

Appendix. Detailed Results for Spearman BDC, Medoid Partitioning, and Fuzzy Analysis for Cenozoic Mammalia

This appendix contains the results of Spearman baraminic distance correlation, medoid partitioning, and fuzzy analysis for the 82 Cenozoic mammal groups of Thompson and Wood (2018). For each group, the results are presented in approximately six pages. The first page contains a written summary of the findings together with the baraminological conclusion for that group and the clusterability statistics. The second page reproduces the original appendix page of Thompson and Wood (2018) with Pearson BDC clusters marked. For abbreviations used on the second page, see the appendix of Thompson and Wood (2018). The third page displays the Spearman BDC results on the top of the page and a diagram showing the average silhouette widths for medoid partitioning as a function of the number of groups (k). The third page also contains a summary of the correspondence between the Pearson BDC clusters and the published phylogeny. The fourth page gives color-coded silhouette plots of the Pearson and Spearman BDC clusters, together with a scatter plot of the first two dimensions of multidimensional scaling (MDS). The fifth page gives color-coded silhouette plots and MDS diagrams for three sets of medoid partitioning. Medoid partitions are done for the same number of clusters as the Pearson BDC plus one more or one fewer clusters. The sixth page gives the color-coded silhouette plots and MDS diagrams for three sets of fuzzy analysis that correspond to the number of clusters used in the medoid partition. If fuzzy analysis fails for a particular number of clusters, that diagram is omitted. If fuzzy analysis fails for all possible cluster numbers shown in the medoid partition, the entire page is omitted. A final optional page may present additional diagrams and addenda as explained on that page. The taxa are classified and ordered as in Thompson and Wood (2018). An index of the mammal taxa is provided below; page numbers are indicated at the bottom right of each page.

Anomaluridae	127	Hegetotheriidae	415	Otariidae	193
Anthracotheriidae	361	Hippopotamidae	355	Palaeoryctidae	151
Aplodontidae	109	Hyaenodontidae	163	Palaeotheriidae	433
Astrapotheriidae	421	Hyopsodontidae	337	Palorchestidae	14
Barbourofelinae	181	Hypsiprymnodontidae	26	Peramelidae	8
Brontotheriidae	439	Interatheriidae	403,409	Phascolarctidae	50
Caenolestidae	62	Lemuridae	283	Phyllostomidae	264
Camelidae	367	Leontiniidae	391	Picrodontidae	270
Carodniidae	427	Lepilemuridae	289	Plesiadapidae	277
Carpolestidae	300	Leporidae	103	Procaviidae	475
Castoridae	115	Lophiodontidae	457	Procyonidae	217
Caviidae	133	Loridae	295	Pseudocheiridae	44
Cebidae	312,318	Louisinidae	331	Pseudorhynchocyonidae	92
Cervidae	379	Macropodidae	32,38	Rhinocerotidae	452
Chalicotheriidae	445	Manidae	157	Rhinolophidae	252
Chrysochloridae	223	Mephitidae	211	Sirenia	463
Cricetidae	121	Mormoopidae	258	Soricidae	246
Dasypodidae	74	Moschidae	373	Suidae	349
Desmostylidae	469	Mustelidae	205	Talpidae	235
Didelphidae	56	Myrmecophagidae	86	Thylacoleonidae	20
Didolodontidae	343	Notohippidae	384	Toxodontidae	397
Echimyidae	145	Nyctitheriidae	241	Ursidae	187
Elephantidae	478	Ochotonidae	98		
Erinaceidae	229	Octodontidae	139		
Felidae	169,175	Odobenidae	199		
Glyptodontidae	80	Omomyidae	306		
Gomphotheriidae	481	Ornithorhynchidae	2		
Hathliacynidae	68	Orycteropodidae	324		

Family Ornithorhynchidae

Order Platypoda

Rowe et al. 2008

Pearson BDC

Negative: 4

Positive: 3

Clusters: 3

Clusterability

Hopkins Statistic: 0.809

Dip test: 0.098

Dip test p-value: 0.2243

Spearman BDC

Negative: 2

Positive: 1

Clusters: 5

Spearman correlation causes four significant BDC observations to go away, two positive and two negative. Result indicates significant, positive correlation only between *Ornithorhynchus* and *Obdurodon*. Evidence for monobaramin of all four ornithorhynchids now gone. This substantially weakens the inferred Ornithorhynchid holobaramin.

By BDC clustering procedure, we find three clusters in the Pearson BDC and five clusters in the Spearman BDC. One third of the taxa get put into different clusters in the Spearman BDC vs. the Pearson BDC. The average silhouette width for these partitions is 0.34 for three-cluster Pearson BDC and 0.12 for five-cluster Spearman BDC. Hence the Pearson seems to do better.

The medoid partition results support the clustering of the Pearson BDC at $k=3$ and the clustering of the Spearman BDC at $k=5$. In both cases, cluster membership is exactly the same. The average silhouette value supports the $k=3$ partitioning (0.34 vs. 0.4 for $k=4$ and 0.12 for $k=5$).

The best average silhouette value for medoid partitioning is 0.42 for $k=2$. In this clustering, the mammaliaform *Hadrocodium* forms a singleton group separated from the rest of the taxa, but the extant echidna *Tachyglossus* has a negative silhouette value.

Fuzzy analysis only worked for $k=2$ and partitioned the taxa in yet a different way, with *Tachyglossus* joining *Hadrocodium*. The average silhouette for this partitioning was 0.54 with no taxa having negative silhouette values. This is the only cluster analysis partition that separated ornithorhynchids from the outgroup taxa *Tachyglossus* and *Hadrocodium*.

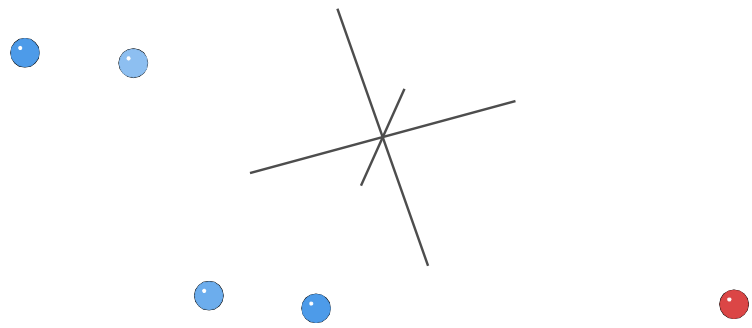
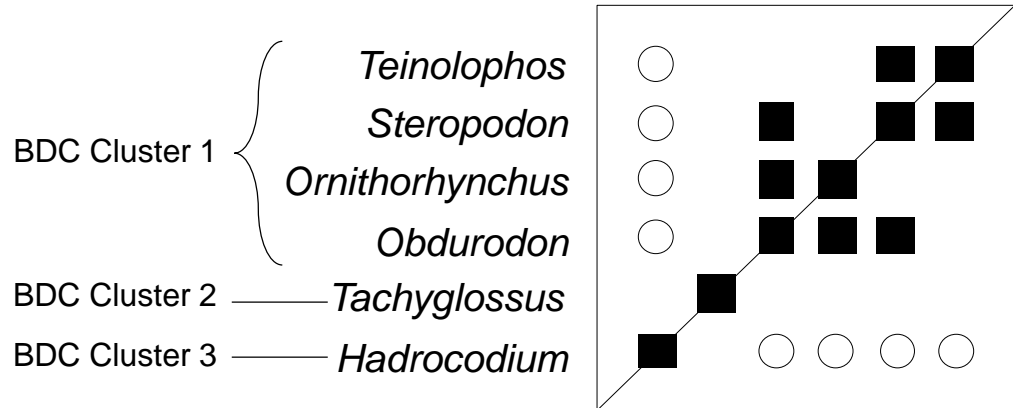
These results reinforce the uncertainty of the original analysis. The Spearman BDC clustering is not consistent with the Pearson BDC clustering, but the Pearson BDC clustering is exactly consistent with the $k=3$ medoid partition. As measured by silhouette value, the best partition by far is the fuzzy analysis at $k=2$, which agrees exactly with the original diagnosis of Ornithorhynchidae as an uncertain holobaramin. These results reinforce both the holobaramin and the uncertainty.

Original conclusion: HB?

Updated conclusion: HB?

Rowe, T., T.H. Rich, P. Vickers-Rich, M. Springer, and M.O. Woodburne. 2008. The oldest platypus and its bearing on divergence timing of the platypus and echidna clades. *Proceedings of the National Academy of Sciences USA* 105:1238-1242.

Characters: Craniodental and postcranial

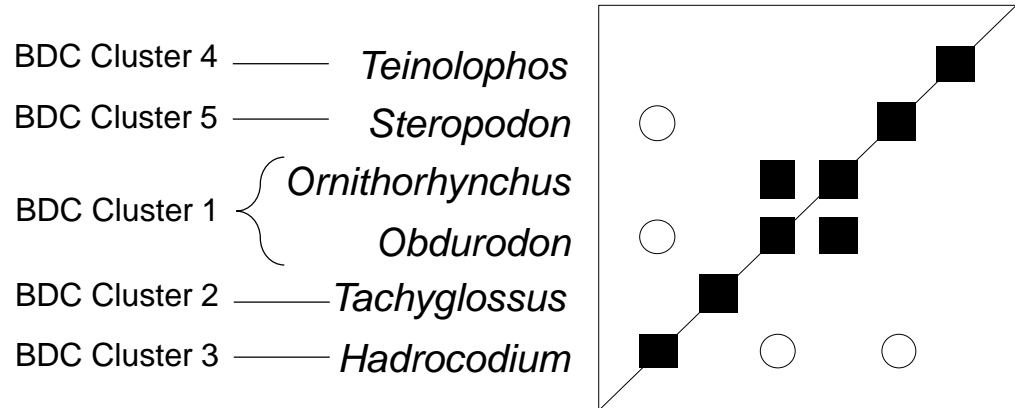


Order Platypoda
Family Ornithorhynchidae

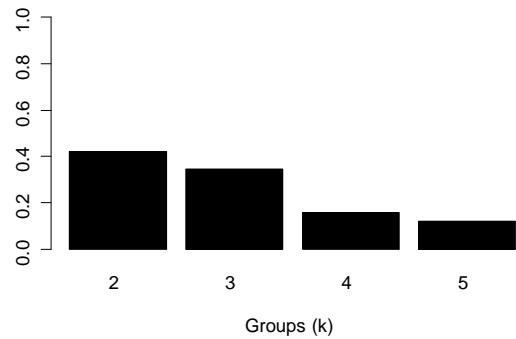
Published taxa	6
Published characters	390
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	6
Characters used for calculations	50
Median bootstrap value	91
F ₉₀	0.53
Stress of 3D MDS	0.15
k _{min}	2
Conclusion	HB?

Notes: Character set has been reduced to just Monotremata from the published dataset. BDC results have poor bootstrap values, and MDS reveals a disperse cloud of taxa. Nevertheless, ornithorhynchids share significant, positive BDC, and are noticeably separated from outgroup taxa in MDS. We may provisionally accept holobaramin Ornithorhynchidae.

Spearman Correlation



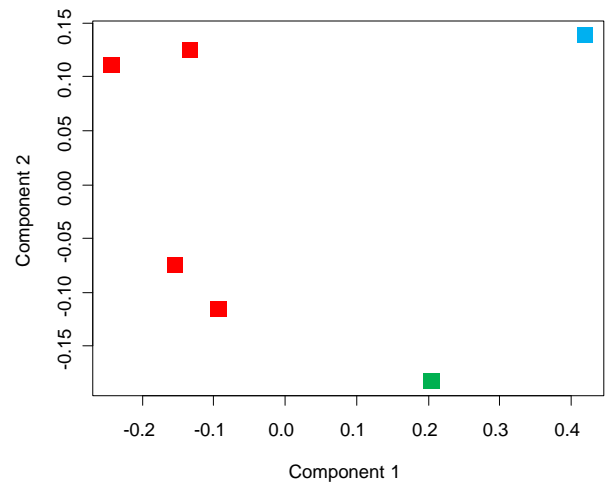
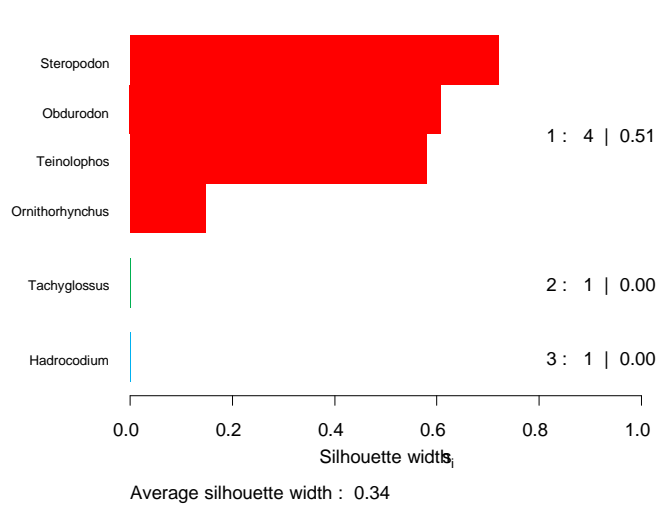
Average Silhouette Widths, Partition Around Medoids



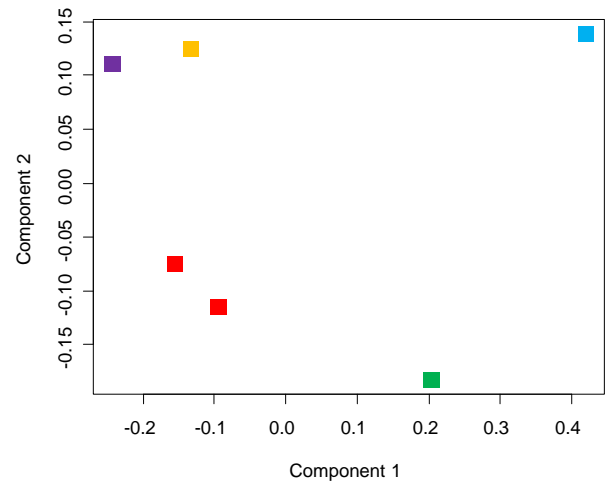
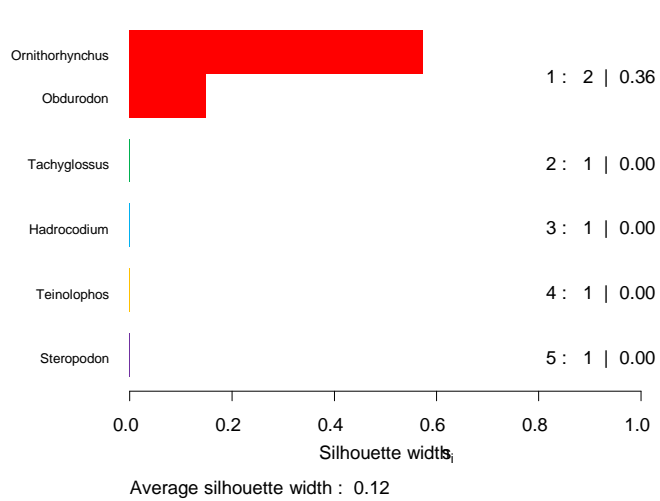
Clade Correspondence: There is one nonsingleton BDC cluster that corresponds to family Ornithorhynchidae, which is monophyletic in the phylogeny shown in Figure 5 of Rowe et al. (2008).

Silhouette plot, BDC partitions

Pearson Correlation

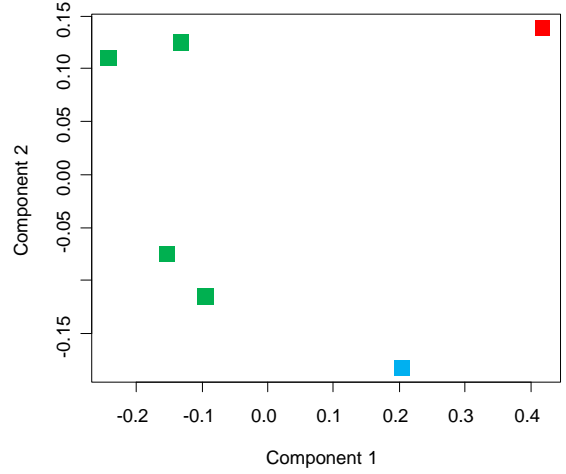
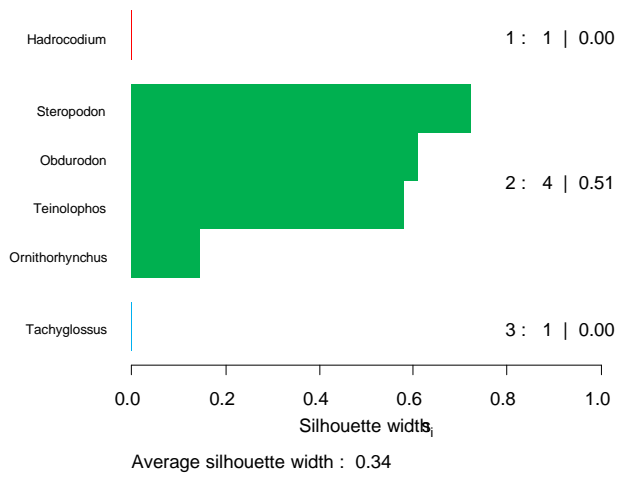


Spearman Correlation

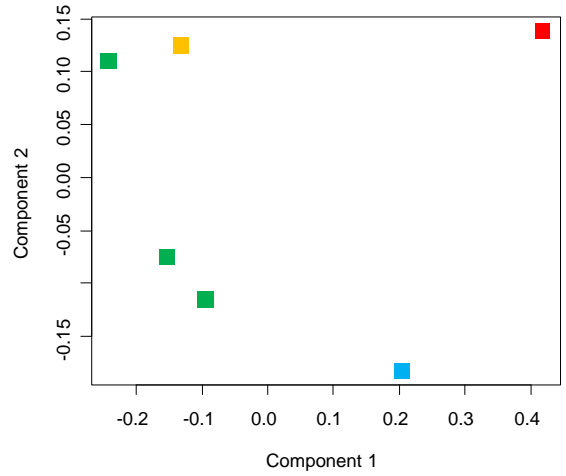
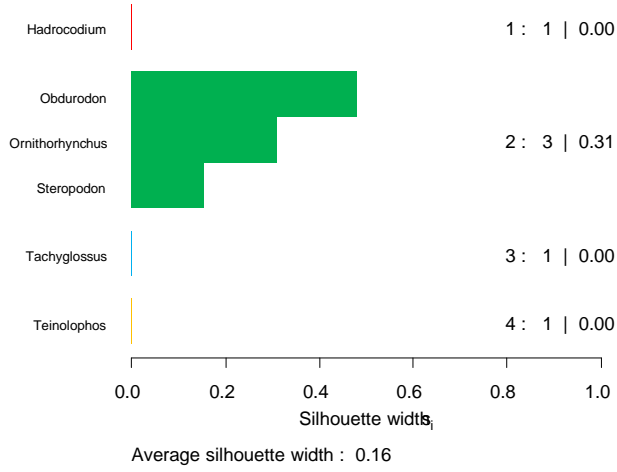


Silhouette plot, Partition Around Medoids

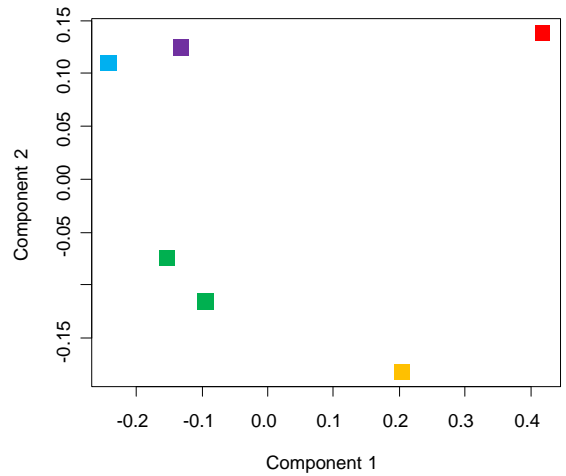
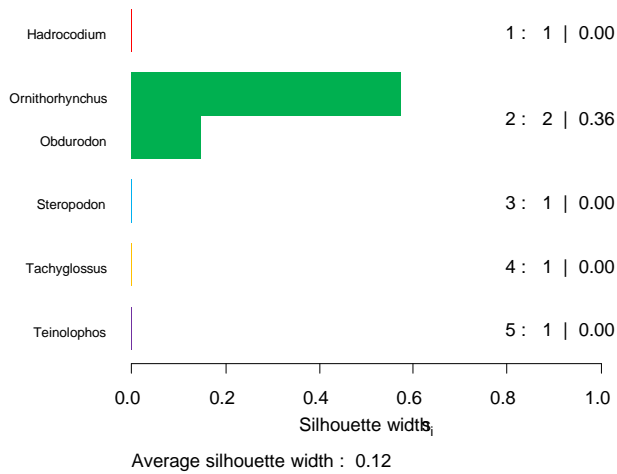
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k=4

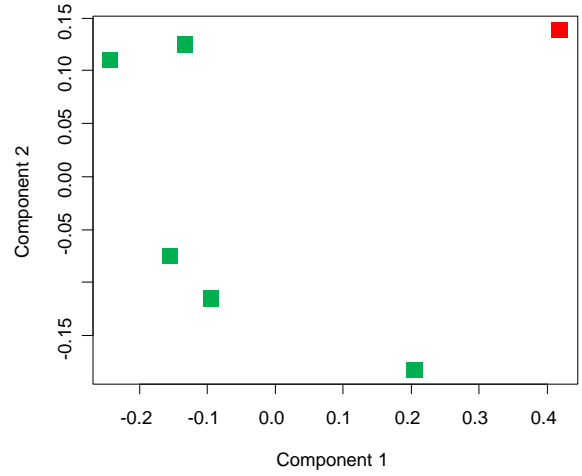
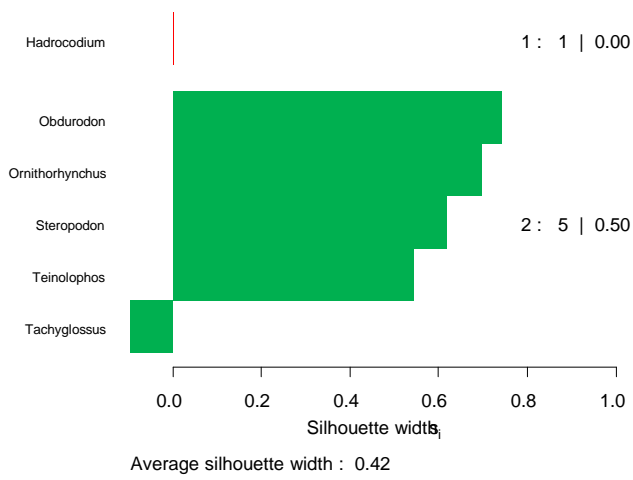


k=5

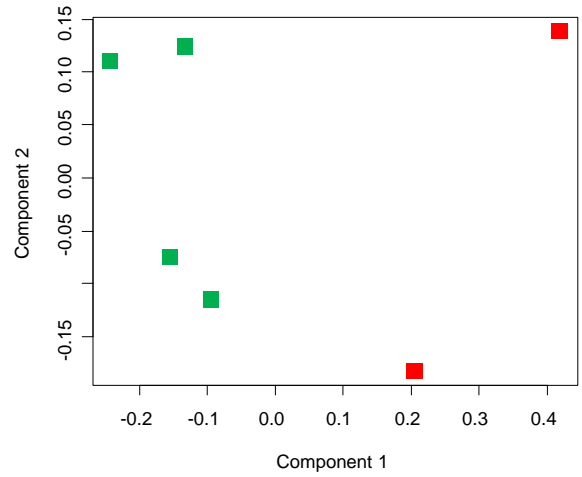
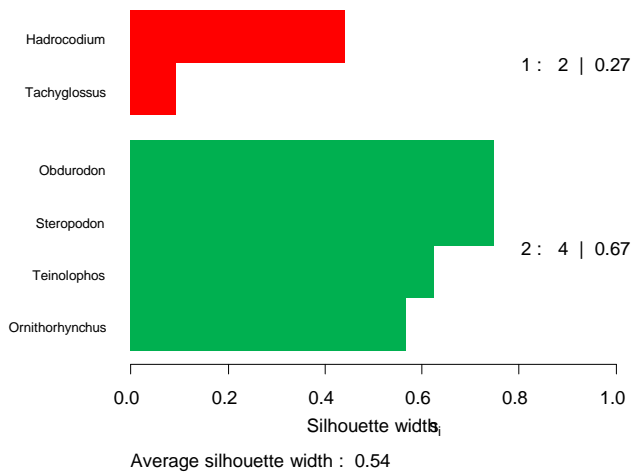


Addendum: Silhouette plots, k=2

Medoid Partition



Fuzzy Analysis



Family Peramelidae

Order Peramelia
Travouillon et al. 2014

Pearson BDC
Negative: 143
Positive: 219
Clusters: 3

Clusterability
Hopkins Statistic: 0.777
Dip test: 0.013
Dip test p-value: 0.764

Spearman BDC
Negative: 114
Positive: 272
Clusters: 2

Spearman BDC reveals more significant, positive BDC and fewer significant, negative BDC. This change results in more observed correlations between the clusters, resulting in the combination of two of the clusters observed in the Pearson BDC.

The average silhouette value for the Pearson BDC clustering is 0.29, with one taxon (*Yarala kida*) having a negative silhouette value. Average silhouette value for the Spearman BDC is the same at 0.29; however, no taxon was observed to have a negative silhouette value. With the combination of three clusters into two, the cluster membership difference is 34.3%.

The medoid partition at k=3 also had an average silhouette of 0.29, but there was one taxon with a negative silhouette value, *Djathia murgonensis*. The cluster membership difference with the Pearson BDC was 5.7%. At k=2, the medoid partition again had an average silhouette of 0.29, but there were two taxa with negative silhouette values (*Y. kida* and *Galadi grandis*). The average silhouette value for medoid partitioning at k=4 was also 0.29.

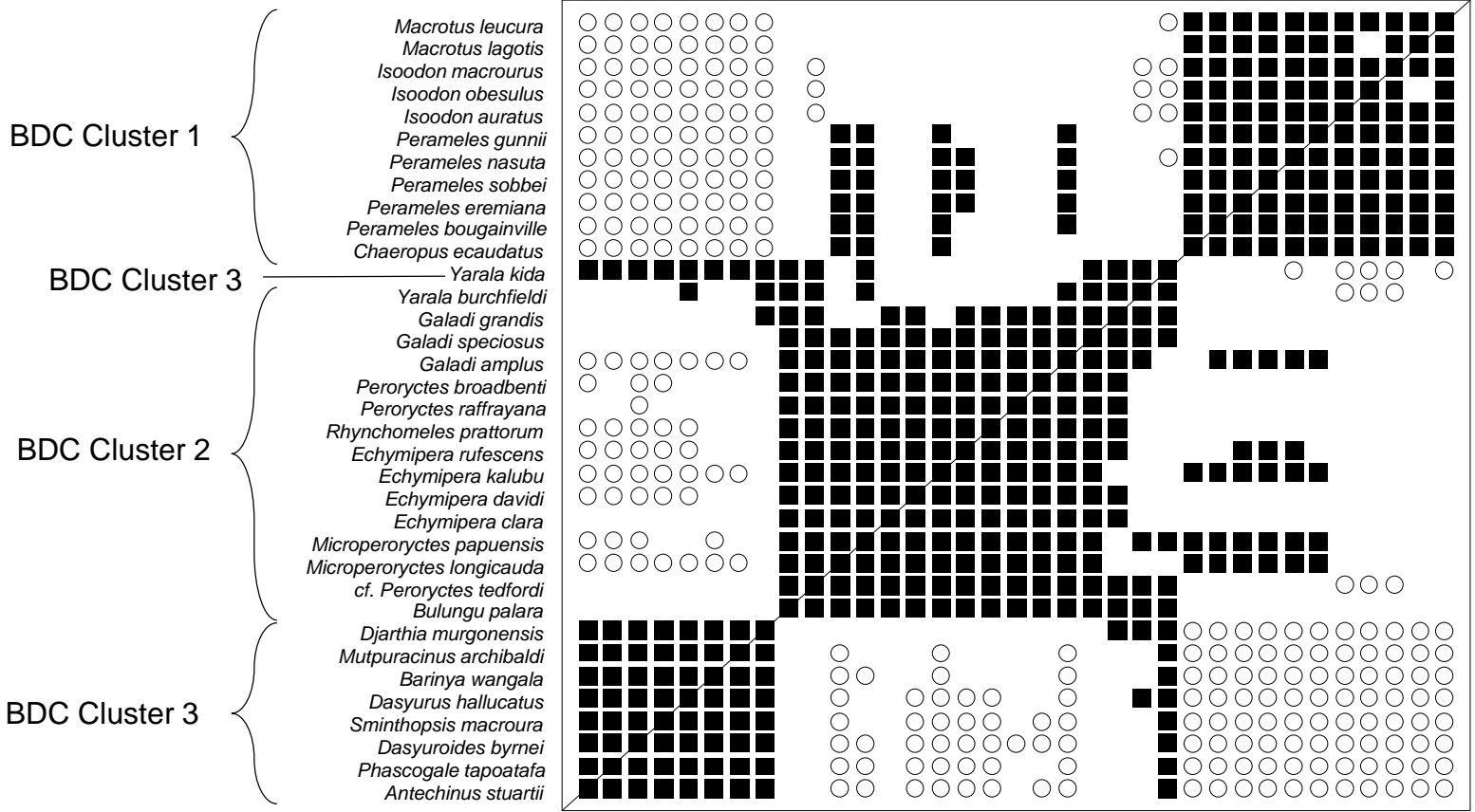
Fuzzy partitioning could only be calculated for k=2, but the average silhouette value of 0.23 was lower than either Pearson BDC or medoid partitioning. In the fuzzy partition, two taxa were observed with negative silhouette values (*Echymipera clara* and *Peroryctes broadbenti*). Fuzzy analysis failed for higher cluster values.

Once again, we find good agreement with the new analyses and the original conclusions. There is no clear medoid partition to be preferred on the basis of average silhouette, and negative silhouette values were routinely observed in every analysis (except for the Spearman BDC partition). Consequently, I conclude that the distances derived from this character set do not support a single clustering partition. These results are consistent with the original conclusion that no holobaramin could be inferred from these characters.

Original conclusion: Inconclusive
Updated conclusion: Inconclusive

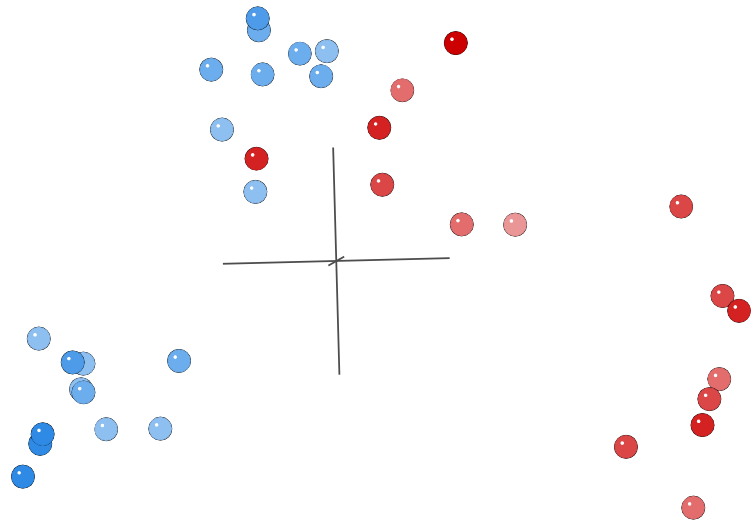
Travouillon, K.J., S.J. Hand, M. Archer, and K.H. Black. 2014. Earliest modern bandicoot and bilby (Marsupialia, Peramelidae, and Thylacomyidae) from the Miocene of the Riversleigh World Heritage Area, Northwestern Queensland, Australia. *Journal of Vertebrate Paleontology* 34:375-382.

Characters: Craniodental



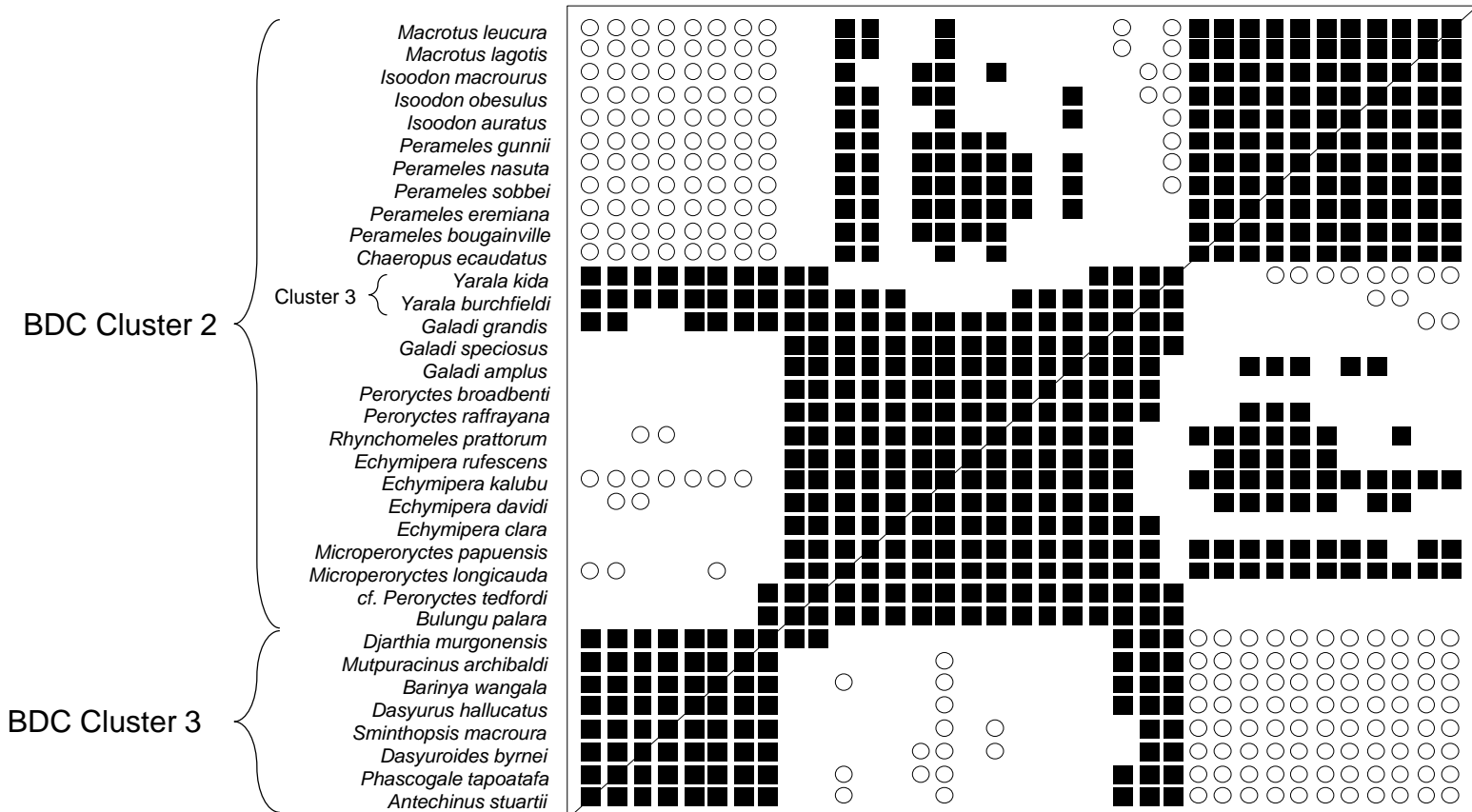
Order Peramelia
Family Peramelidae

Published taxa	42
Published characters	156
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	35
Characters used for calculations	140
Median bootstrap value	91
F ₉₀	0.52
Stress of 3D MDS	0.26
k _{min}	12
Conclusion	Inc

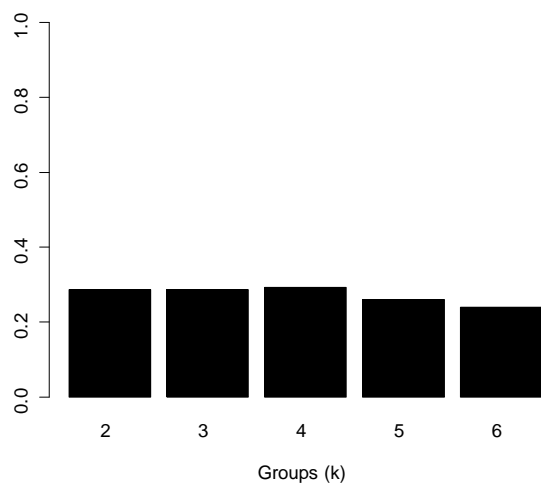


Notes: Three groups appear in both BDC and MDS: one with only peramelids, one with only outgroup taxa, and one with both. BDC and MDS do not support a clear holobaramin, even provisionally.

Spearman Correlation



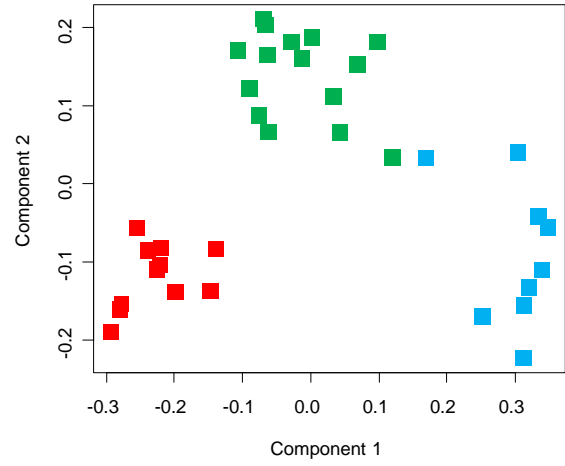
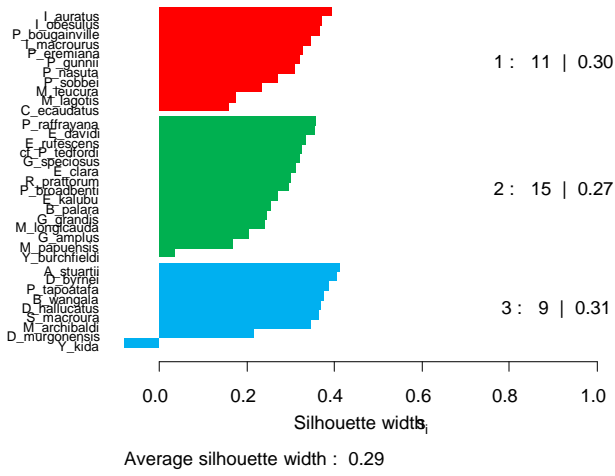
Average Silhouette Widths, Partition Around Medoids



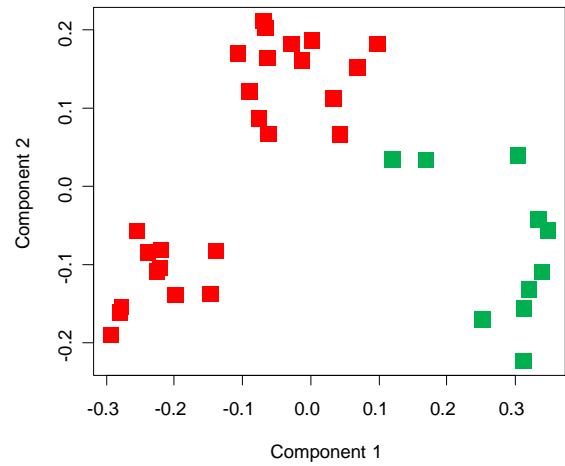
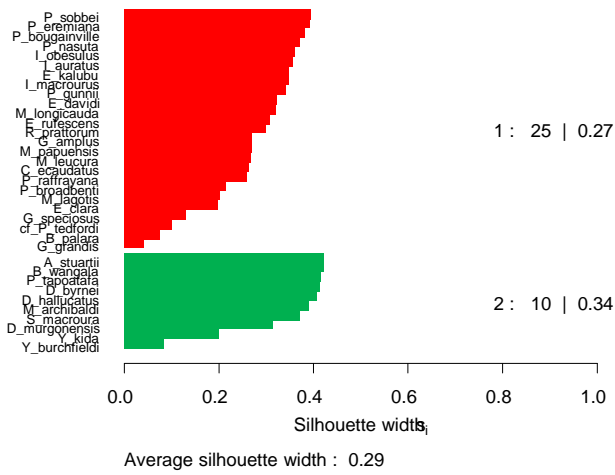
Clade Correspondence: There are three sizeable BDC clusters, none of which are singletons. Cluster 1 corresponds to one of the clades of crown Peramelemorphia in Figure 4A of Travouillon et al. (2014). Cluster 2 corresponds to the remaining peramelemorphans and outgroup of genera *Bulungu*, *Galadi*, and *Yarala*. Cluster 3 contains the remaining outgroup taxa, including *Yarala kida*. In both published phylogenies, the two species of *Yarala* are sister taxa, and for that reason, neither cluster 2 nor 3 corresponds to a clade of the published phylogenies. If *Y. kida* was placed in cluster 2 instead of cluster 3, cluster 3 would correspond to a clade, but cluster 2 would not.

Silhouette plot, BDC partitions

Pearson Correlation

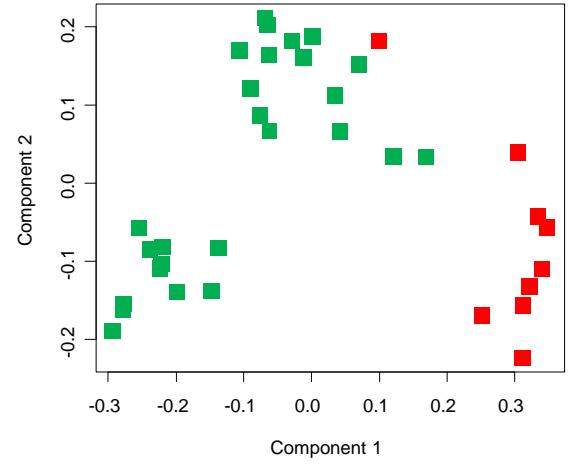
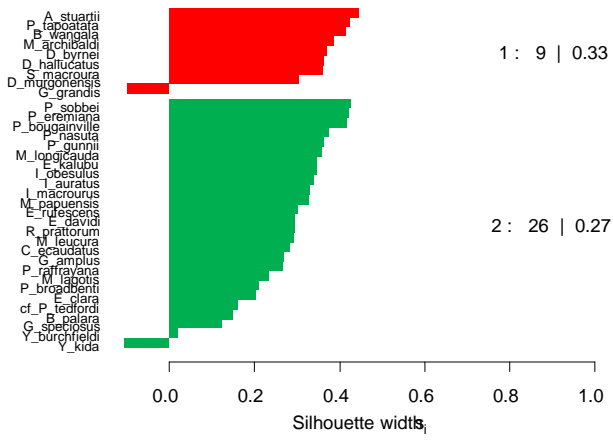


Spearman Correlation

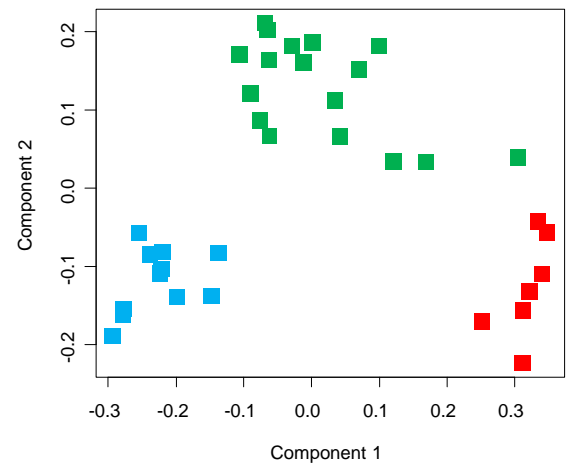
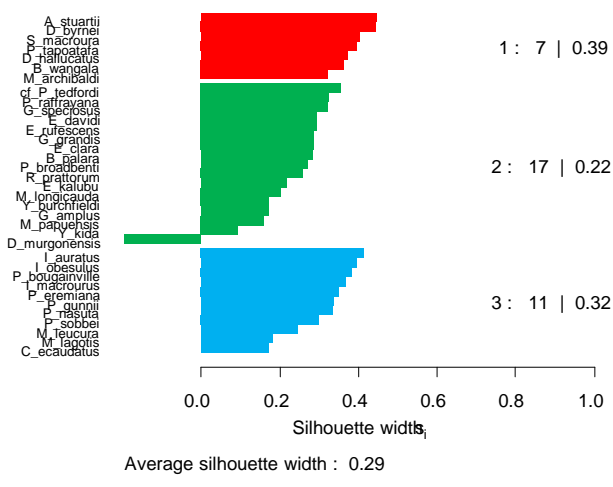


Silhouette plot, Partition Around Medoids

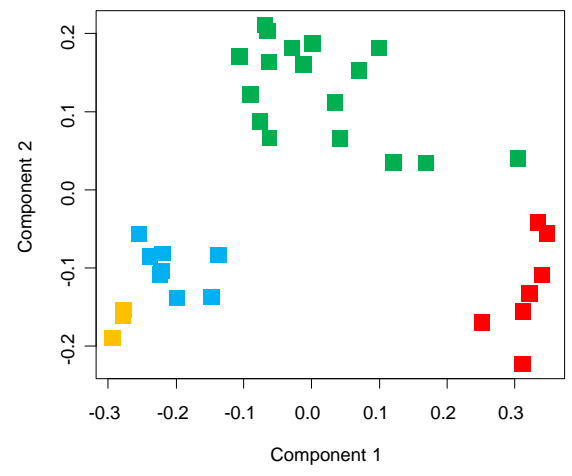
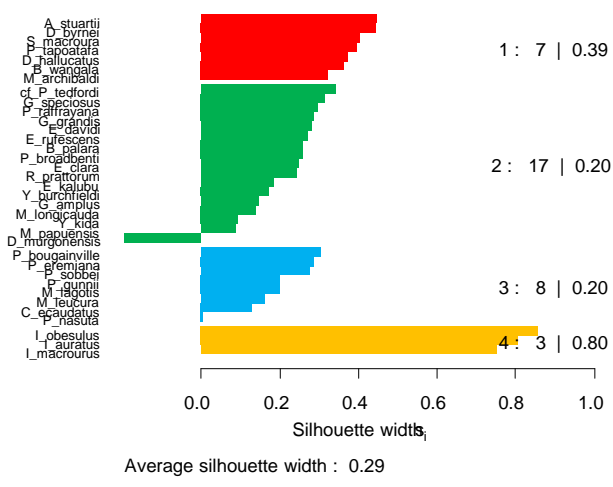
k=2



k=3

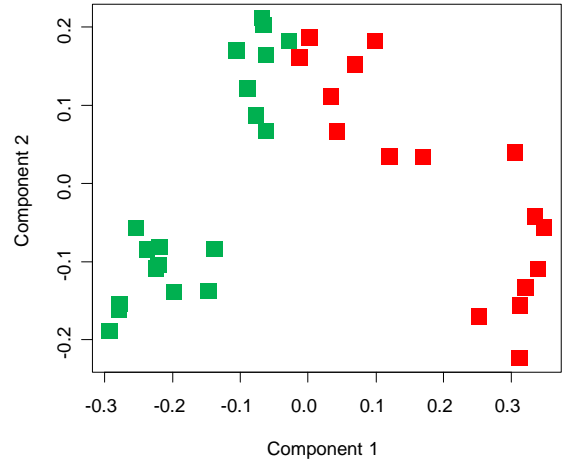
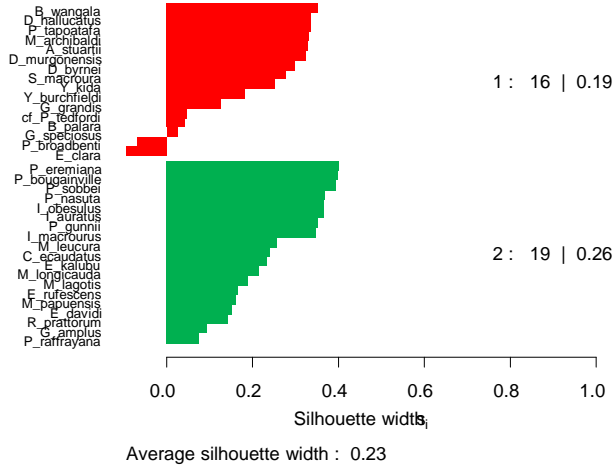


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Palorchestidae

Order Diprotodontia

Black 2008

Pearson BDC

Negative: 117

Positive: 191

Clusters: 3

Clusterability

Hopkins Statistic: 0.893

Dip test: 0.015

Dip test p-value: 0.676

Spearman BDC

Negative: 99

Positive: 201

Clusters: 3

The Spearman BDC did not alter the observed clusters from the Pearson BDC.

