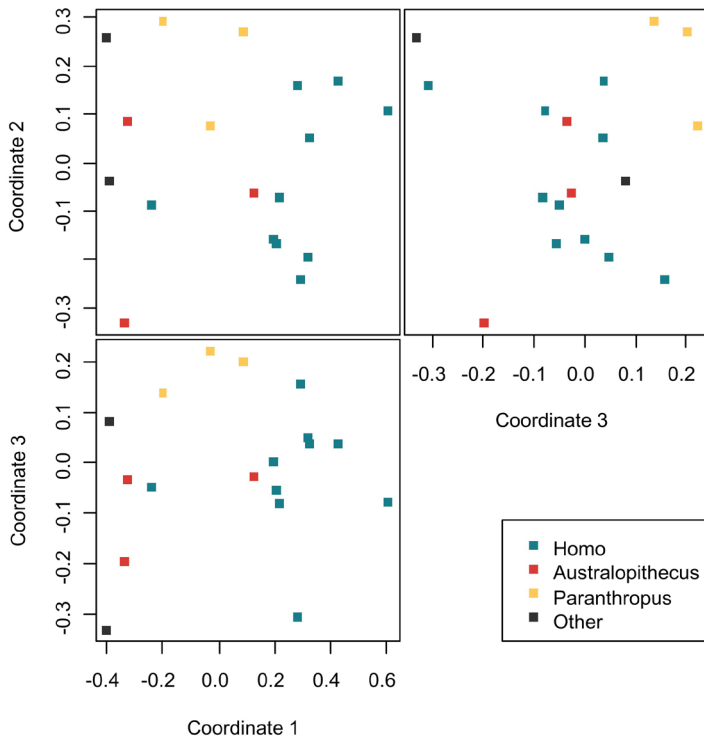
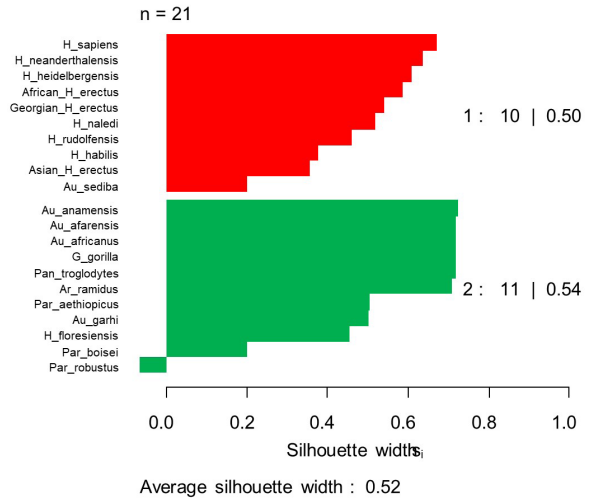
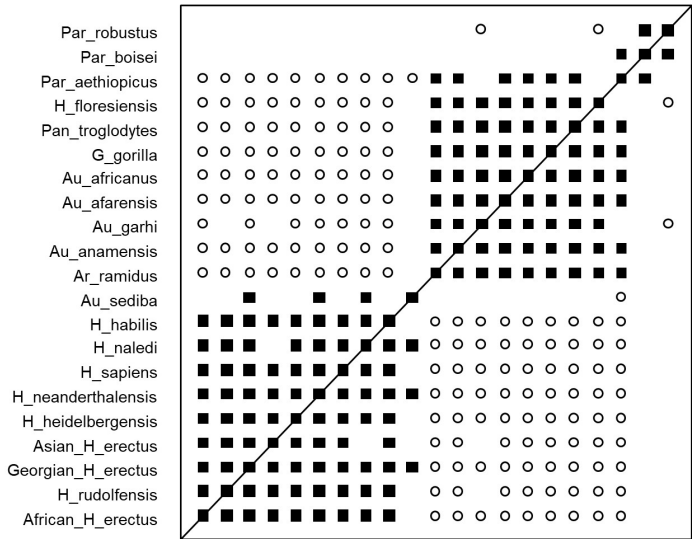


Figure 14. Clustering for simple matching distances using the FA character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

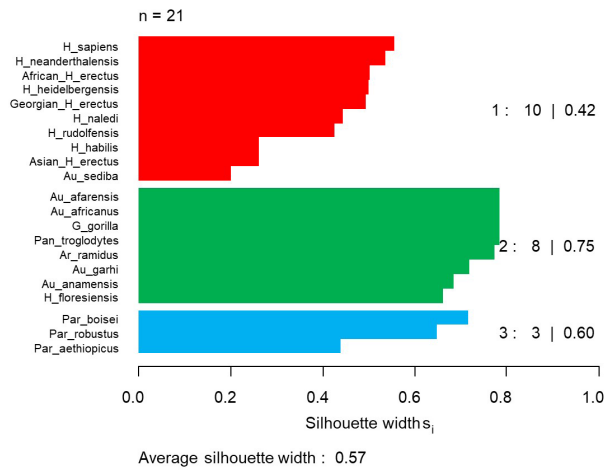
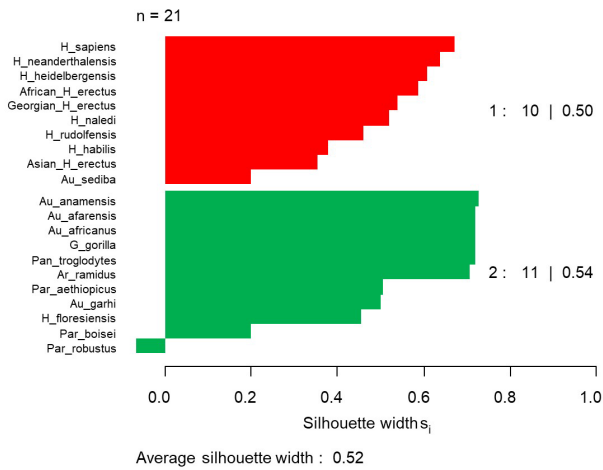