The average silhouette widths for the BDC clusters (Spearman and Pearson) were 0.47, and one taxon *Namilamadeta albivenator* had a negative silhouette value. At $k=3$, the average silhouette width for the medoid partition of 0.48 was only slightly higher than the BDC; however, none of the taxa in the medoid partition had negative silhouette widths. The one difference was that *Namilamadeta albivenator* was placed in a different cluster. This change resulted in a cluster membership difference of 3% between the BDC and medoid partition at $k=3$. The medoid partition for $k=2$ yielded an average silhouette width of 0.4, and at $k=4$, the average silhouette width for the medoid partition was 0.45. At $k=4$, there were two taxa with negative silhouette widths. Hence we may conclude that the $k=3$ partition is to be preferred over $k=2$ or $k=4$.

The fuzzy partition at $k=3$ was substantially worse than either the BDC or the medoid partition. The average silhouette width for fuzzy partitioning at $k=3$ was 0.44, and three taxa had negative silhouette widths (*Maokopia ronaldi*, *Hulitherium tomasetti*, and *Alkwertatherium webbi*). Despite these differences, the cluster membership difference at $k=3$ was only 9%. Three taxa were transferred from one cluster to another: *Hulitherium tomasetti*, *Maokopia ronaldi*, and *Namilamadeta albivenator*. The fuzzy partitioning at $k=2$ and $k=4$ resulted in an average silhouette widths of 0.4 and 0.49 respectively.

For these characters, the close match between the Pearson BDC, Spearman BDC, medoid partition, and fuzzy analysis firmly supports the original results. This would seem to confirm the original baraminology conclusion that the Palorchestidae is a holobaramin, for much the same reasons as given in the original comments on this character set.

Original conclusion: HB

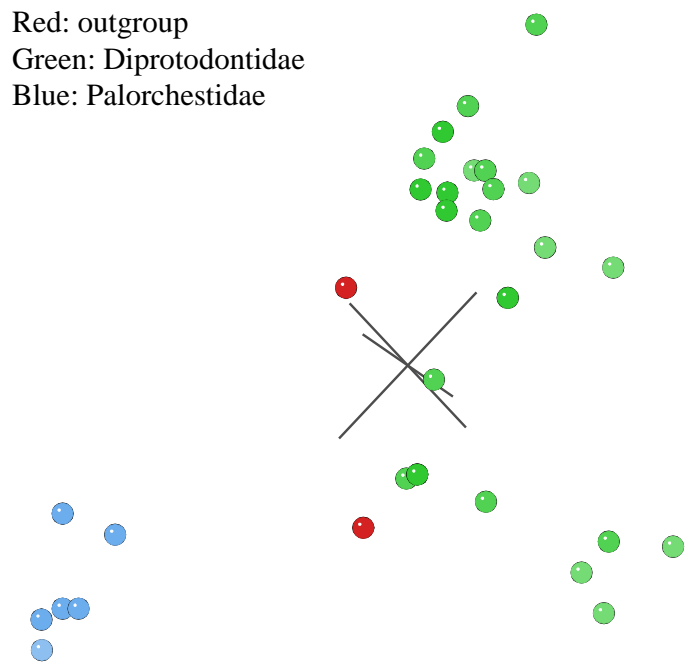
Updated conclusion: HB

Black, K. 2008. Diversity, Phylogeny and biostratigraphy of Diprotodontoids (Marsupialia: Diprotodontidae, Palorchestidae) from the Riversleigh World Heritage Area. Ph.D. Dissertation. Sydney, Australia: University of New South Wales.

Characters: Craniodental



Red: outgroup
Green: Diprotodontidae
Blue: Palorchestidae



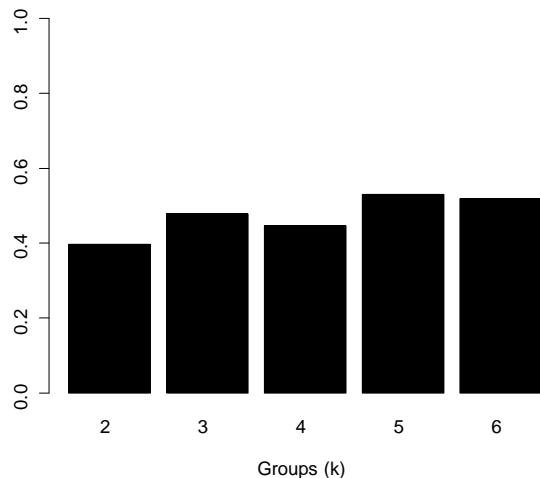
Order Diprotodontia
Family Palorchestidae

Published taxa	35
Published characters	77
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	32
Characters used for calculations	57
Median bootstrap value	79
F ₉₀	0.39
Stress of 3D MDS	0.1
k _{min}	4
Conclusion	HB

Notes: This character set is taken from chapter ten of Black's dissertation. BDC appears to support clear separation of palorchestids from outgroup taxa, except for *Vombatus ursinus*, which is correlated positively with two palorchestids (but with low bootstrap values). The MDS definitely supports an inference of discontinuity between Palorchestidae and the outgroup taxa. Palorchestidae is probably a holobaramin.



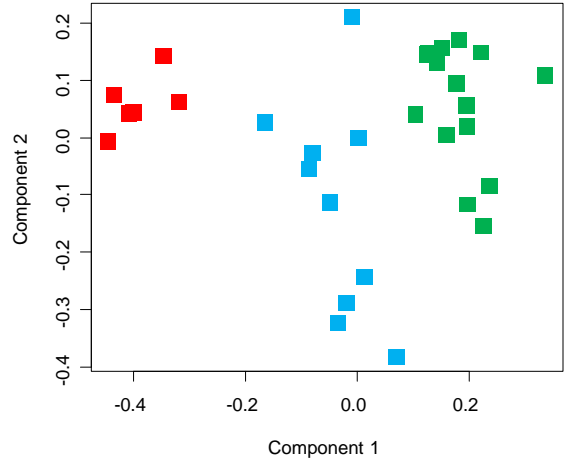
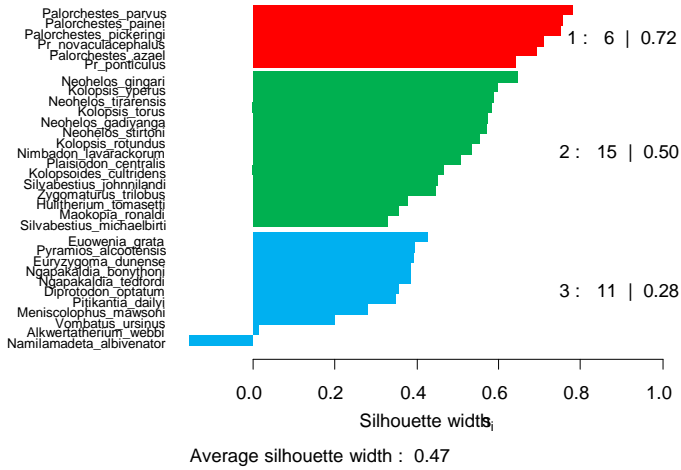
Average Silhouette Widths, Partion Around Medoids



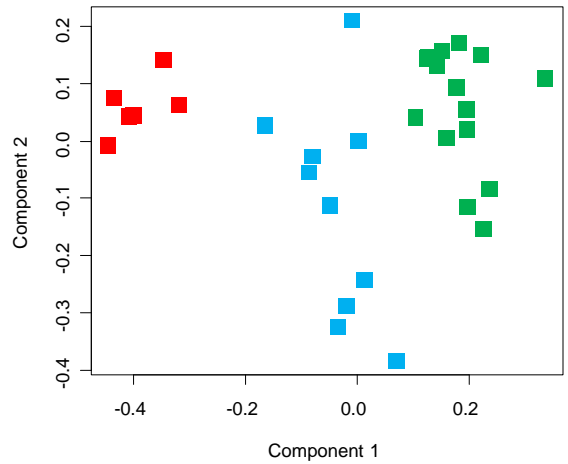
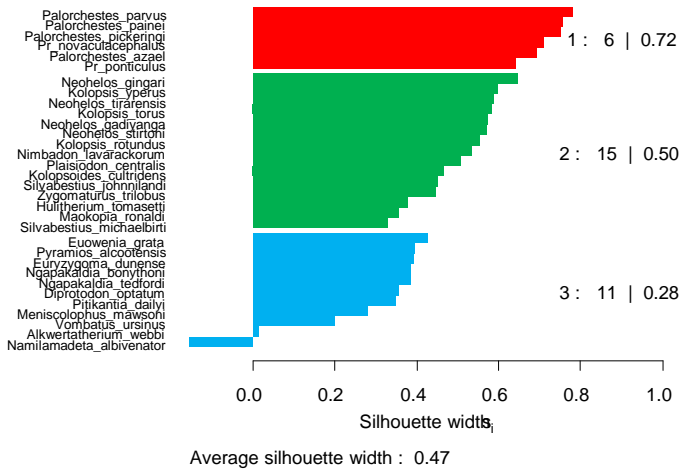
Clade Correspondence: There are three BDC clusters. Cluster 1 corresponds to clade 26 (family Palorchestidae) in figure 10.7 of Black (2008). Cluster 2 corresponds to clade 3 (subfamily Zygomaturinae of family Diprotodontidae) of the same figure, and cluster 3 contains all of clade 18 (subfamily Diprotodontinae) and the outgroup taxa *Vombatus* and *Namilamadeta* and is not monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

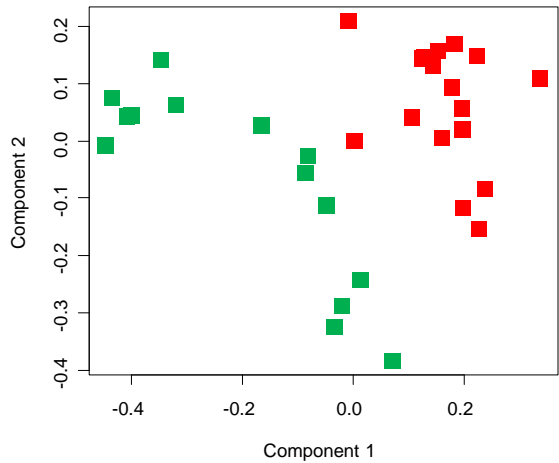
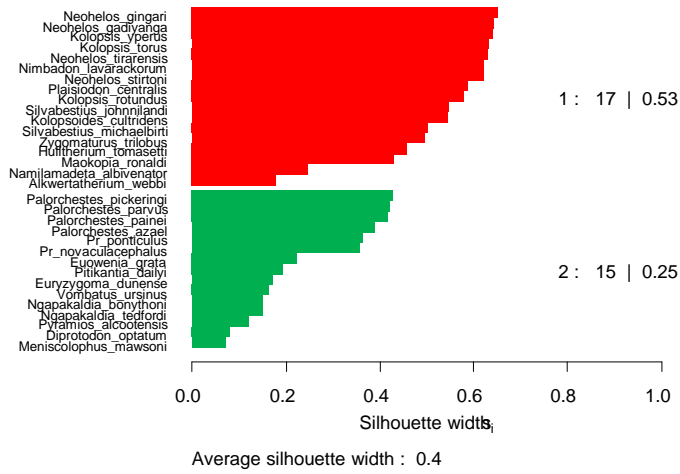


Spearman Correlation

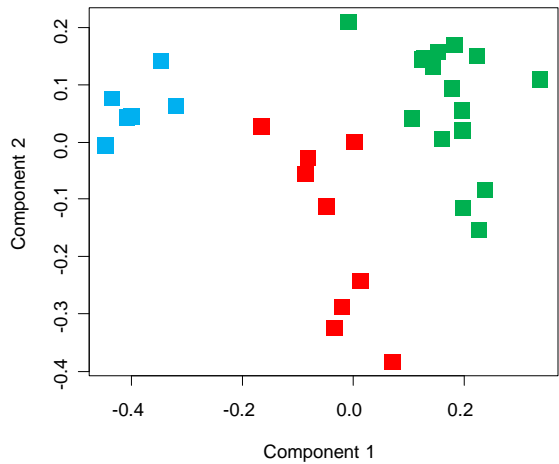
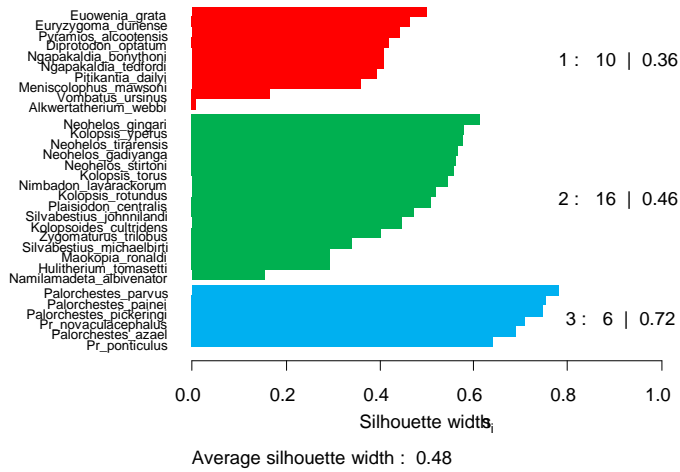


Silhouette plot, Partition Around Medoids

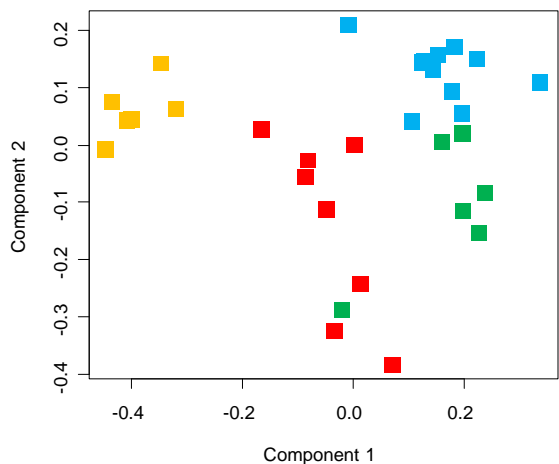
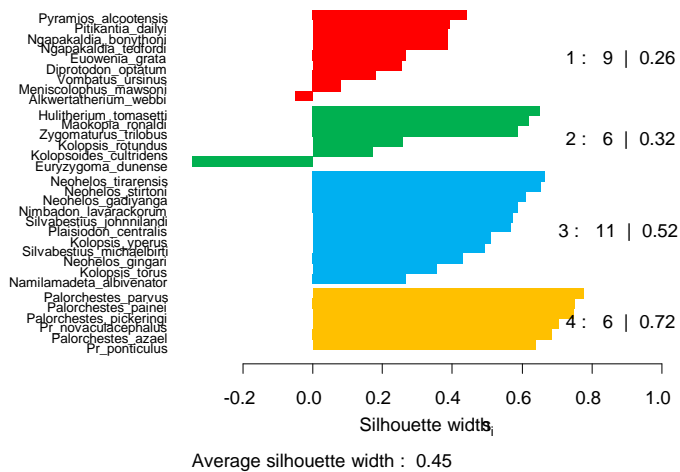
k=2



k=3

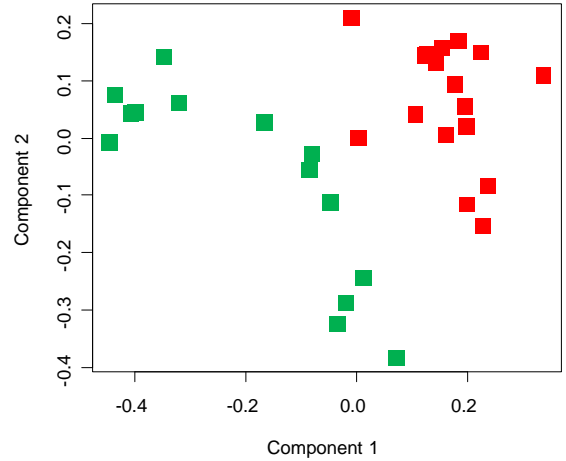
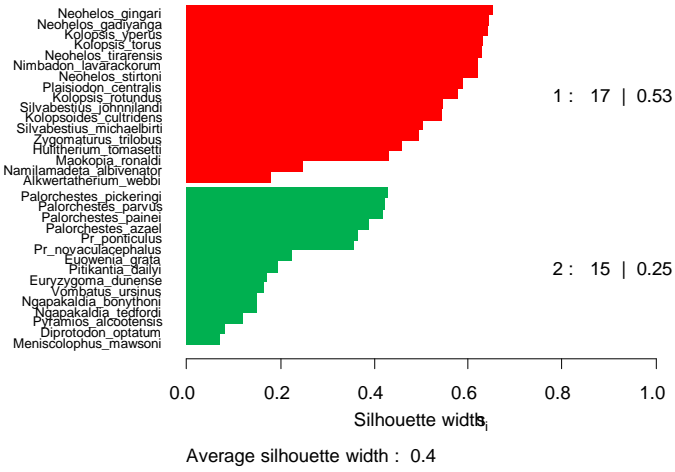


k=4

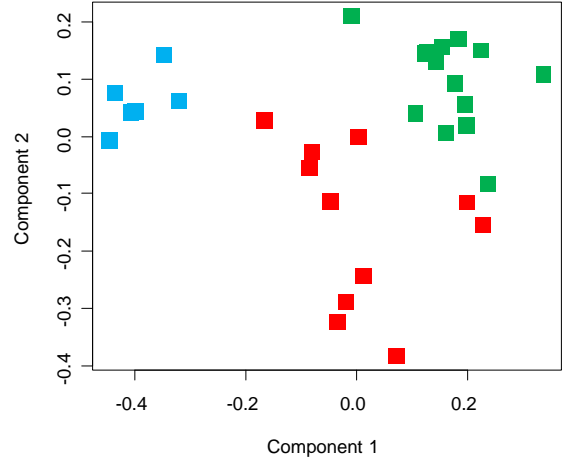
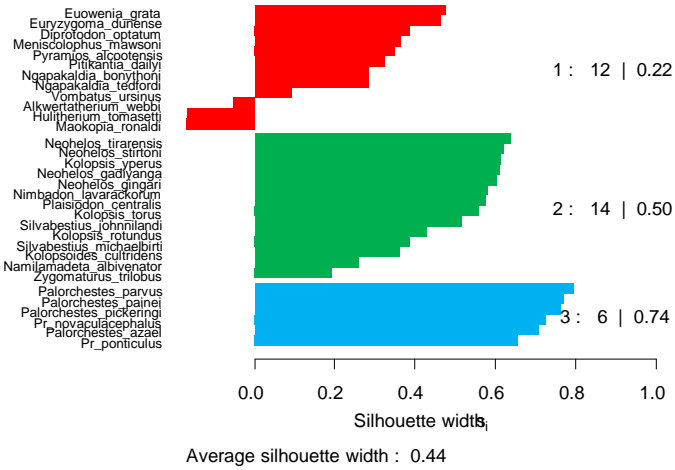


Silhouette plot, Fuzzy Analysis

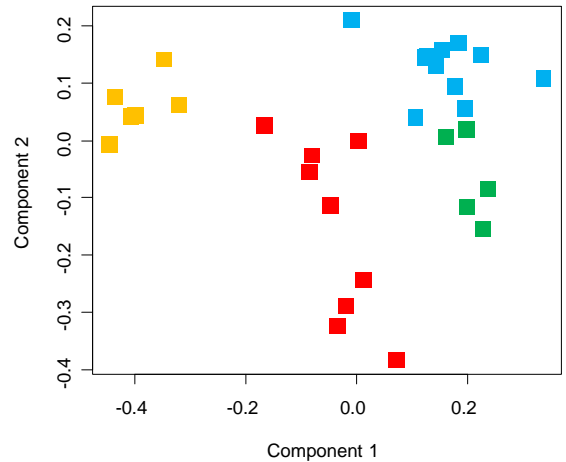
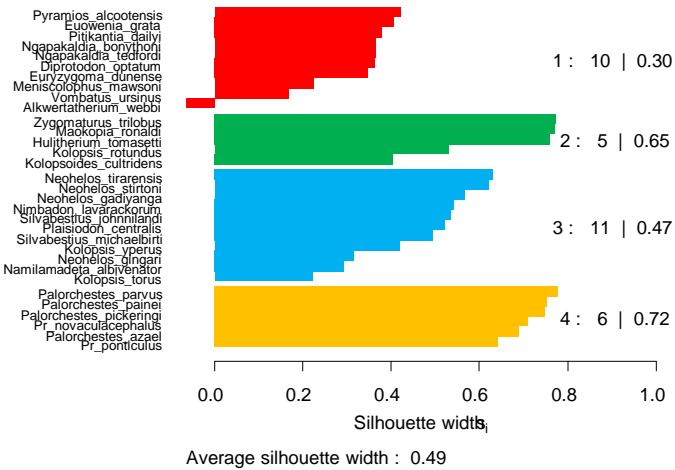
k=2



k=3



k=4



Family Thylacoleonidae

Order Diprotodontia

Gillespie 2007

Pearson BDC

Negative: 22

Positive: 17

Clusters: 4

Clusterability

Hopkins Statistic: 0.762

Dip test: 0.031

Dip test p-value: 0.956

Spearman BDC

Negative: 22

Positive: 21

Clusters: 3

Spearman BDC added four instances of significant, positive BDC to the original Pearson BDC results. The new instances of positive BDC collapsed two clusters into one, and connected genus *Thylacoleo* to genus *Wakaleo*. The average silhouette widths for the Pearson and Spearman BDC clusters were 0.48 and 0.27, respectively. The lower value for the Spearman BDC is a result of combining genera which appear to be at a notable distance in the MDS.

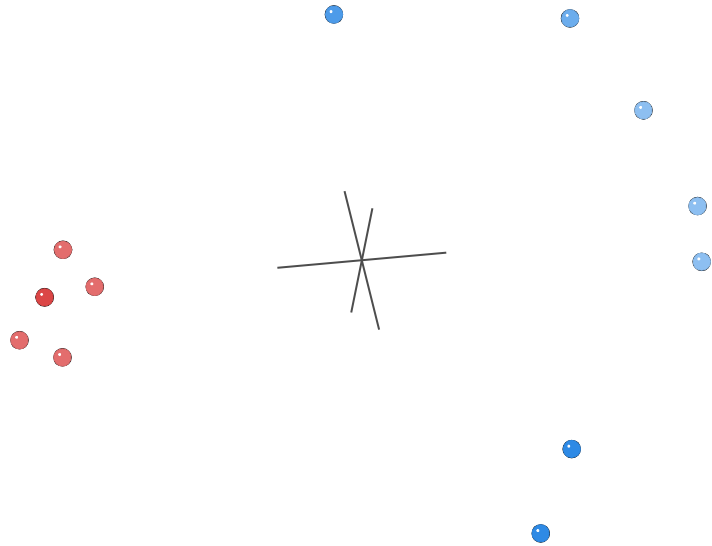
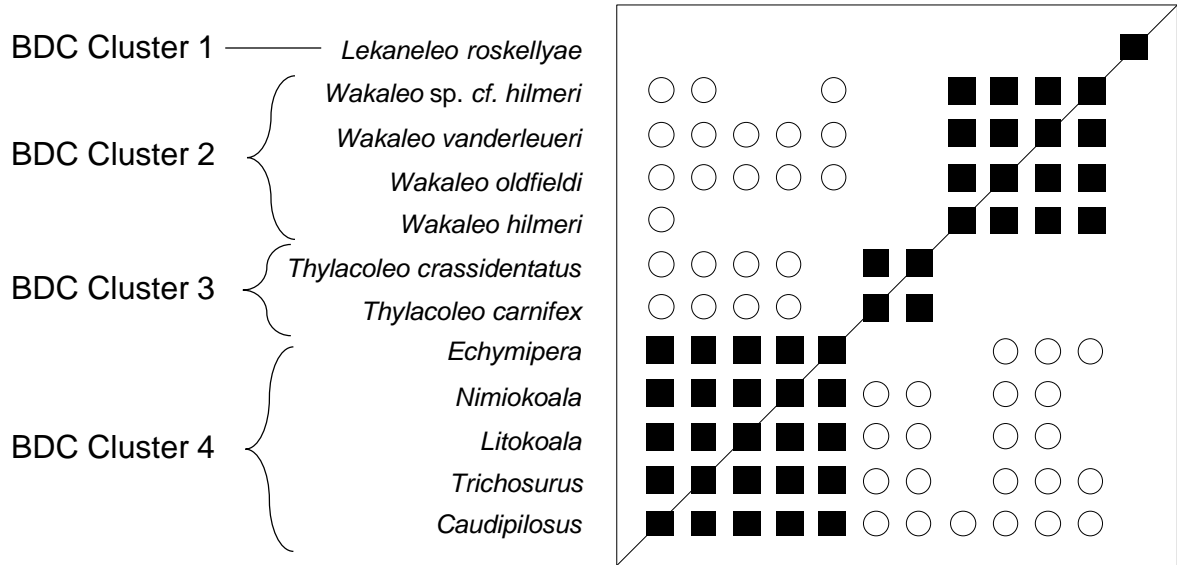
The medoid partition at k=4 agrees exactly with the Pearson clustering, but the medoid partition at k=3 does not agree with the Spearman clustering. At k=3, the medoid partition produces the highest average silhouette width of 0.55 and puts the Miocene *Lekaneleo roskellyae* in a cluster with the outgroup taxa. In doing so, however, *L. roskellyae* exhibits a negative silhouette value.

Fuzzy analysis at k=4 also agrees exactly with the Pearson clustering, but the k=3 fuzzy clustering once again does not agree with the Spearman clustering. As in the medoid partitioning, the average silhouette width at k=3 for the fuzzy partition is 0.56, but no taxa have negative silhouette widths. At k=3, the fuzzy partition places *L. roskellyae* in a cluster with the species of genus *Wakaleo*.

In the original results, a lack of significant, positive BDC in the ingroup taxa was attributed to an arc-shaped distribution as revealed in the 3D MDS. The provisional holobaraminic status concluded for the ingroup was based on that and on the frequent occurrence of significant, negative BDC between the ingroup and outgroup taxa. Here the Spearman BDC still exhibits frequent significant, negative correlation between the ingroup and outgroup, but there is little consistency on which taxa belong together when examined with fuzzy analysis and medoid partitioning. The status of *L. roskellyae* remains particularly unresolved. Hence we may classify these results as inconclusive.

Original conclusion: HB?

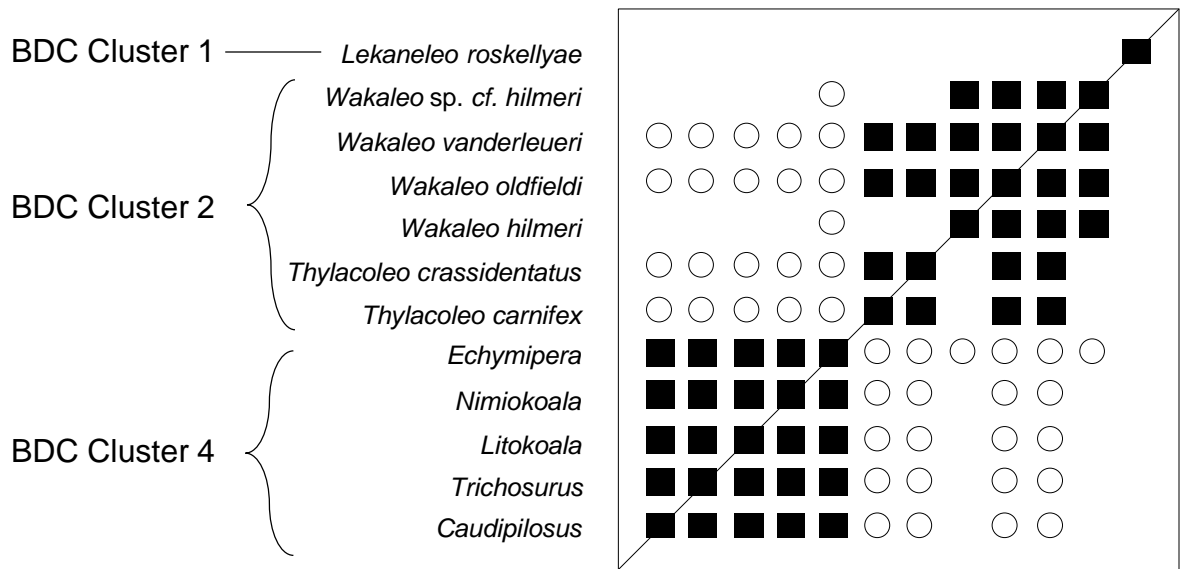
Updated conclusion: Inconclusive



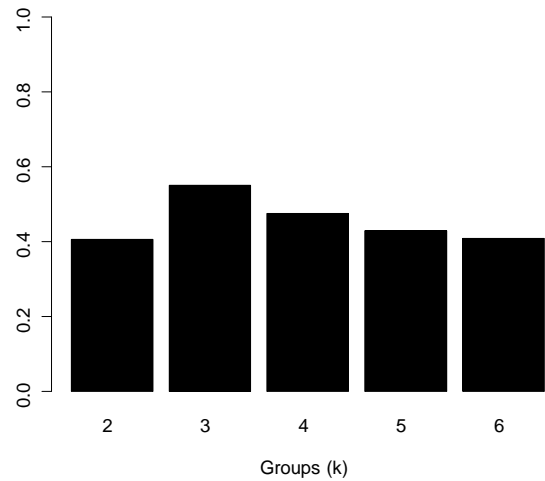
Order Diprotodontia
Family Thylacoleonidae

Published taxa	17
Published characters	72
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	12
Characters used for calculations	51
Median bootstrap value	89
F ₉₀	0.47
Stress of 3D MDS	0.12
k _{min}	6
Conclusion	HB?

Notes: This dataset comes from chapter 11 of Gillespie’s dissertation. The BDC shows what appear to be four groups of thylacoleonids all negatively correlated with the outgroup taxa but with little evidence of positive correlation with each other. The MDS reveals an arc of thylacoleonid taxa surrounding a tight cluster of outgroup taxa. The curvilinear distribution of thylacoleonid taxa might account for the poor intrafamilial BDC results. Hence we may provisionally accept Thylacoleonidae as a holobaramin.



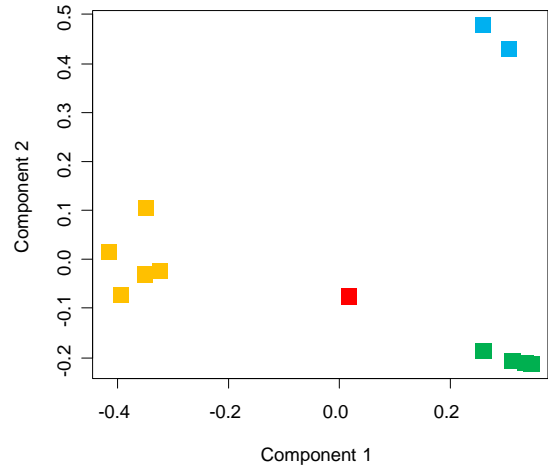
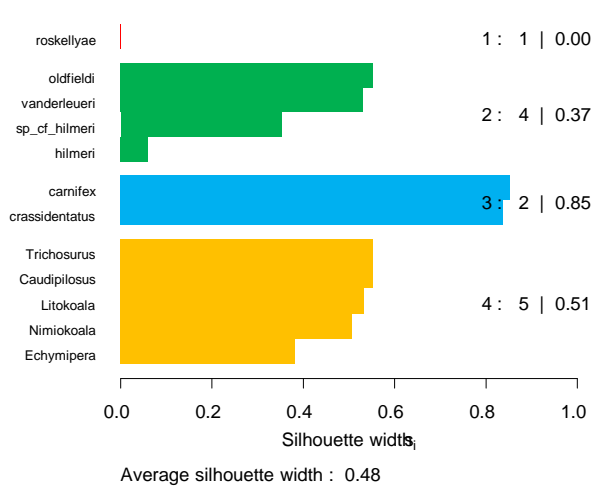
Average Silhouette Widths, Partion Around Medoids



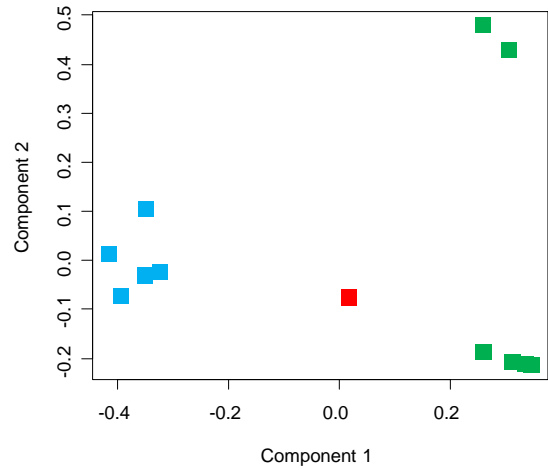
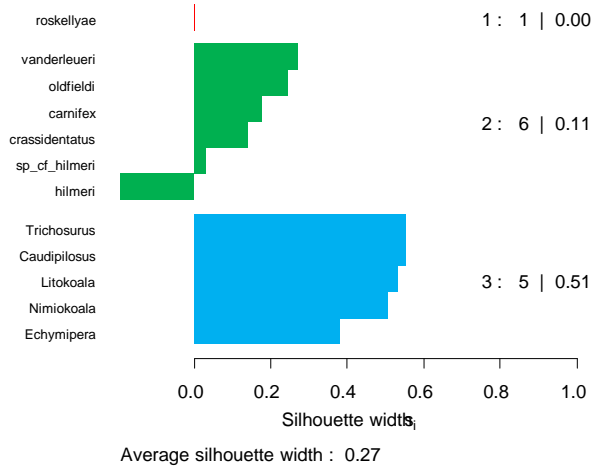
Clade Correspondence: Three of the four clusters (2-4) identified in the BDC analysis consist of more than one taxon. Cluster 2 corresponds to genus *Wakaleo* and is monophyletic in figure 11.2a of Gillespie (2007). Cluster 3 consists of the species of *Thylacoleo* and is also monophyletic in figure 11.2a. The outgroup taxa are found in cluster 4 and correspond to a clade if figure 11.2a were drawn unrooted. Hence, all clusters correspond to clades in the published phylogeny.

Silhouette plot, BDC partitions

Pearson Correlation

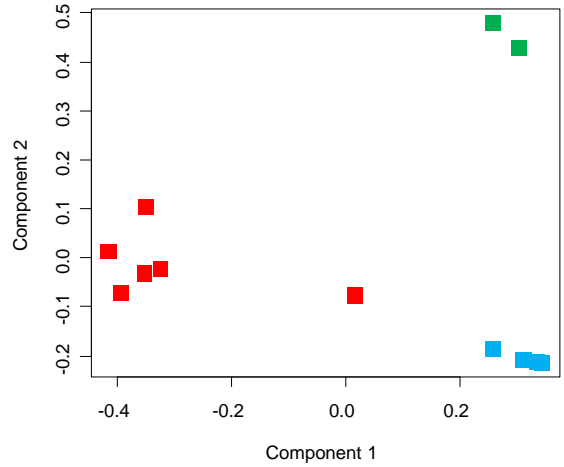
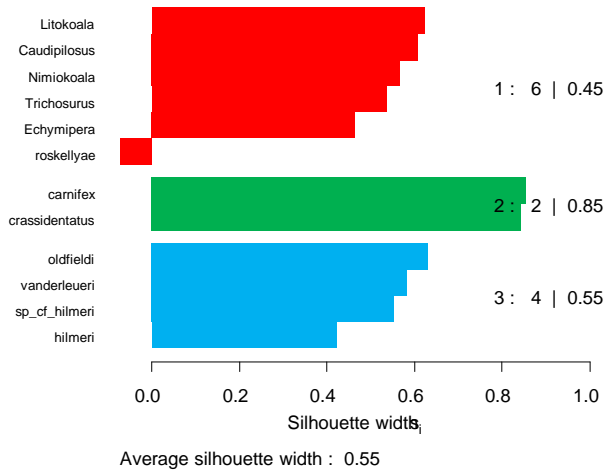


Spearman Correlation

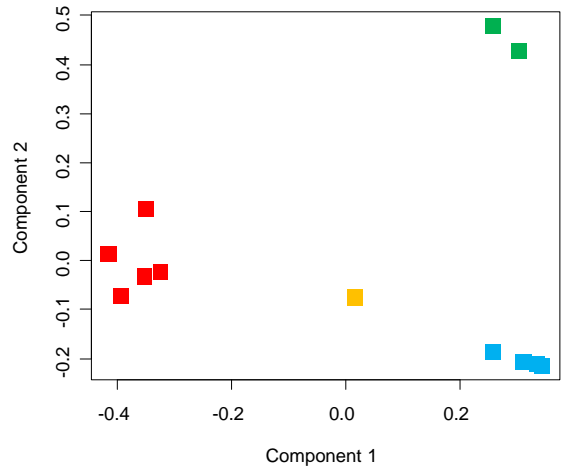
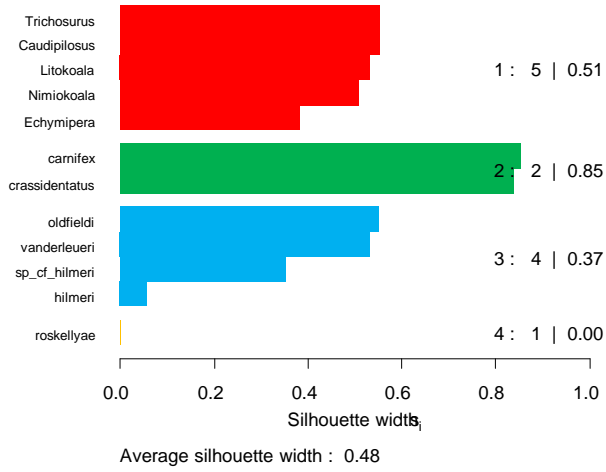


Silhouette plot, Partition Around Medoids

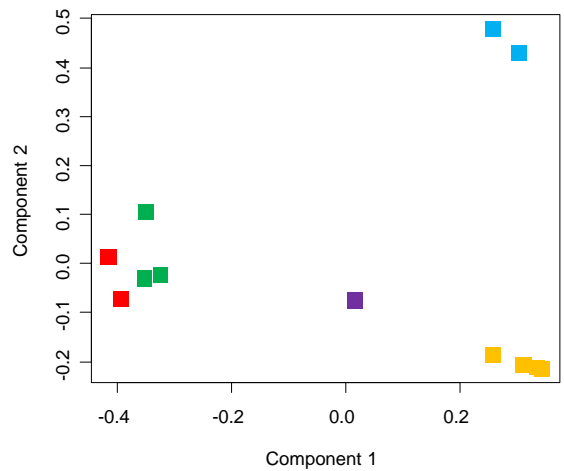
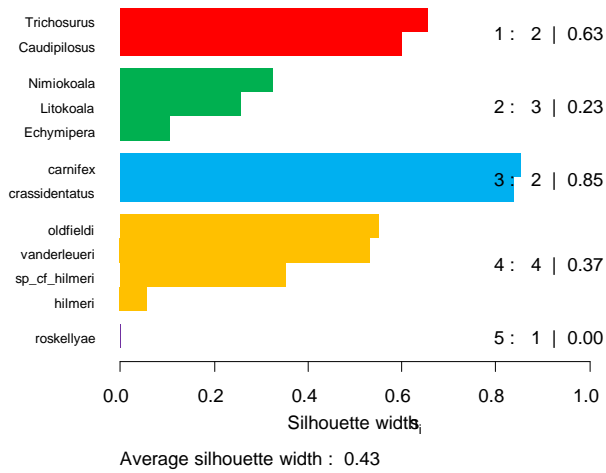
k=3



k=4

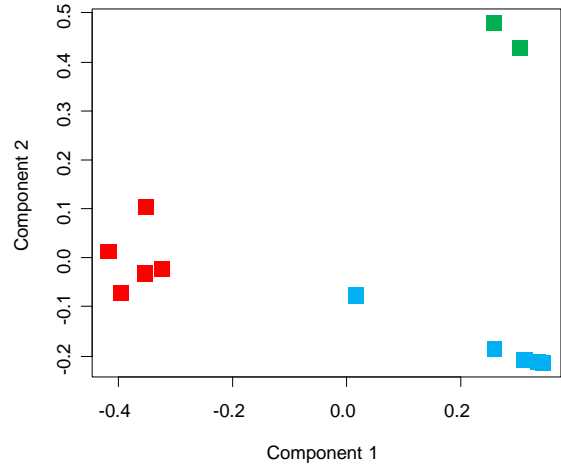
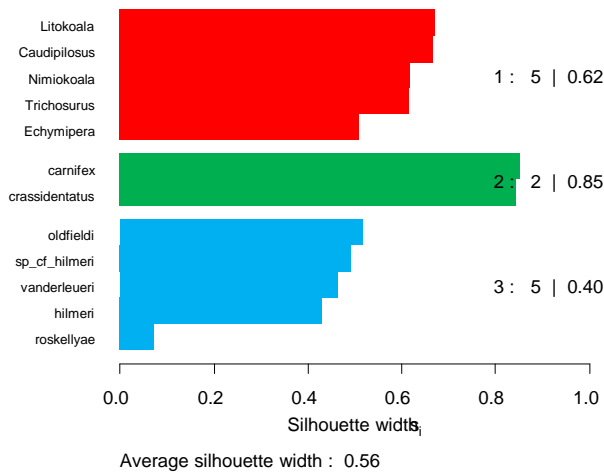


k=5

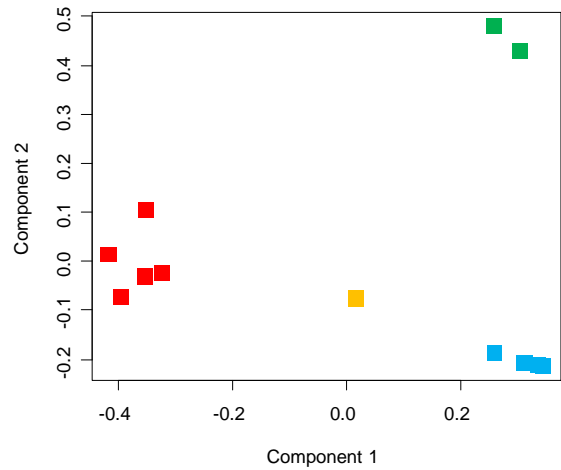
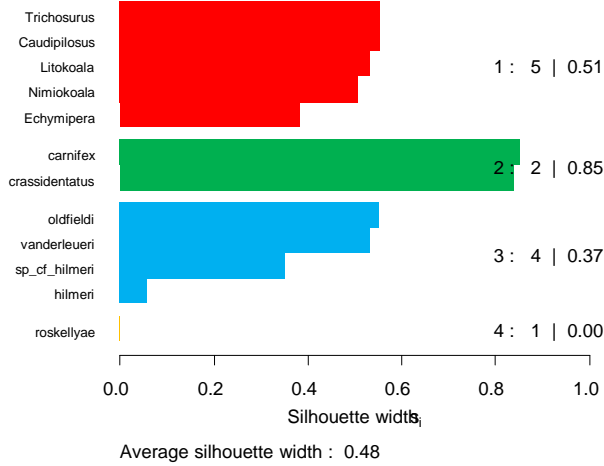


Silhouette plot, Fuzzy Analysis

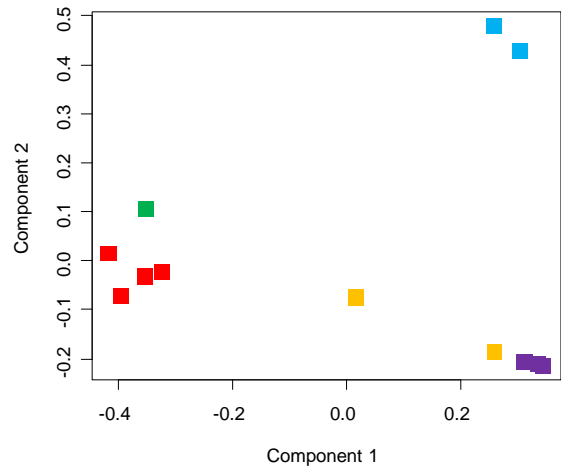
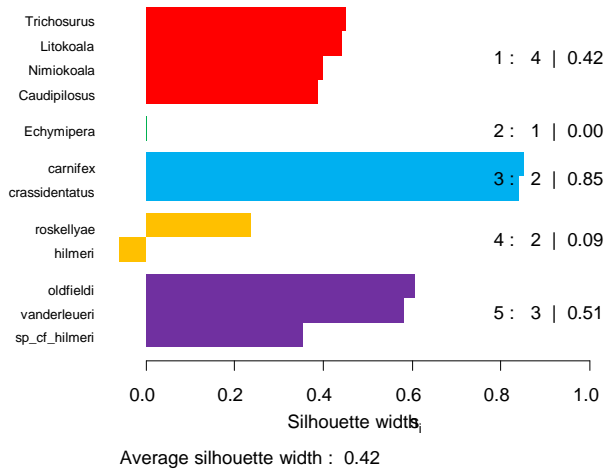
k=3



k=4



k=5



Family Hypsiprymnodontidae

Order Diprotodontia

Bates et al. 2014

Pearson BDC

Negative: 50

Positive: 58

Clusters: 3

Clusterability

Hopkins Statistic: 0.796

Dip test: 0.02

Dip test p-value: 0.906

Spearman BDC

Negative: 49

Positive: 73

Clusters: 3

The Spearman BDC increases the instances of significant, positive BDC over the Pearson BDC by 15 taxon pairs, but the clustering remains the same, with three clusters discernible. The average silhouette width for this three-cluster partition is 0.34, with one taxon *Potorous tridactylus* exhibiting a negative silhouette width.