**Figure 15.** Orthogonal views of the 3D MDS results for the simple matching distances using the FA character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

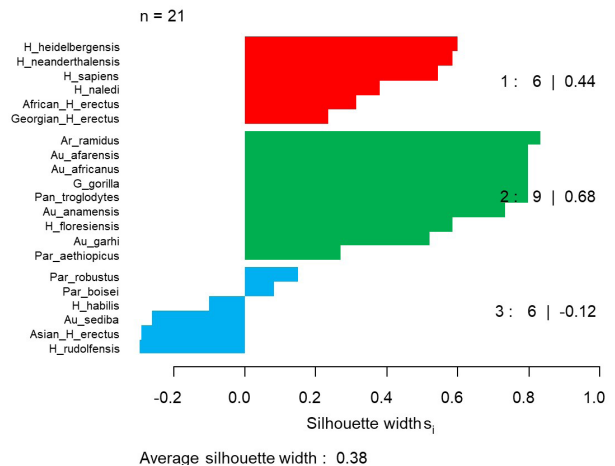
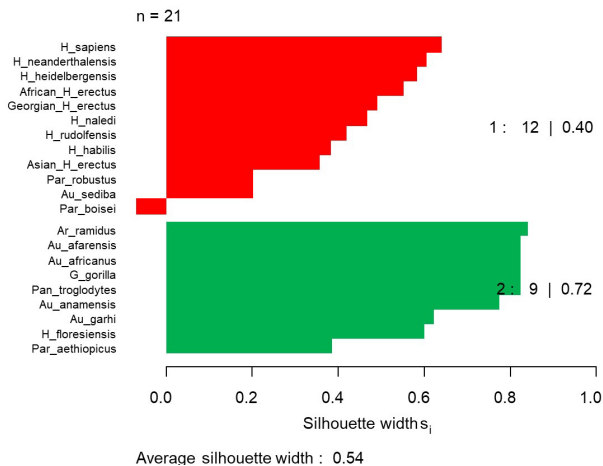
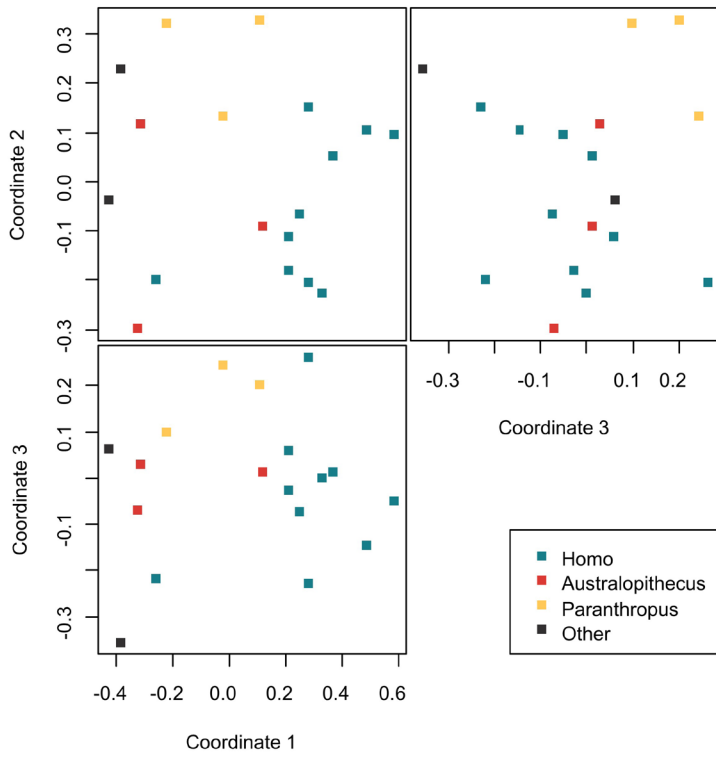
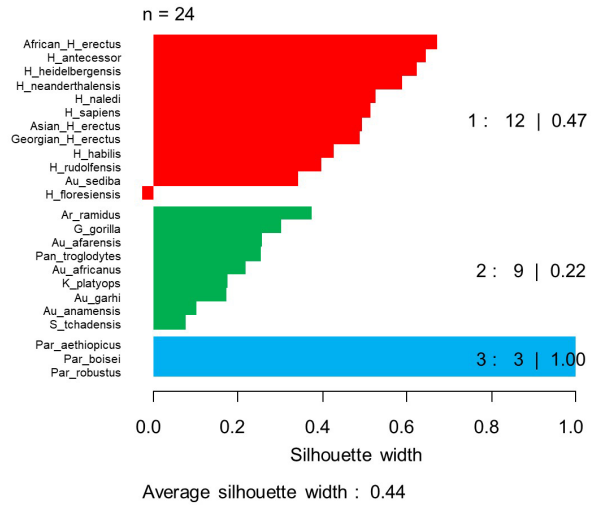
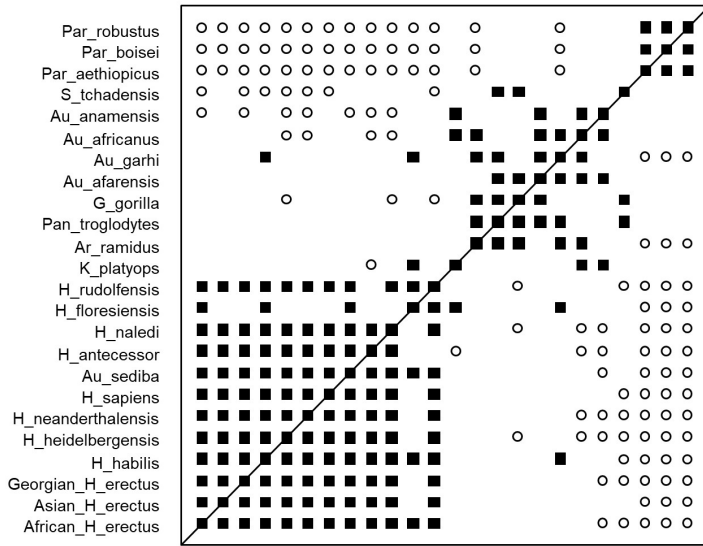