The medoid partition at $k=3$ exhibits substantial differences from this partition, with a cluster membership difference of 25%. Where both BDC analyses split the ingroup into two clusters and place macropodids and *Hadronomas* into the outgroup, the medoid partition at $k=3$ splits the outgroup into two clusters and places *Bulungamaya* and *Ganguroo* in one of the outgroup clusters. The average silhouette width for medoid partitioning at $k=3$ is 0.39, but one taxon *Bettongia* has a negative silhouette width. The average silhouette width increases as the number of medoid partition clusters increases.

Fuzzy analysis at $k=3$ presents a third means of partitioning the taxa, with yet again two clusters of outgroup taxa and one of the ingroup. Fuzzy analysis at $k=3$ places *Bulungamaya*, *Ganguroo*, and *Bettongia* in a cluster with outgroup taxa. The average silhouette width for the $k=3$ fuzzy partition is 0.37. As with the medoid partition, the average silhouette width increases dramatically with an increase in cluster number.

It should be noted, however, that both fuzzy and medoid partitioning at $k=2$ very nearly supports the division between the ingroup Hypsiprymnodontidae and the outgroup macropodids and *Hadronomas*. The only exception to this is that the medoid partition places *Bulungamaya* in the outgroup. The average silhouette widths for the $k=2$ fuzzy and medoid partition is 0.38 and 0.37 respectively, not substantially different from the $k=3$ partition.

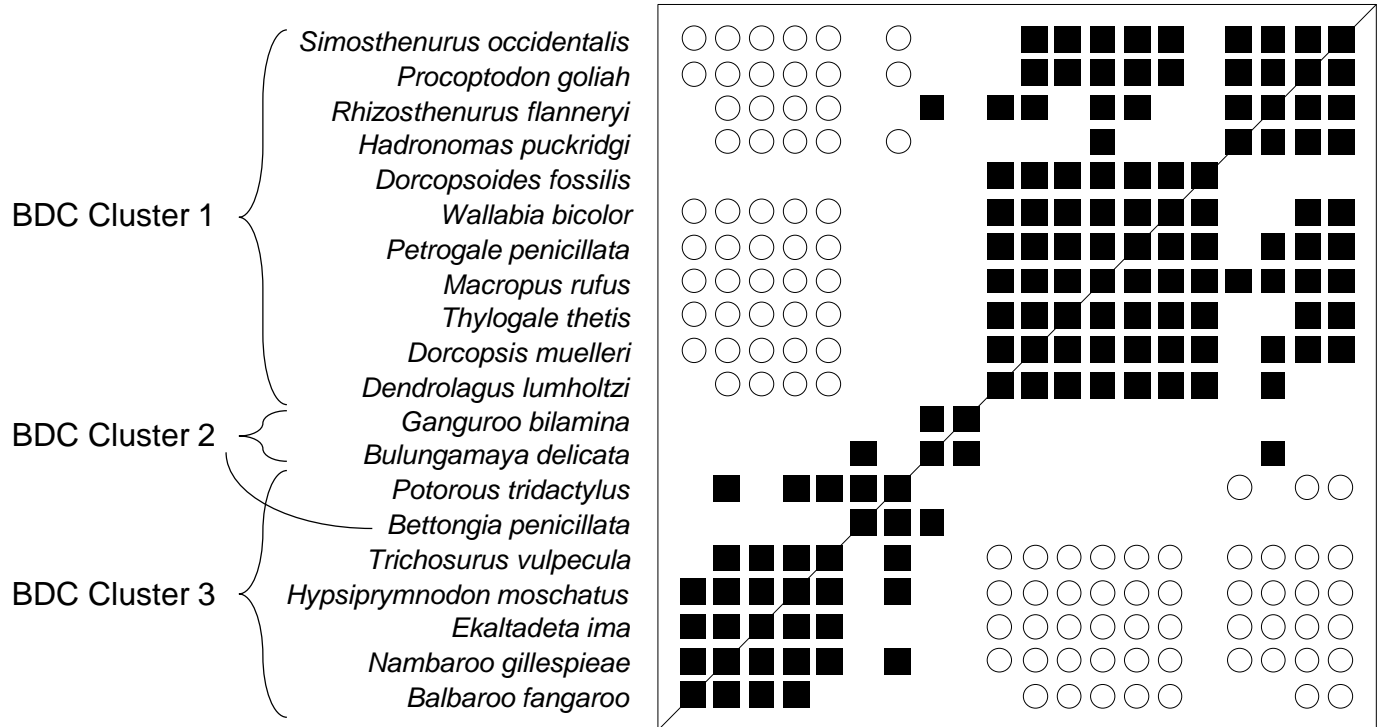
The original conclusion of a holobaraminic Hypsiprymnodontidae was based on significant, positive BDC between the two clusters of ingroup taxa and the frequent occurrence of significant, negative BDC between the ingroup and outgroup taxa. The new Spearman BDC agrees substantially with this original conclusion, as do the medoid and fuzzy partitions at $k=2$. The only question remaining is the status of *Bulungamaya*, which exhibits significant, positive BDC with three members of the outgroup in the Spearman BDC and was placed with the outgroup in the medoid partition at $k=2$. Hence these results confirm the original diagnosis with the sole provision that the status of *Bulungamaya* is uncertain.

Original conclusion: HB

Updated conclusion: HB

Bates, H., K.J. Travouillon, B. Cooke, R.M.D. Beck, S.J. Hand, and M. Archer. 2014. Three new Miocene species of musky rat-kangaroos (Hypsiprymnodontidae, Macropodoidea): description, phylogenetics, and paleoecology. *Journal of Vertebrate Paleontology* 34:383-396.

Characters: Craniodental



Bulungamaya delicata ●

Ganguroo bilamina ●

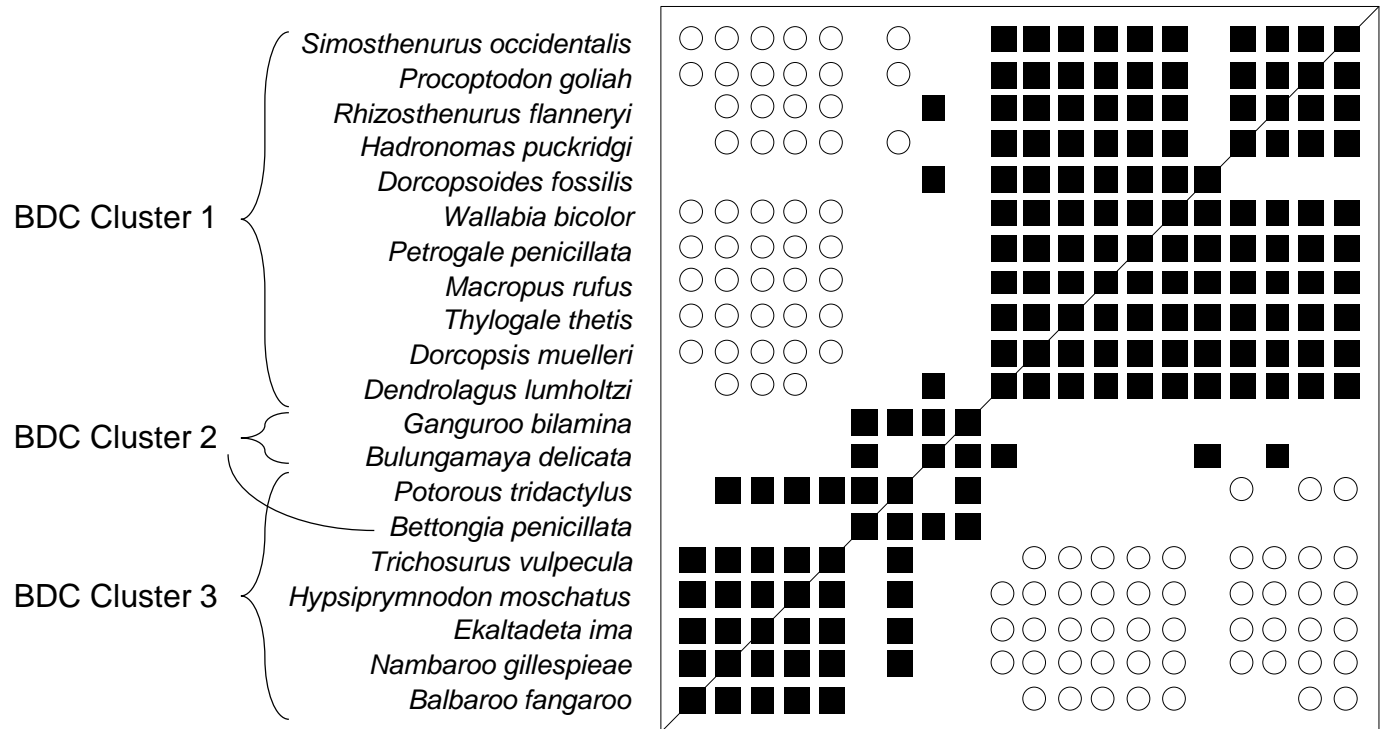
Hadronomas puckridgi ●

Order Diprotodontia
Family Hypsiprymnodontidae

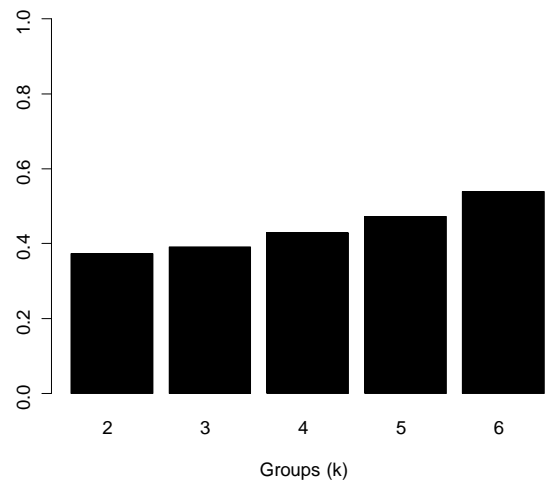
Published taxa	33
Published characters	107
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	20
Characters used for calculations	93
Median bootstrap value	84
F ₉₀	0.36
Stress of 3D MDS	0.12
k _{min}	5
Conclusion	HB

Red: outgroup
Green: Macropodidae
Blue: Hypsiprymnodontidae

Notes: MDS reveals a disperse cluster of ingroup taxa, but BDC supports recognizing a discontinuity between ingroup and outgroup. There is only one taxon pair with significant, positive BDC between the Macropodidae and Hypsiprymnodontidae: *Rhizosthenurus flanneryi* and *Bulungamaya delicata* respectively. Since the bootstrap value for that correlation is only 79% and the MDS reveals that *Bulungamaya* is an outlier from the hypsiprymnodontids and not adjacent to the macropodids, we may consider that correlation spurious. Hypsiprymnodontidae is probably a holobaramin.



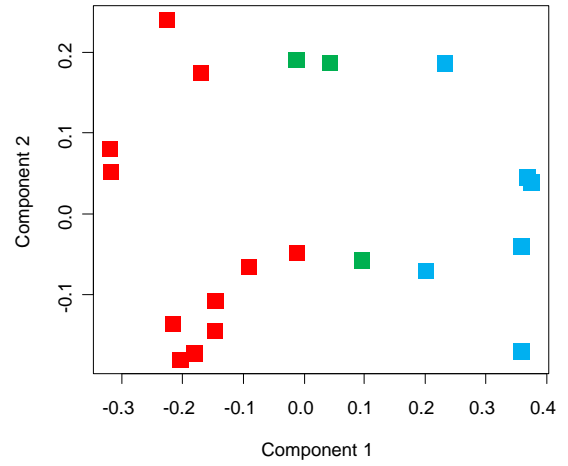
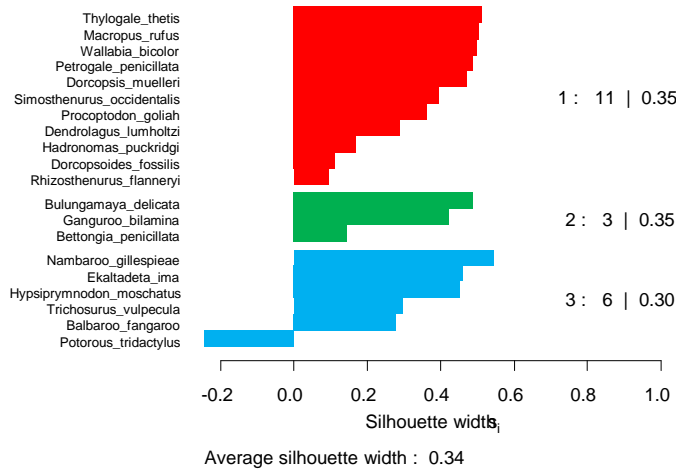
Average Silhouette Widths, Partion Around Medoids



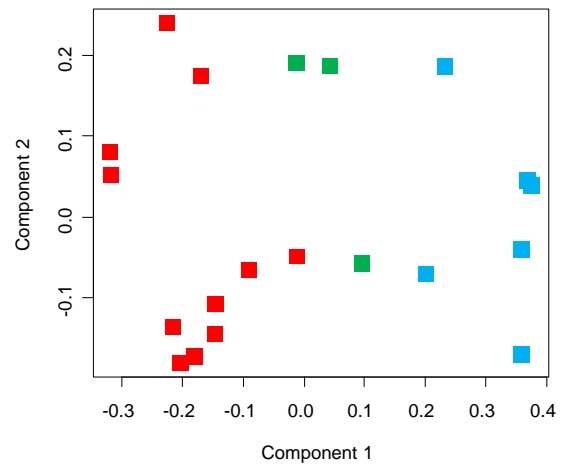
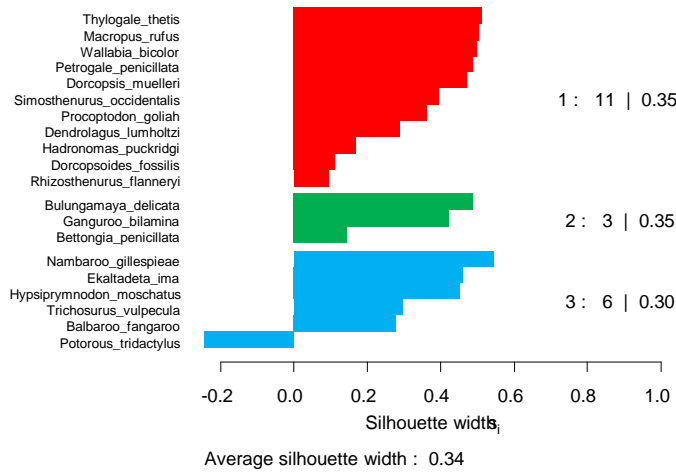
Clade Correspondence: All three clusters identified in the BDC analysis contain more than one taxon. Cluster 1 corresponds to a clade in figure 6 of Bates et al. (2014), but the remaining clusters do not correspond to clades in the figure. The published phylogeny is a strict consensus of 6,960 most parsimonious trees, and most of the relationships are unresolved polytomies.

Silhouette plot, BDC partitions

Pearson Correlation

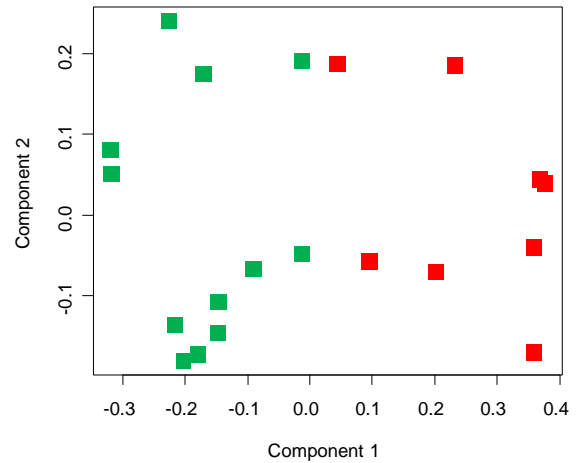
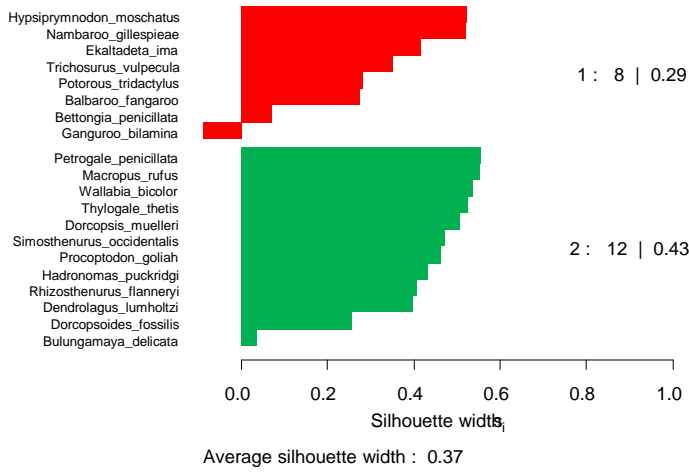


Spearman Correlation

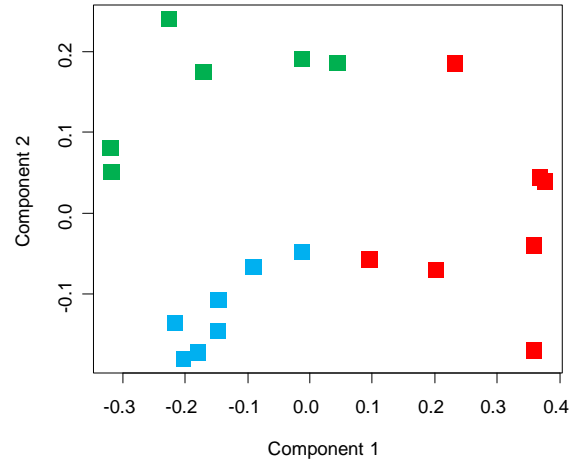
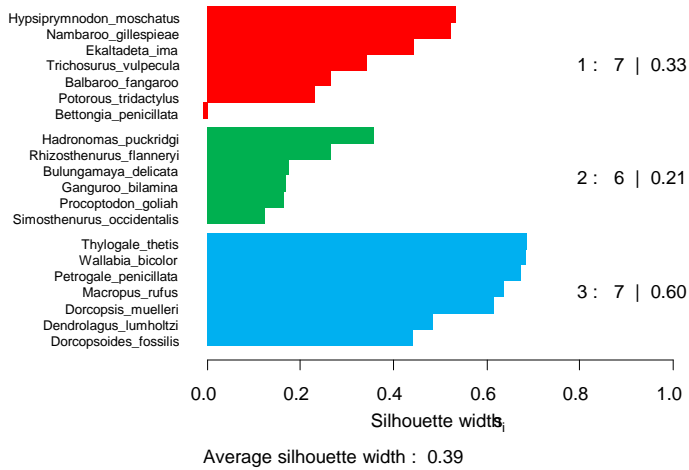


Silhouette plot, Partition Around Medoids

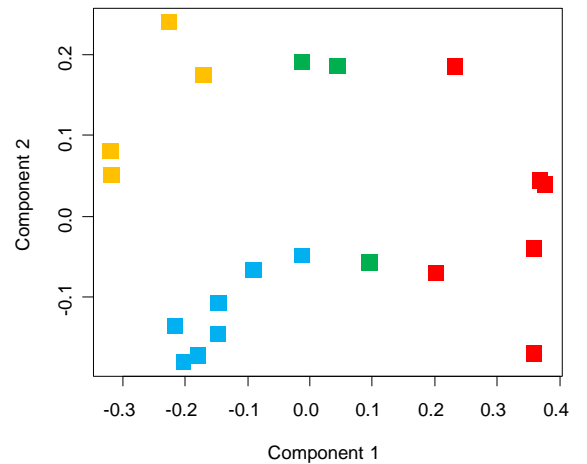
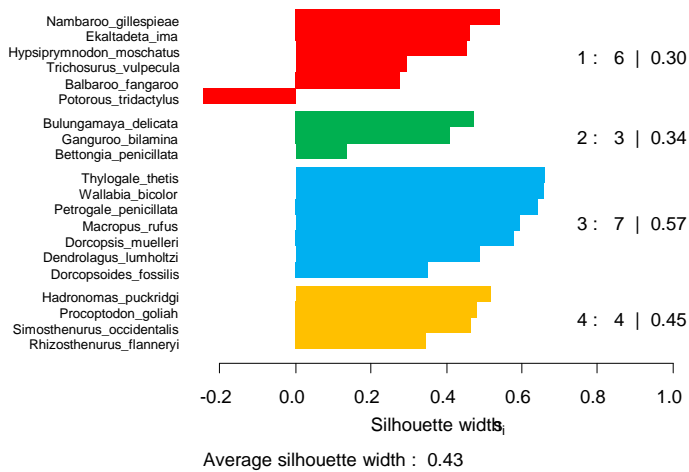
k=2



k=3

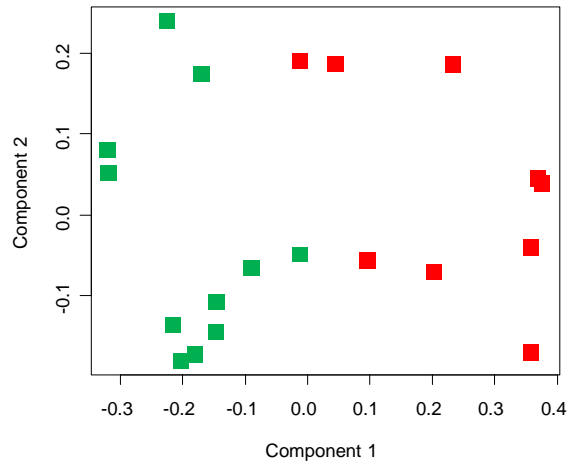
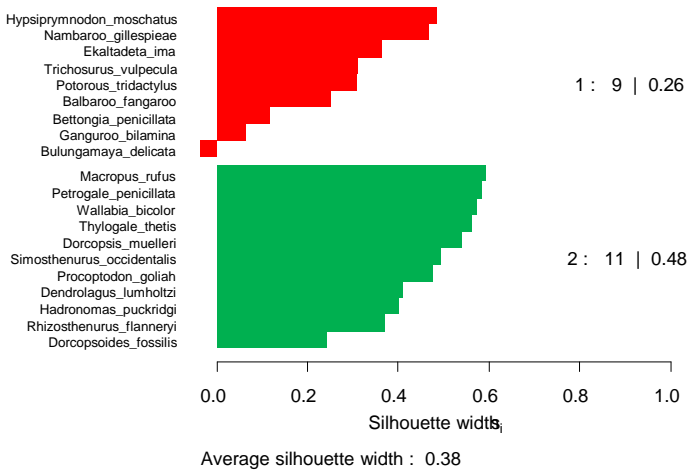


k=4

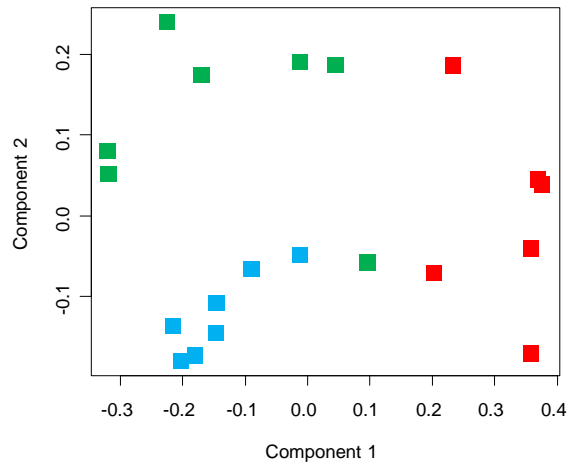
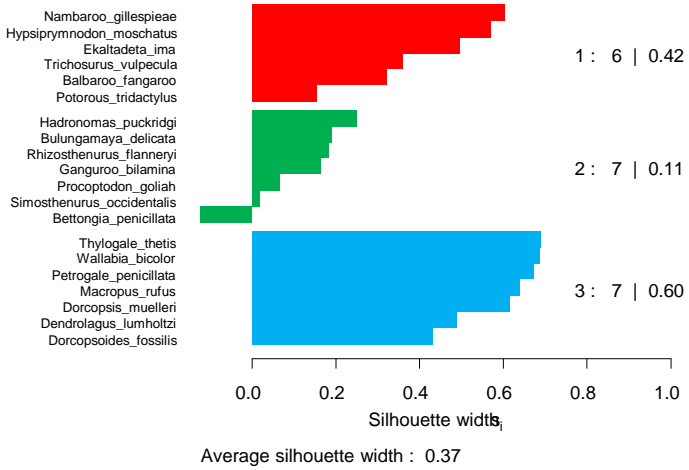


Silhouette plot, Fuzzy Analysis

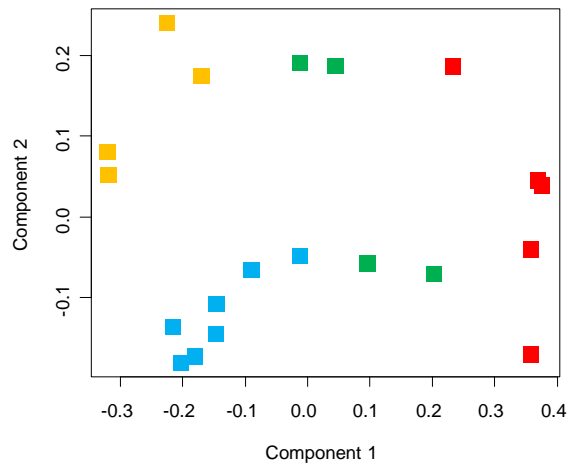
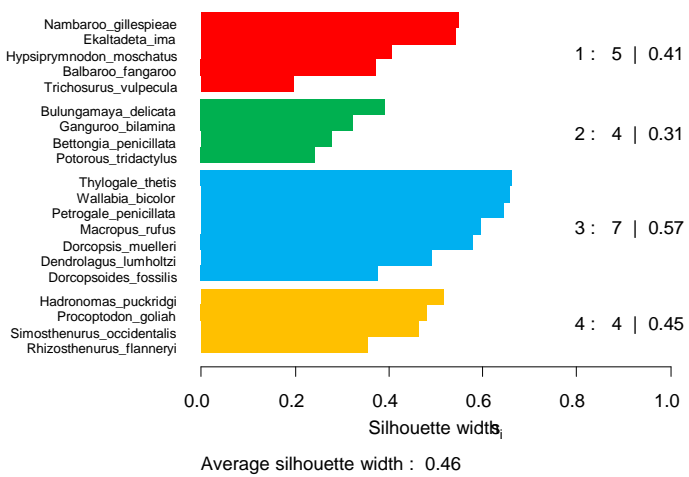
k=2



k=3



k=4



Family Macropodidae

Order Diprotodontia

Prideaux and Tedford 2012

Pearson BDC

Negative: 73

Positive: 184

Clusters: 3

Clusterability

Hopkins Statistic: 0.845

Dip test: 0.016

Dip test p-value: 0.722

Spearman BDC

Negative: 10

Positive: 227

Clusters: 3

The Spearman BDC results recognize the same three clusters recognized in the Pearson BDC. The major difference between the two is a dearth of significant, negative correlation in the Spearman BDC. Significant, negative correlation can be observed between 73 different taxon pairs in the Pearson BDC but only between 10 taxon pairs in the Spearman BDC. The average silhouette width of this three-cluster partition is 0.46 and no taxa exhibited negative silhouette widths.

The medoid partition at $k=3$ yields the same clustering as the Pearson and Spearman BDC. Medoid partitioning at $k=2$ or $k=4$ had notably lower average silhouette widths (0.35 and 0.31 respectively).

Fuzzy analysis did not produce a three-cluster partition, and the two-cluster partition had the worst average silhouette width at 0.26. Six taxa in the two-cluster partition exhibited negative silhouette widths.

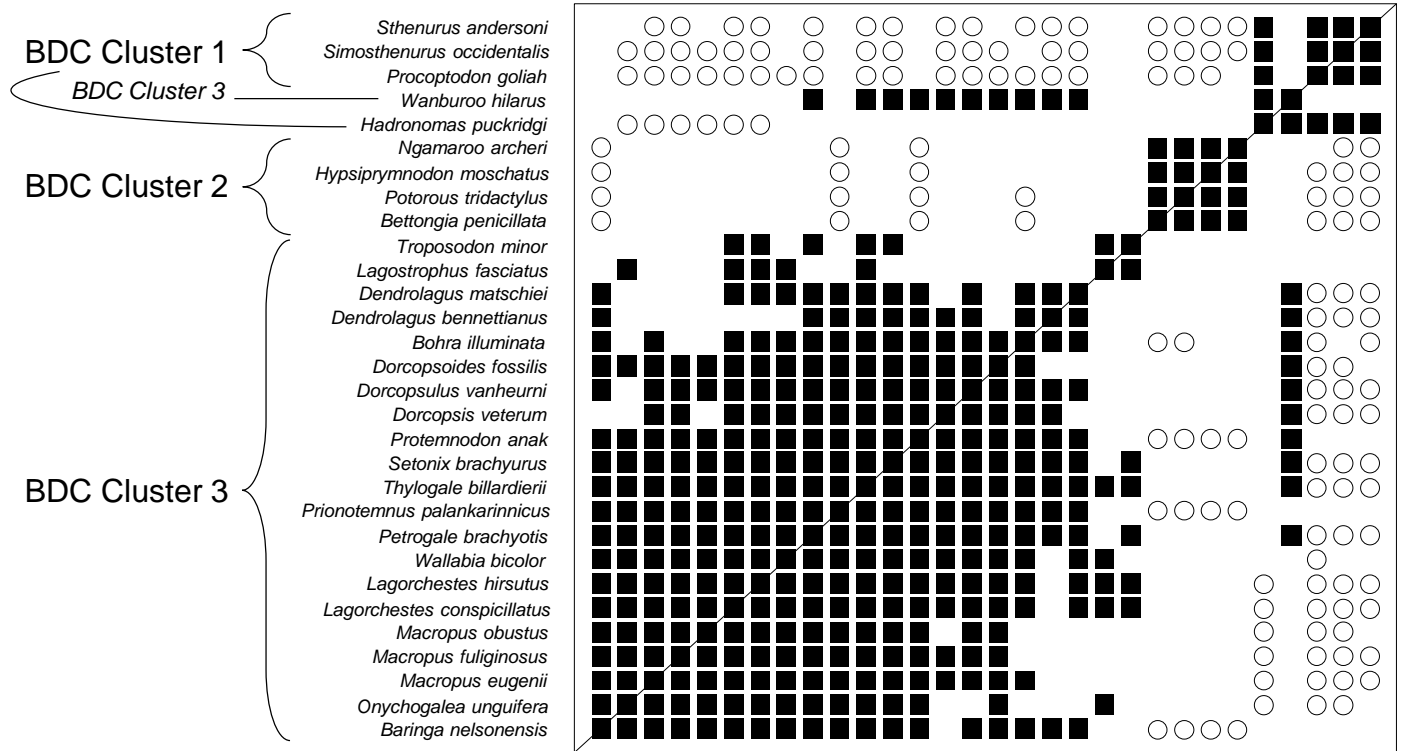
The original conclusion was based on significant positive correlation between two ingroup clusters (particularly involving *Wanburoo hilarus*) and the significant, negative correlation observed between the outgroup and ingroup taxa. Here the significant, negative correlation has largely disappeared in the Spearman BDC, and there are six instances of significant, positive correlation between outgroup taxa and the ingroup taxa *Dorcopsis veterum* and *Lagostrophus fasciatus*. The medoid partition seems to most strongly support a three-cluster partition rather than recognizing the ingroup and outgroup clusters. Hence I judge these updated results to be inconclusive.

Original conclusion: HB?

Updated conclusion: Inconclusive

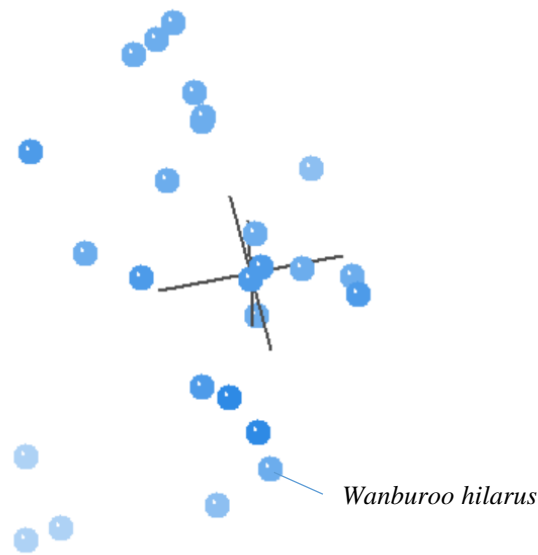
Prideaux, G.J. and R.H. Tedford. 2012. *Tjukuru wellsii*, gen. et sp. nov., a lagostrophine kangaroo (Diprotodontia, Macropodidae) from the Pliocene (Tirarian) of northern South Australia. *Journal of Vertebrate Paleontology* 32:717-721.

Characters: Craniodental and postcranial



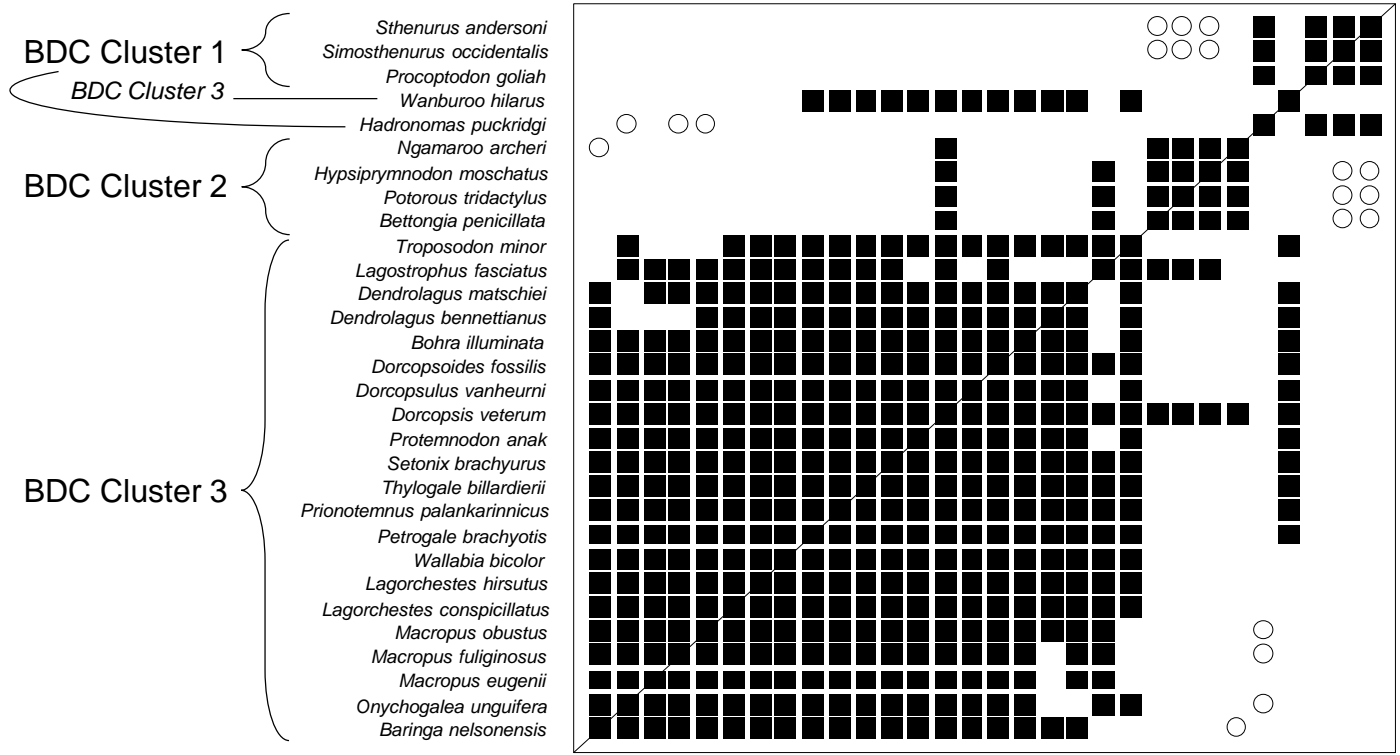
Order Diprotodontia
Family Macropodidae

Published taxa	36
Published characters	83
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	30
Characters used for calculations	80
Median bootstrap value	81
F ₉₀	0.34
Stress of 3D MDS	0.18
k _{min}	6
Conclusion	HB?

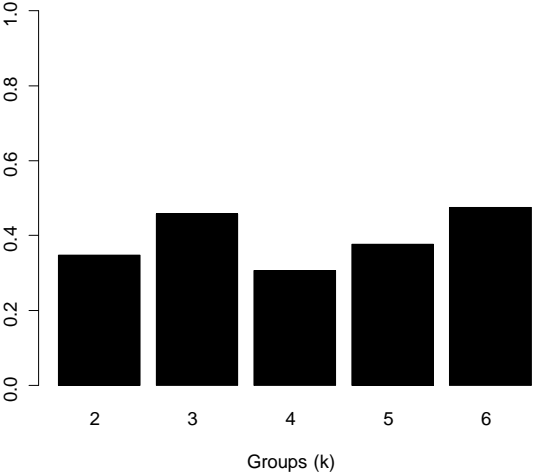


Notes: The outgroup indicated in the MDS results is only the hypsiprymnodontid *Hypsiprymnodon moschatus*. Other non-macropodid taxa include the potoroids *Bettongia* and *Potorous*.

The BDC results indicate a clear separation between macropodids and the three outgroup taxa. Also, BDC shows positive BDC between stem macropodoid *Ngamaroo* and the outgroup taxa and negative BDC between *Ngamaroo* and the ingroup. Macropodoid *Wanburoo* appears to correlate with the outgroup and ingroup taxa, but the MDS results reveal that *Wanburoo* is not actually part of the outgroup cluster. Instead, it appears to be part of the Macropodidae holobaramin.



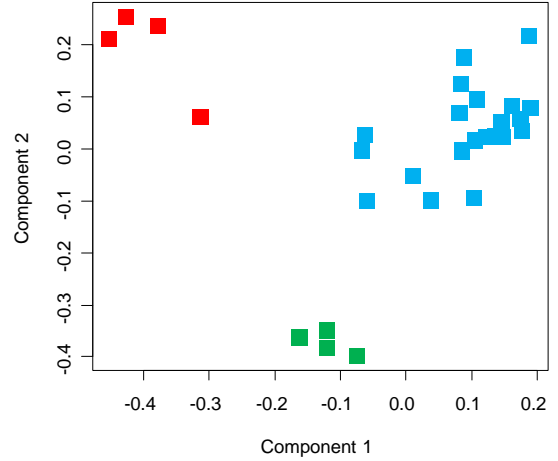
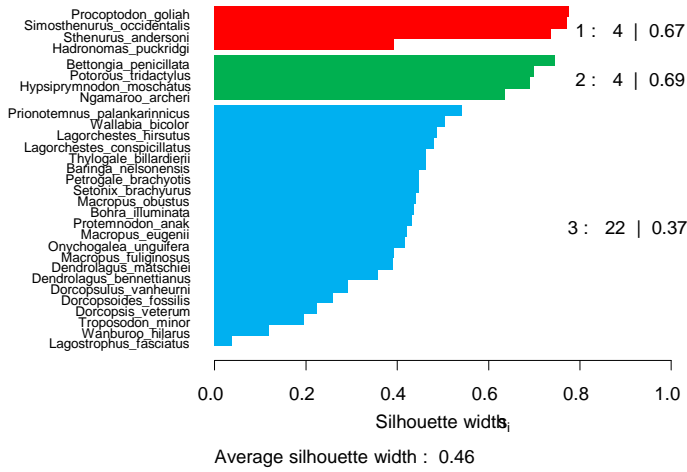
Average Silhouette Widths, Partion Around Medoids



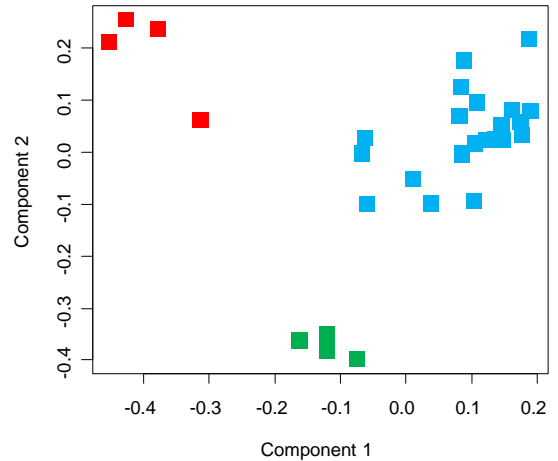
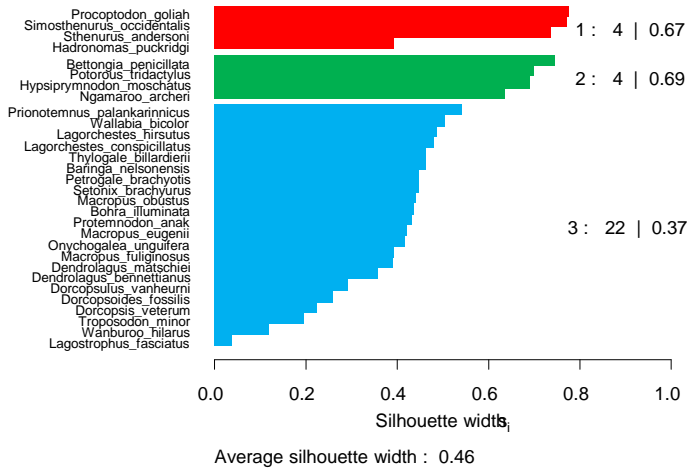
Clade Correspondence: The three BDC clusters all contain more than one taxon. Cluster 1 corresponds to the crown Sthenurinae and is monophyletic in Figure 3 of Prideaux and Tedford (2012). Cluster 2 corresponds to the outgroup *Hypsiprymnodon* together with the basal macropodid *Ngamaroo archeri* and subfamily Potoroinae. If the published phylogeny were unrooted, cluster 2 would be monophyletic. Cluster 3 consists of the remaining taxa and is not monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

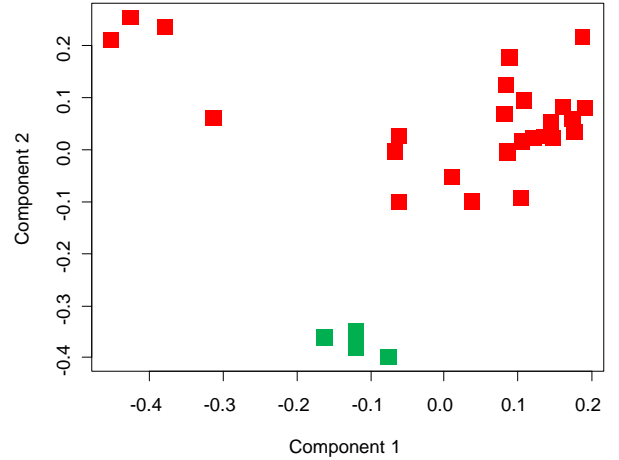
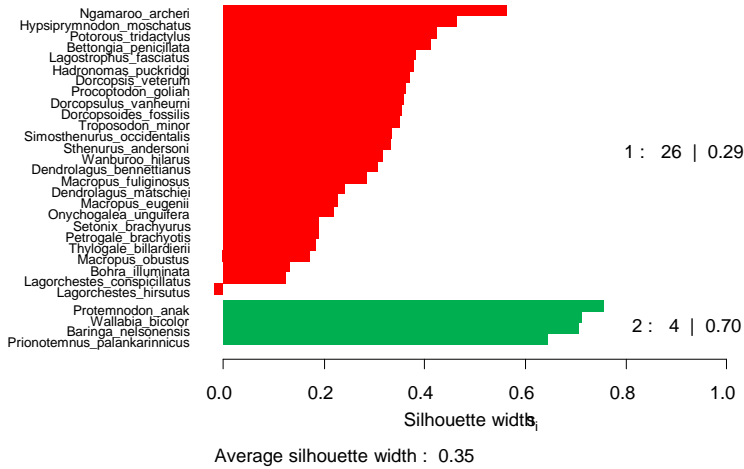


Spearman Correlation

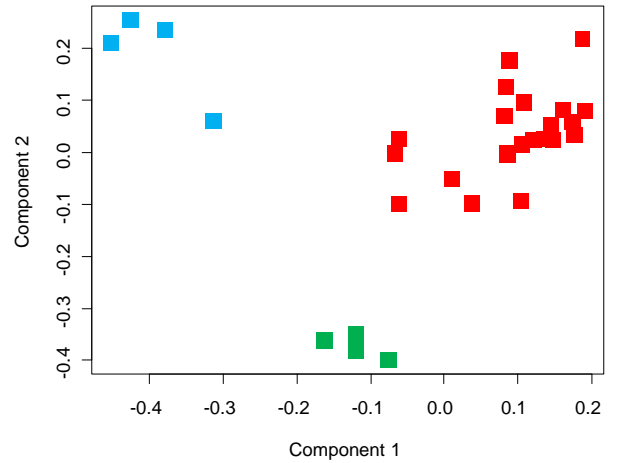
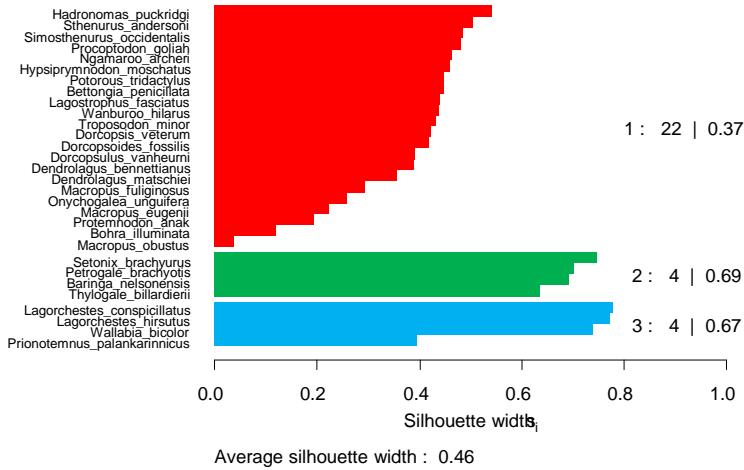


Silhouette plot, Partition Around Medoids

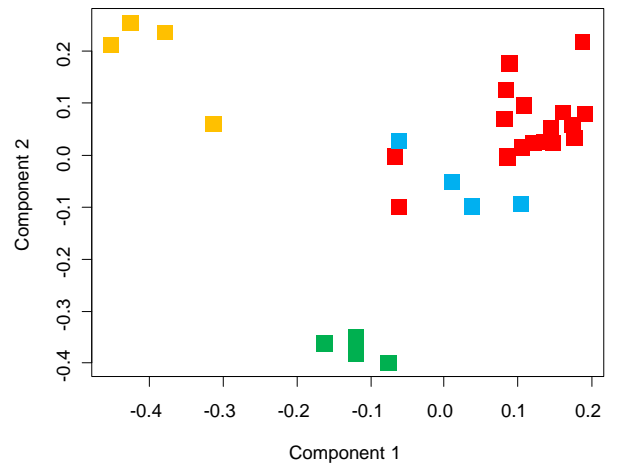
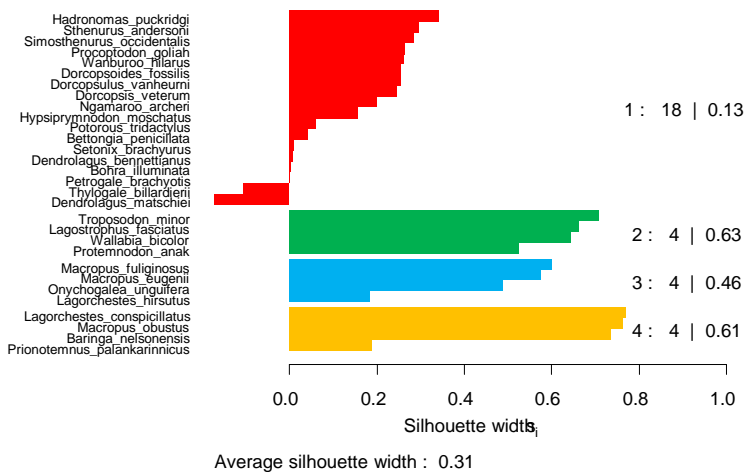
k=2



k=3

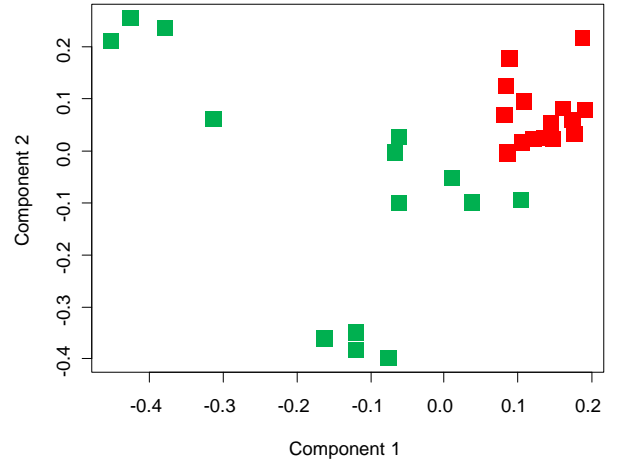
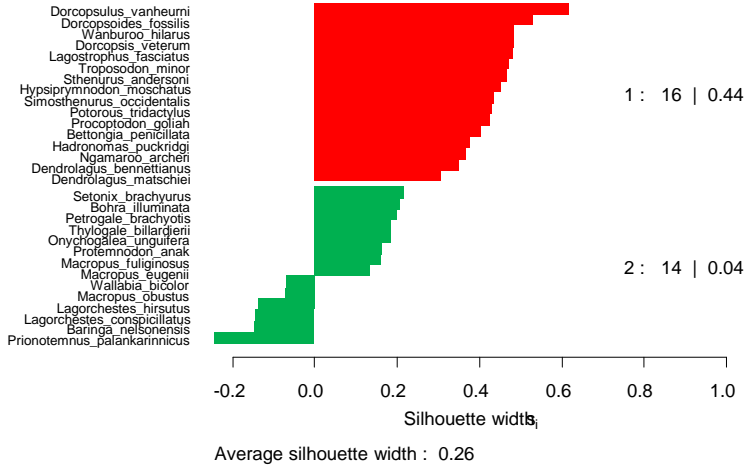


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Macropodidae

Order Diprotodontia

Kear et al. 2007

Pearson BDC

Negative: 45

Positive: 49

Clusters: 3

Clusterability

Hopkins Statistic: 0.739

Dip test: 0.029

Dip test p-value: 0.474

Spearman BDC

Negative: 45

Positive: 66

Clusters: 2

The Spearman BDC results add 17 instances of significant, positive correlation to the result of the Pearson BDC, resulting in the joining of two clusters recognized in the Pearson BDC into a single cluster. This larger cluster recognized in the Spearman results consists of all of the macropodids, where the Pearson BDC places macropodids *Ganguroo* and *Bulungamaya* in a separate cluster. The average silhouette width for the Spearman clusters of 0.42 is slightly better than the average silhouette width of 0.4 for the three-cluster partition of the Pearson BDC. No taxa exhibited negative silhouette widths in either the Pearson or Spearman partitions.