Figure 16. Clustering for Jaccard distances using the FA character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

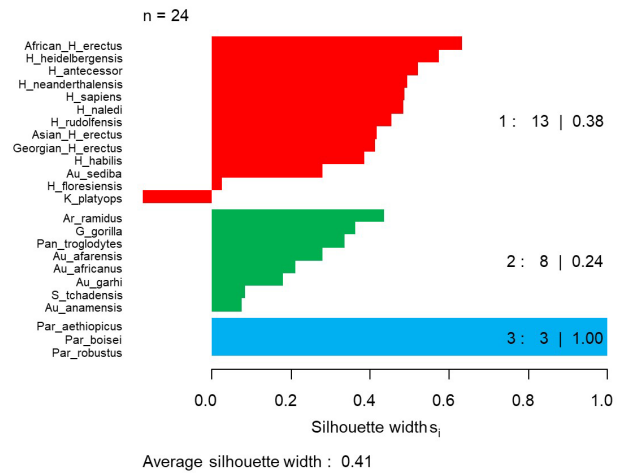
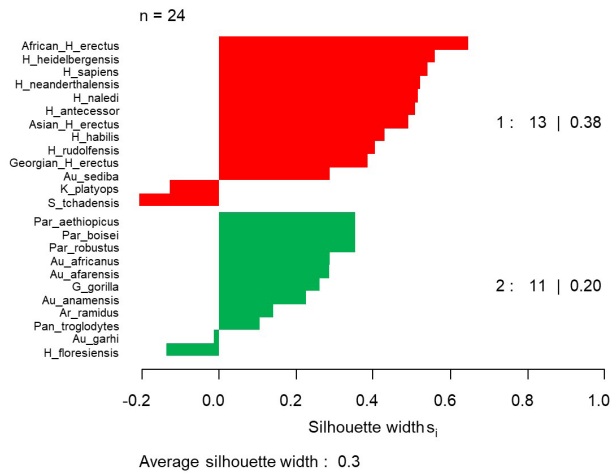


**Figure 17.** Orthogonal views of the 3D MDS results for the Jaccard distances using the FA character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

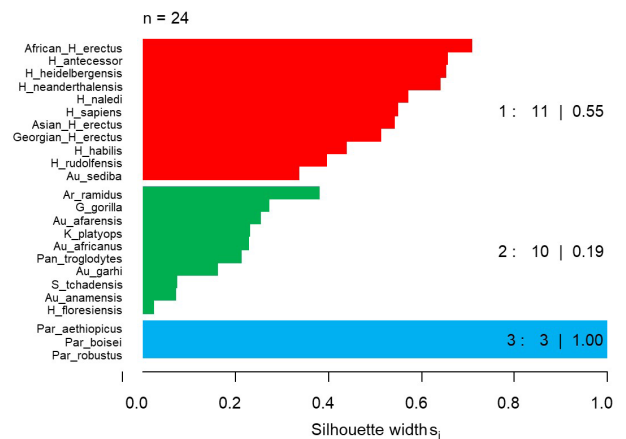
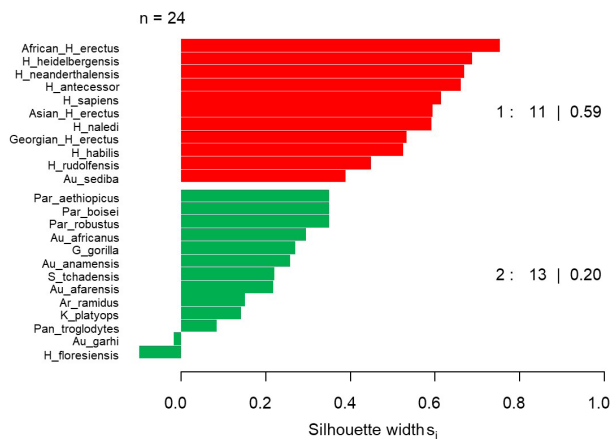
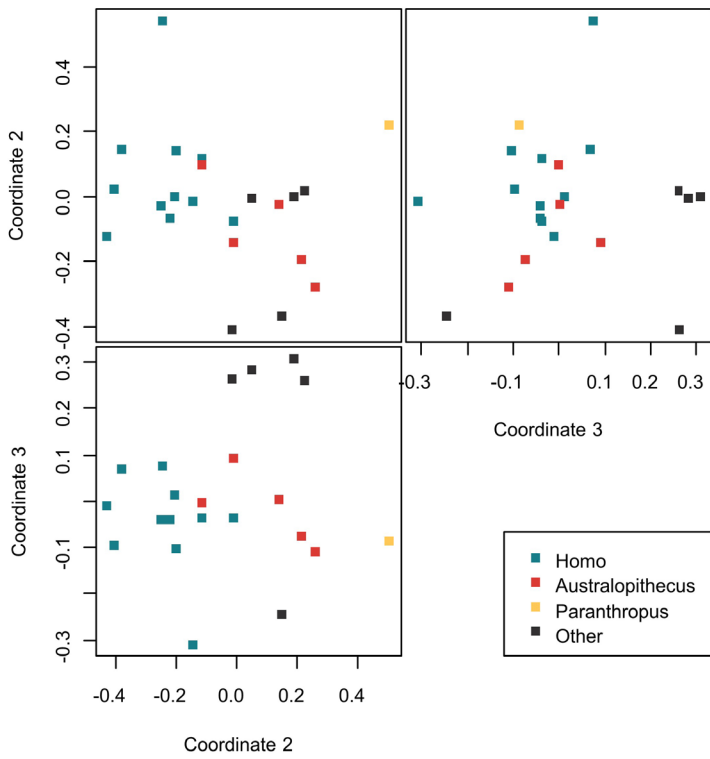
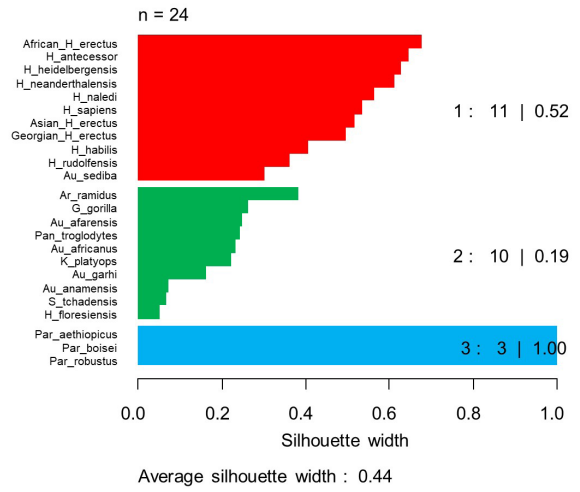
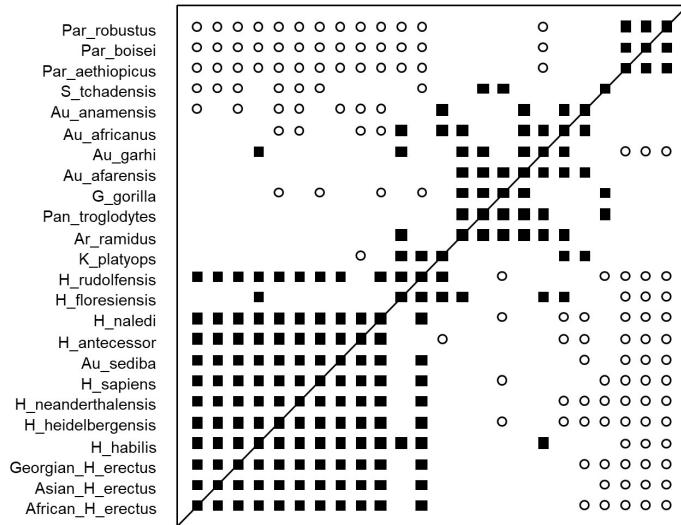


Figure 18. Clustering for simple matching distances using the PO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

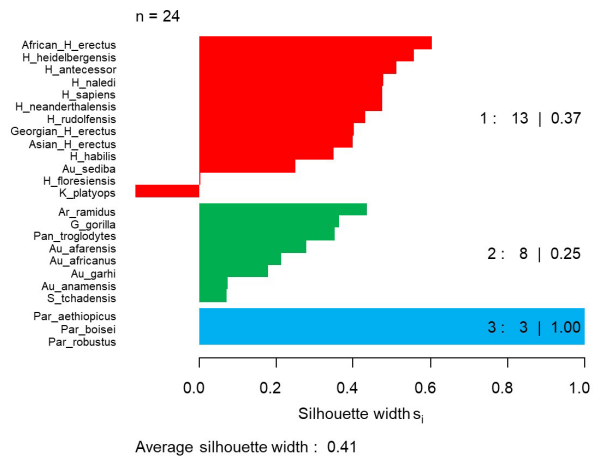
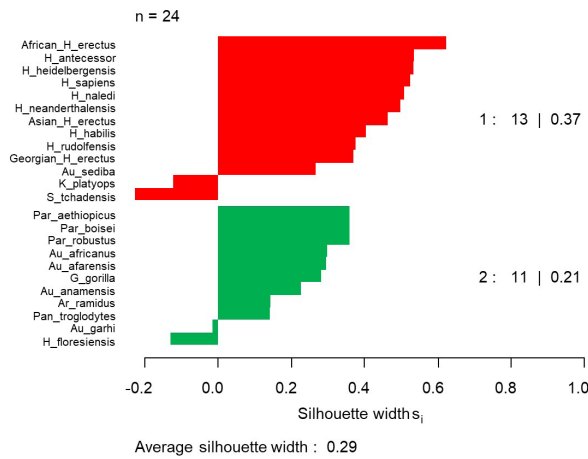


**Figure 19.** Orthogonal views of the 3D MDS results for the simple matching distances using the PO character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