The medoid partition at $k=3$ does not agree with the partition of the Pearson BDC. The cluster membership difference is 28%, but the medoid partition has a notably lower average silhouette value at 0.38. The only cluster they share in common is a cluster of outgroup taxa that includes *Hypsiprymnodon*. With $k=2$, the medoid partition agrees precisely with the Spearman BDC clusters.

Fuzzy analysis at $k=3$ presents yet a third way of partitioning the taxa with an average silhouette width of 0.38. At $k=2$, however, the clusters very nearly agree with the Spearman BDC clusters. The only difference is the inclusion of *Ganguroo* with the outgroup taxa, rendering *Ganguroo*'s silhouette width negative. The average silhouette width for the two-cluster fuzzy analysis is then only 0.38.

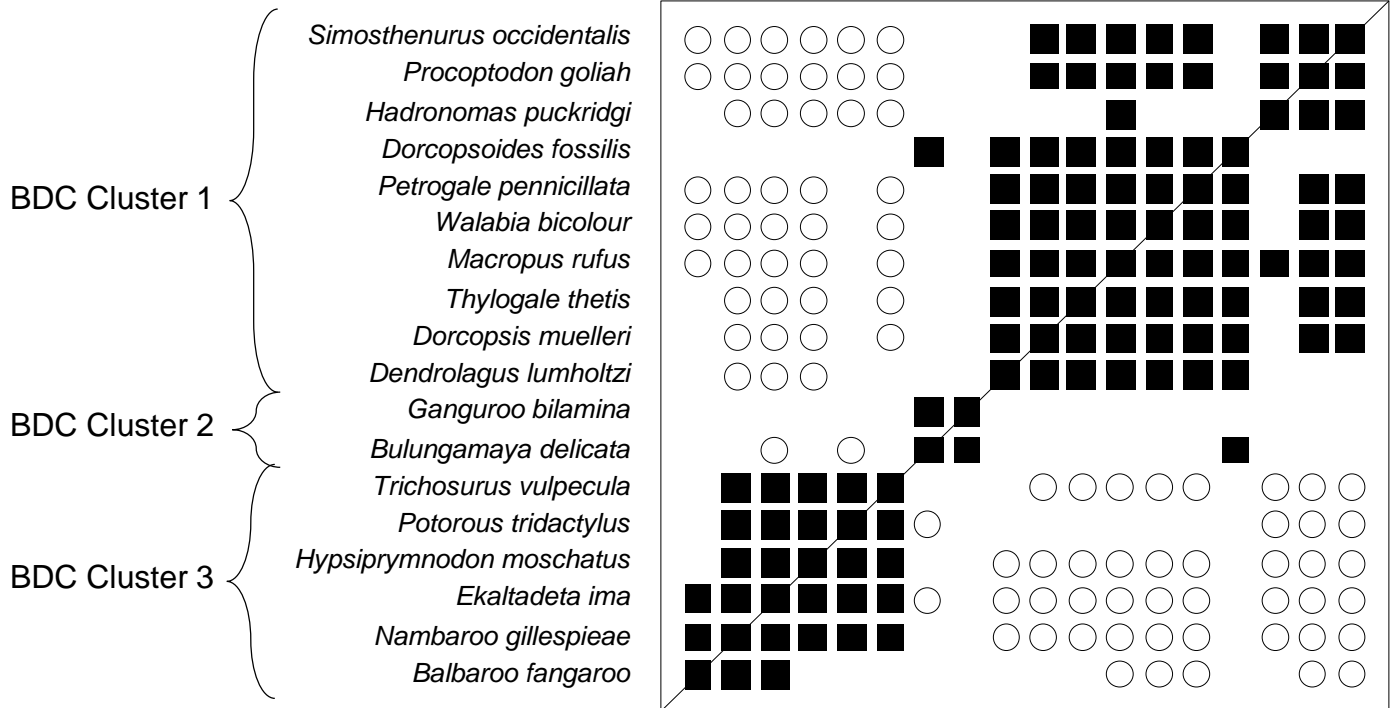
Given all of these results, Spearman BDC, medoid partitioning, and fuzzy analysis support recognizing two clusters consisting respectively of macropodids and outgroup taxa. Hence this is better support for a macropodid monobaramin than the original Pearson BDC. The holobaraminic status of Macropodidae using these taxa, characters, and newer analytical methods is confirmed.

Original conclusion: HB

Updated conclusion: HB

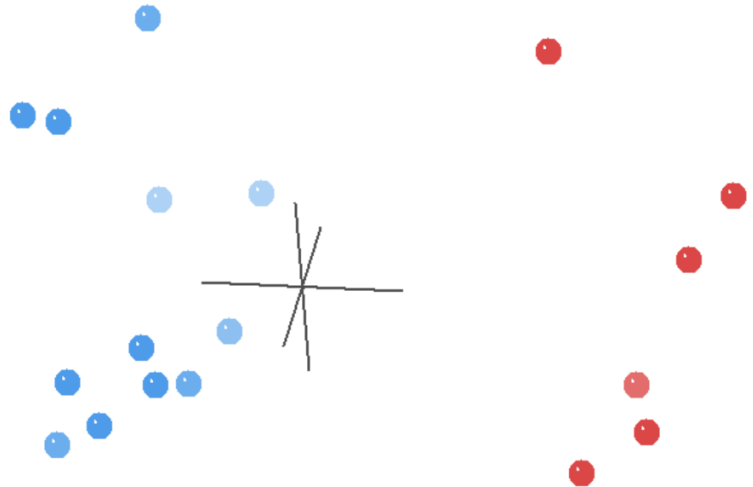
Kear, B.P., B.N. Cooke, M. Archer, and T.F. Flannery. 2007. Implications of a new species of the Oligo-Miocene kangaroo (Marsupialia: Macropodoidea) *Nambaroo*, from the Riversleigh World Heritage Area, Queensland, Australia. *Journal of Paleontology* 81:1147-1167.

Characters: Craniodental and postcranial

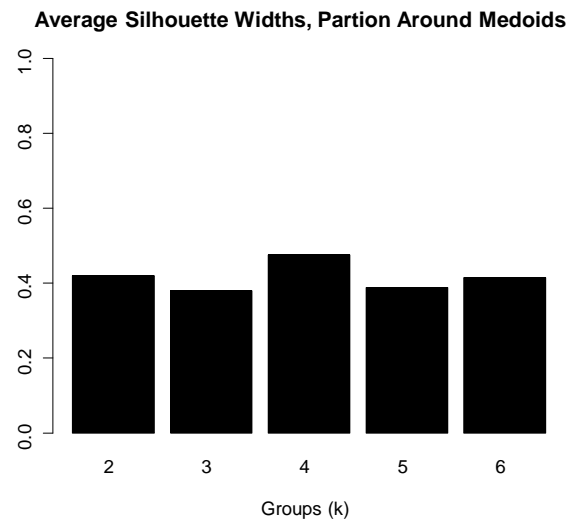
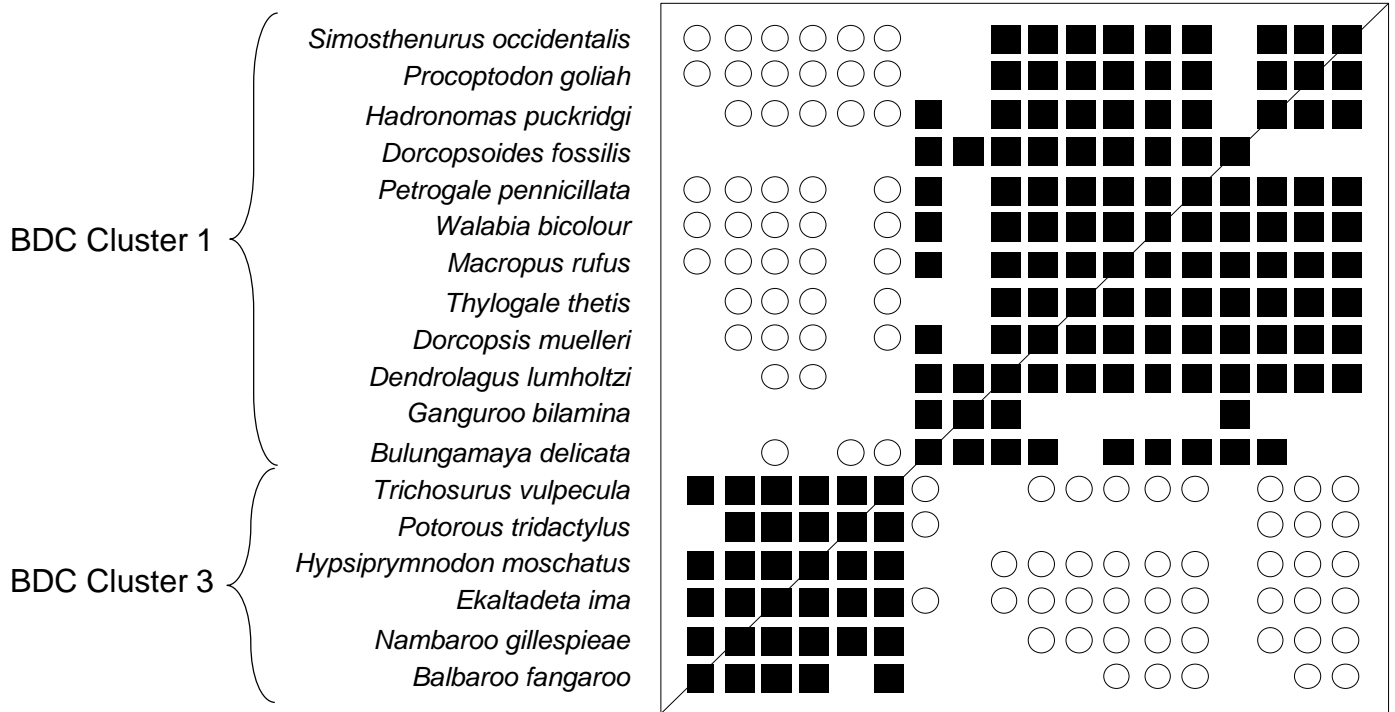


Order Diprotodontia
Family Macropodidae

Published taxa	25
Published characters	104
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	18
Characters used for calculations	85
Median bootstrap value	83
F ₉₀	0.34
Stress of 3D MDS	0.15
k _{min}	6
Conclusion	HB



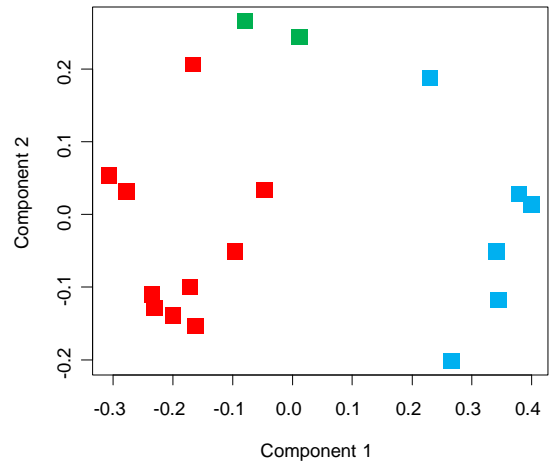
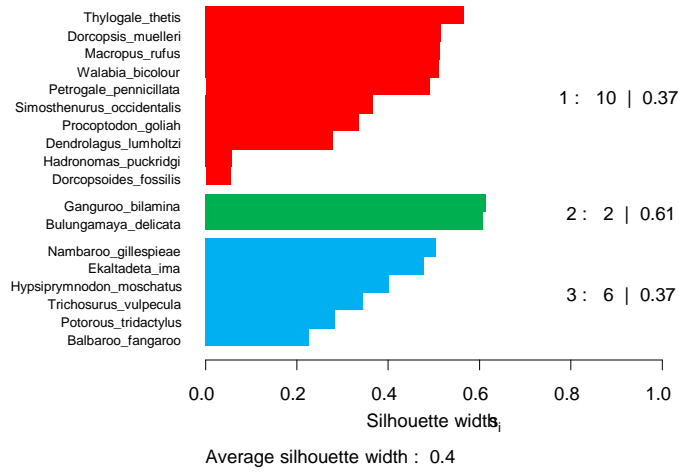
Notes: This second macropodid dataset is included because it contains fewer taxa than the previous Prideaux and Tedford dataset but more characters. In this case, the outgroups and macropodids are definitely separated in both BDC and MDS results, supporting the inference that Macropodidae is a holobaramin.



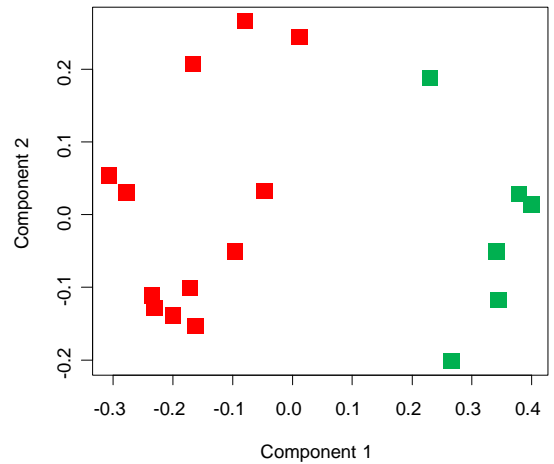
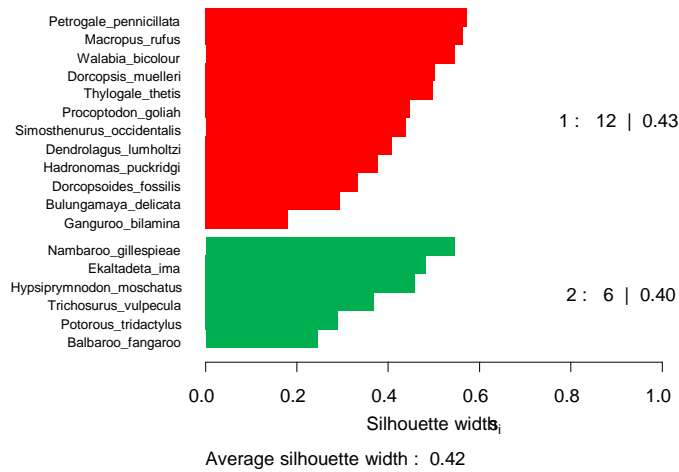
Clade Correspondence: All three BDC clusters contain more than one taxon. In Figure 11.1 of Kear et al. (2007), taxa of clusters 1 and 3 are monophyletic, but cluster 2 is not. Cluster 1 consists of crown macropodids, and cluster 3 contains the non-macropodid outgroups, which are monophyletic if the tree were drawn unrooted. Cluster 2 contains two basal macropodids, which would be paraphyletic with the rest of the macropodids.

Silhouette plot, BDC partitions

Pearson Correlation

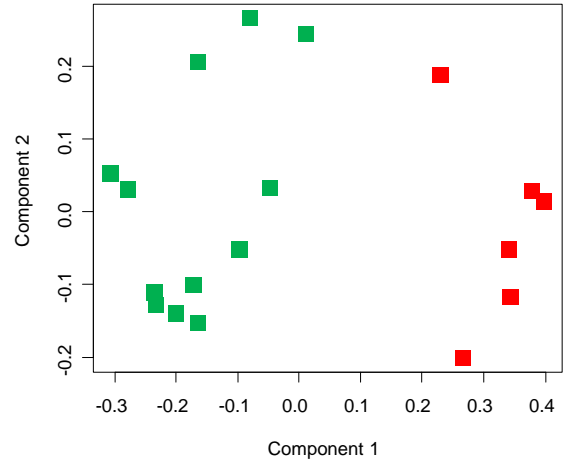
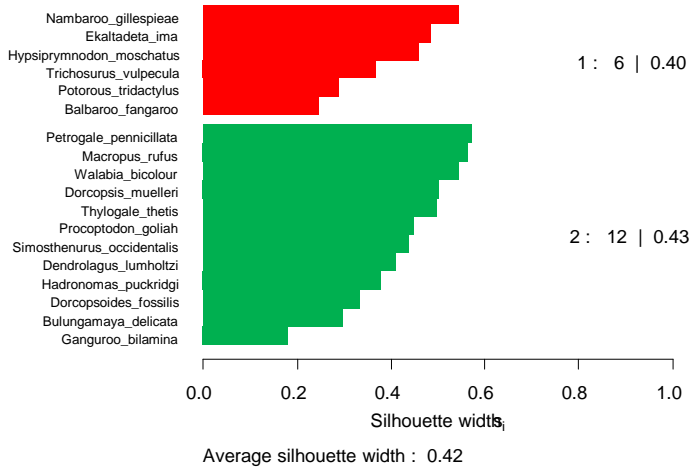


Spearman Correlation

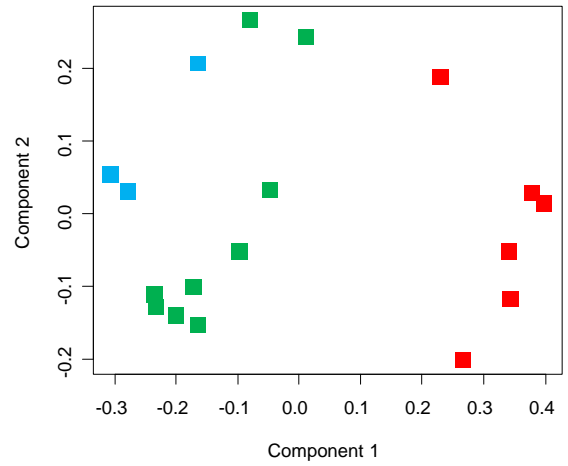
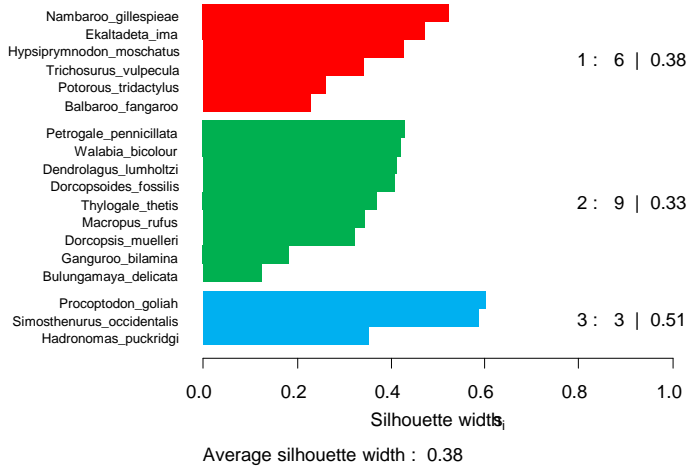


Silhouette plot, Partition Around Medoids

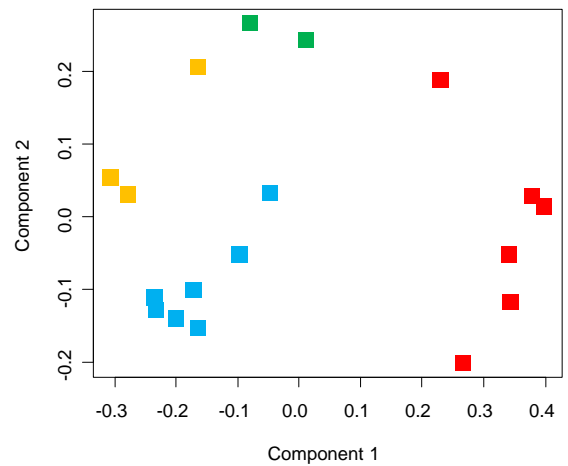
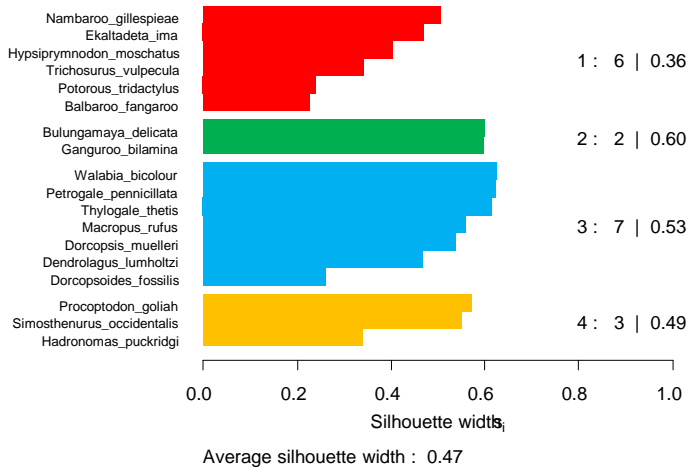
k=2



k=3

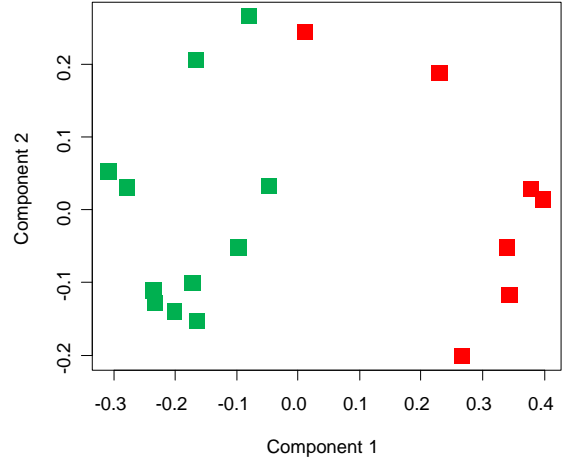
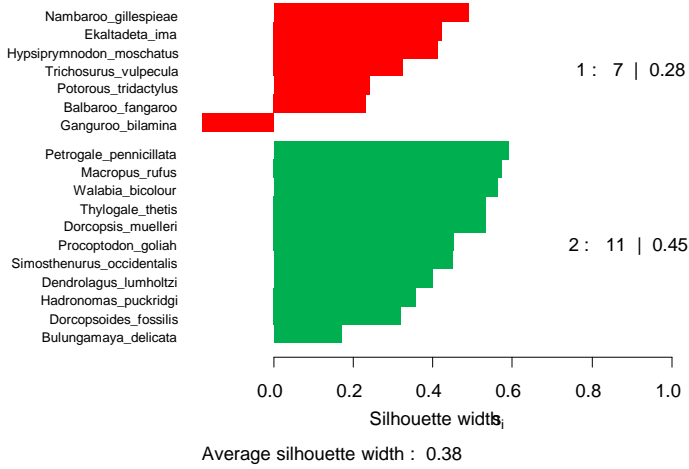


k=4

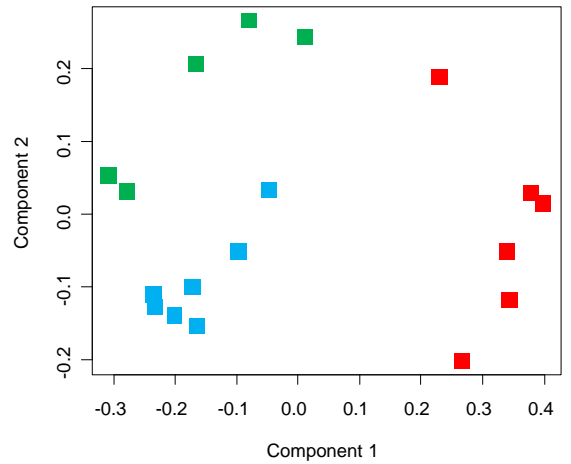
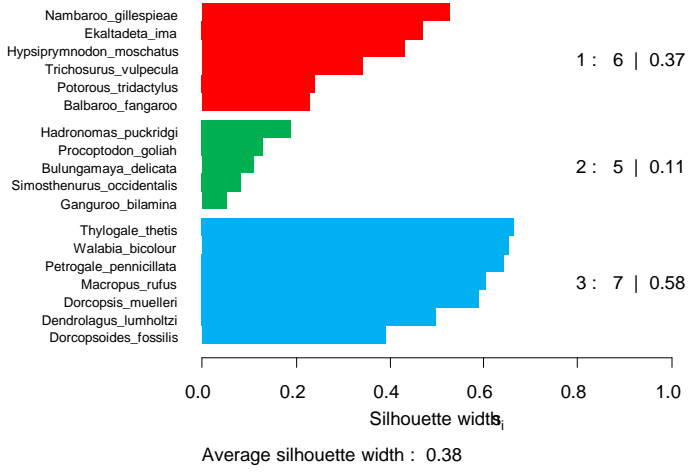


Silhouette plot, Fuzzy Analysis

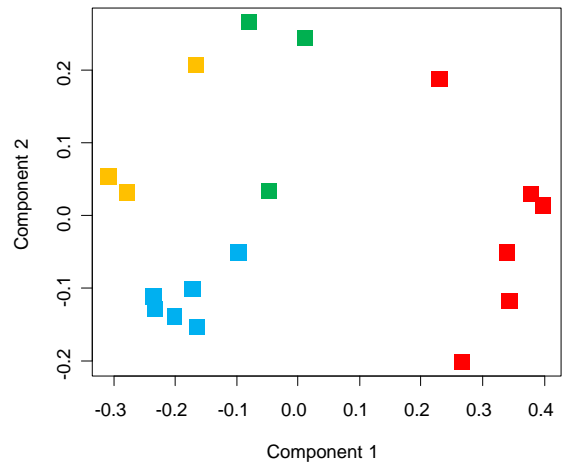
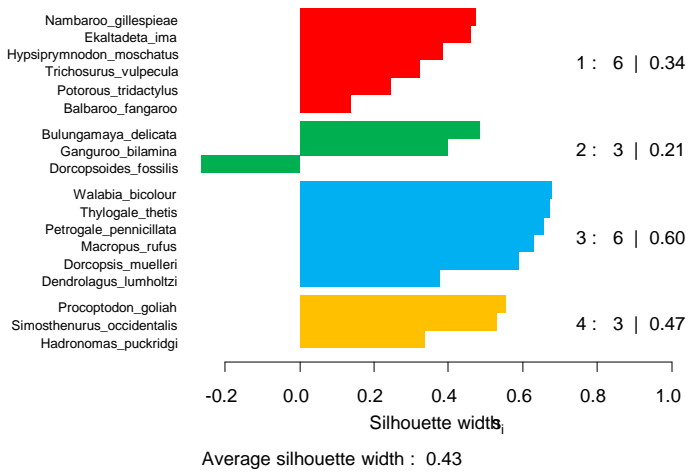
k=2



k=3



k=4



Family Pseudocheiridae

Order Diprotodontia

Springer 1993

Pearson BDC

Negative: 45

Positive: 49

Clusters: 3

Clusterability

Hopkins Statistic: 0.789

Dip test: 0.028

Dip test p-value: 0.784

Spearman BDC

Negative: 44

Positive: 54

Clusters: 2

The Spearman BDC results are very similar to the Pearson BDC. The only difference is additional instances of significant, positive BDC that unite two of the three clusters evident in the Pearson BDC. The average silhouette widths for the Pearson BDC clusters is 0.46 and for the Spearman BDC is 0.56. Hence the Spearman BDC is a substantially better clustering.

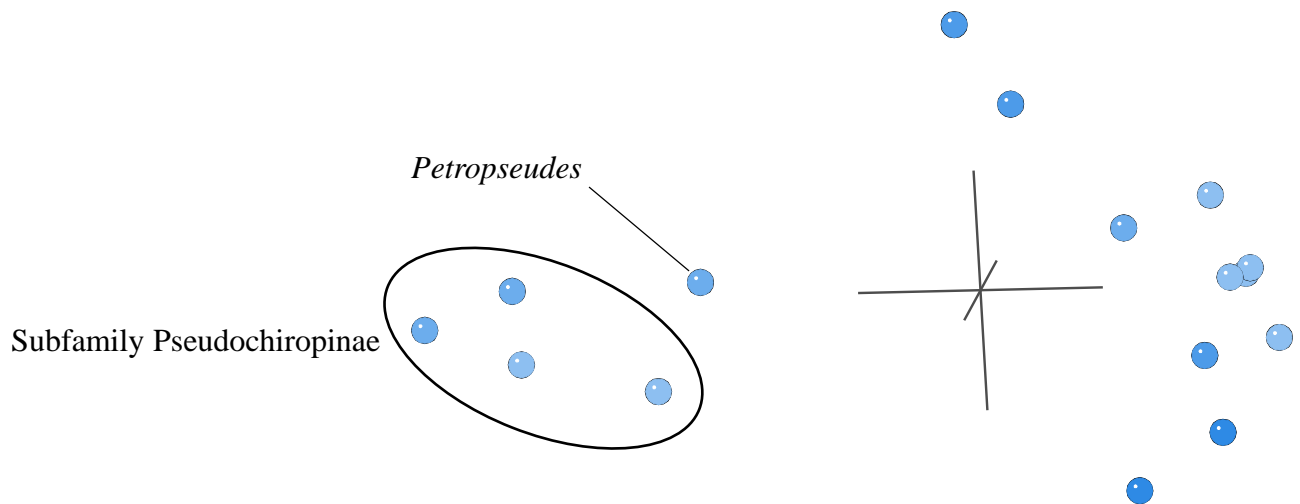
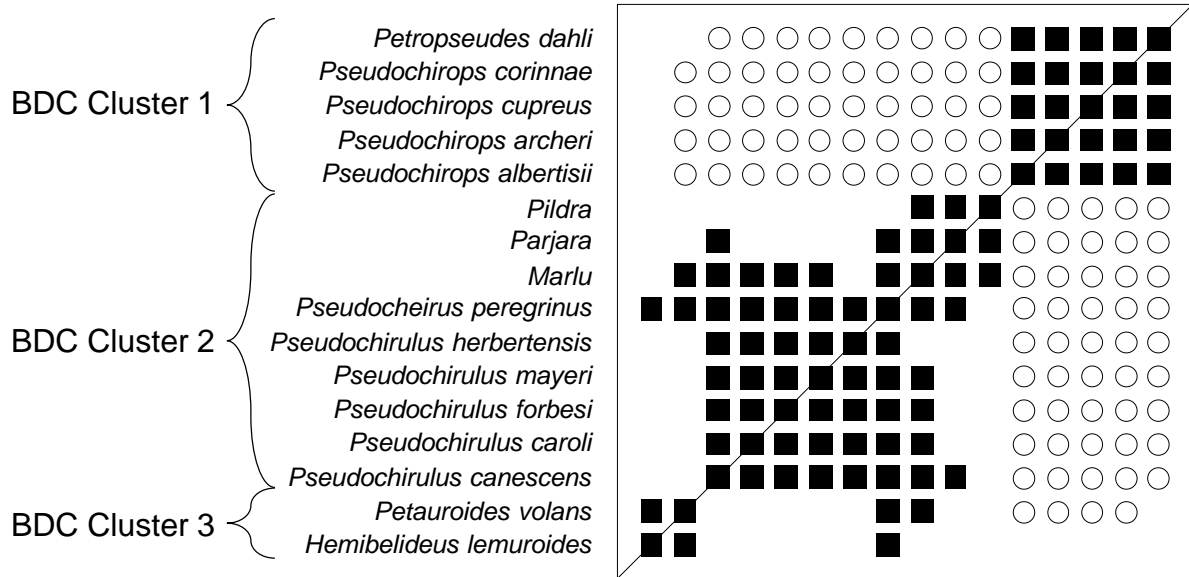
The medoid partitioning and fuzzy analyses produce identical clusters at $k=3$. The medoid and fuzzy partition is not the same as the Pearson BDC partition, with a cluster membership difference of 19%. The three-cluster medoid and fuzzy partition is substantially better than the Pearson BDC clusters, with an average silhouette width of 0.54. At $k=2$, however, the medoid partition, fuzzy analysis, and Spearman BDC agree exactly.

The original conclusion for this dataset are confirmed by these new analyses.

Original conclusion: HB

Updated conclusion: HB

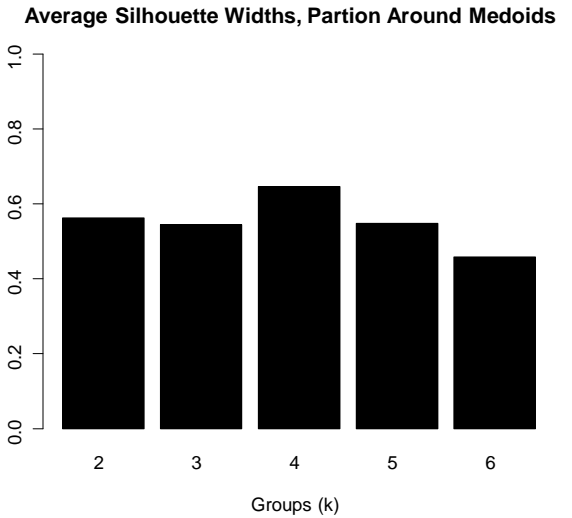
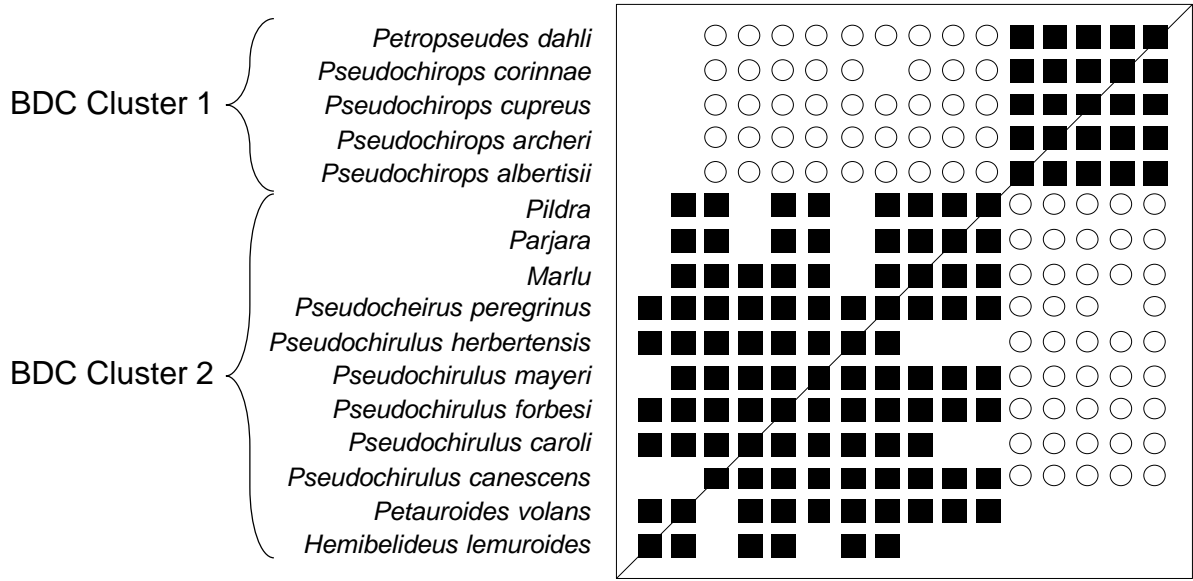
Characters: Craniodental



Order Diprotodontia
Family Pseudocheiridae

Published taxa	16
Published characters	56
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	16
Characters used for calculations	56
Median bootstrap value	87.5
F ₉₀	0.46
Stress of 3D MDS	0.04
k _{min}	4
Conclusion	HB

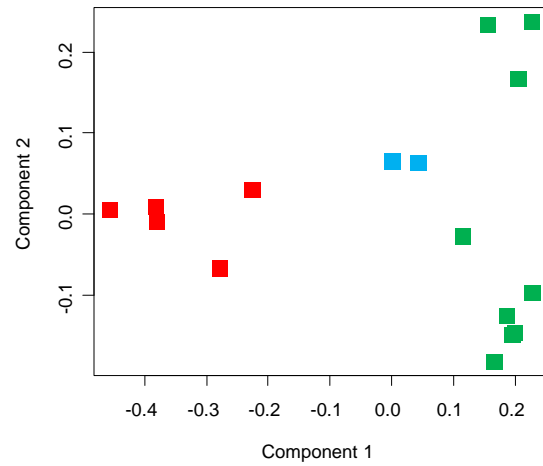
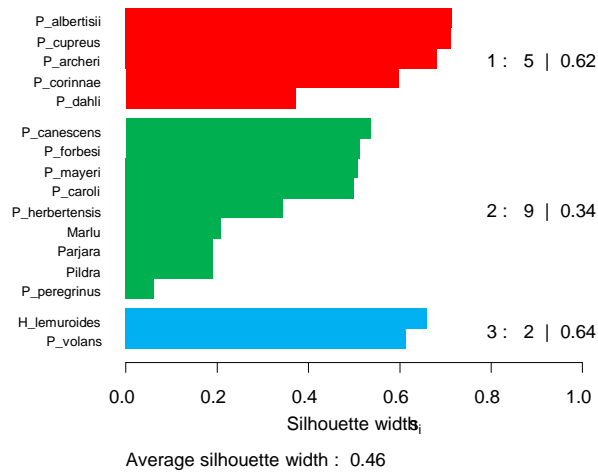
Notes: Two holobaramins: Subfamily Pseudochiropinae + *Petropseudes*, and all other taxa.



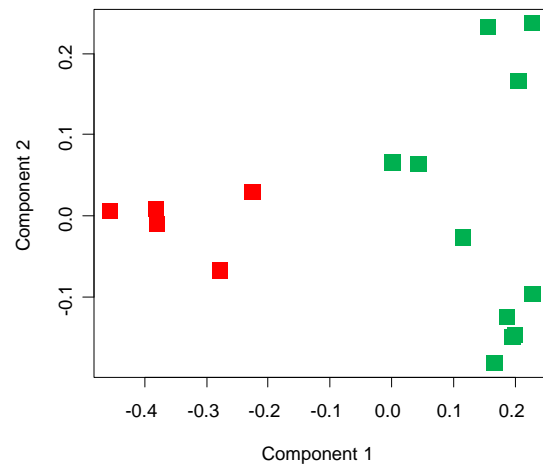
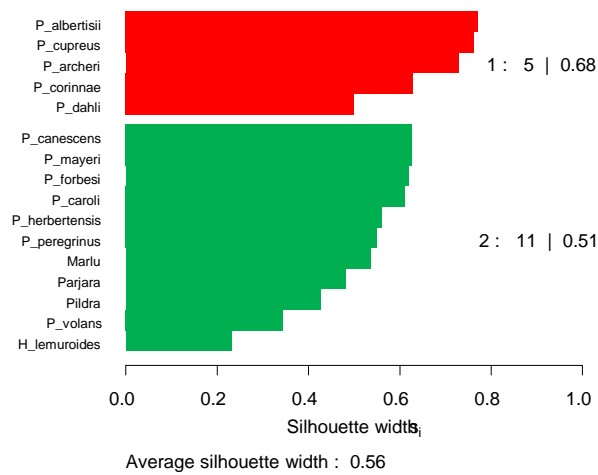
Clade Correspondence: All three BDC clusters contain more than one taxon, and all three are monophyletic in the majority rule consensus tree shown in figure 2b of Springer (1993).

Silhouette plot, BDC partitions

Pearson Correlation

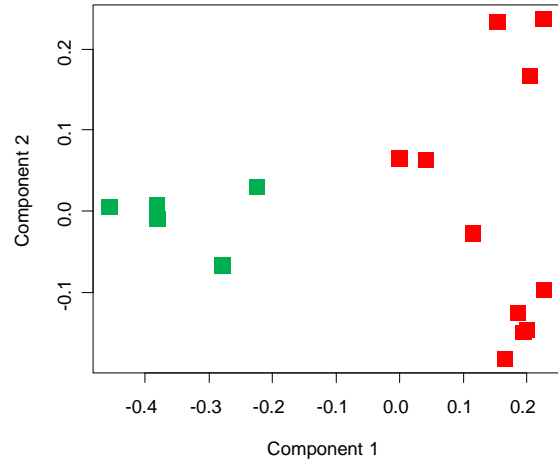
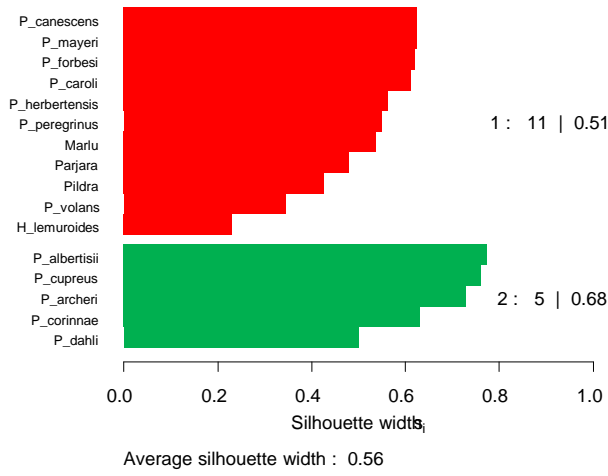


Spearman Correlation

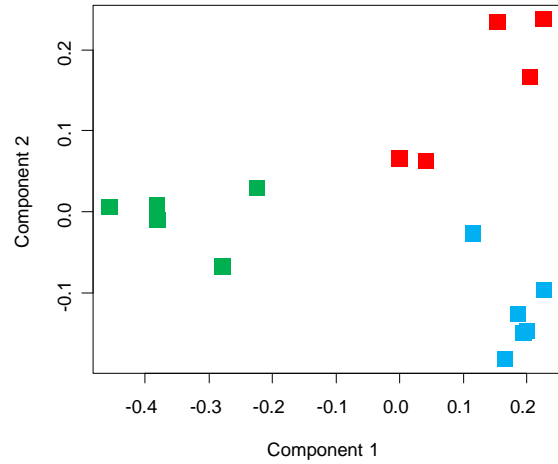
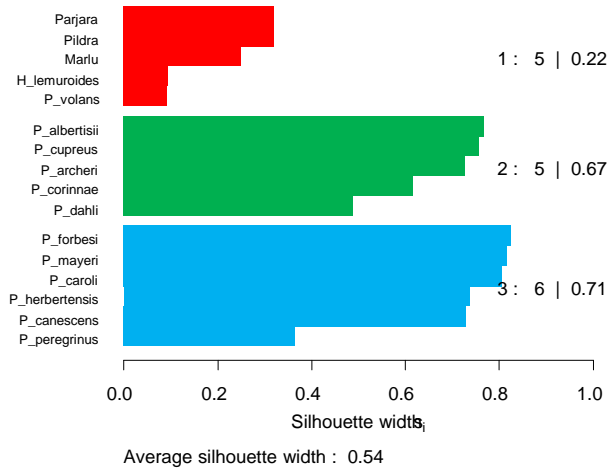


Silhouette plot, Partition Around Medoids

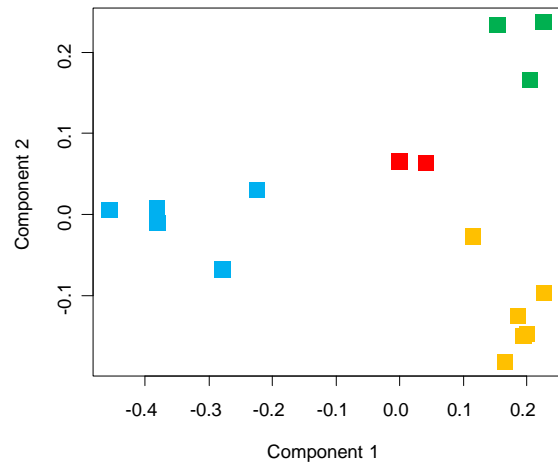
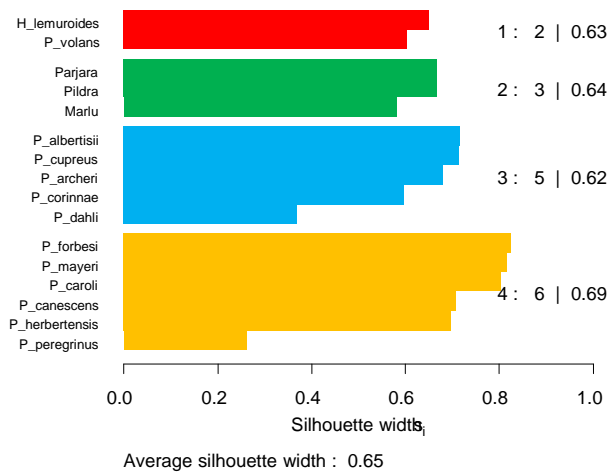
k=2



k=3

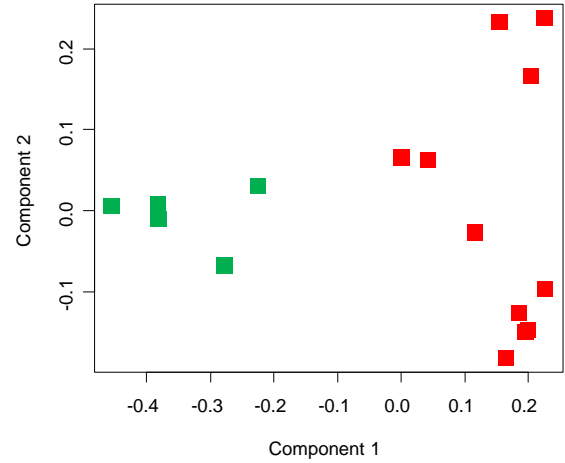
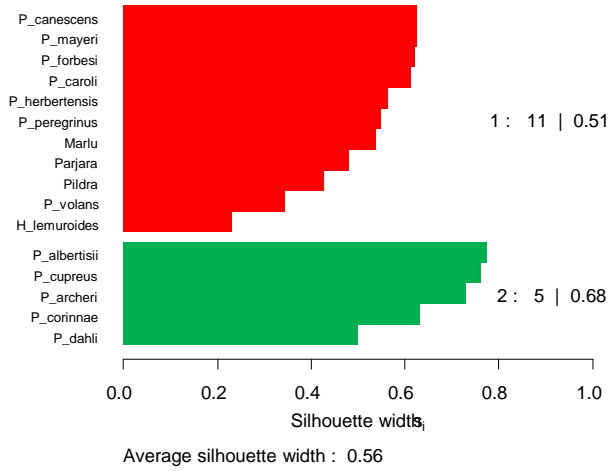


k=4

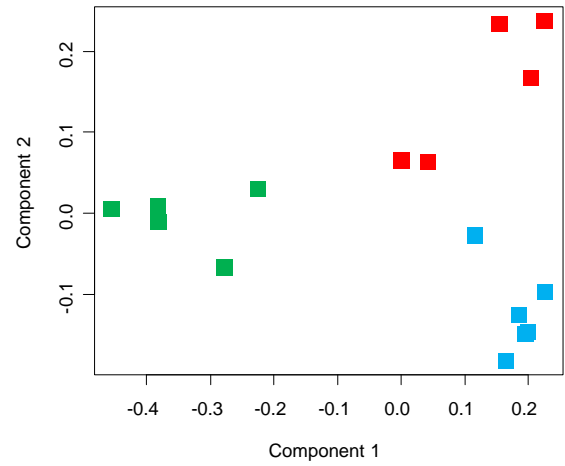
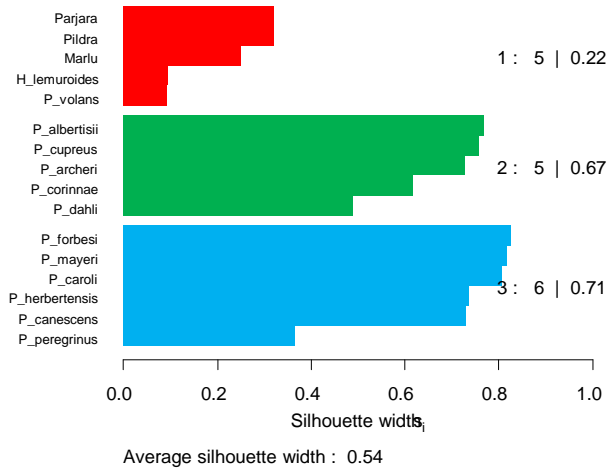


Silhouette plot, Fuzzy Analysis

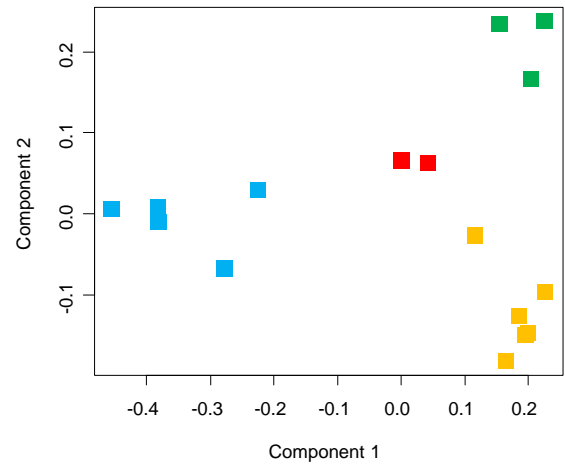
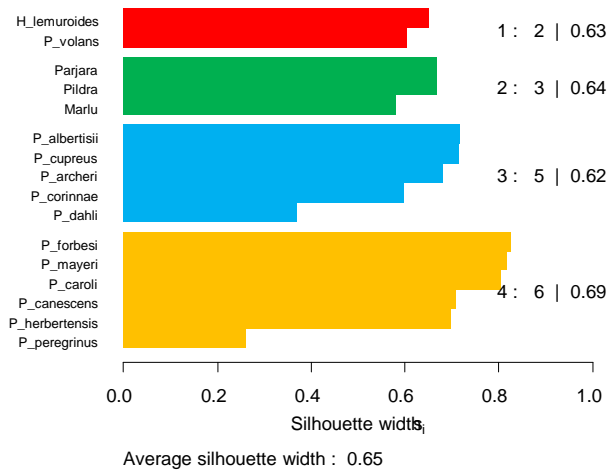
k=2



k=3



k=4



Fossil Phascolarctidae

Order Diprotodontia

Black et al. 2012

Pearson BDC

Negative: 30

Positive: 32

Clusters: 3

Clusterability

Hopkins Statistic: 0.795

Dip test: 0.045

Dip test p-value: 0.136

Spearman BDC

Negative: 30

Positive: 38

Clusters: 3

The Spearman BDC adds only six new instances of significant, positive correlation compared to the Pearson BDC results. These new correlations do not alter the three clusters that are evident in the Pearson BDC results. Those clusters consist of two outgroup clusters and one cluster of phascolarctids. The average silhouette widths for this three-cluster partition is 0.38.

The medoid partition at $k=3$ has an average silhouette value of 0.39 but does not correspond to the partition of the BDC results. The medoid partition at $k=3$ and the BDC results recognize the phascolarctids as a single cluster, but they divide the outgroup taxa into different clusters, resulting in a cluster membership difference of 27%. At $k=2$, however, the medoid partition is substantially better with an average silhouette width of 0.43 and divides the taxa into clusters corresponding to the Phascolarctidae and the outgroup taxa.

The fuzzy analysis at $k=3$ yields a partition identical to the medoid partition at $k=3$, but at $k=2$ the fuzzy partition differs from the medoid partition. The fuzzy analysis places the outgroup *Cercartetus* in the phascolarctid cluster, but this results in a negative silhouette width for *Cercartetus* and an average silhouette width of 0.37. Hence the two-cluster medoid partition is superior to the two-cluster fuzzy partition.

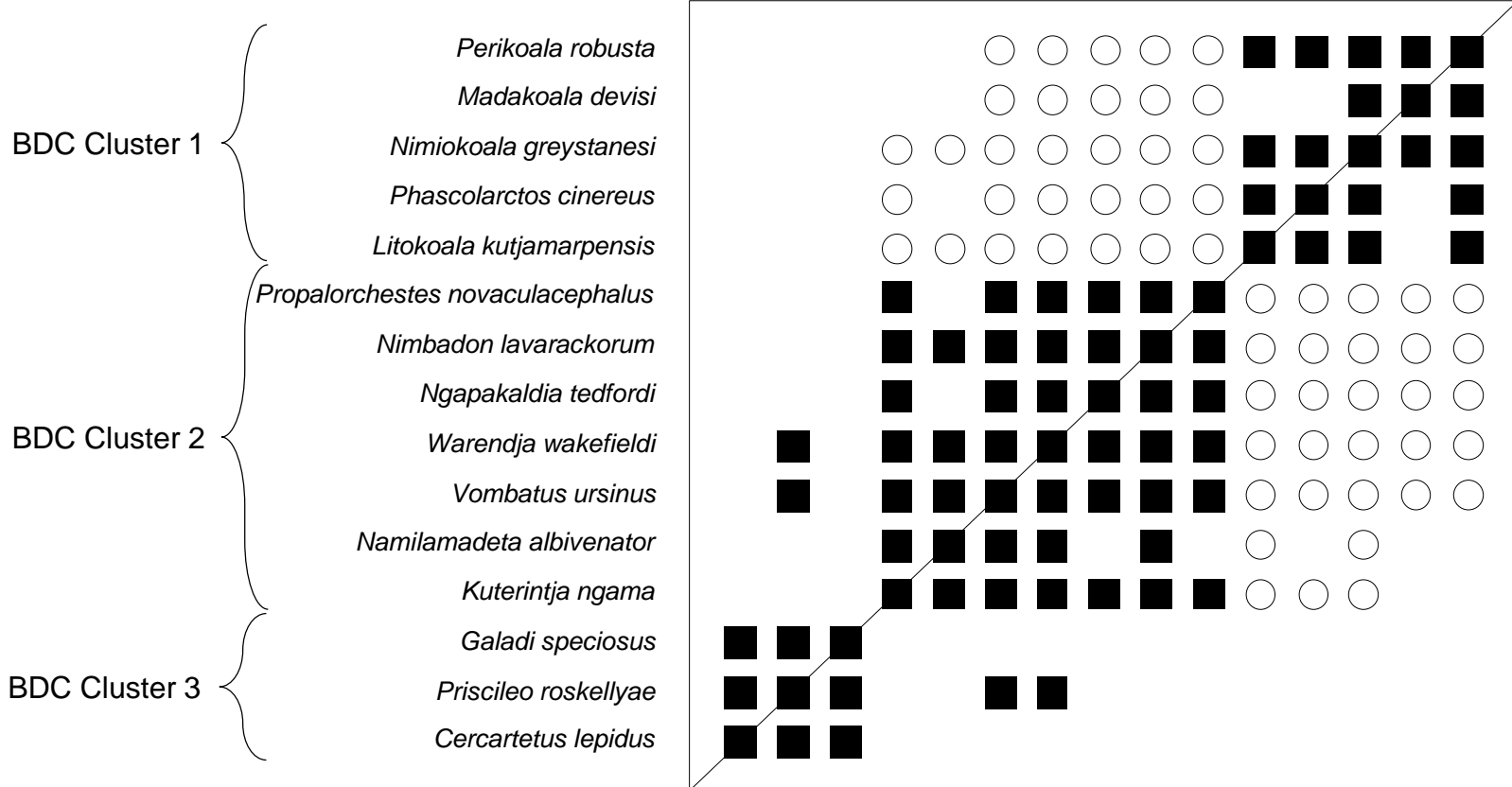
Since all of these analyses (except the two-cluster fuzzy analysis) recognize the phascolarctid cluster, these results confirm the original conclusion of holobaramin.

Original conclusion: HB

Updated conclusion: HB

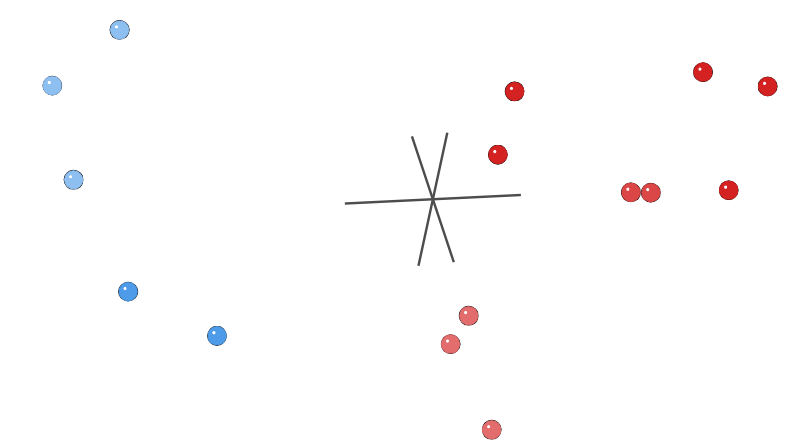
Black, K.H., M. Archer, and S.J. Hand. 2012. New Tertiary koala (Marsupialia, Phascolarctidae) from Riversleigh, Australia, with a revision of phascolarctid phylogenetics, paleoecology, and paleobiodiversity. *Journal of Vertebrate Paleontology* 32:125-138.

Characters: Craniodental

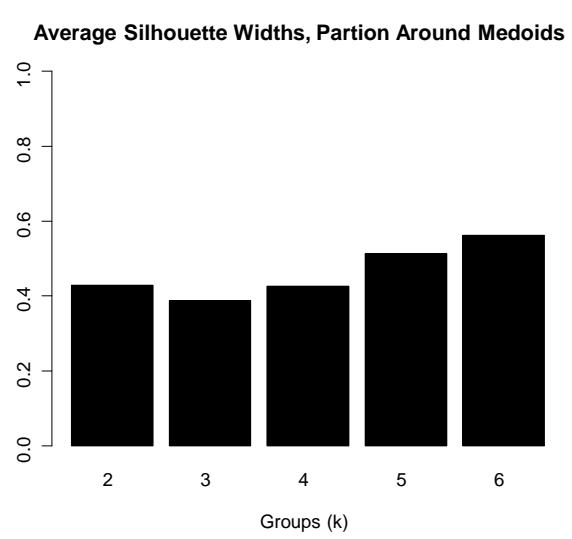
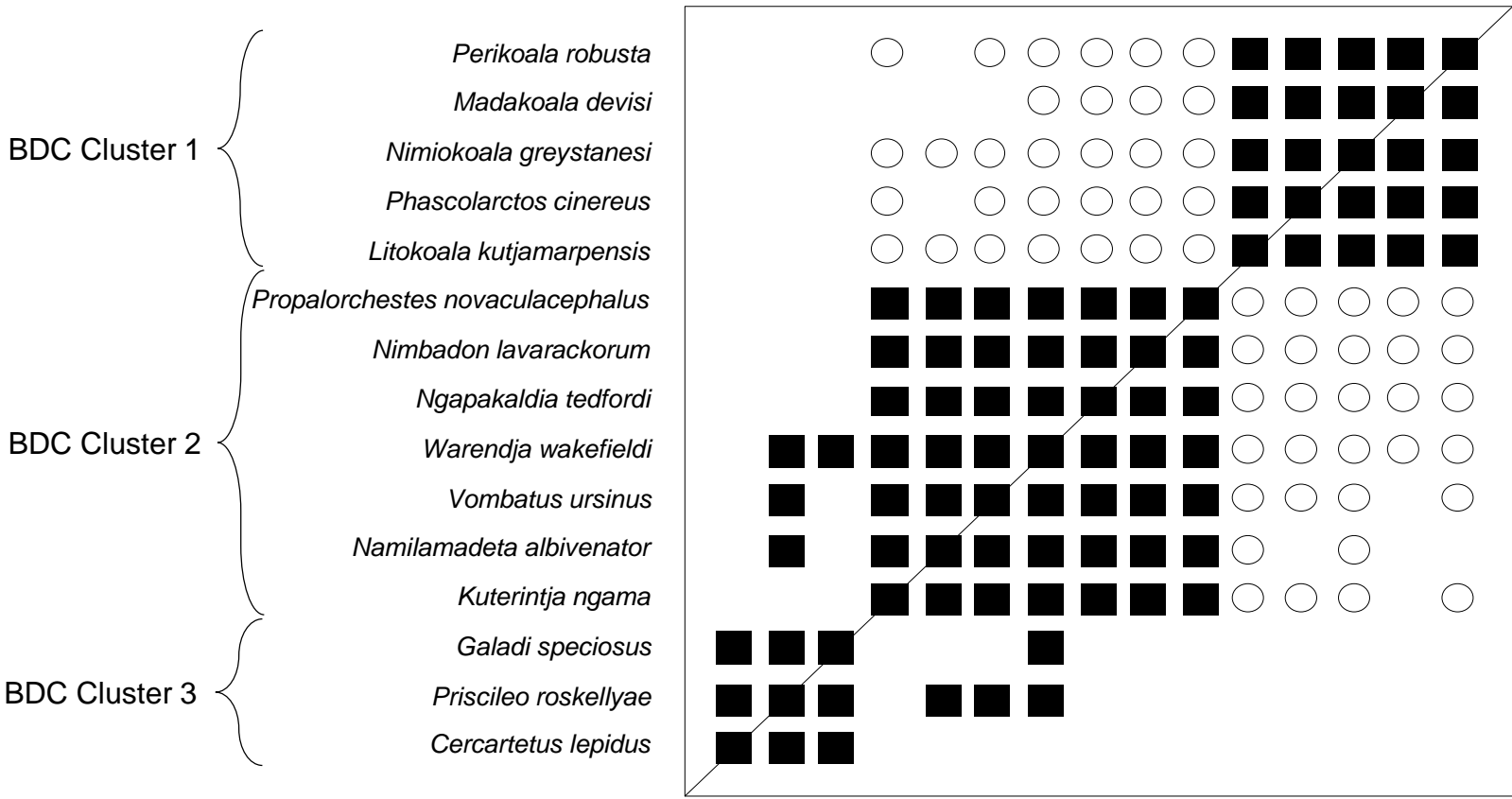


Order Diprotodontia
Family Phascolarctidae

Published taxa	19
Published characters	71
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	15
Characters used for calculations	50
Median bootstrap value	86
F ₉₀	0.38
Stress of 3D MDS	0.1
k _{min}	6
Conclusion	HB



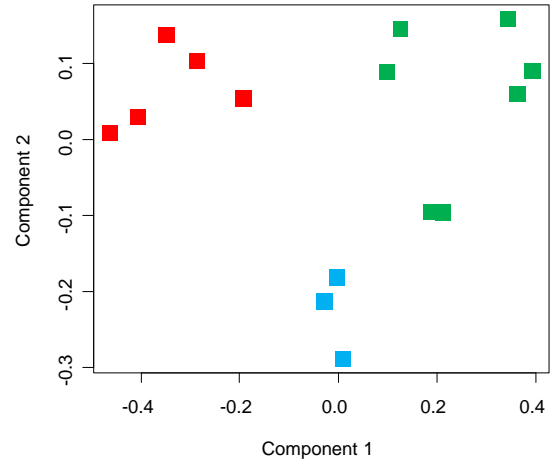
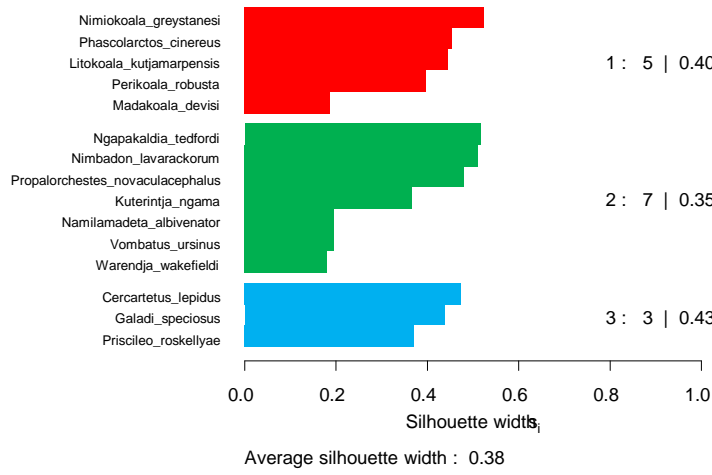
Notes: Phascolarctidae is a holobaramin.



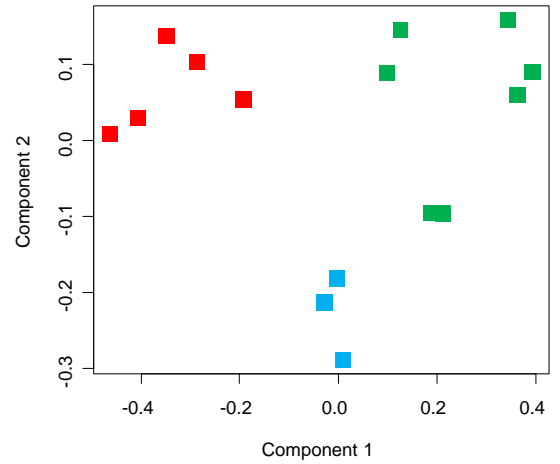
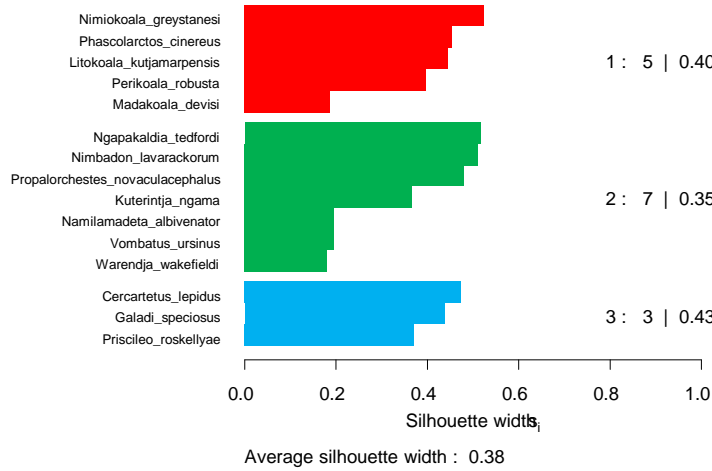
Clade Correspondence: Three BDC clusters are found, all with two or more taxa. Cluster 1 corresponds to clade 4 (Phascolarctidae) of the phylogeny in Figure 2B of Black et al. (2012). Cluster 2 corresponds to clade 8 (Vombatimorphs excluding the basal *Priscileo*) of the same phylogeny. Cluster 3 is not monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

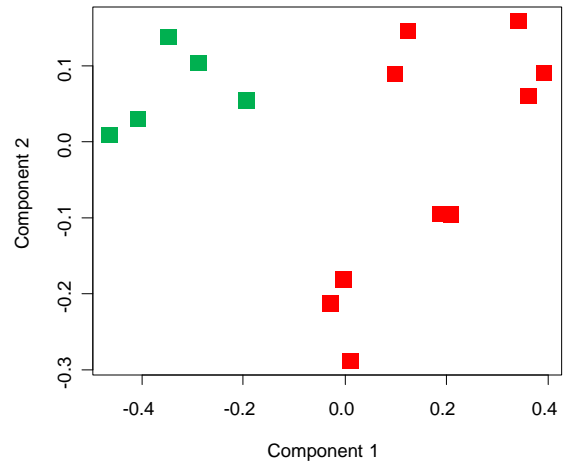
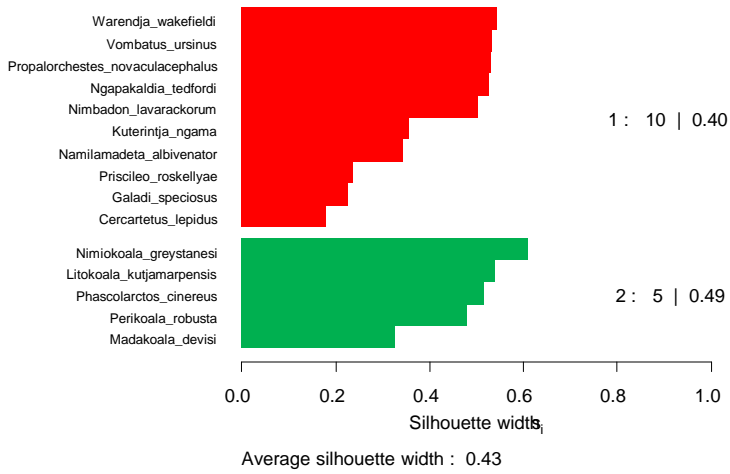


Spearman Correlation

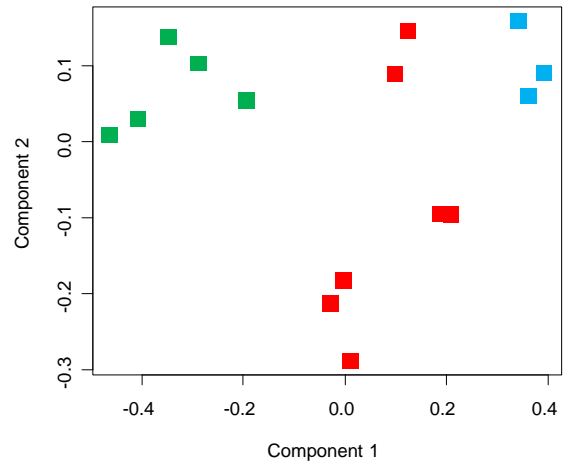
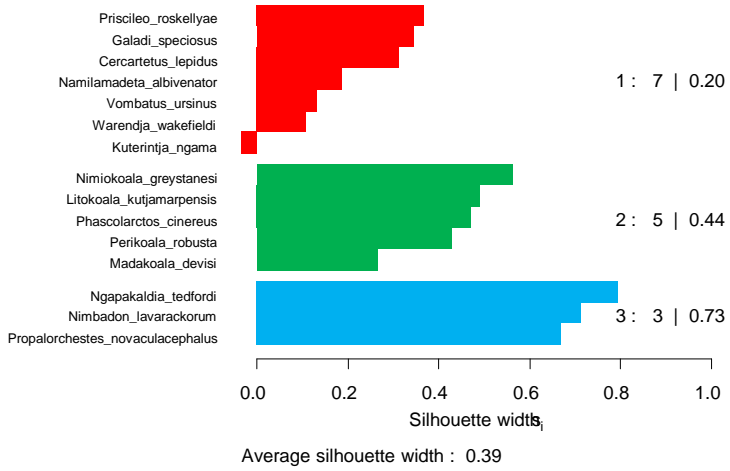


Silhouette plot, Partition Around Medoids

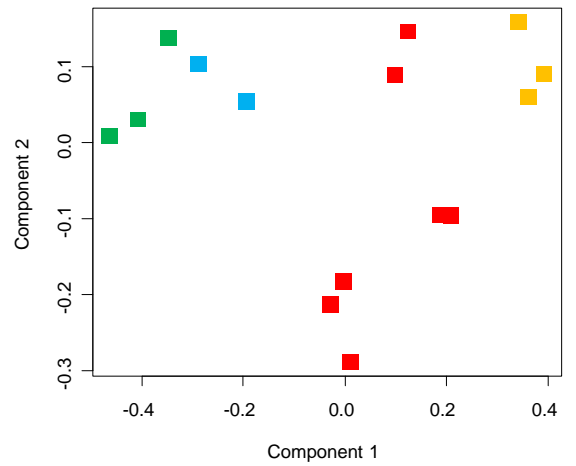
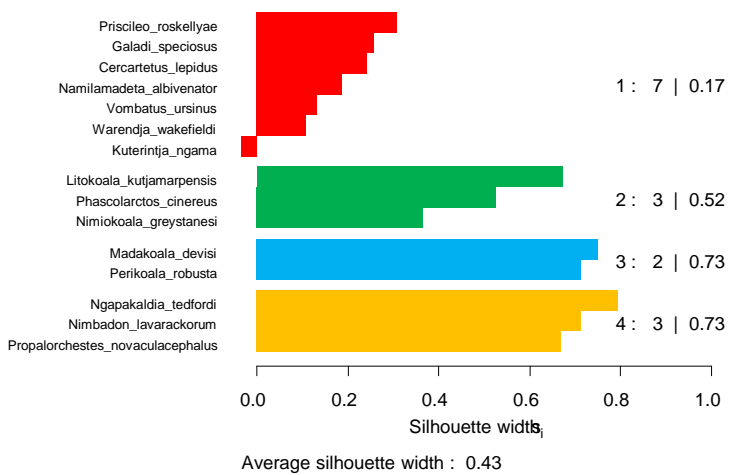
k=2



k=3

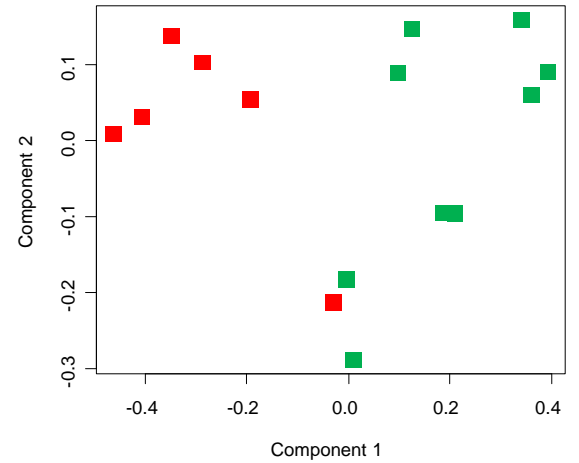
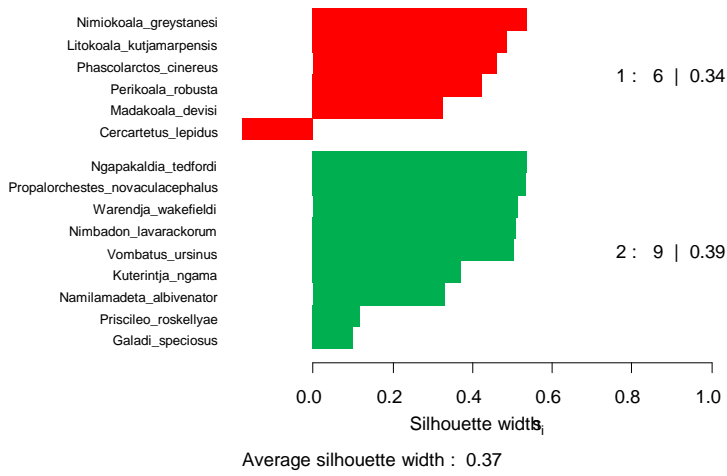


k=4

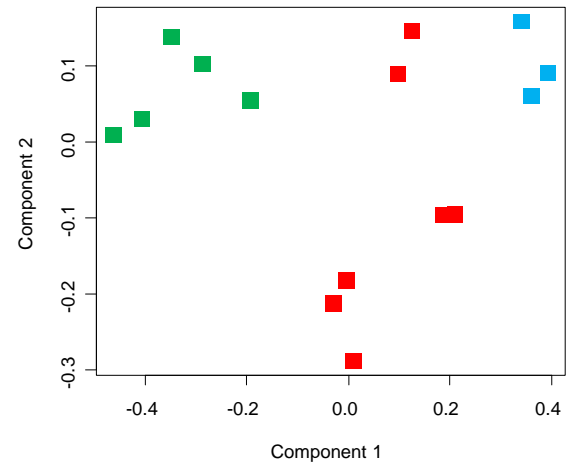
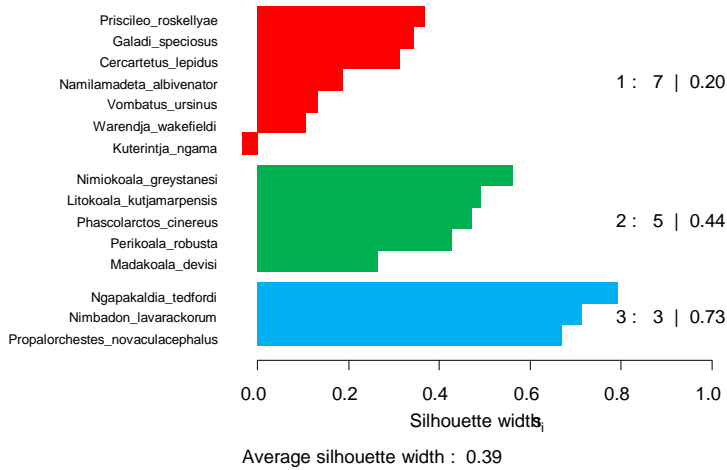


Silhouette plot, Fuzzy Analysis

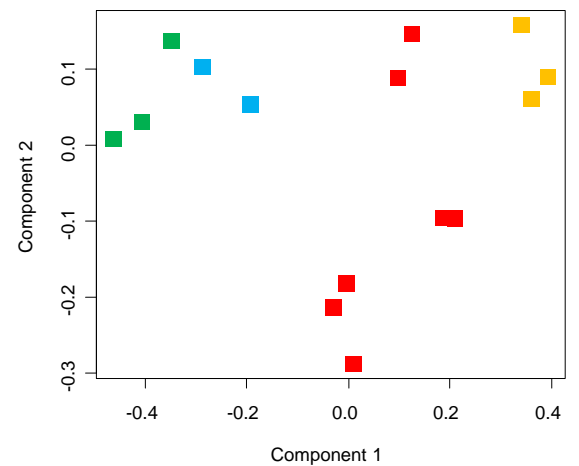
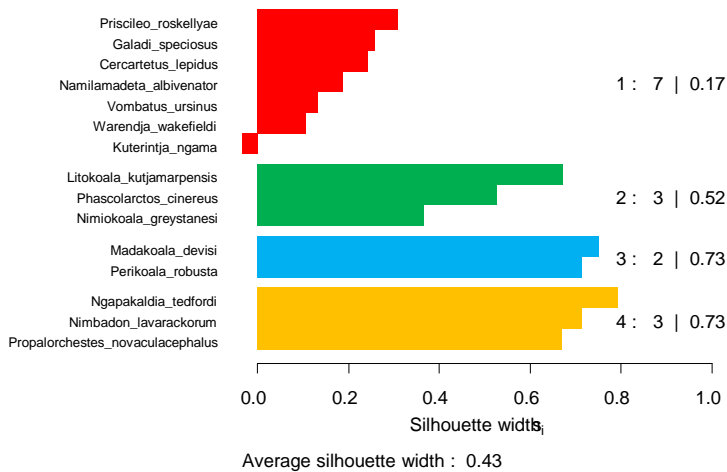
k=2



k=3



k=4



Family Didelphidae

Order Didelphimorphia

Voss and Jansa 2009

Pearson BDC

Negative: 185

Positive: 1013

Clusters: 3

Clusterability

Hopkins Statistic: 0.904

Dip test: 0.018

Dip test p-value: 0.047

Spearman BDC

Negative: 55

Positive: 922

Clusters: 2

Spearman BDC results reveal fewer instances of significant correlation but also support the lumping of two clusters from the Pearson BDC results into one. The common cluster between the two contains four outgroup taxa of Caenolestidae and Peramelidae. In addition, 139 instances of significant, negative BDC separating two of the clusters in the Pearson BDC disappear in the Spearman BDC, and in their place, sixteen instances of significant, positive BDC appear. The average silhouette width for the three clusters in the Pearson BDC results is 0.47, but for the Spearman BDC results, the average silhouette width is 0.59.

The medoid partition for $k=3$ is substantially different from the Pearson BDC results, with an average silhouette width of 0.42 and a cluster membership difference of 22%. Only the cluster of Caenolestidae + Peramelidae is common to both. At $k=2$, the medoid partition is substantially worse than at $k=3$, with an average silhouette width of 0.32. The medoid partition at $k=2$ also does not match the Spearman BDC clustering.

The fuzzy analysis is perhaps most surprising of all. At $k=3$, the average silhouette width is 0.2, and the clusters do not match the medoid partition nor the Pearson BDC. At $k=2$, the average silhouette width is 0.26, and the clusters do not match the medoid partition nor the Spearman BDC.

Given the lack of consistency with these analyses, I suggest that the original conclusion of a possible holobaramin has been rendered much more uncertain. These results are inconclusive.

Original conclusion: HB?

Updated conclusion: Inconclusive

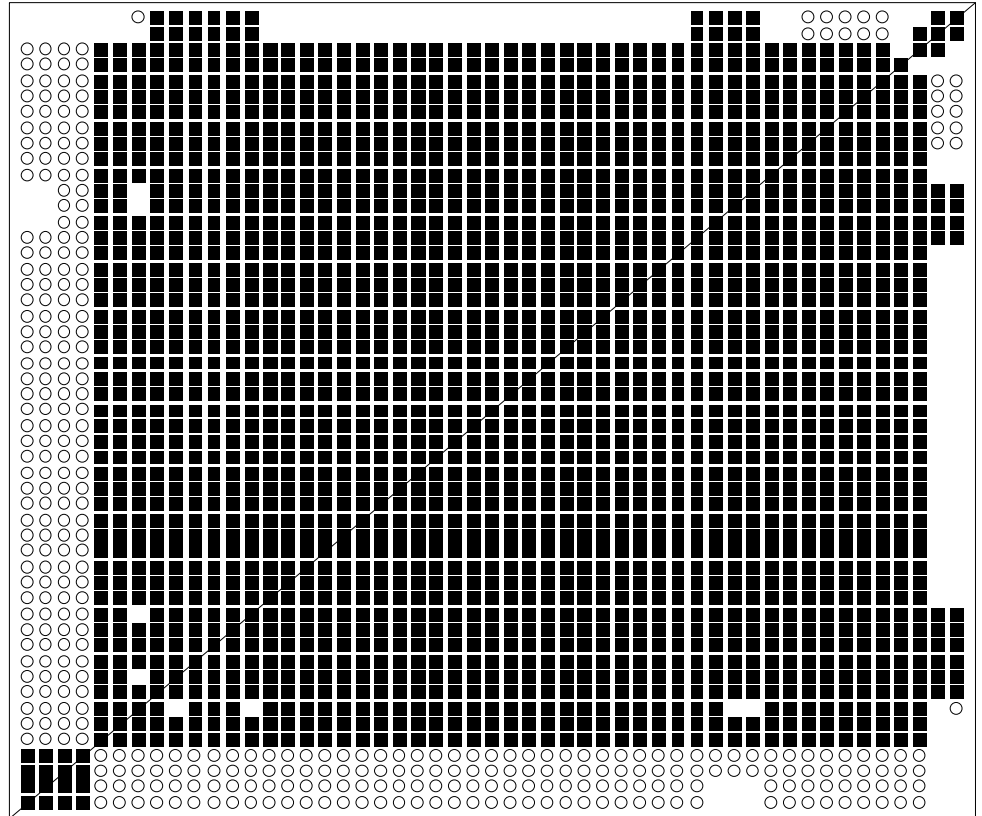
Voss, R.S. and S.A. Jansa. 2009. Phylogenetic relationships and classification of didelphid marsupials, an extant radiation of New World metatherian mammals. *Bulletin of the American Museum of Natural History* 322:1-177. Characters: External morphology, craniodental, karyotype

BDC Cluster 3

Sminthopsis crassicaudata
Murexia longicaudata
Dromiciops gliroides
Lutreolina crassicaudata
Philander opossum
Philander mcilhennyi
Philander frenata
Didelphis marsupialis
Didelphis virginiana
Didelphis albiventris
Chironectes minimus
Monodelphis theresa
Monodelphis peruviana
Monodelphis emiliae
Monodelphis brevicaudata
Metachirus nudicaudatus
Hyladelphys kalinowskii
Gironia venusta
Marmosa rubra
Tlacuatzin canescens
Marmosa robinsoni
Marmosa mexicana
Micoureus paraguayanus
Micoureus regina
Micoureus demerarae
Marmosa murina
Marmosa lepida
Marmosops pinheiroi
Marmosops parvidens
Marmosops incanus
Marmosops noctivagus
Marmosops impavidus
Gracilinanus emiliae
Gracilinanus microtarsus
Gracilinanus agilis
Gracilinanus aceramarcae
Cryptonanus unduaviensis
Cryptonanus chacoensis
Thylamys pallidior
Thylamys venustus
Thylamys pusillus
Thylamys macrurus
Lestodelphys halli
Chacodelphys formosa
Caluromysops irrupta
Caluromys philander
Caluromys lanatus
Perameles gunnii
Echymipera kalubu
Rhyncholestes raphanurus
Caenolestes fuliginosus

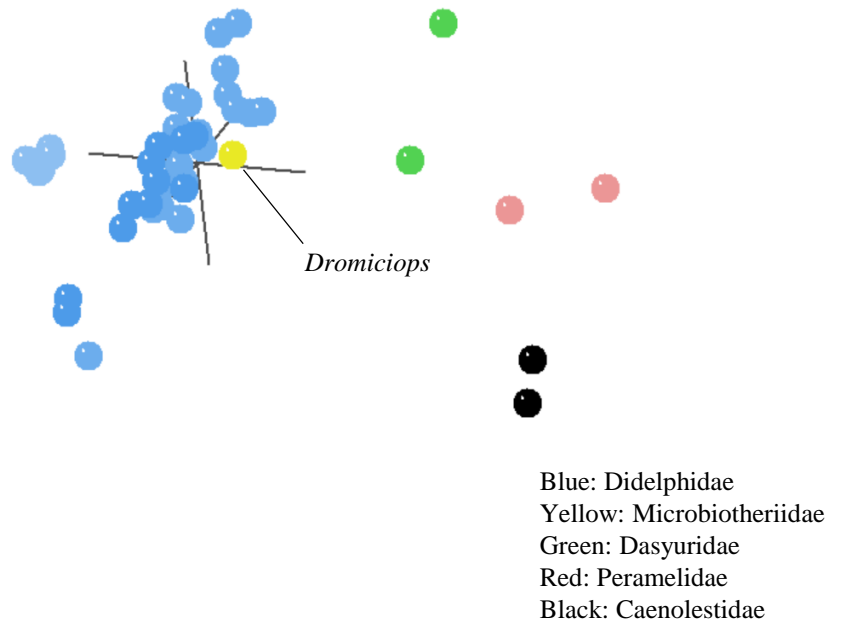
BDC Cluster 1

BDC Cluster 2

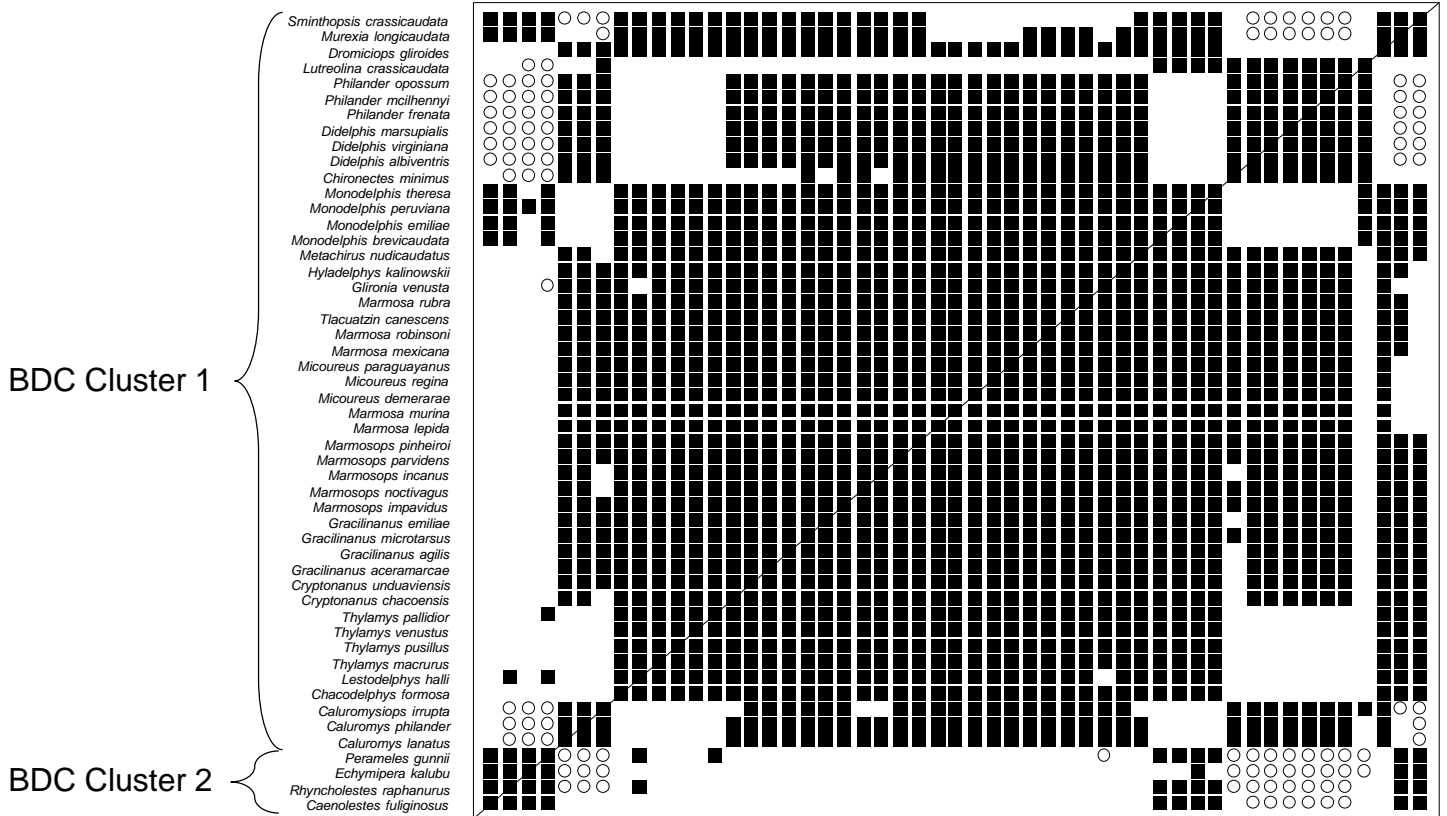


Order Didelphimorphia
 Family Didelphidae

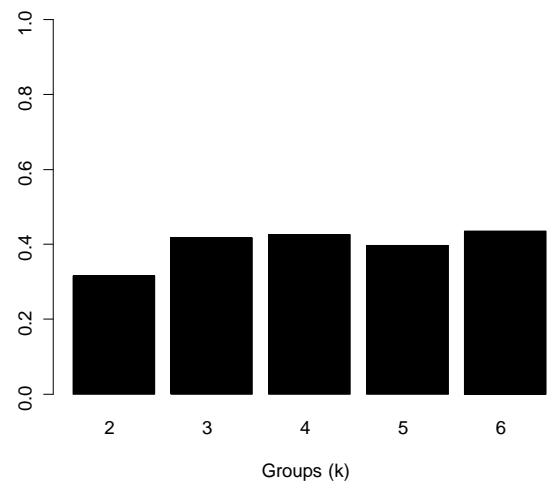
Published taxa	51
Published characters	129
Character relevance	0.95
Taxic relevance	0
Taxa used for calculations	51
Characters used for calculations	115
Median bootstrap value	97
F ₉₀	0.61
Stress of 3D MDS	0.21
k _{min}	8
Conclusion	HB?