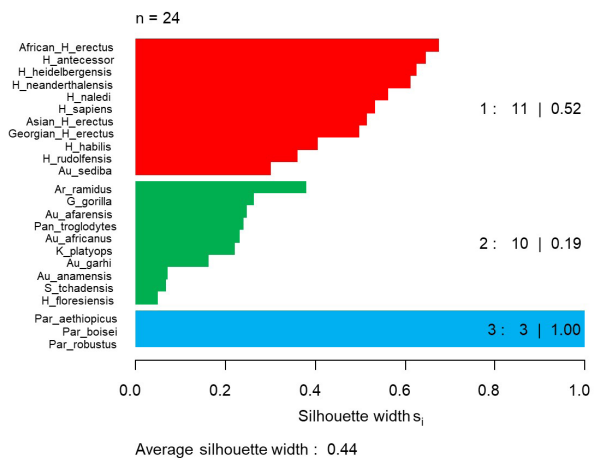
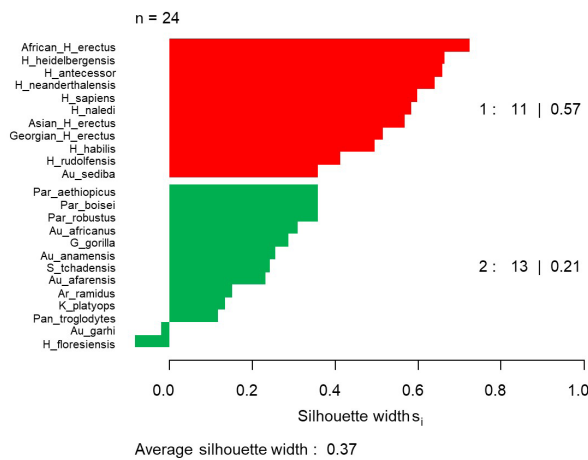
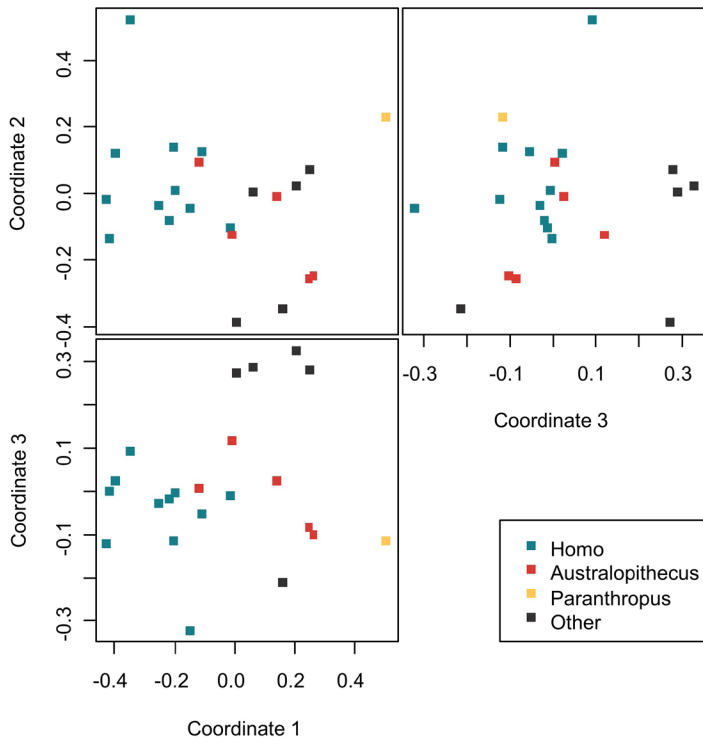
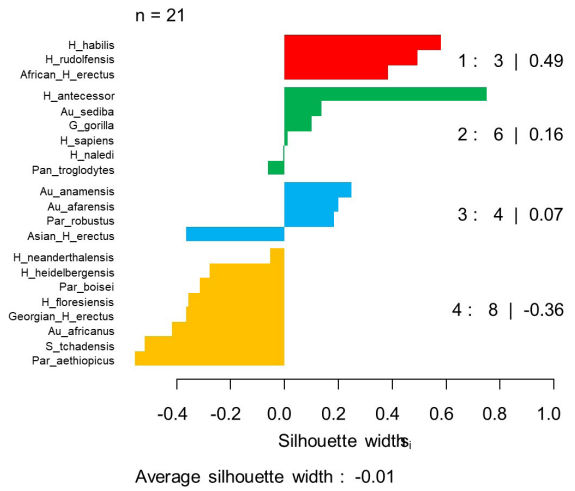
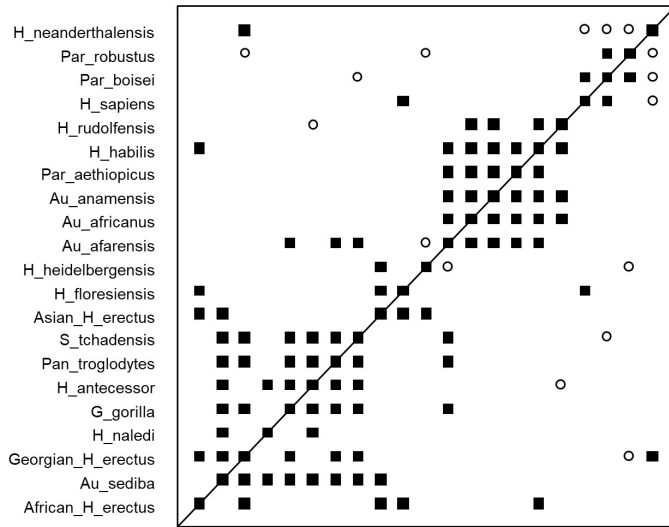


Figure 20. Clustering for Jaccard distances using the PO character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