Notes: BDC supports inference of discontinuity between two groups: 1. Peramelidae + Caenolestidae and 2. Didelphidae + Microbiotheriidae + Dasyuridae. MDS supports including microbiotheriid *Dromiciops* in Didelphidae, but dasyurids are more distant. Either Didelphidae + *Dromiciops* or Didelphidae + *Dromiciops* + Dasyuridae is a holobaramin.



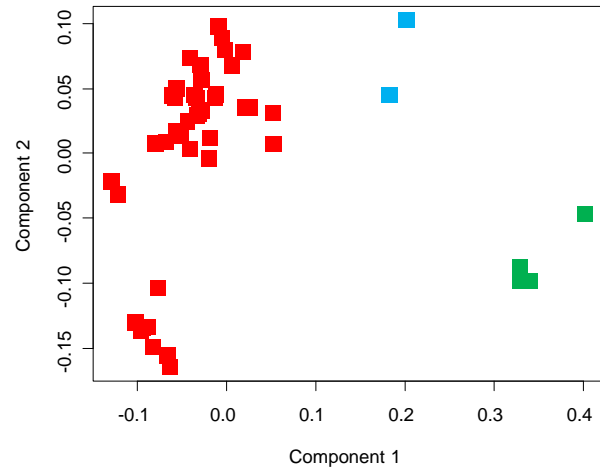
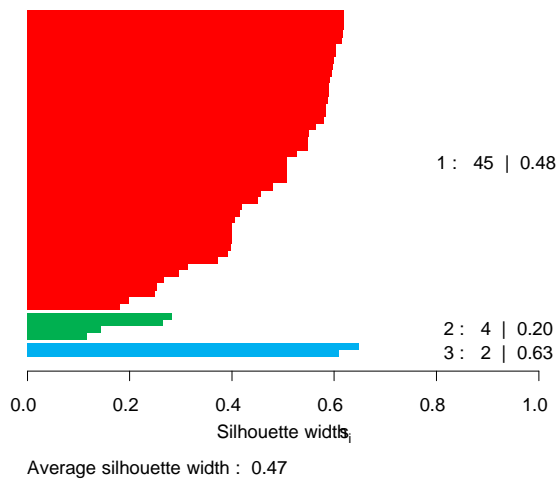
Average Silhouette Widths, Partion Around Medoids



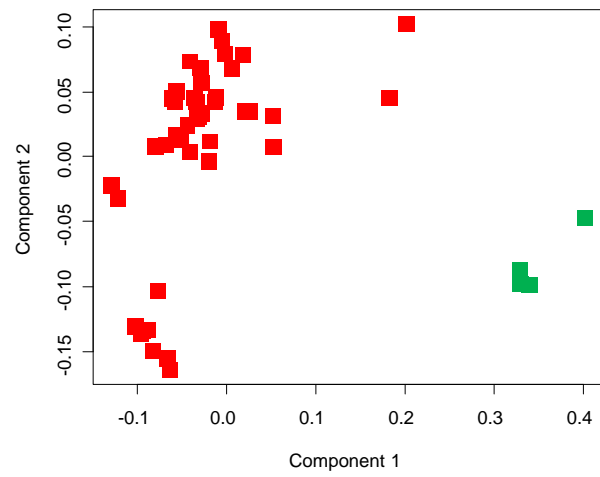
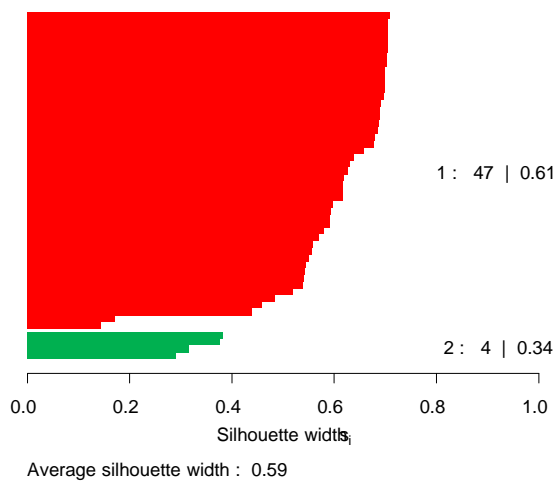
Clade Correspondence: Three BDC clusters can be identified, none of which are singletons. Clusters 2 and 3 consist of outgroup taxa. The phylogeny recorded in Figure 27 of Voss and Jansa (2009) omits the outgroup from the topology, showing only the relationships of the ingroup taxa, which corresponds to Cluster 1. Hence we can only say that Cluster 1 is decisively monophyletic in the published phylogeny.

Silhouette plot, BDC partitions

Pearson Correlation

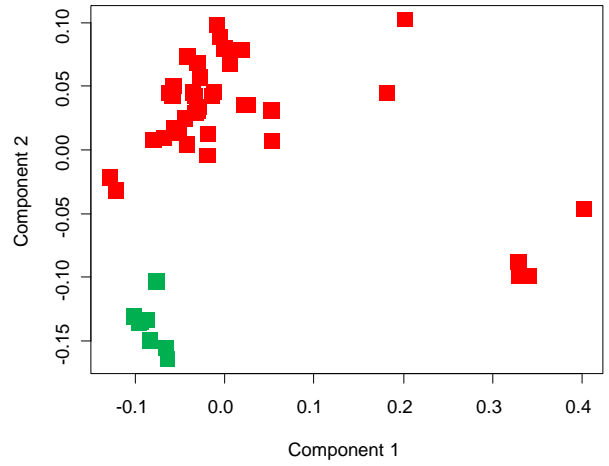
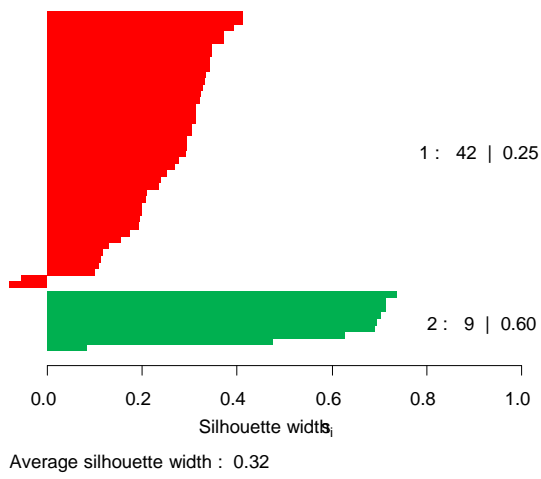


Spearman Correlation

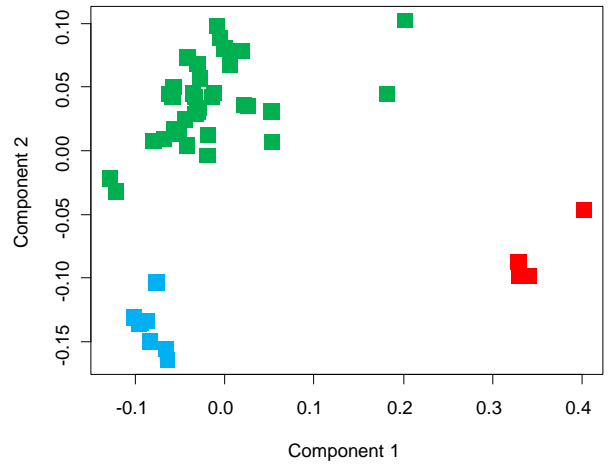
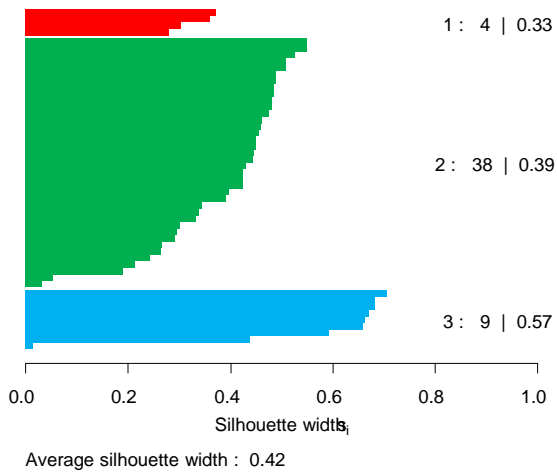


Silhouette plot, Partition Around Medoids

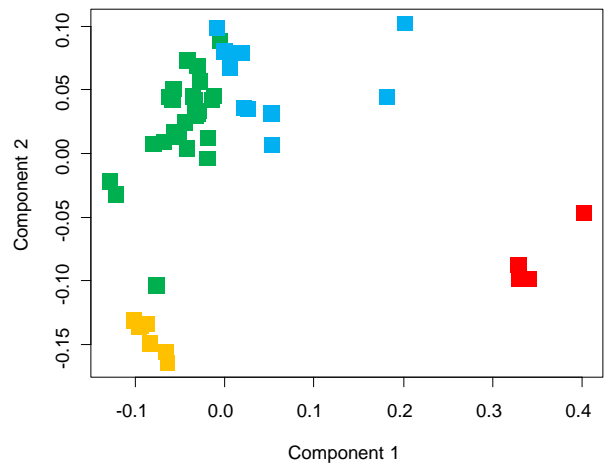
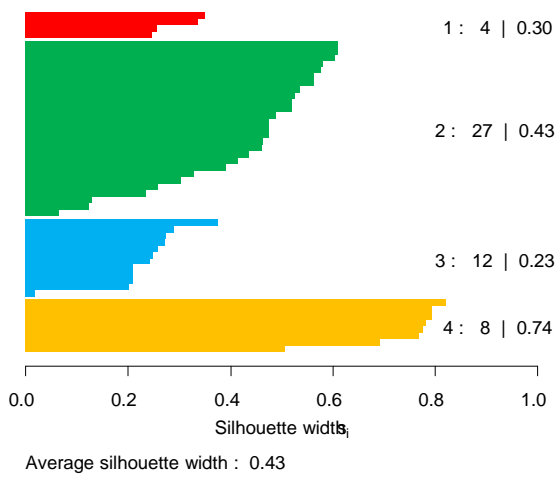
k=2



k=3

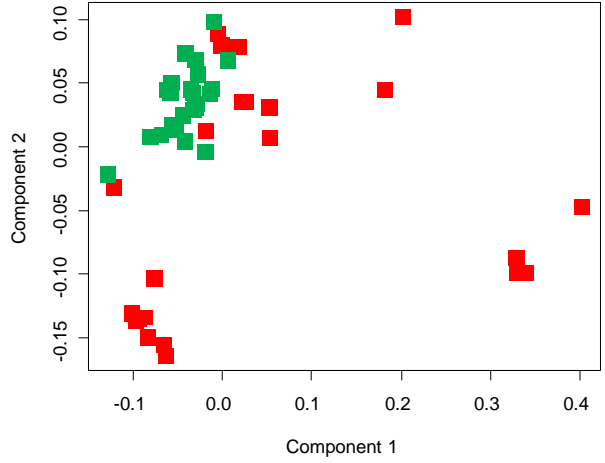
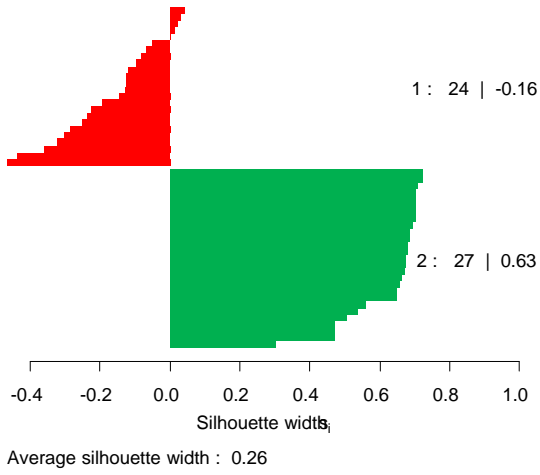


k=4

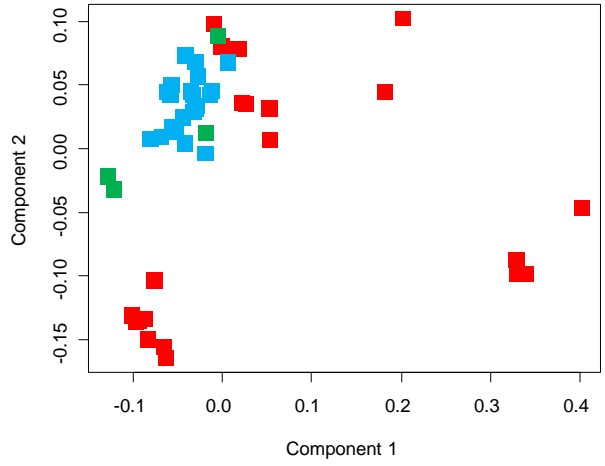
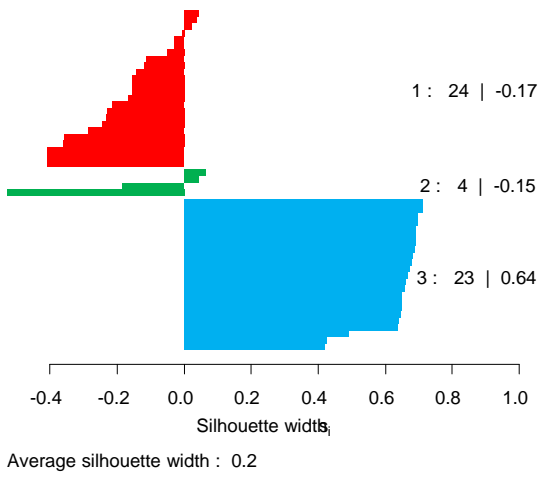


Silhouette plot, Fuzzy Analysis

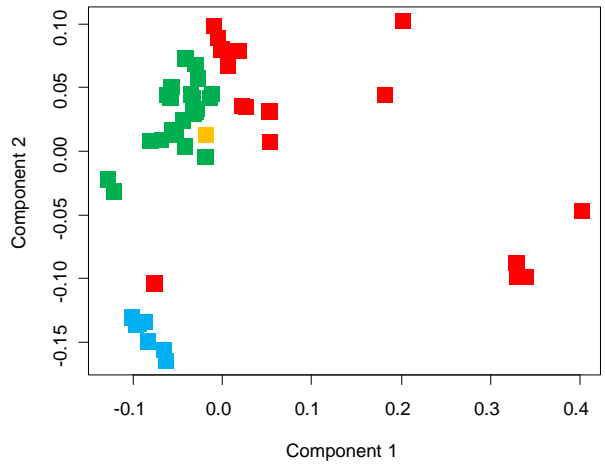
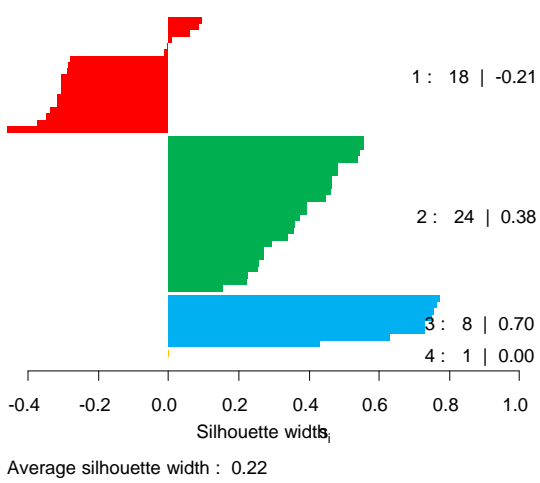
k=2



k=3



k=4



Family Caenolestidae

Order Paucituberculata
Ojala-Barbour et al. 2013

Pearson BDC

Negative: 2
Positive: 11
Clusters: 4

Clusterability

Hopkins Statistic: 0.672
Dip test: 0.075
Dip test p-value: 0.1

Spearman BDC

Negative: 5
Positive: 12
Clusters: 3

The Spearman BDC results add one new instance of significant, positive BDC, uniting two singletons from the Pearson BDC (*Rhyncholestes* and *Lestoros*) into a single cluster. The four-cluster Pearson BDC partition has an average silhouette width of 0.54, and the three-cluster Spearman BDC partition is substantially better with an average silhouette width of 0.65.

Medoid partitioning at k=4 renders clusters exactly the same as the Pearson BDC clusters, and medoid partitioning at k=3 yields clusters exactly the same as the Spearman BDC clusters. Fuzzy analysis at k=3 gave clusters exactly the same as three-cluster medoid partitioning and the Spearman BDC clusters. Fuzzy analysis at k=4 failed.

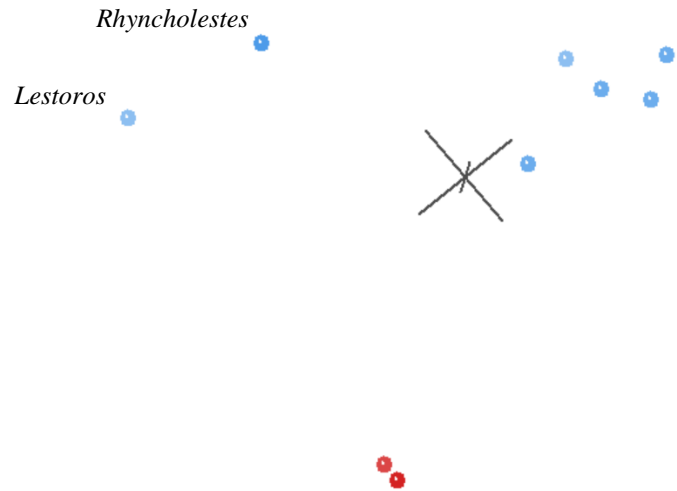
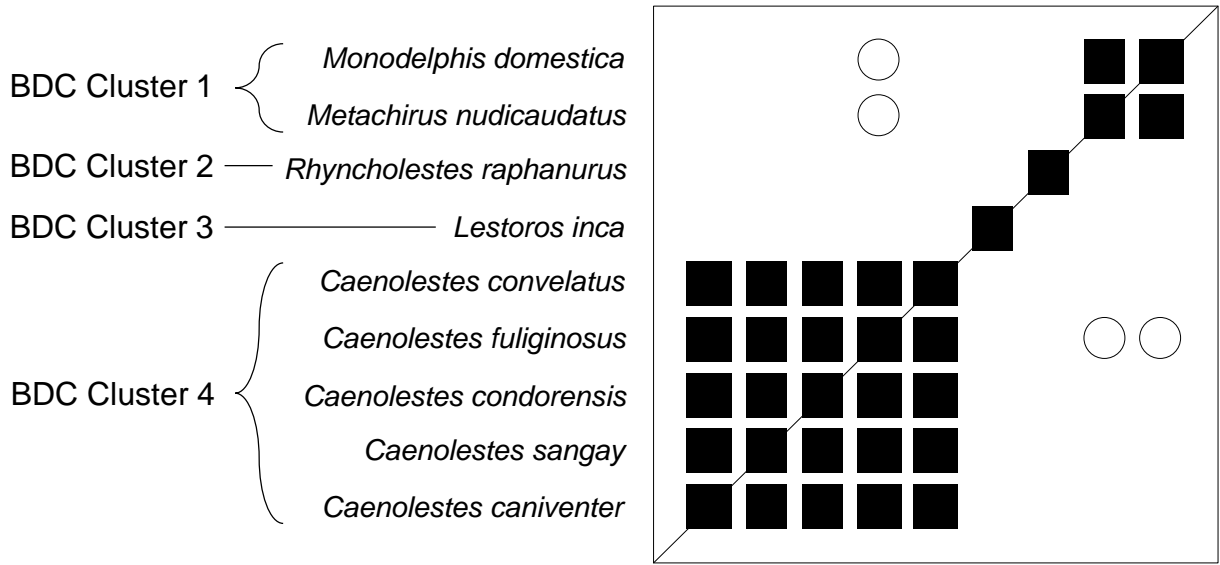
These results reinforce the original conclusion that genus *Caenolestes* is a monobaramin. Significant, negative BDC remains sporadic and insufficient to conclude a discontinuity is present.

Original conclusion: MB

Updated conclusion: MB

Ojala-Barbour, R., C.M. Pinto, M.J. Brito V.L. Albuja T.E. Lee Jr, and B.D. Patterson. 2013. A new species of shrew-opossum (Paucituberculata: Caenolestidae) with a phylogeny of extant caenolestids. *Journal of Mammalogy* 94:967-982.

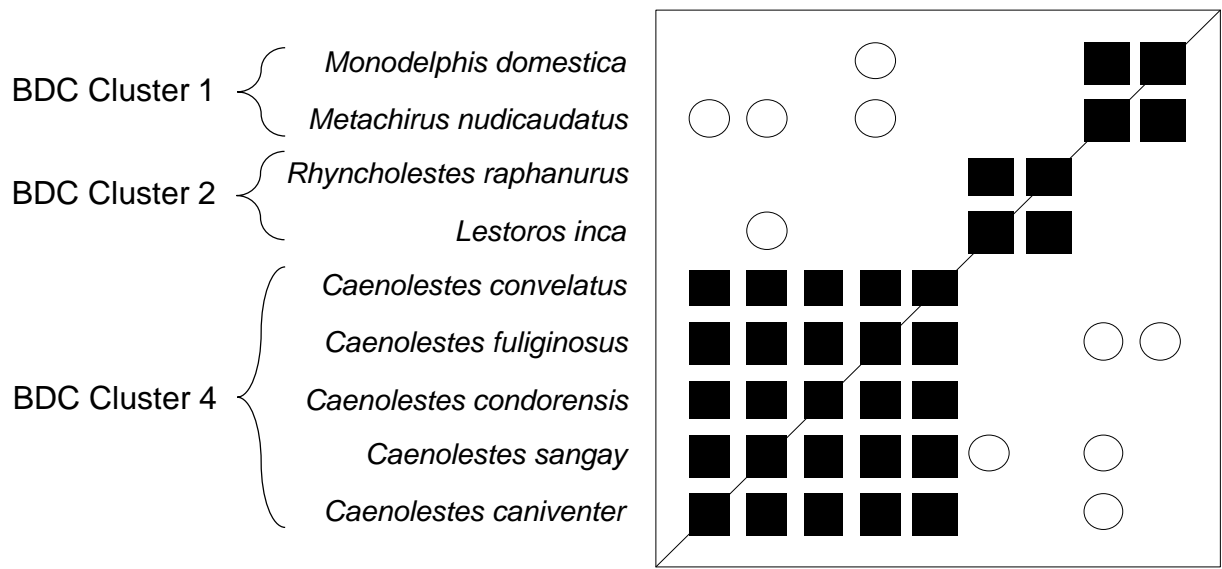
Characters: External morphology, craniodental



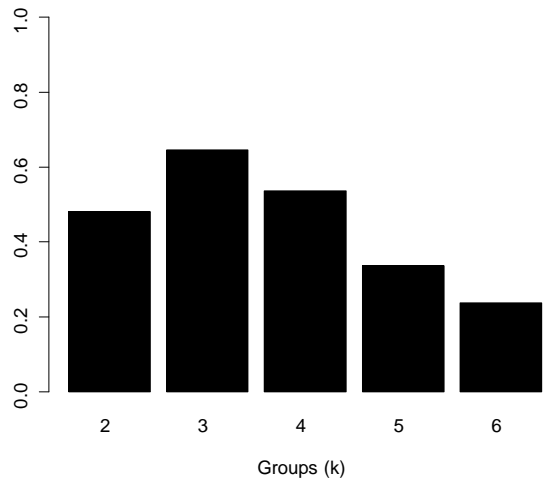
Order Paucituberculata
Family Caenolestidae

Published taxa	9
Published characters	33
Character relevance	0.95
Taxic relevance	0
Taxa used for calculations	9
Characters used for calculations	33
Median bootstrap value	94
F ₉₀	0.56
Stress of 3D MDS	0.08
k _{min}	5
Conclusion	MB

Notes: BDC correlations between *Caenolestes* species suggests that at minimum, *Caenolestes* is a monobaramin. There is no evidence that would suggest continuity between the three caenolestid genera or discontinuity of any kind.



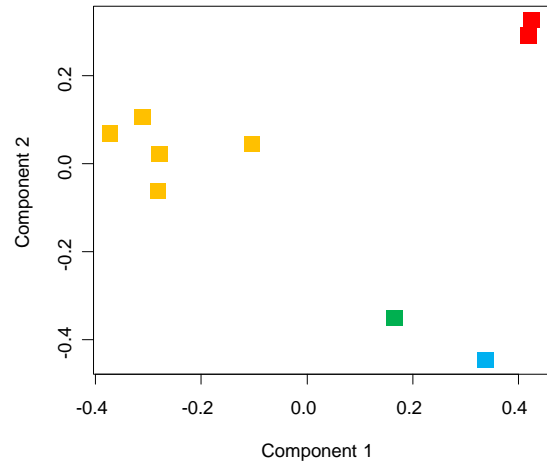
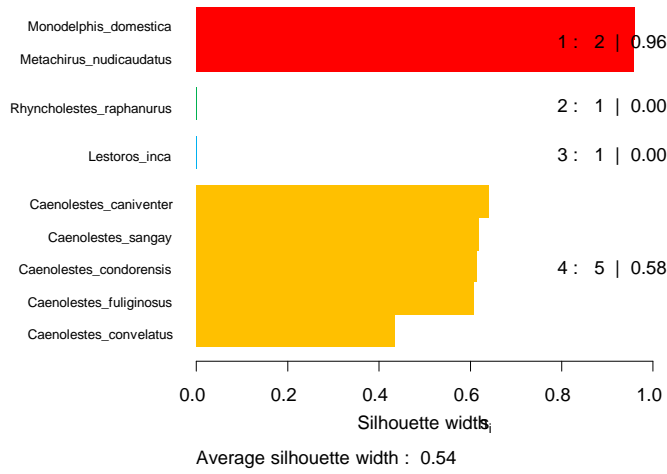
Average Silhouette Widths, Partion Around Medoids



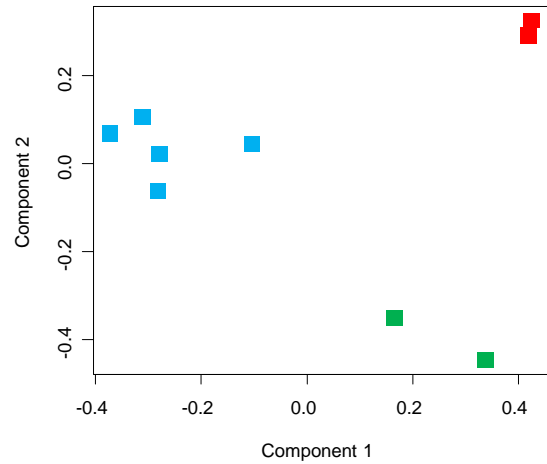
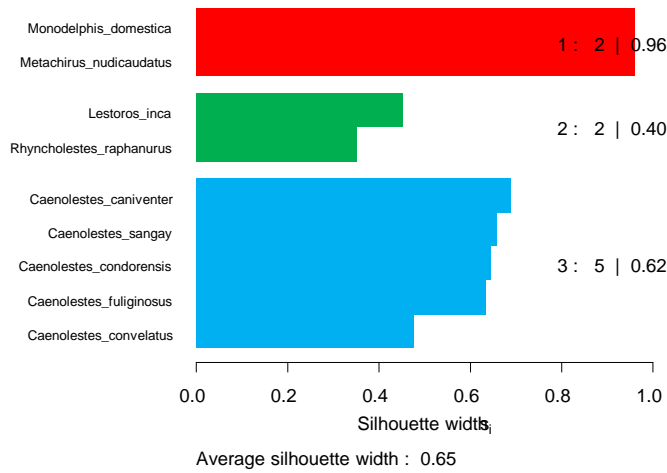
Clade Correspondence: Of the four clusters identified in the BDC, clusters 2 and 3 are both singletons. In the phylogeny in Figure 7b of Ojala-Barbour et al. (2013), clusters 1 and 4 are both monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

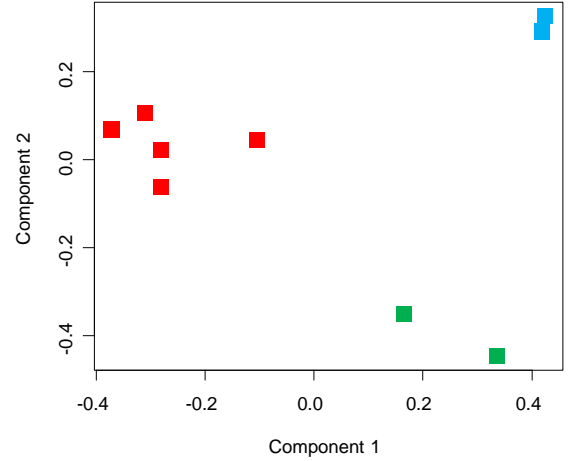
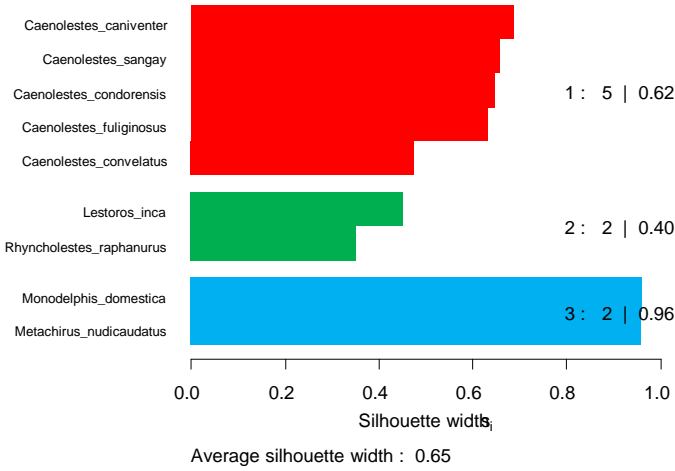


Spearman Correlation

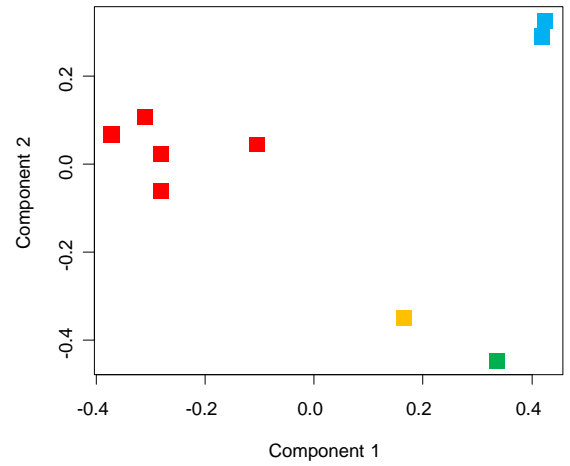
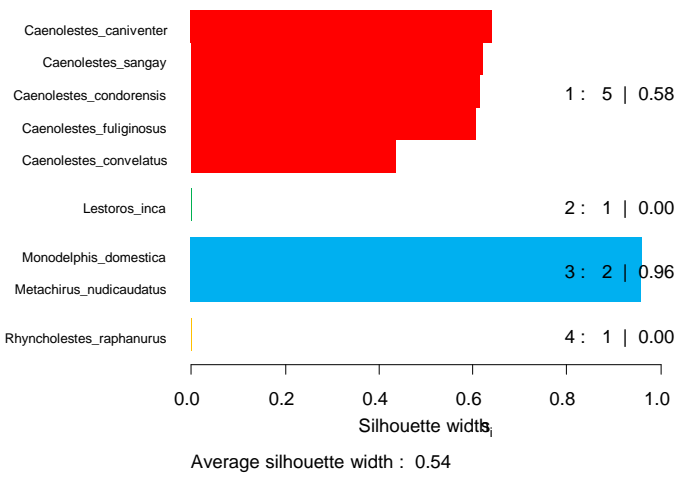


Silhouette plot, Partition Around Medoids

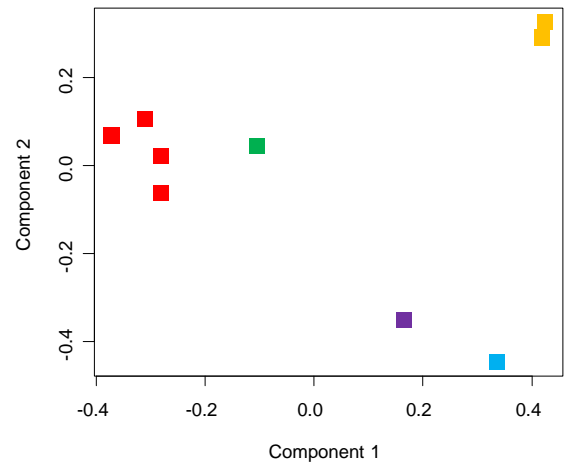
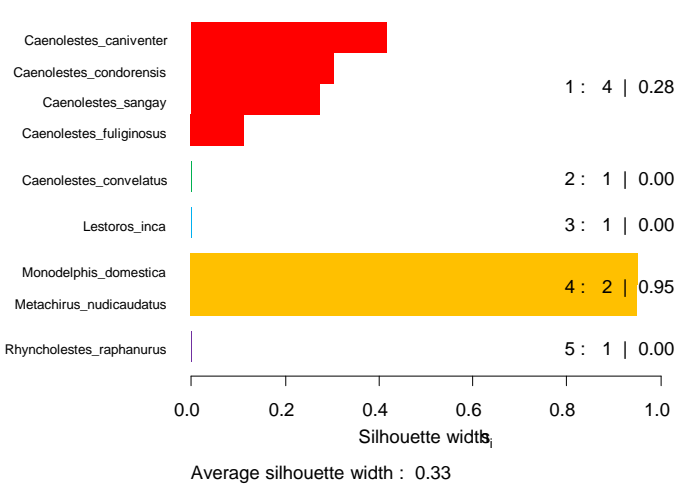
k=3



k=4

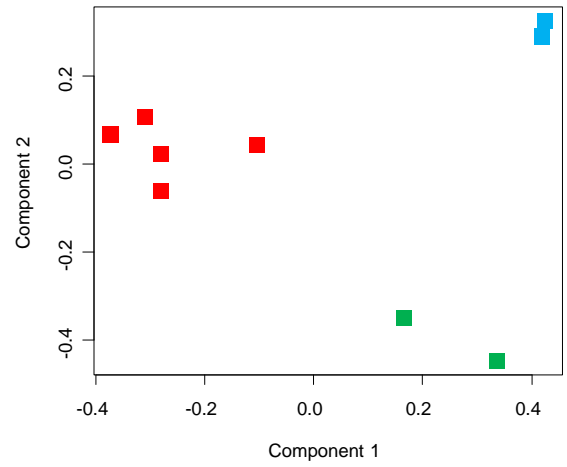
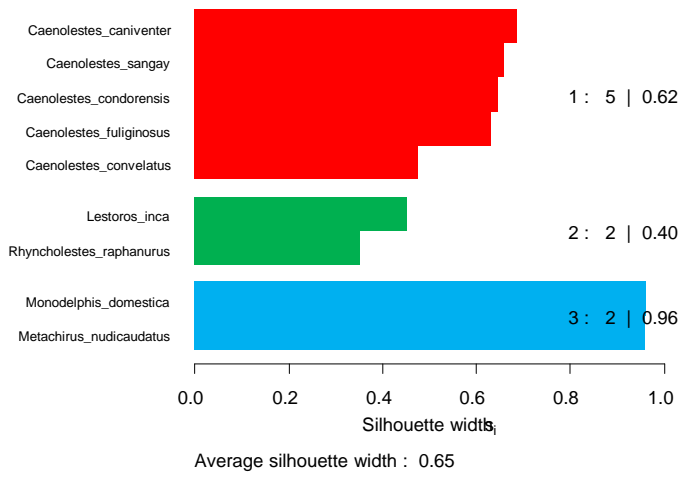


k=5



Silhouette plot, Fuzzy Analysis

k=3



Family Hathliacynidae

Order Sparassodonta

Forasiepi et al. 2006

Pearson BDC

Negative: 8

Positive: 16

Clusters: 4

Clusterability

Hopkins Statistic: 0.77

Dip test: 0.057

Dip test p-value: 0.323

Spearman BDC

Negative: 3

Positive: 15

Clusters: 3

Pearson BDC results indicate four clusters with an average silhouette width of 0.52. The Spearman BDC results are very similar, except that *Prothylacynus*, a singleton in the Pearson BDC results, is definitively joined to a cluster also containing *Borhyaena* and *Arctodictis*. The average silhouette width for the three-cluster Spearman BDC results is 0.58, which is slightly higher than the Pearson BDC partition. The presence of significant, negative correlation between the clusters in the Pearson BDC is largely absent in the Spearman BDC.

Clusters identified from a medoid partitioning at k=4 are exactly the same as those identified in the Pearson BDC results. Clusters identified in a medoid partitioning at k=3 are exactly the same as those identified in the Spearman BDC results.

Fuzzy analysis for k=3 agrees exactly with the three-cluster medoid partition and the Spearman BDC clusters. Fuzzy analysis for k=4 presents a different partition from the other four-cluster analyses, but the average silhouette width was 0.33, which is substantially worse.

The original conclusion that Hathliacynidae + *Lycopsis* could be a holobaramin seems partially vindicated by these results. The Spearman BDC, medoid partitioning at k=3 and k=4, and fuzzy analysis at k=3 all support recognizing this group of taxa. However, unlike the Pearson BDC, the significant, negative correlations that implied the presence of a discontinuity surrounding this group of taxa is largely absent from the Spearman BDC. Hence, the conclusion should probably be downgraded to a monobaramin.

Original conclusion: HB?

Updated conclusion: MB

Forasiepi, A.M., M.R. Sánchez-Villagra, F.J. Goin, M. Takai, N. Shigehara, and R.F. Kay. 2006. A new species of Hathliacynidae (Metatheria, Sparassodonta) from the middle Miocene of Quebrada Honda, Bolivia. *Journal of Vertebrate Paleontology* 26:670-684.

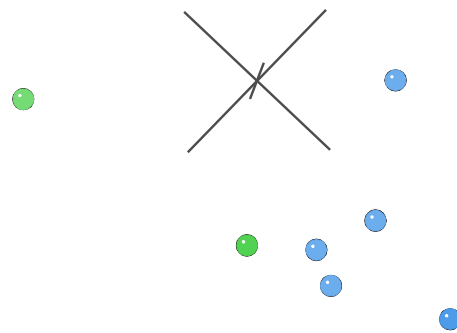
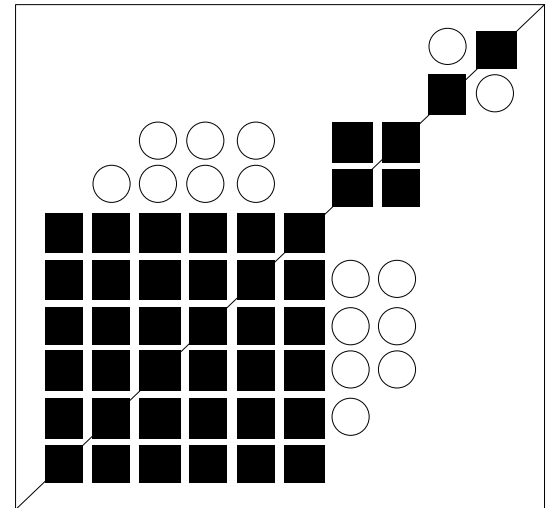
Characters: Craniodental

BDC Cluster 1 — *Mayulestes*

BDC Cluster 2 — *Prothylacynus*

BDC Cluster 3 { *Borhyaena*
Arctodictis

BDC Cluster 4 { *Lycopsis*
Sallacyon
Sipalocyon
Notogale
Cladosictis
Acyon

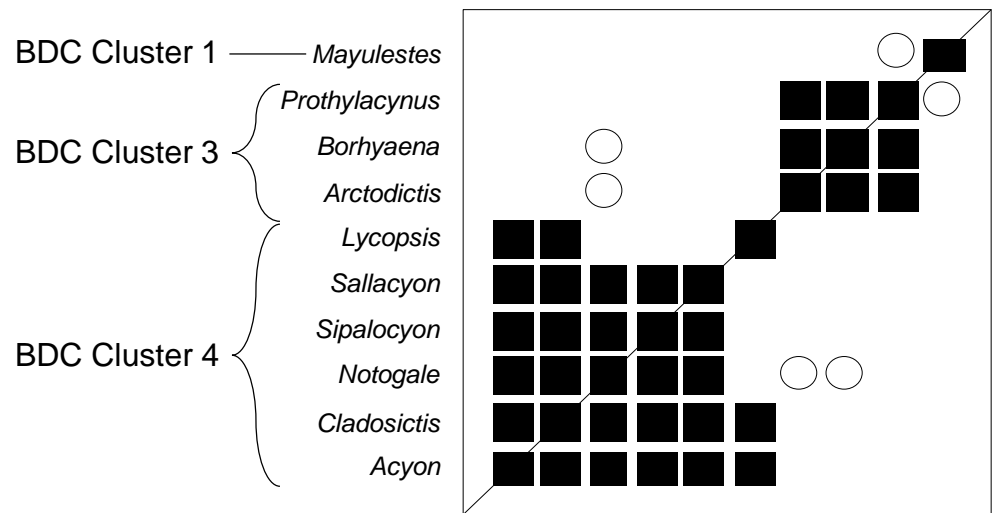


Order Sparassodonta
Family Hathliacynidae

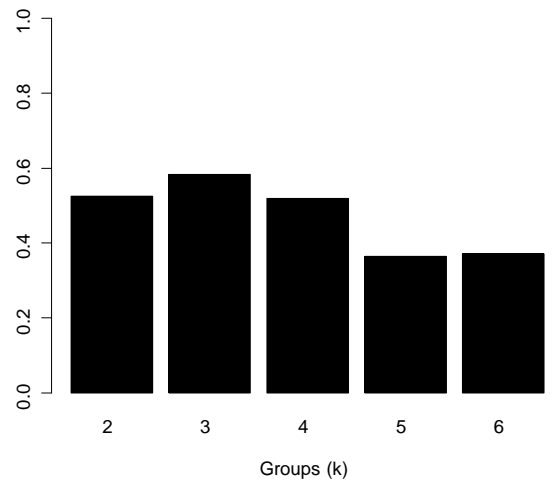
Published taxa	10
Published characters	47
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	10
Characters used for calculations	39
Median bootstrap value	89
F ₉₀	0.4
Stress of 3D MDS	0.08
k _{min}	3
Conclusion	HB?

Red: outgroup
Green: Borhyaenidae
Blue: Hathliacynidae

Notes: Hathliacynidae + *Lycopsis* could be a holobaramin; evidence of discontinuity has poor bootstrap values.



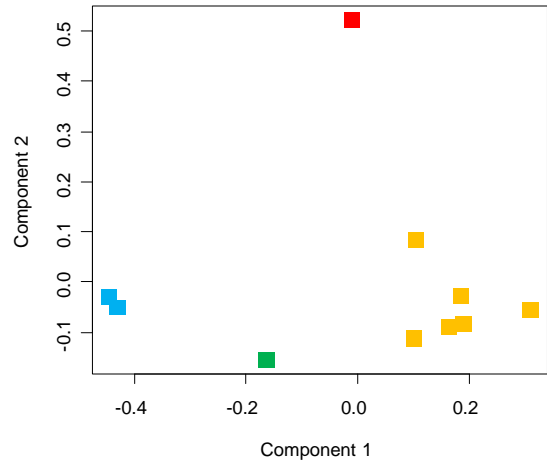
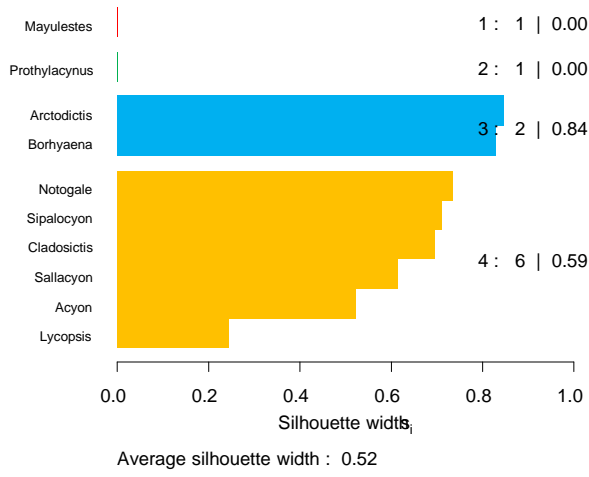
Average Silhouette Widths, Partion Around Medoids



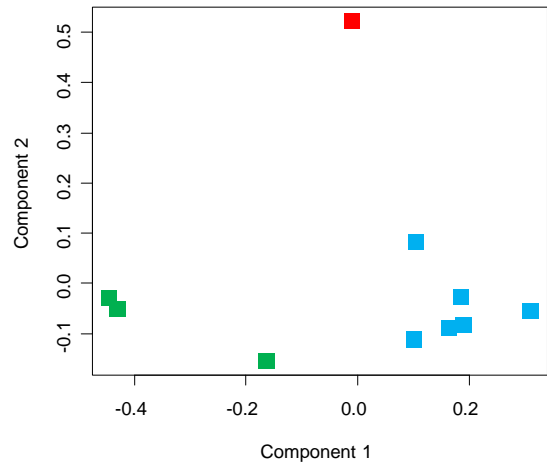
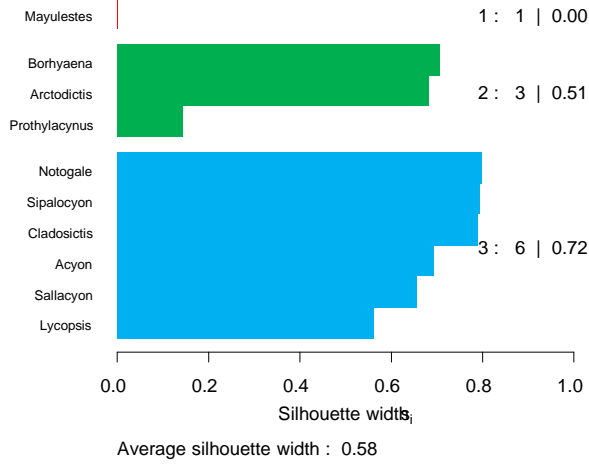
Clade Correspondence: Of the four BDC clusters identified, only clusters 3 and 4 contain more than one taxon. Only cluster 3 appears as a clade in the phylogeny of Figure 10 in Forasiepi et al. (2006).