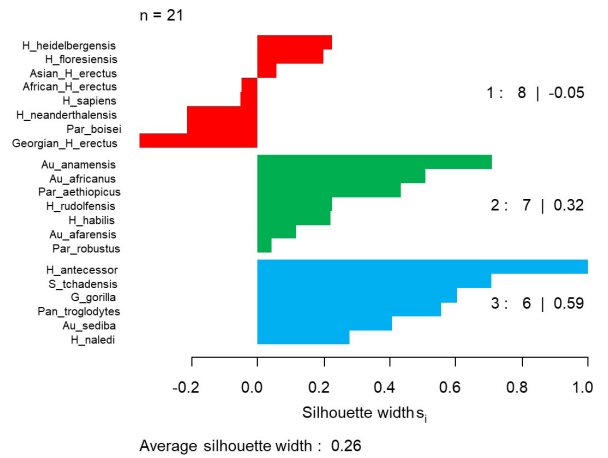
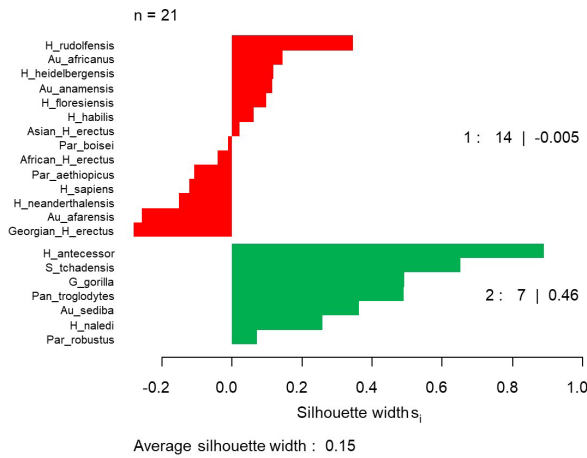


**Figure 21.** Orthogonal views of the 3D MDS results for the Jaccard distances using the PO character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

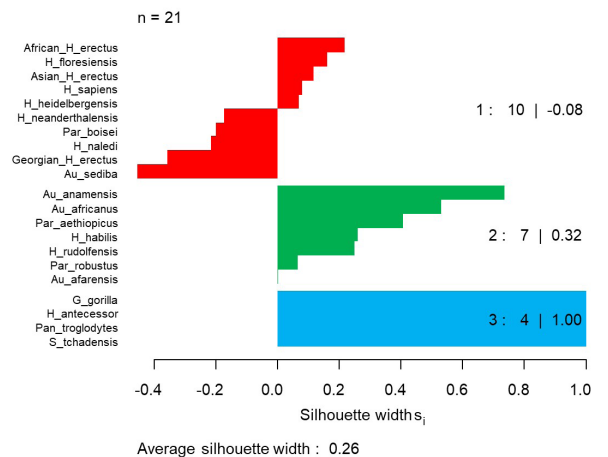
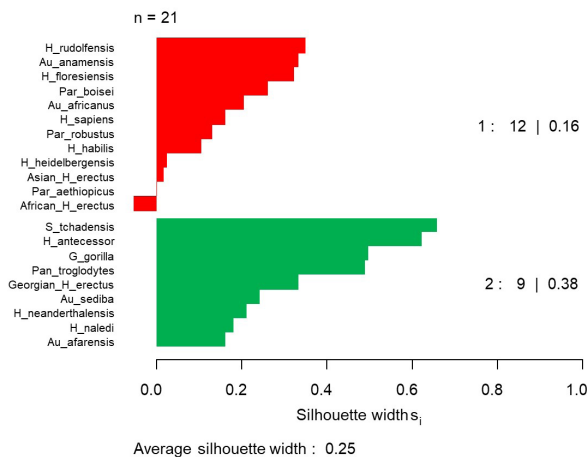
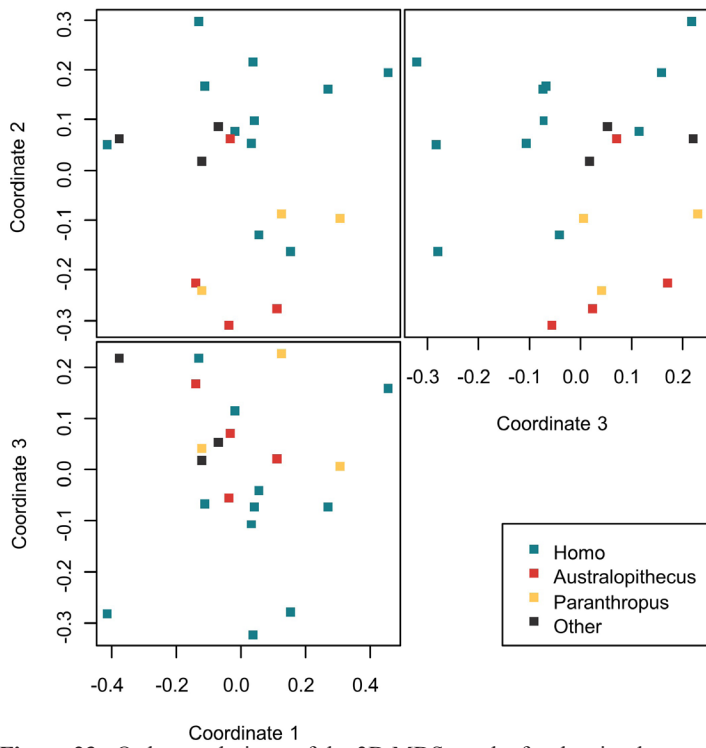
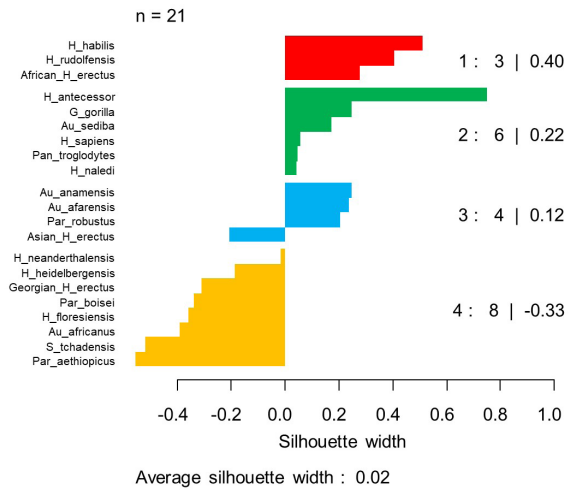
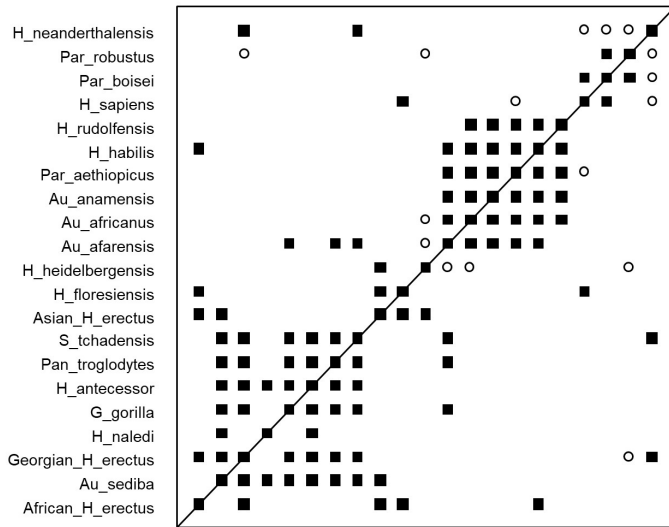