Silhouette plot, BDC partitions

Pearson Correlation

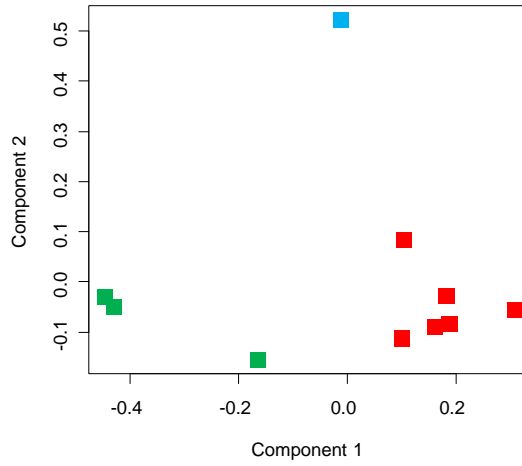
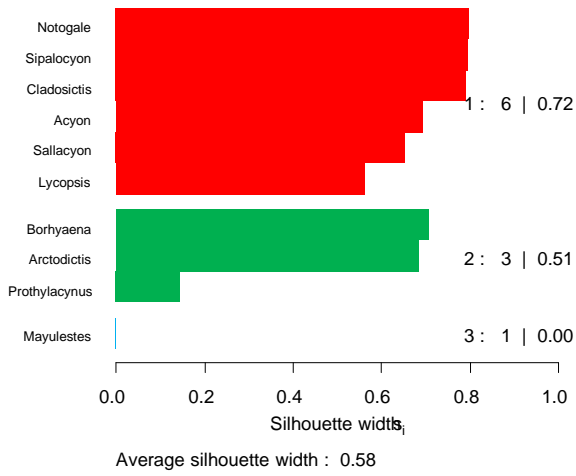


Spearman Correlation

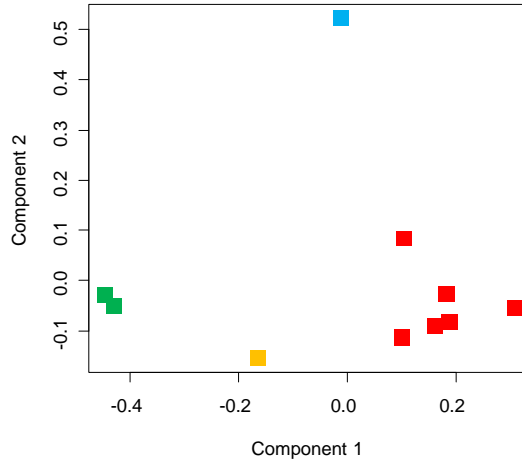
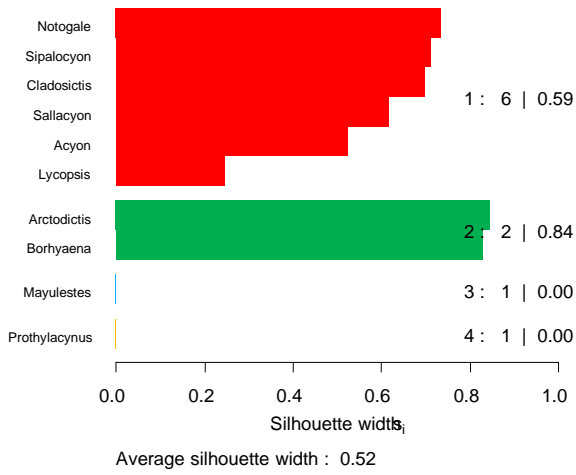


Silhouette plot, Partition Around Medoids

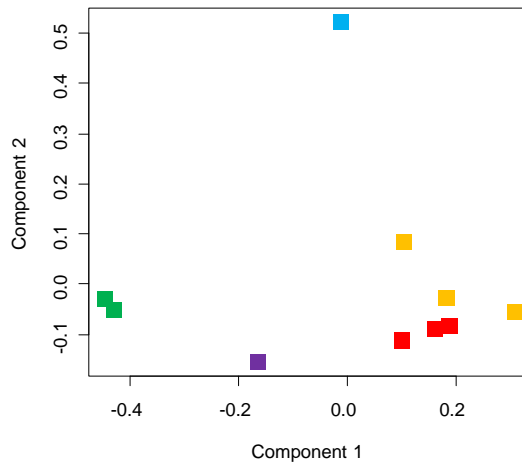
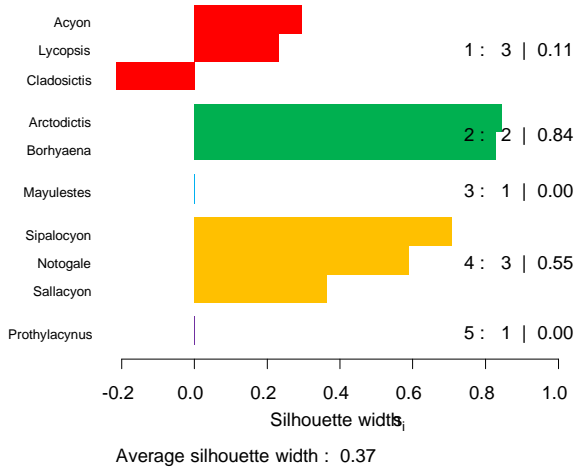
k=3



k=4

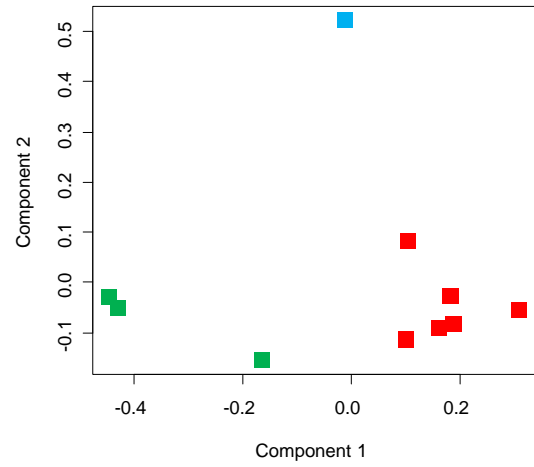
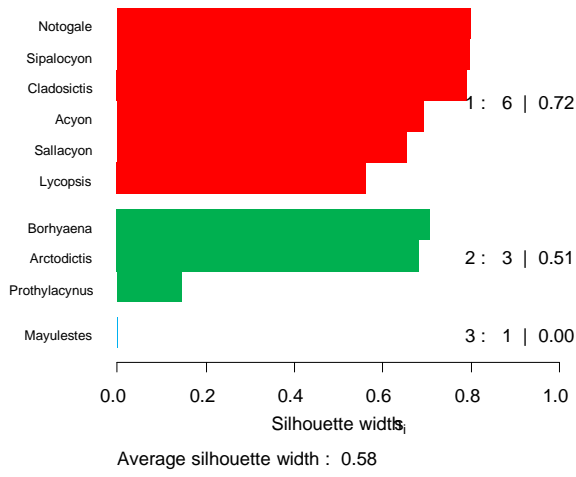


k=5

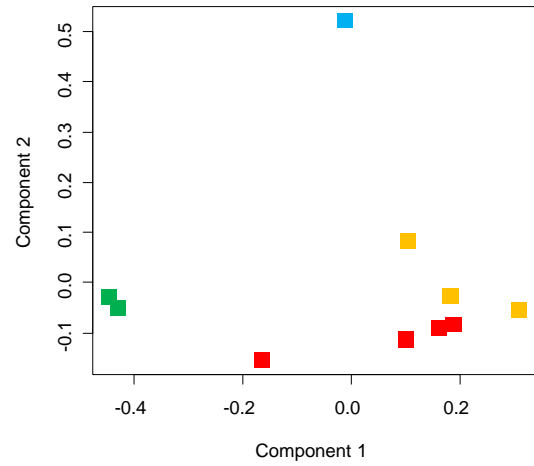
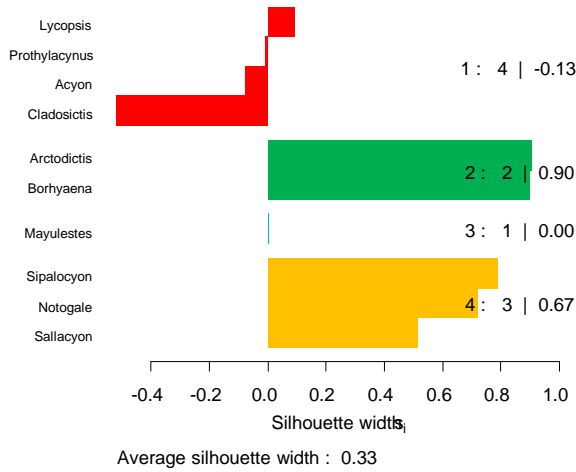


Silhouette plot, Fuzzy Analysis

k=3



k=4



Family Dasypodidae

Order Cingulata

Herrera et al. 2017

Pearson BDC

Negative: 26

Positive: 48

Clusters: 5

Clusterability

Hopkins Statistic: 0.687

Dip test: 0.019

Dip test p-value: 0.974

Spearman BDC

Negative: 9

Positive: 75

Clusters: 3

Pearson BDC can distinguish five clusters with an average silhouette width of 0.25. The Spearman BDC results add 27 more instances of significant, negative correlation, resulting in three clusters instead of five. The Spearman BDC clustering has an average silhouette width of 0.24, not much different from the Pearson BDC partition.

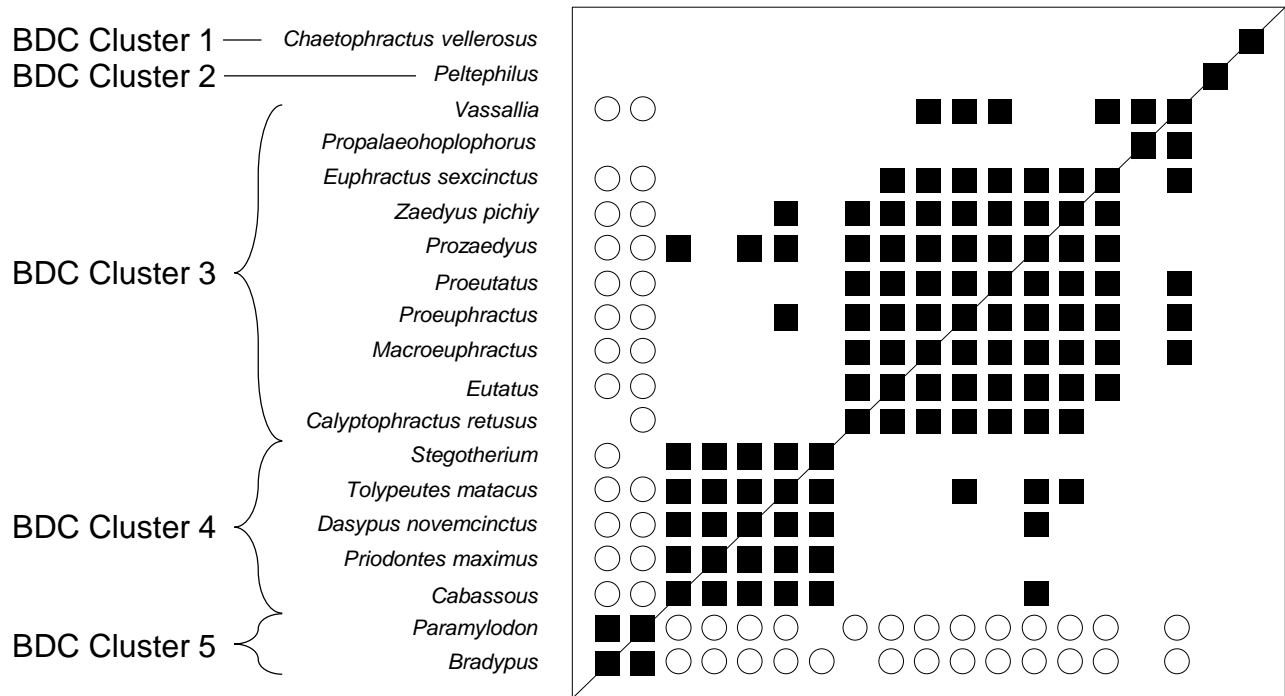
Medoid partitioning at $k=5$ is not consistent with the Pearson BDC clusters. They have a cluster membership difference of 16%. At $k=3$, however, the medoid partition matches the Spearman BDC clusters exactly.

Fuzzy analysis was not possible for $k>2$. At $k=2$, the medoid partition divided the taxa into clusters corresponding to the putative holobaramin and outgroup taxa identified in the original analysis. The fuzzy analysis at $k=2$, however, differed significantly, giving clusters of roughly equal membership. The average silhouette width for the two-cluster medoid partition was 0.37, better than any of the partitions giving a higher number of clusters, and the average silhouette width for the two-cluster fuzzy analysis was 0.18.

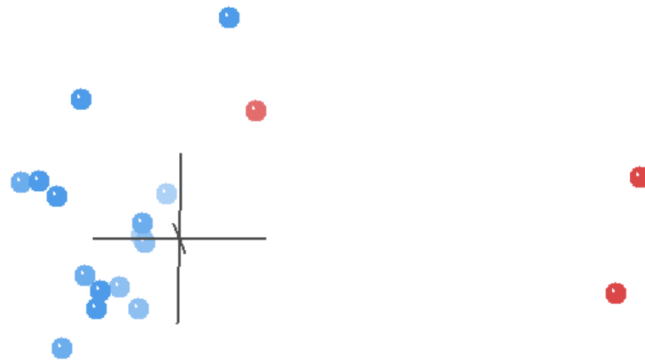
Given these results, especially the two-cluster medoid partition and the Spearman BDC, we may provisionally confirm the original conclusion of a holobaramin consisting of Dasypodidae + *Peltephilus* with one exception: The evidence of discontinuity around this group is weakened. Hence the updated analyses supports a possible or uncertain holobaramin.

Original conclusion: HB

Updated conclusion: HB?

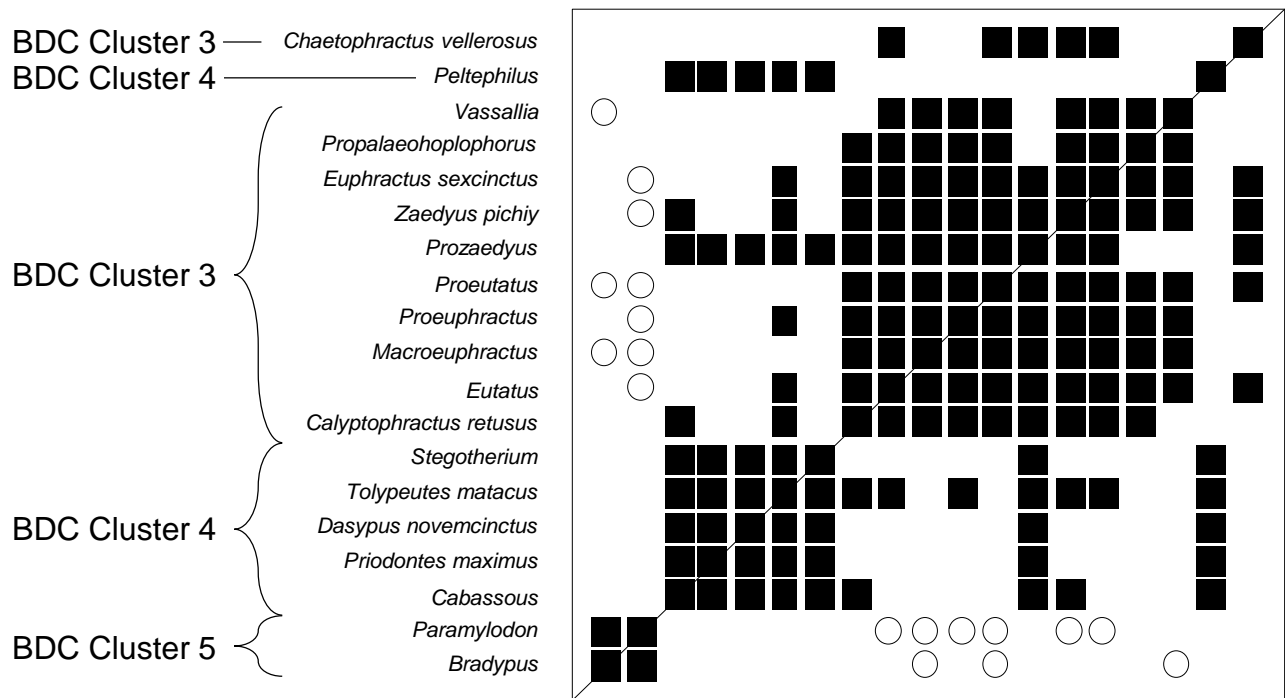


Order Cingulata
Family Dasypodidae

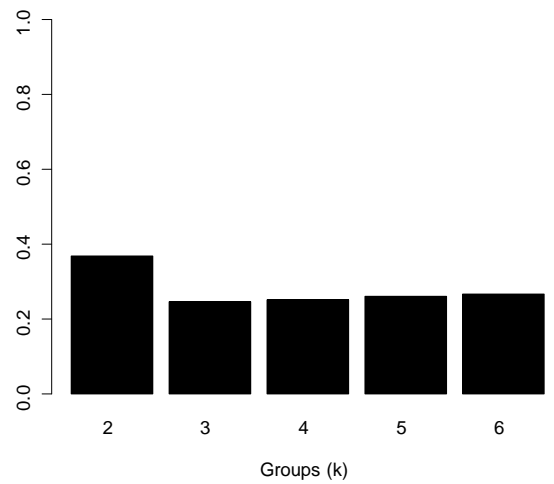


Published taxa	22
Published characters	144
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	19
Characters used for calculations	106
Median bootstrap value	94
F ₉₀	0.58
Stress of 3D MDS	0.29
k _{min}	11
Conclusion	HB

Notes: Significant, negative BDC between two outgroup taxa and the ingroup taxa is widespread but has poor bootstrap values. Chlamyphorid *Peltephilus* clusters with the dasypodids in both BDC and MDS results. Dasypodidae + *Peltephilus* are a holobaramin. Dasypodid *Chaetophractis* appears to be separate from the holobaramin.



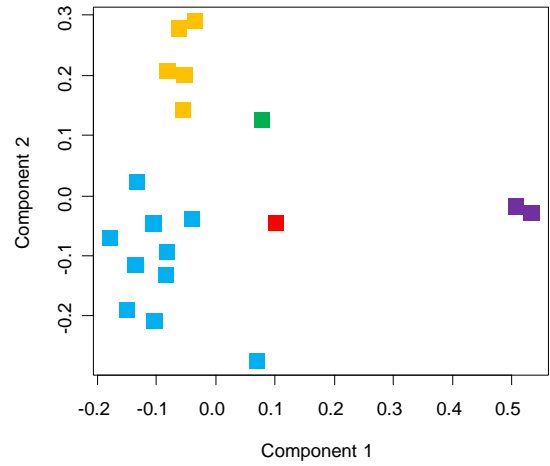
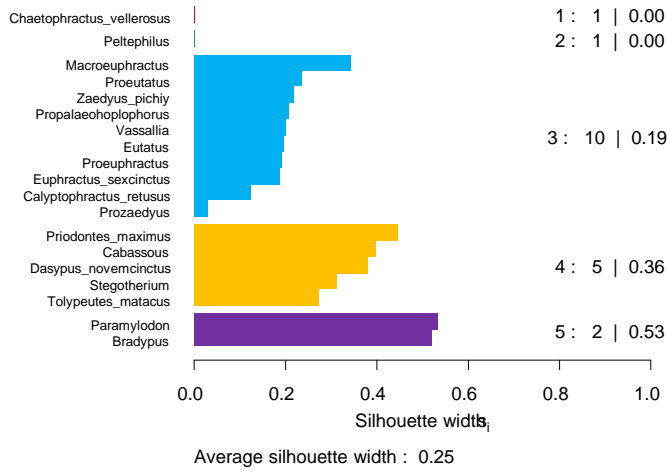
Average Silhouette Widths, Partion Around Medoids



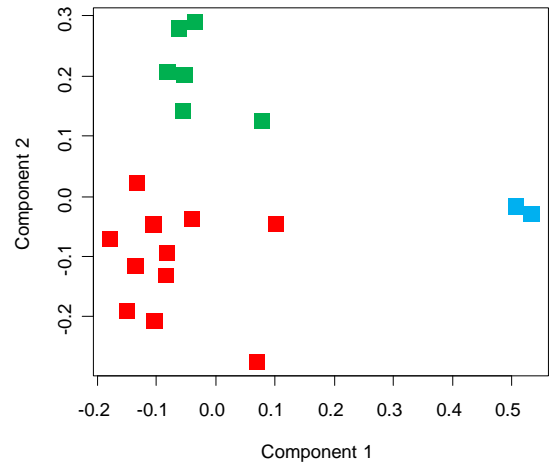
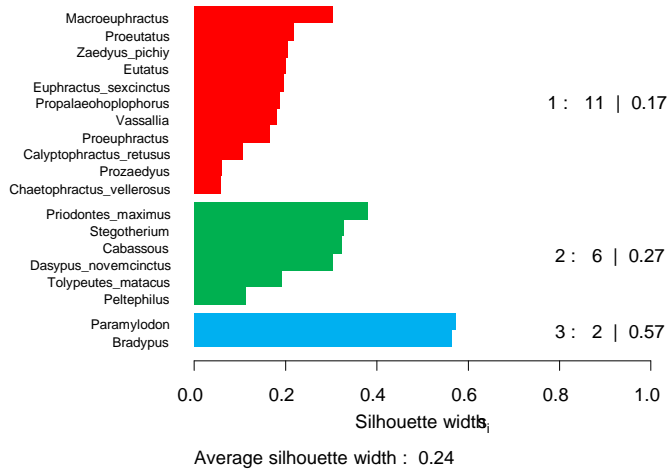
Clade Correspondence: There are five clusters in the BDC results, three of which (clusters 3-5) contain more than one taxon. The phylogeny in Figure 9 of Herrera et al. (2017) shows that Cluster 4 is a clade. Cluster 5 consists of two outgroup taxa that would be monophyletic if the tree were drawn unrooted. Cluster 3 is not monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

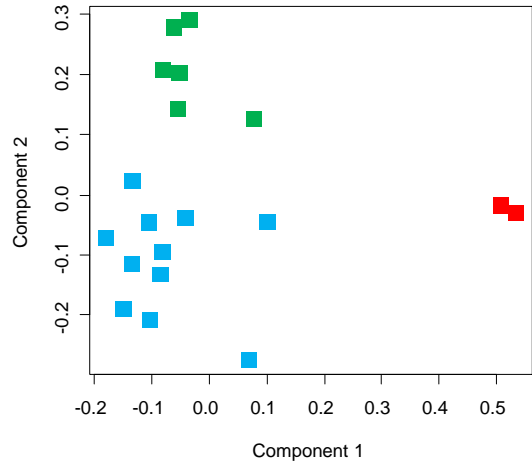
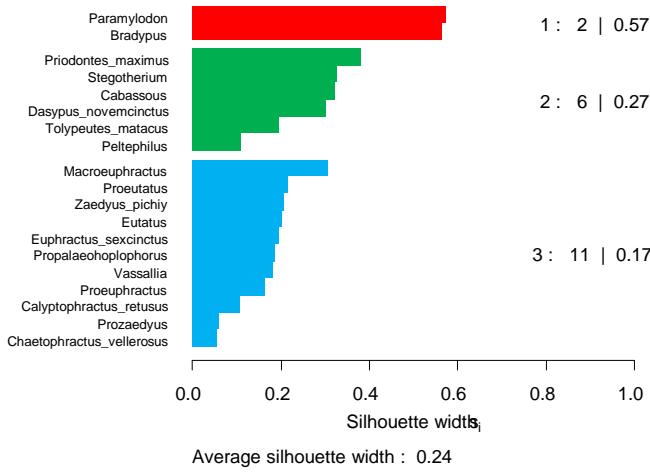


Spearman Correlation

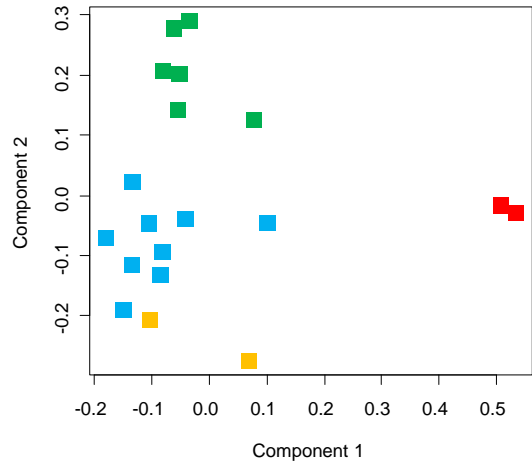
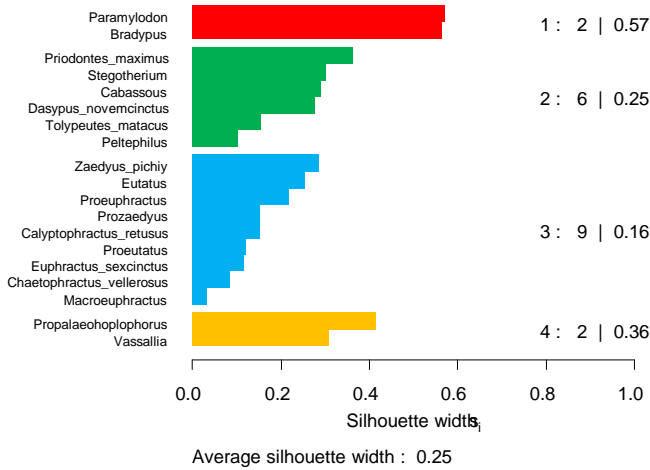


Silhouette plot, Partition Around Medoids

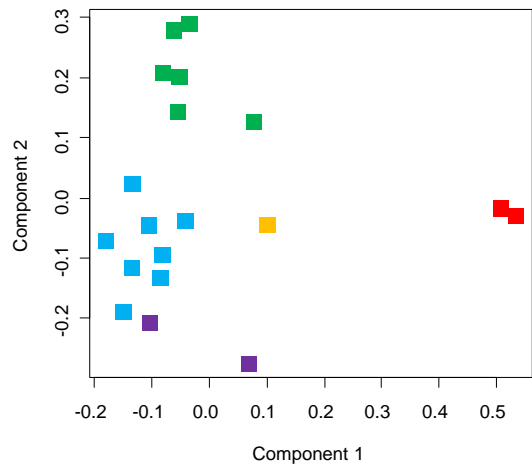
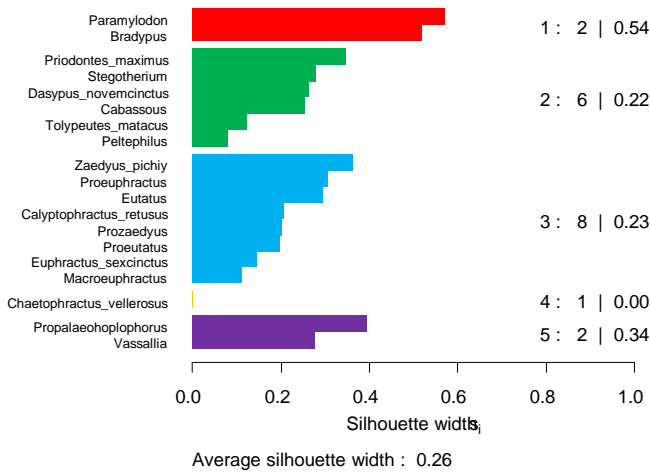
k=3



k=4

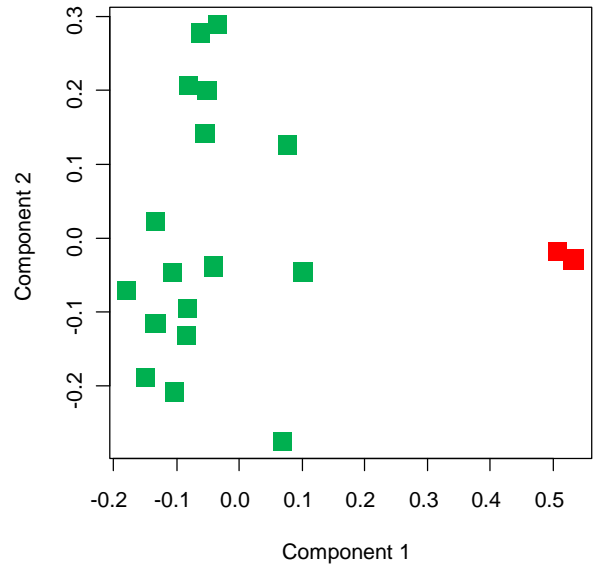
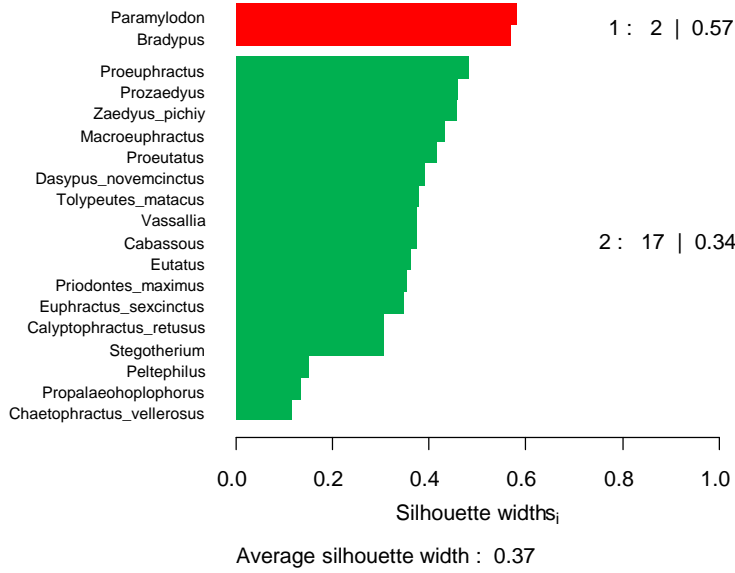


k=5

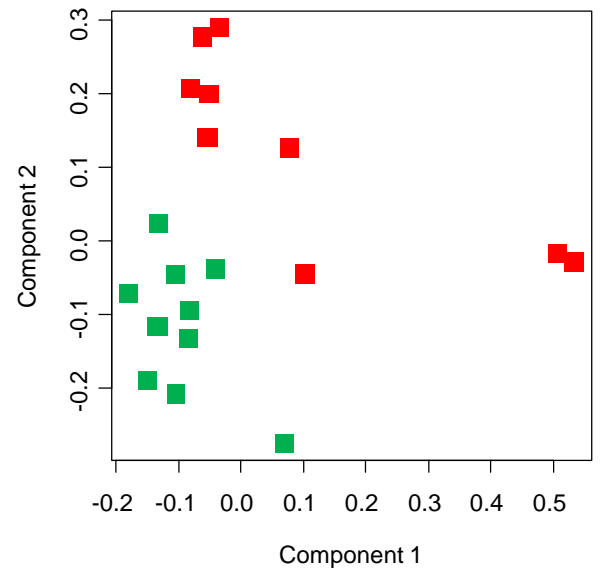
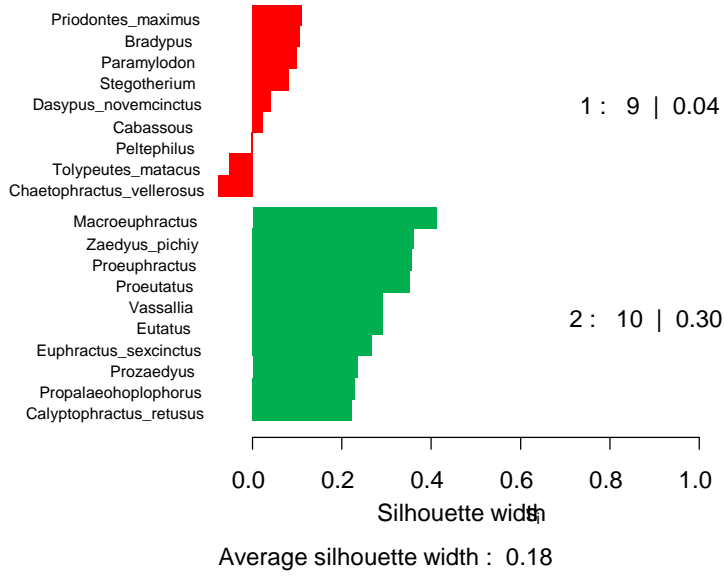


Addendum: Clustering at k=2

Medoid Partition



Fuzzy Analysis



Family Glyptodontidae

Order Cingulata
Zurita et al. 2013

Pearson BDC

Negative: 58
Positive: 55
Clusters: 2

Clusterability

Hopkins Statistic: 0.875
Dip test: 0.026
Dip test p-value: 0.695

Spearman BDC

Negative: 54
Positive: 70
Clusters: 2

The Spearman BDC results add fifteen instances of significant, positive correlation to the results of the Pearson BDC, but the cluster membership is identical. Both BDC results reveal two clusters with an average silhouette width of 0.54.

Medoid partitioning at $k=2$ is very similar but puts *Boreostemma acostae* in a different cluster, giving it a negative silhouette width and making the average silhouette width 0.5. Fuzzy analysis at $k=2$ yields an identical partition to both BDC results.

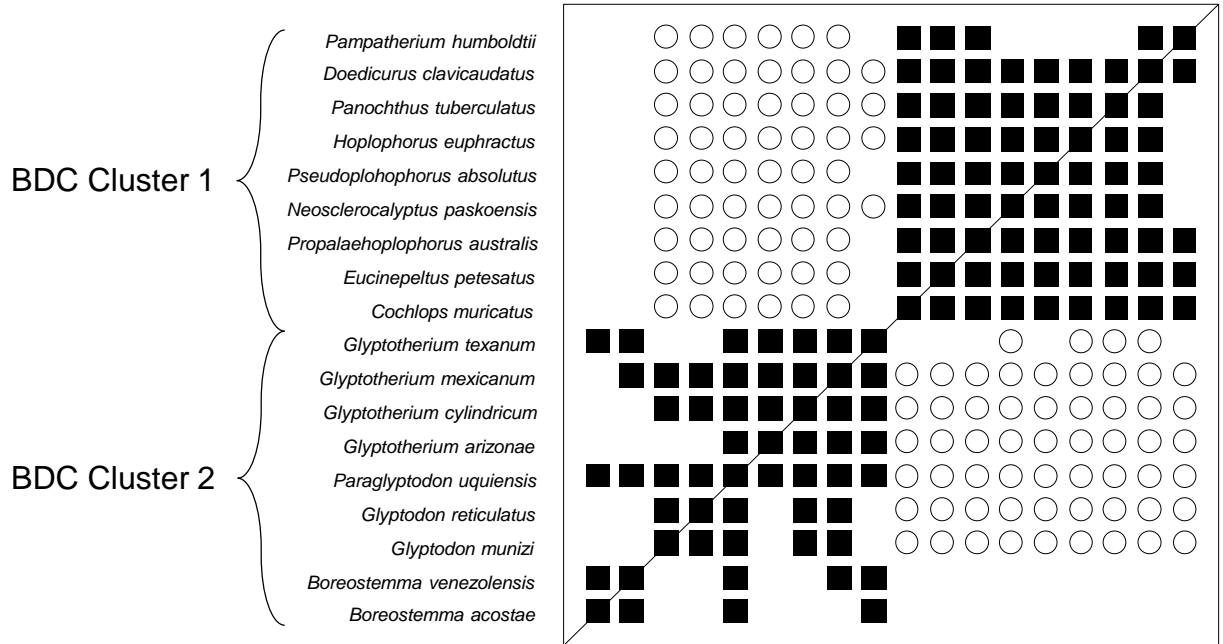
All of these new results support the original conclusion that Glyptodontinae as a holobaramin.

Original conclusion: HB

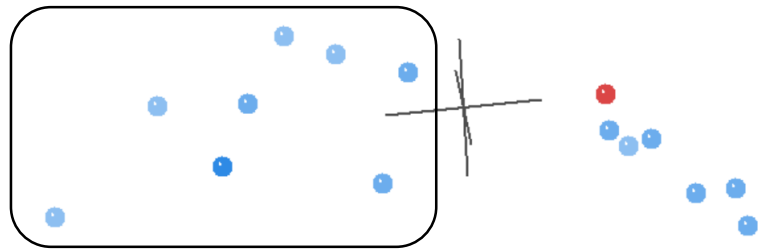
Updated conclusion: HB

Zurita, A.E., L.R.G. Ruiz, A.J. Gómez-Cruz, and J.E. Arenas-Mosquera. 2013. The most complete known Neogene Glyptodontidae (Mammalia, Xenarthra, Cingulata) from northern South America: taxonomic, paleobiogeographic, and phylogenetic implications. *Journal of Vertebrate Paleontology* 33:696-708.

Characters: Cranial and postcranial



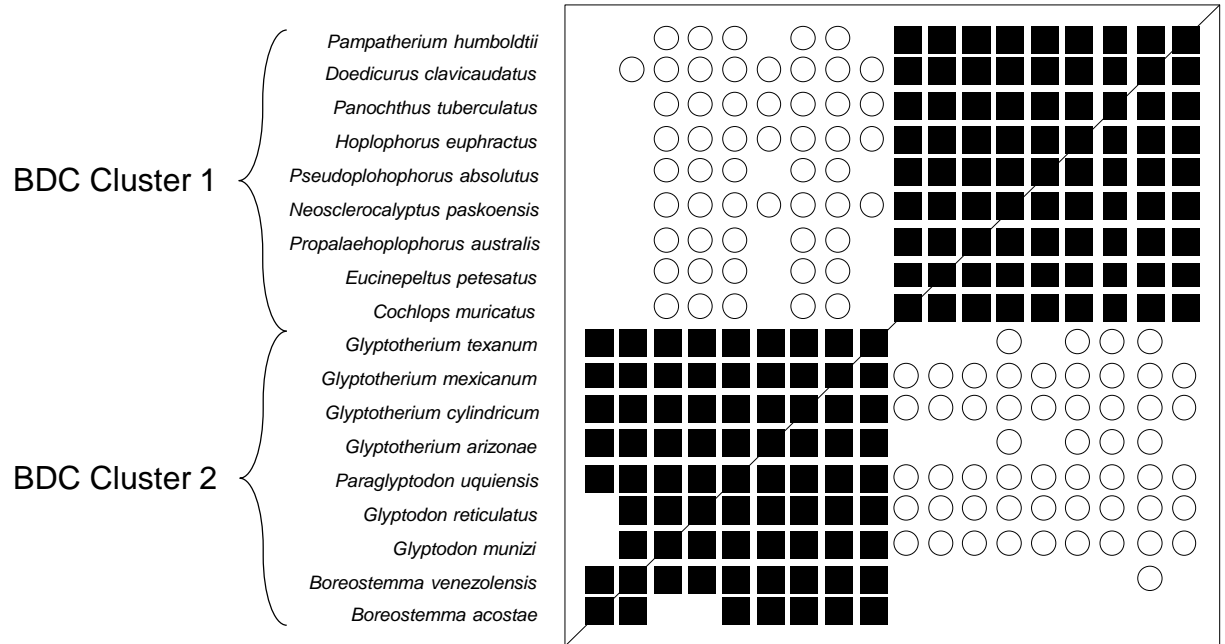
Glyptodontinae



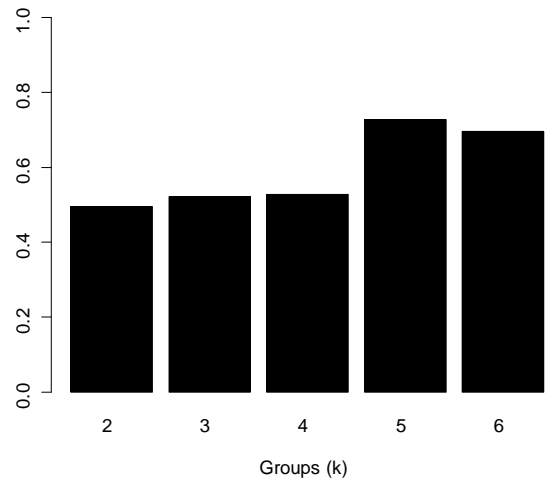
Order Cingulata
Family Glyptodontidae

Published taxa	18
Published characters	26
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	18
Characters used for calculations	23
Median bootstrap value	75
F ₉₀	0.31
Stress of 3D MDS	0.13
k _{min}	4
Conclusion	HB

Notes: Subfamily Glyptodontinae is well-separated in both BDC and MDS analyses. Glyptodontinae is probably a holobaramin.



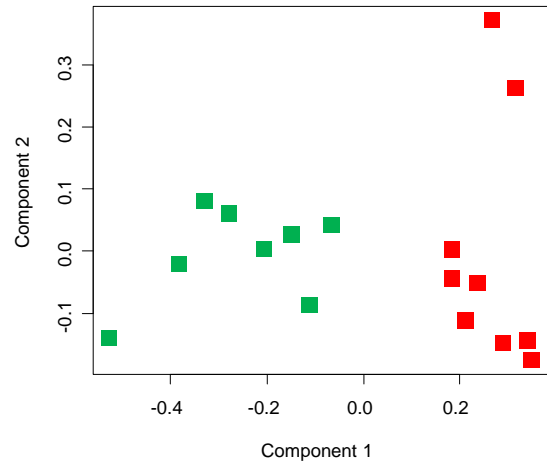
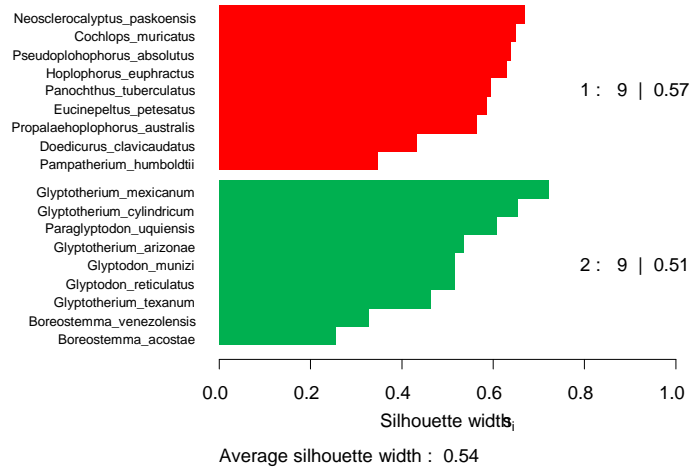
Average Silhouette Widths, Partion Around Medoids



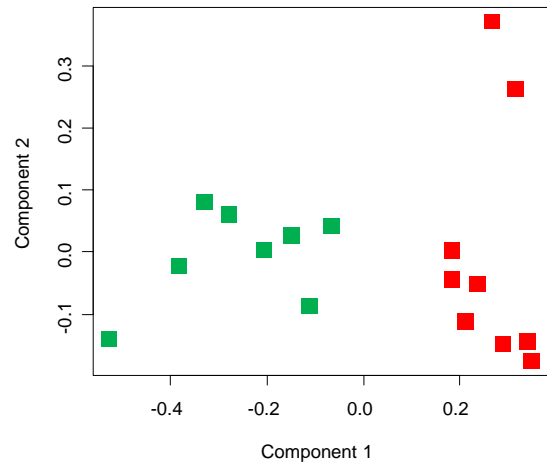
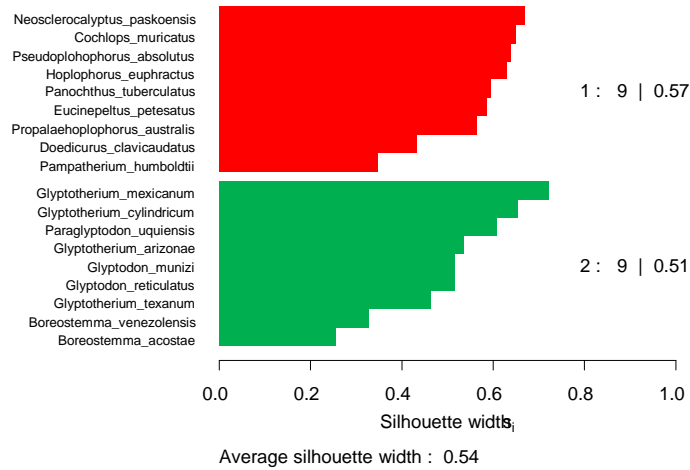
Clade Correspondence: The two BDC clusters both have more than one taxon. Both are monophyletic in the phylogeny in Figure 5 of Zurita et al. (2013).