Figure 22. Clustering for simple matching distances using the HN character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.

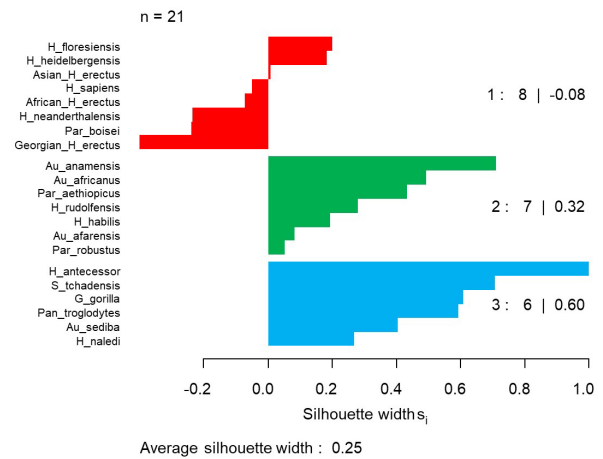
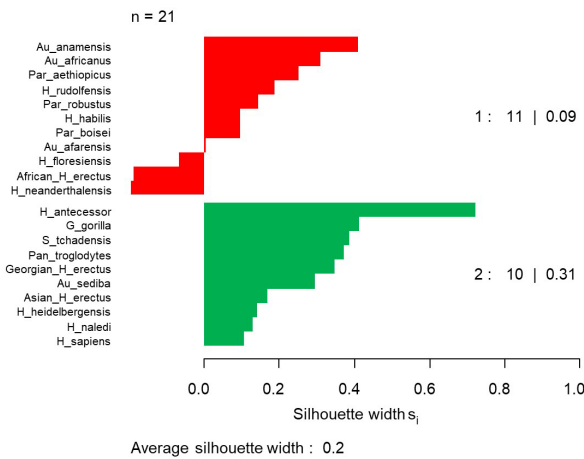


**Figure 23.** Orthogonal views of the 3D MDS results for the simple matching distances using the HN character subset.

Distance Correlation



Medoid Partition



Fuzzy Analysis

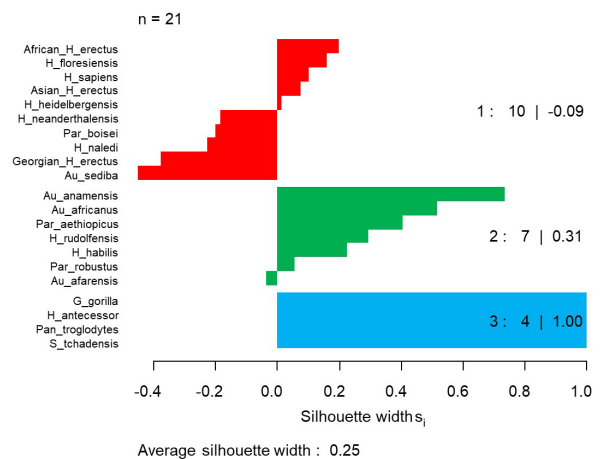
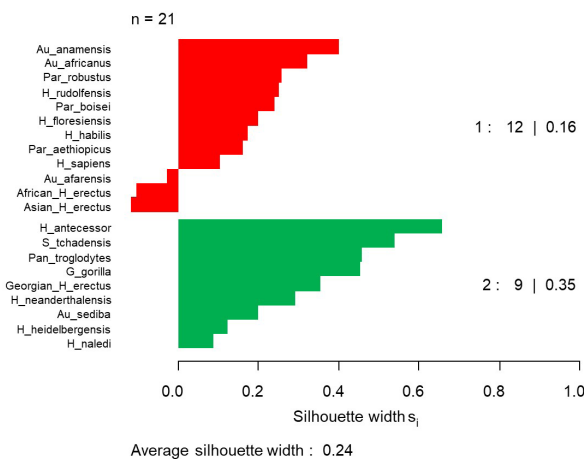
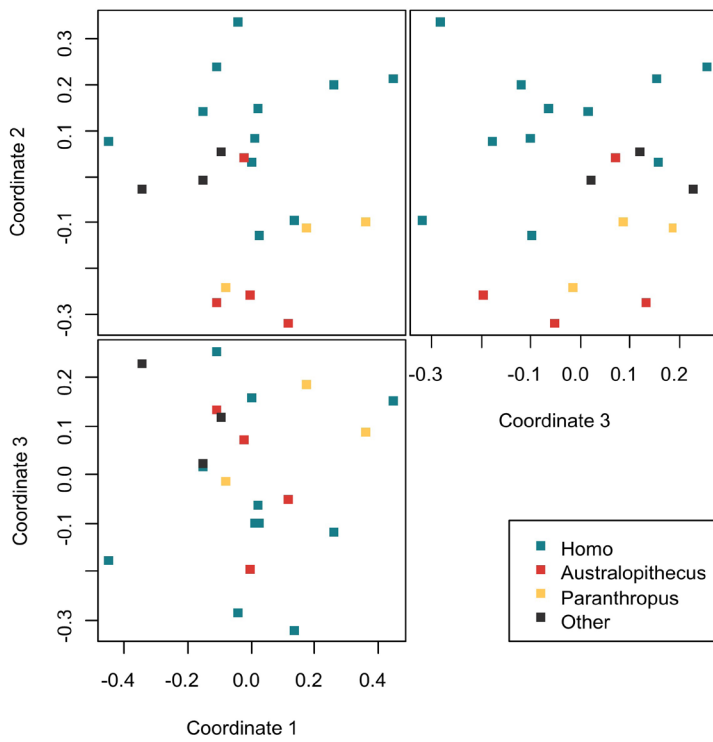
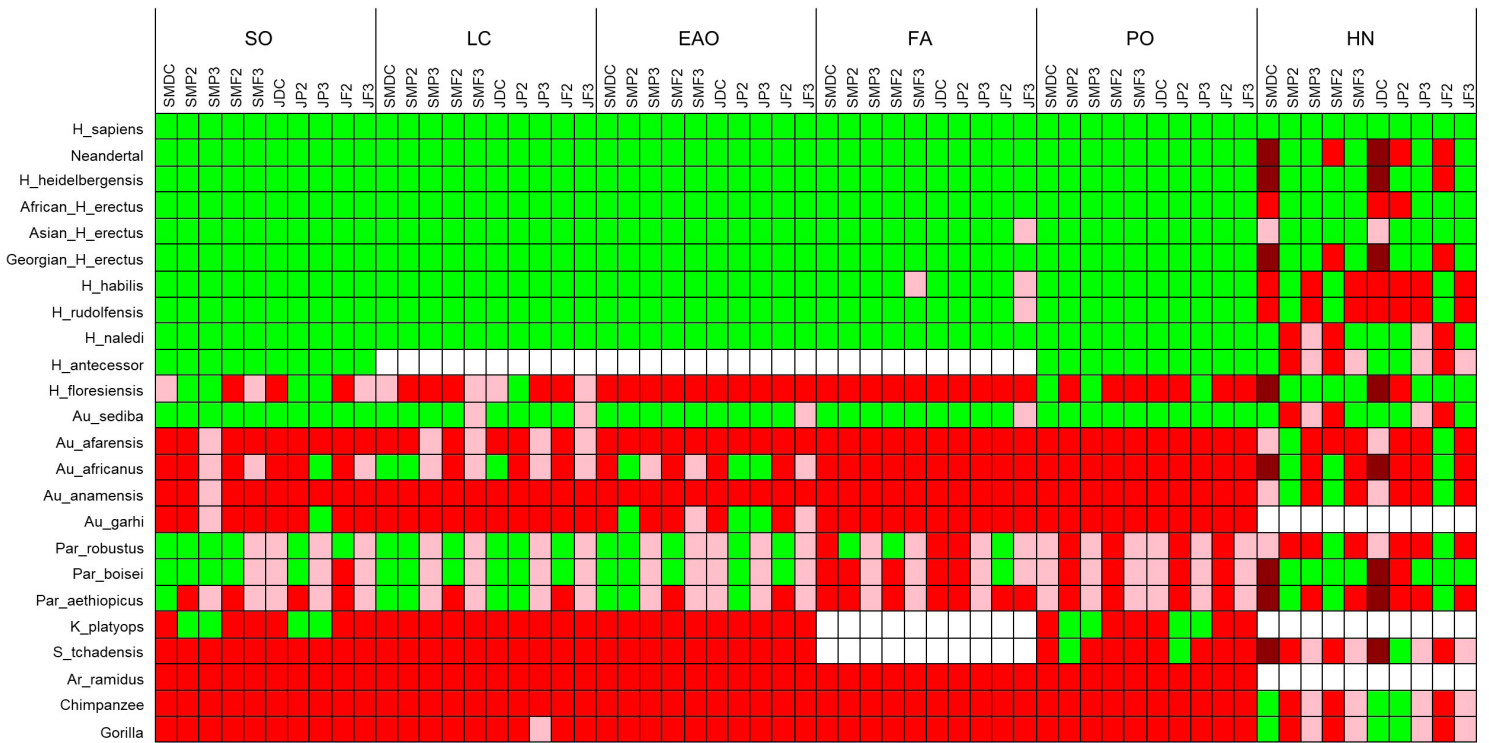


Figure 24. Clustering for Jaccard distances using the HN character subset as indicated. For distance correlation, closed squares indicate significant, positive correlation and open circles indicate significant, negative correlation.



**Figure 25.** Orthogonal views of the 3D MDS results for the Jaccard distances using the HN character subset.



**Figure 26.** Summary of all sixty clustering partitions generated in this study. Each column is a different clustering procedure, indicated by the code at the top of the column. The code prefixes SM and J refer to simple matching and Jaccard distances respectively. DC indicates distance correlation. P2 indicates two-cluster medoid partition, and P3 is three-cluster medoid partition. F2 and F3 indicate fuzzy analysis partitions with two and three clusters respectively. Clusters are indicated by color, with green representing the cluster that contains *Homo sapiens*, and the remaining clusters shown as shades of red. White represents taxa omitted because they do not have any of their characters scored for that character subset.