Silhouette plot, BDC partitions

Pearson Correlation

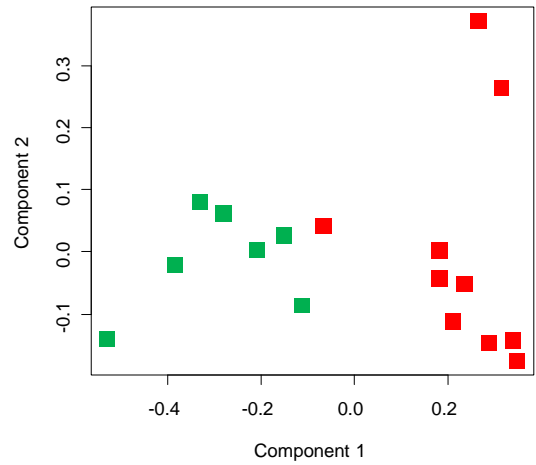
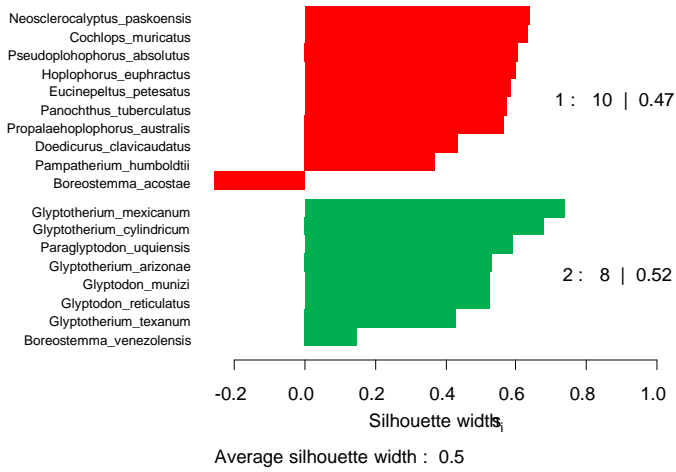


Spearman Correlation

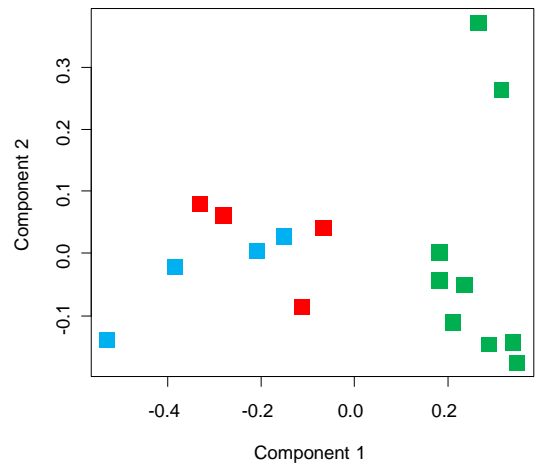
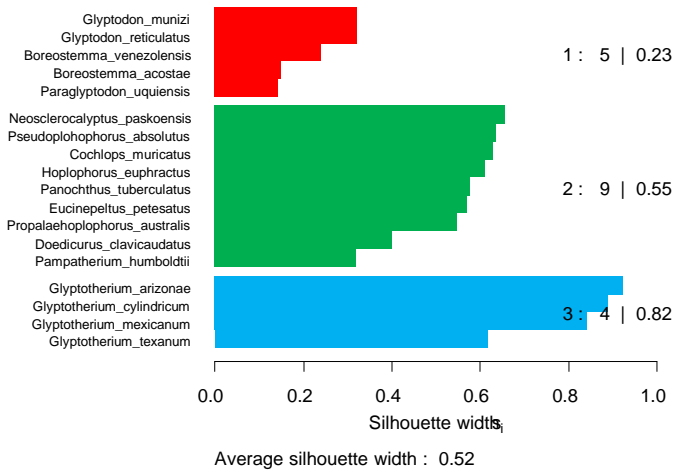


Silhouette plot, Partition Around Medoids

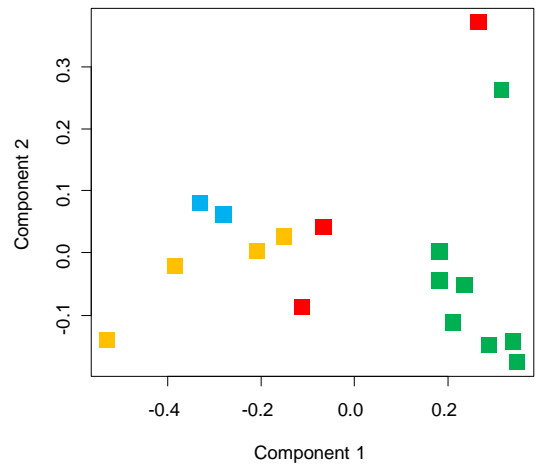
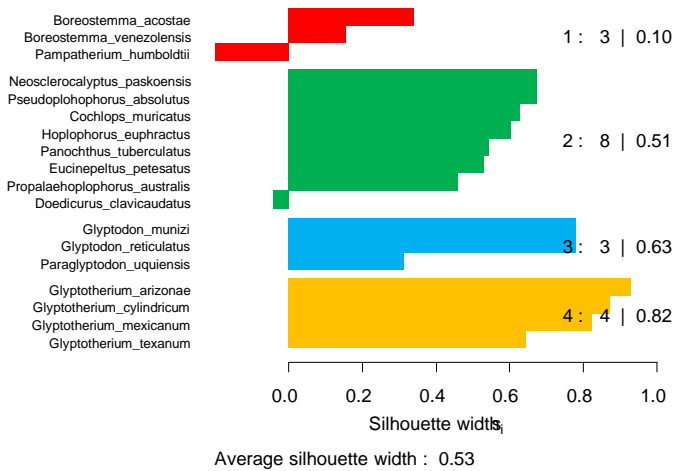
k=2



k=3

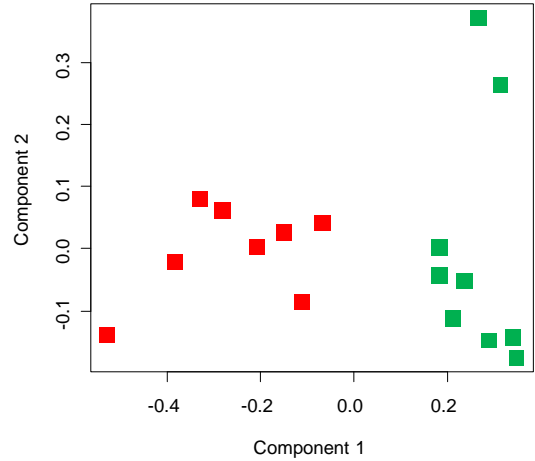
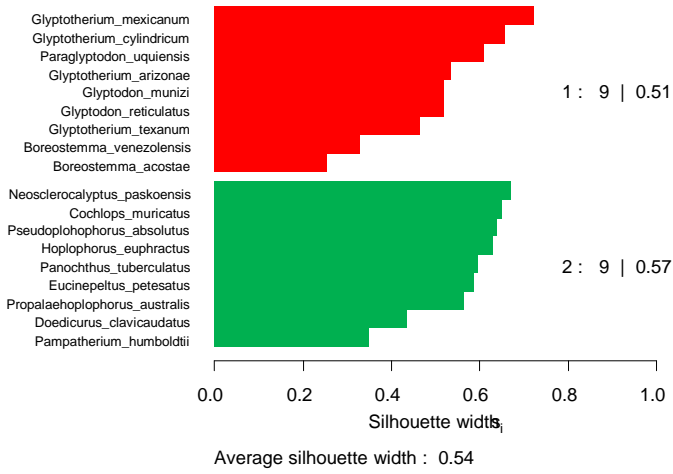


k=4

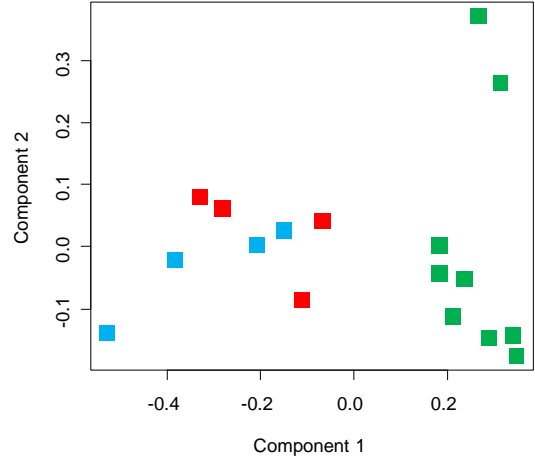
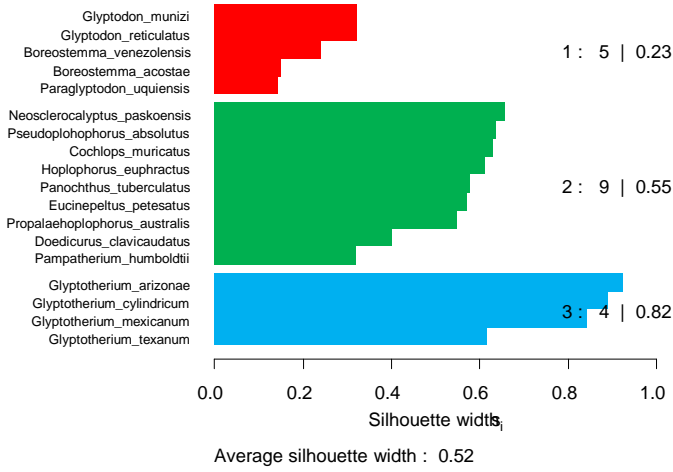


Silhouette plot, Fuzzy Analysis

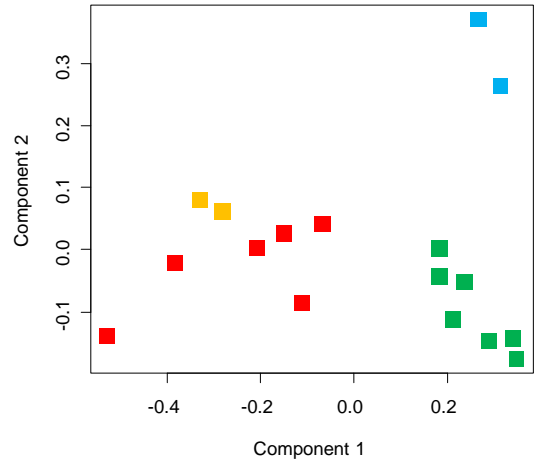
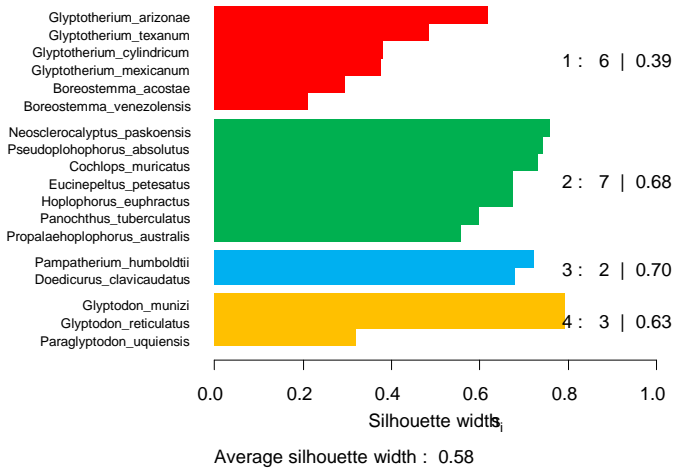
k=2



k=3



k=4



Family Myrmecophagidae

Order Pilosa

Gaudin and Branham 1998

Pearson BDC

Negative: 17

Positive: 9

Clusters: 6

Clusterability

Hopkins Statistic: 0.642

Dip test: 0.048

Dip test p-value: 0.458

Spearman BDC

Negative: 24

Positive: 20

Clusters: 3

The Pearson BDC yields six clusters, four of which are singletons, with an average silhouette width of 0.27. The Spearman BDC reveals an additional eleven instances of significant, positive BDC which reduces the number of clusters to three. Additionally, there are seven more instances of significant, negative correlation revealed by the Spearman BDC that reinforce the separation between the Myrmecophaginae and all other taxa. However, the average silhouette width of 0.29 for the Spearman BDC partition is not much better than the six-cluster Pearson BDC partition.

Medoid partition at $k=6$ matches the Pearson BDC clusters exactly. Medoid partition at $k=3$, however, does not match the Spearman BDC results. The average silhouette width for the Medoid partition at $k=3$ is 0.34, which is better than the Spearman BDC clustering. The highest average silhouette width for medoid partition of 0.38 occurs at $k=2$, where *Cyclopes* is included with the Myrmecophaginae.

Fuzzy analysis at $k=2$ separates the Myrmecophaginae from all other taxa, with an average silhouette width of 0.42. At $k=3$, the fuzzy analysis is not consistent with the Spearman BDC results or the medoid partition at $k=3$. The average silhouette width is 0.33 for the fuzzy partition at $k=3$.

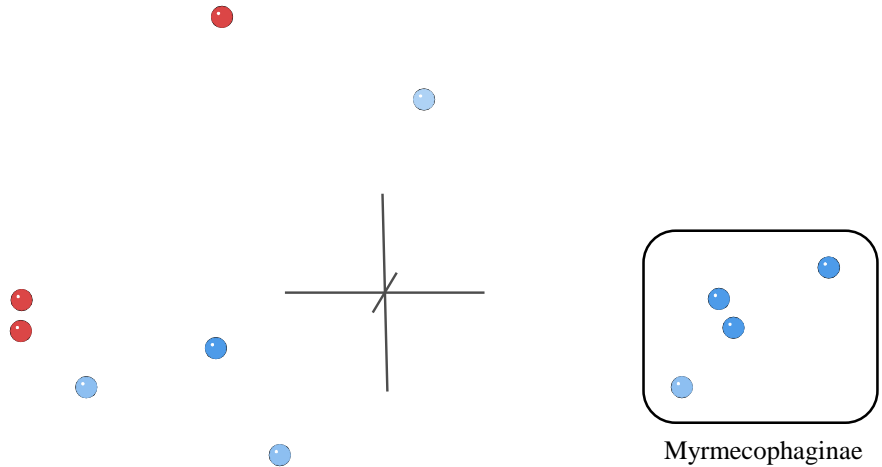
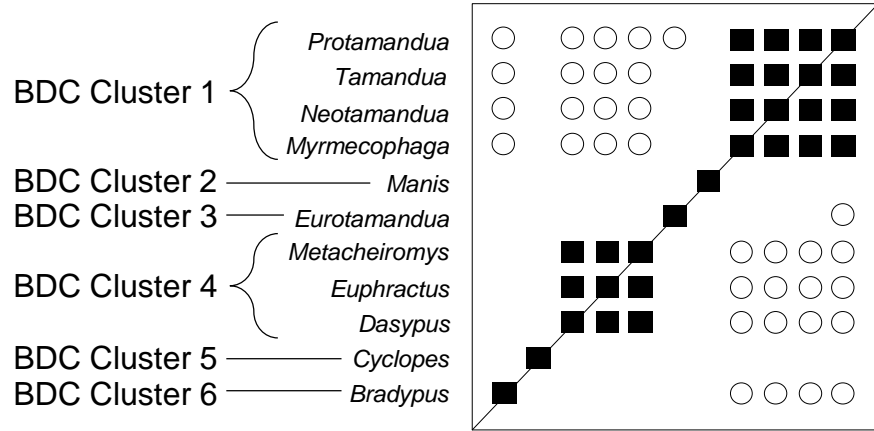
These results reinforce the original conclusion that Myrmecophaginae is a holobaramin. Myrmecophaginae were identified as a group in every analysis except the two-cluster medoid partition, and the additional significant, negative correlations observed in the Spearman BDC supports the inference of discontinuity around the Myrmecophaginae.

Original conclusion: HB

Updated conclusion: HB

Gaudin, T.J. and D.G. Branham. 1998. The phylogeny of the Myrmecophagidae (Mammalia, Xenarthra, Vermilingua) and the relationship of *Eurotamandua* to the Vermilingua. *Journal of Mammalian Evolution* 5:237-265.

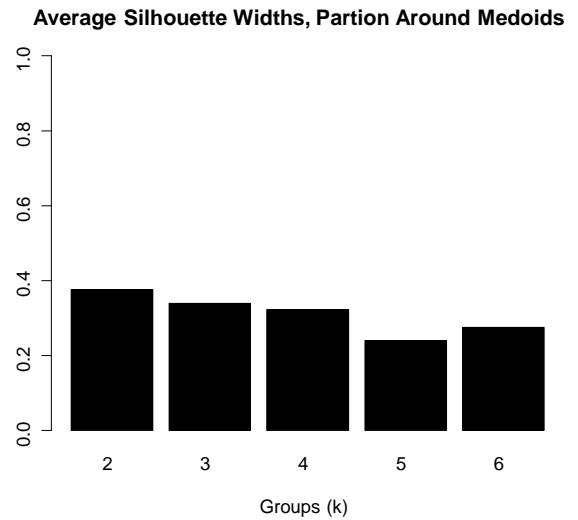
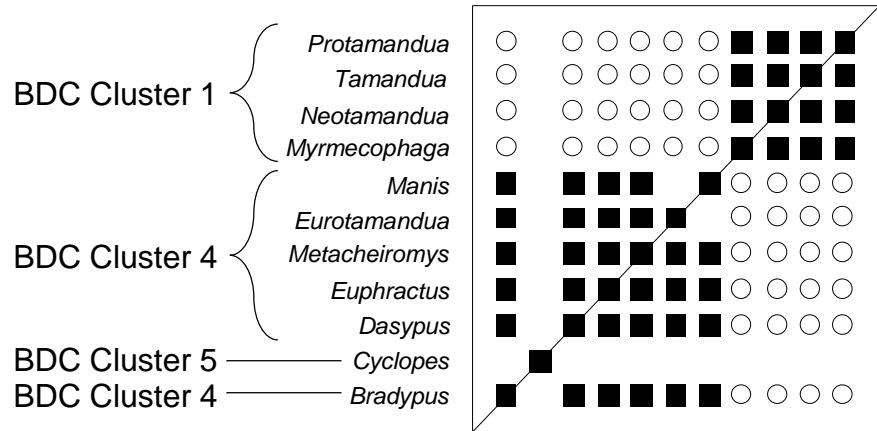
Characters: Cranial and postcranial



Order Pilosa
Family Myrmecophagidae

Published taxa	12
Published characters	107
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	11
Characters used for calculations	88
Median bootstrap value	92
F ₉₀	0.58
Stress of 3D MDS	0.13
k _{min}	6
Conclusion	HB?

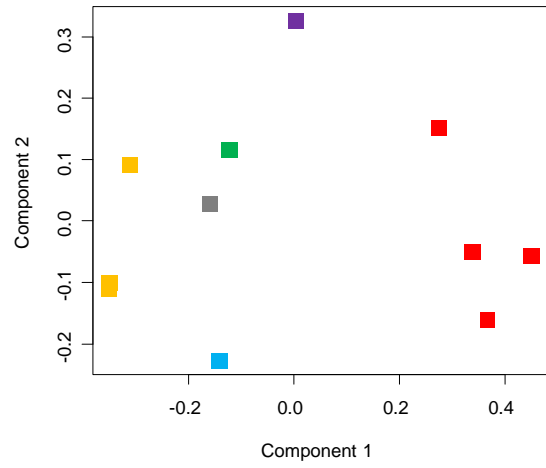
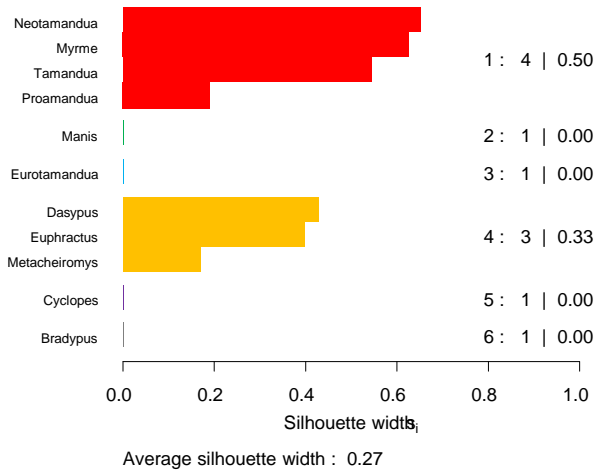
Notes: Both the MDS and BDC results appear to show a separation between the subfamily Myrmecophaginae (*Myrmecophaga*, *Neotamandua*, *Tamandua*, *Protamandua*) and all other taxa. Myrmecophaginae appears to be a holobaramin.



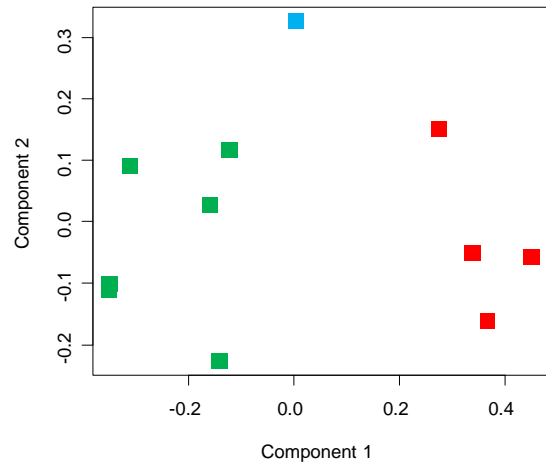
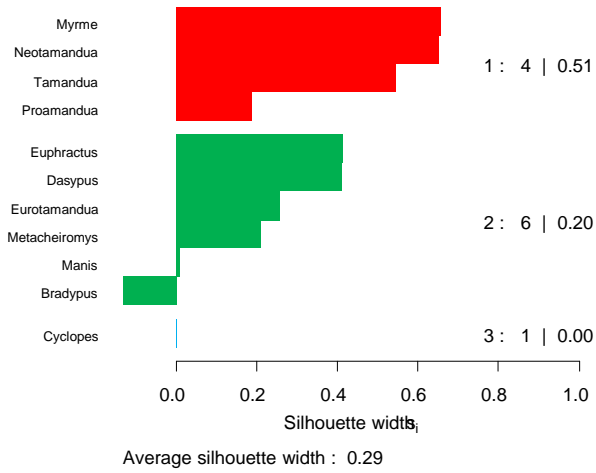
Clade Correspondence: Of the six BDC clusters, only clusters 1 and 4 contain more than one taxon. Cluster 1 corresponds to a clade in Figure 1 of Gaudin and Branham (1998), but one of the taxa from cluster 4 has been omitted from the phylogeny.

Silhouette plot, BDC partitions

Pearson Correlation

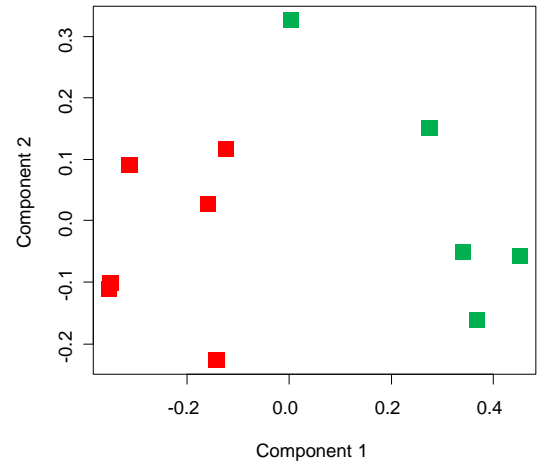
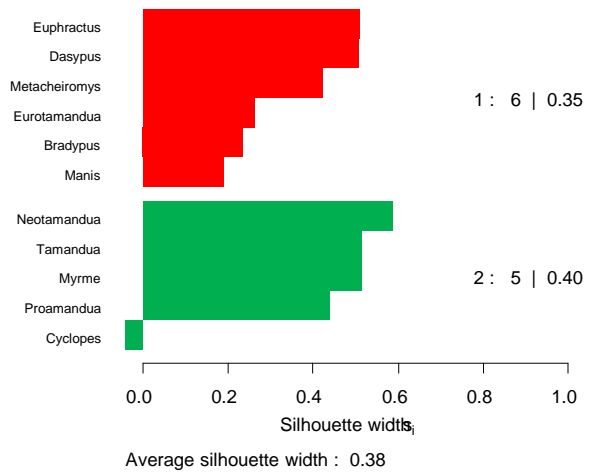


Spearman Correlation

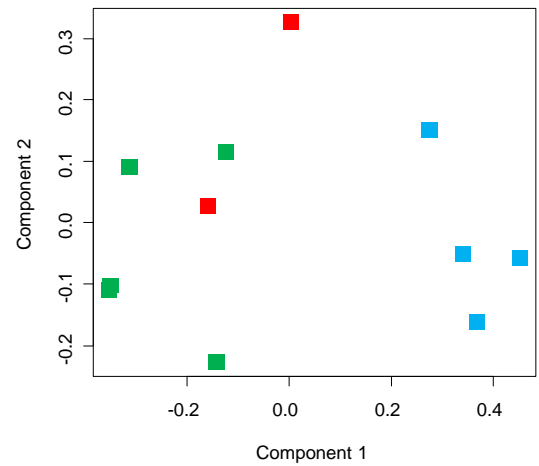
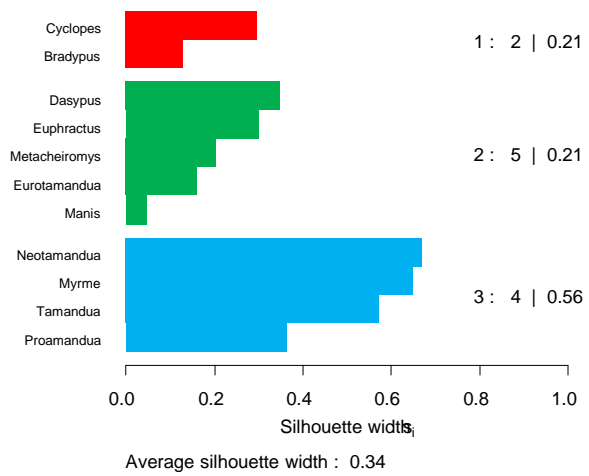


Silhouette plot, Partition Around Medoids

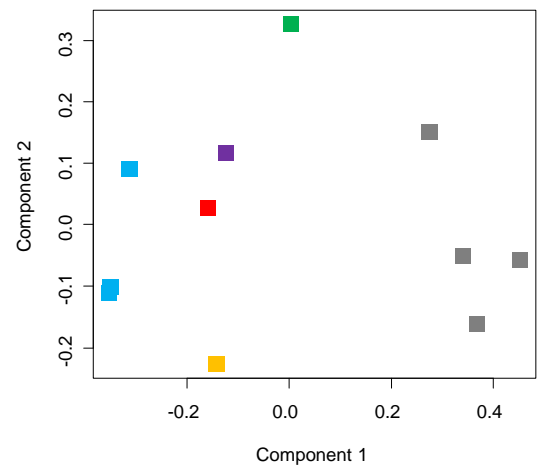
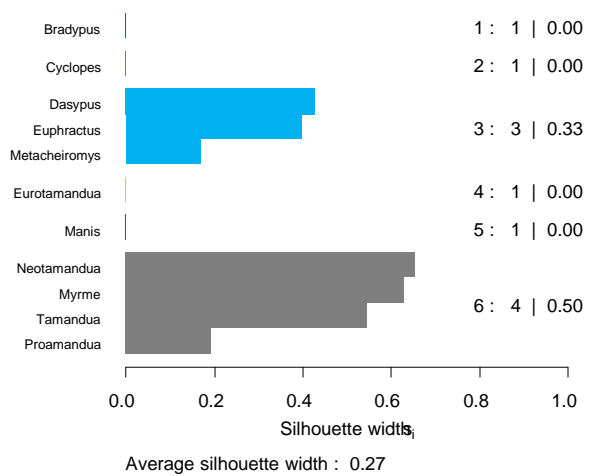
k=2



k=3

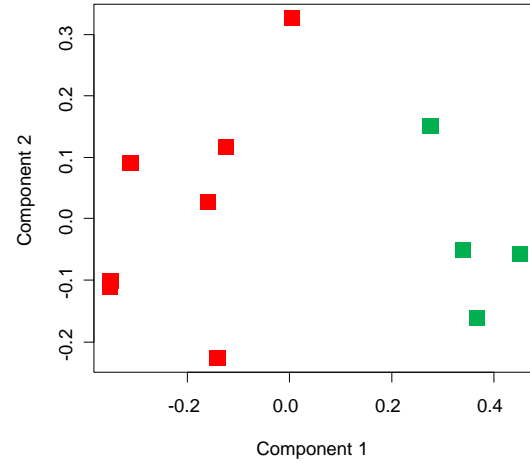
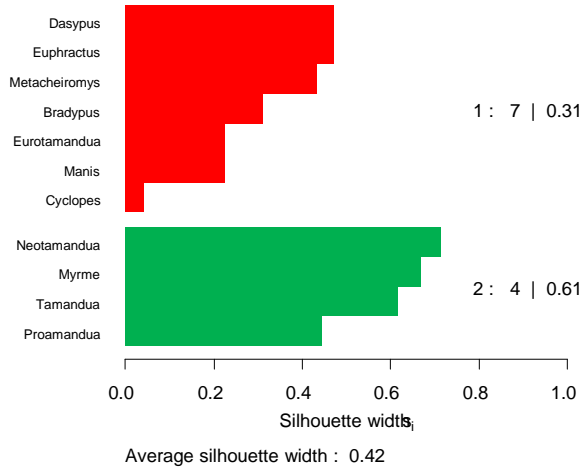


k=6

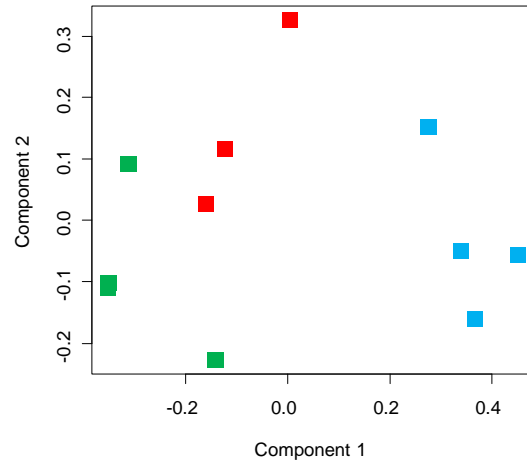
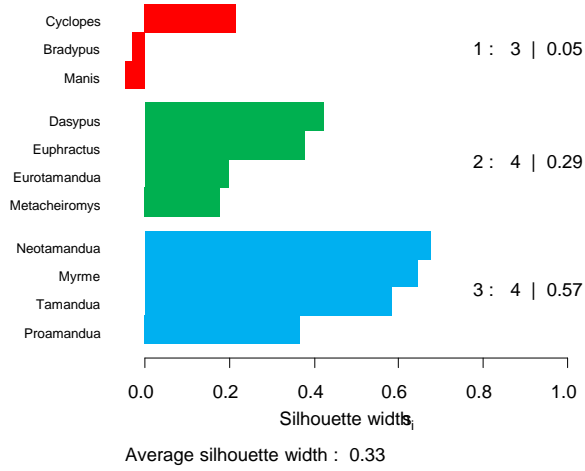


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Pseudorhynchocyoniidae

Order Leptictida

Hooker 2013

Pearson BDC

Negative: 36

Positive: 51

Clusters: 3

Clusterability

Hopkins Statistic: 0.744

Dip test: 0.024

Dip test p-value: 0.698

Spearman BDC

Negative: 27

Positive: 61

Clusters: 3

The Pearson BDC results reveal three clusters of taxa, one of which corresponds to all the pseudorhynchocyonids except *Diadophyodectes*. The Spearman BDC reduce the instances of significant, negative correlation by nine and increase the instances of significant, positive correlation by ten, but the cluster membership is unchanged. The average silhouette width for this partition is 0.33, with the taxon *Aphrononus* having a negative silhouette width.

The medoid partition at k=3 has an average silhouette width of 0.38 and does not agree with the three clusters of the BDC results. The cluster membership difference is 10%, and none of the clusters are exactly the same.

The fuzzy analysis for k=3 has an average silhouette value of 0.28 and agrees with none of the other three-cluster analyses. Compared to the BDC results, the cluster membership difference is 25%.

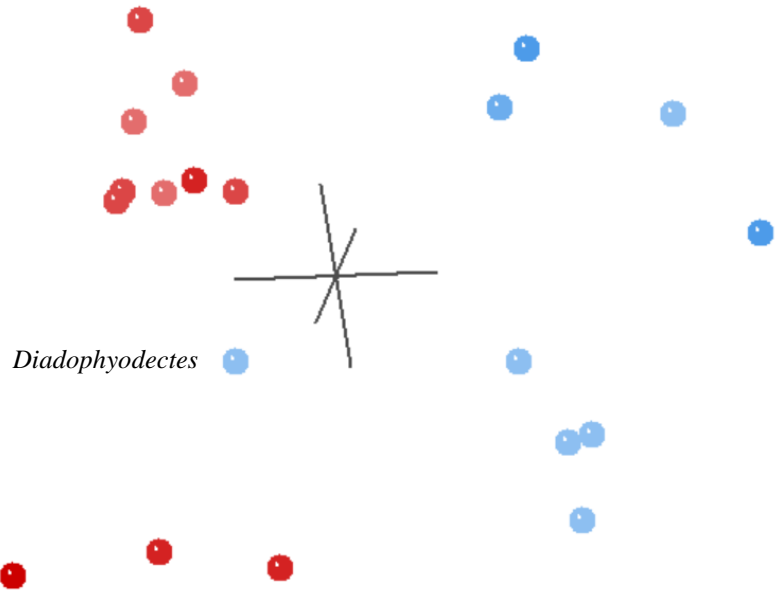
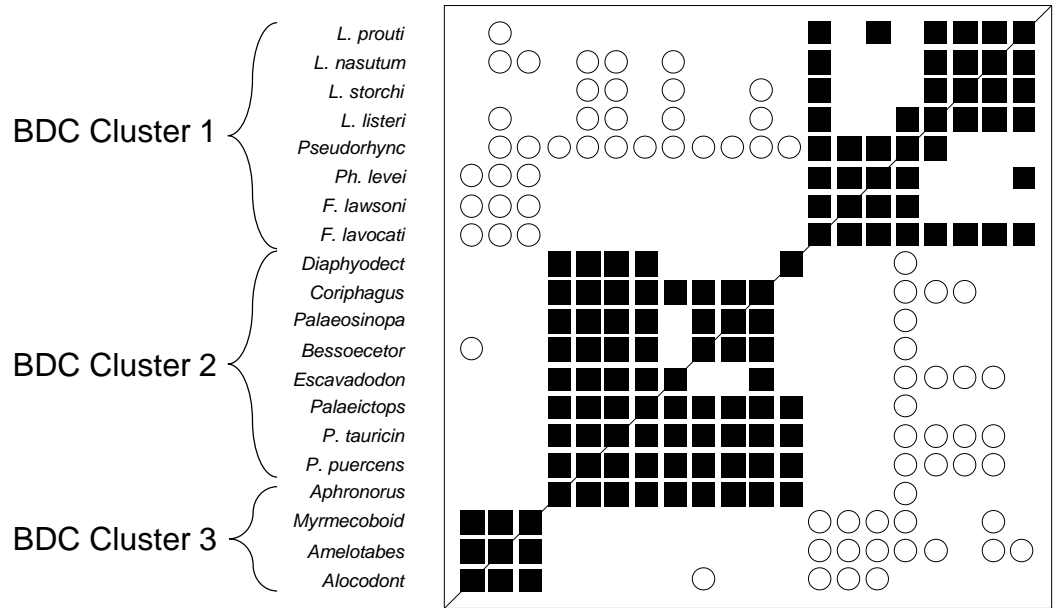
The original conclusion from these results was that Pseudorhynchocyoniidae (except *Diadophyodectes*) might be a holobaramin is reinforced by these results. The Spearman BDC is consistent with the Pearson BDC, reinforcing the conclusion of continuity and discontinuity, but the lack of consistency with the medoid partition and the fuzzy analysis reinforces the uncertainty.

Original conclusion: HB?

Updated conclusion: HB?

Hooker, J.J. 2013. Origin and evolution of the Pseudorhynchocyoniidae, a European Paleogene family of insectivorous placental mammals. *Palaeontology* 56:807-835.

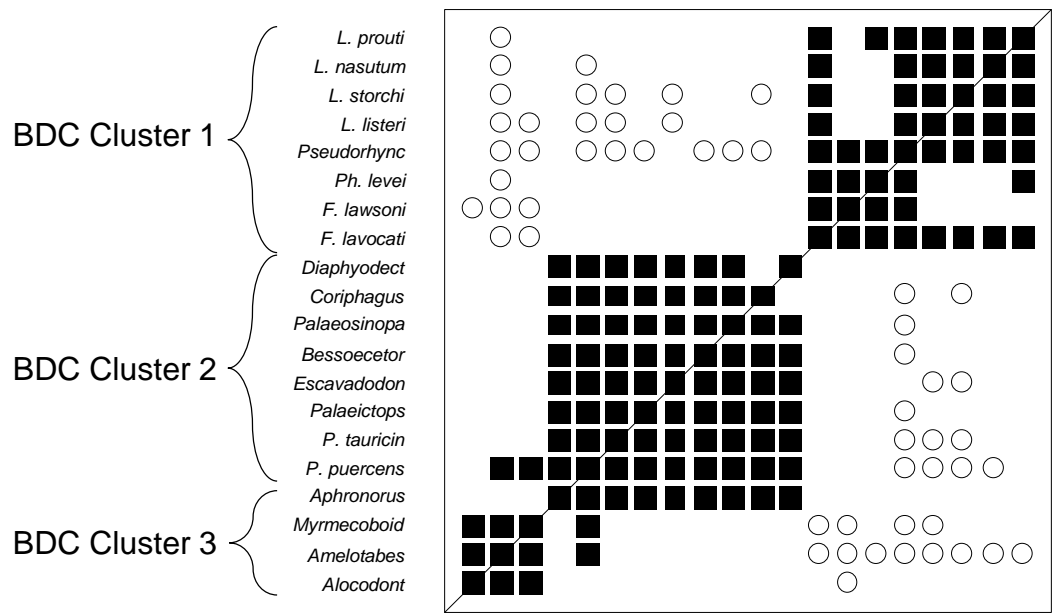
Characters: Craniodental



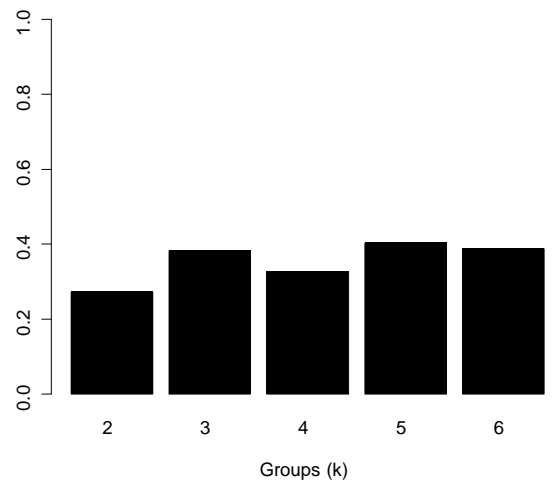
Order Leptictida
Family Pseudorhynchocyoniidae

Published taxa	21
Published characters	56
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	20
Characters used for calculations	38
Median bootstrap value	78
F ₉₀	0.12
Stress of 3D MDS	0.19
k _{min}	4
Conclusion	HB?

Notes: BDC reveals significant, negative BDC with poor bootstrap values, and the MDS shows a diffuse cluster of taxa. Nevertheless, the data support recognizing Pseudorhynchocyoniidae as a provisional holobaramin. The position of *Diadophyodectes*, which clusters with the outgroup in MDS and BDC results, remains uncertain.



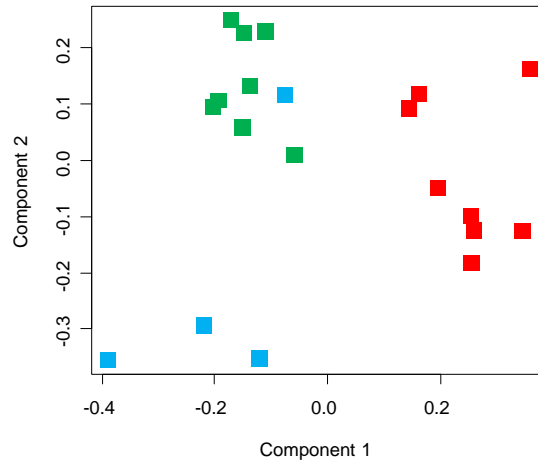
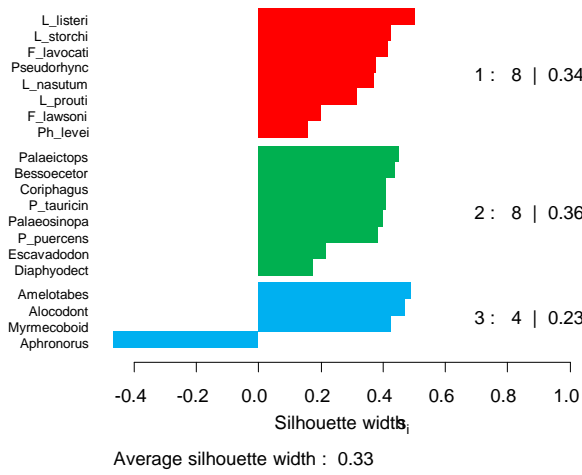
Average Silhouette Widths, Partion Around Medoids



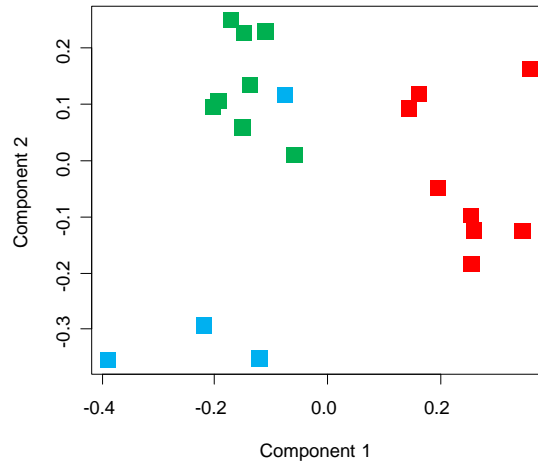
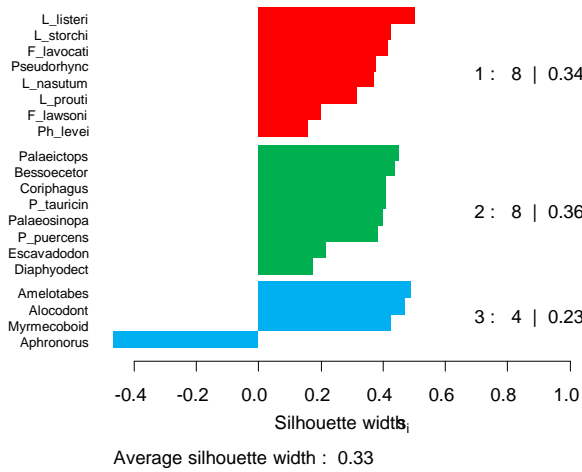
Clade Correspondence: All three BDC clusters contain more than one taxon. Only one (cluster 3) is monophyletic in any of the phylogenies published in Hooker (2013, figures 10-12).

Silhouette plot, BDC partitions

Pearson Correlation

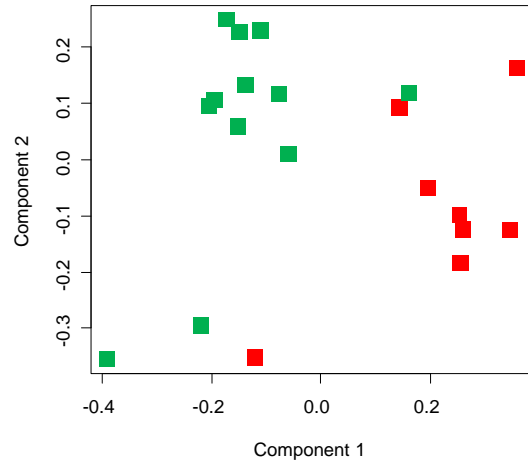
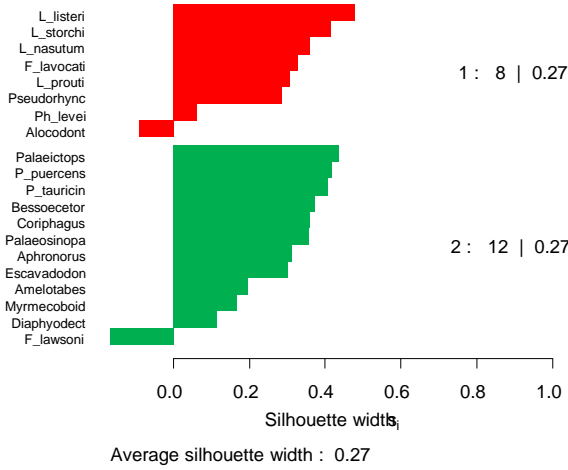


Spearman Correlation

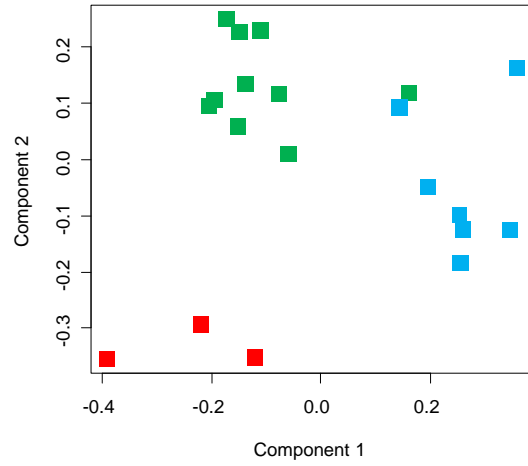
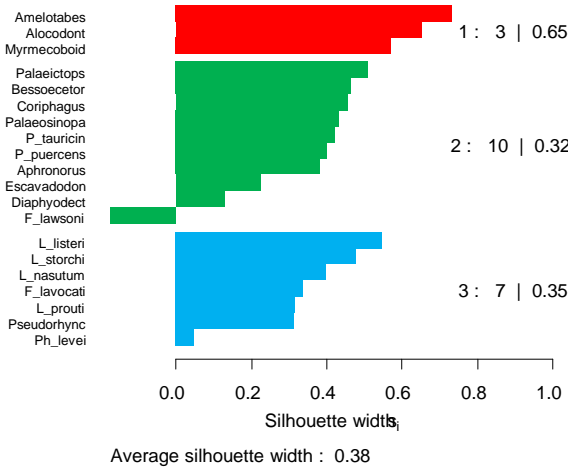


Silhouette plot, Partition Around Medoids

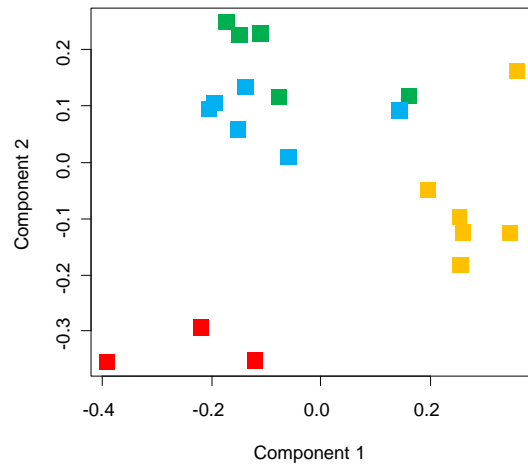
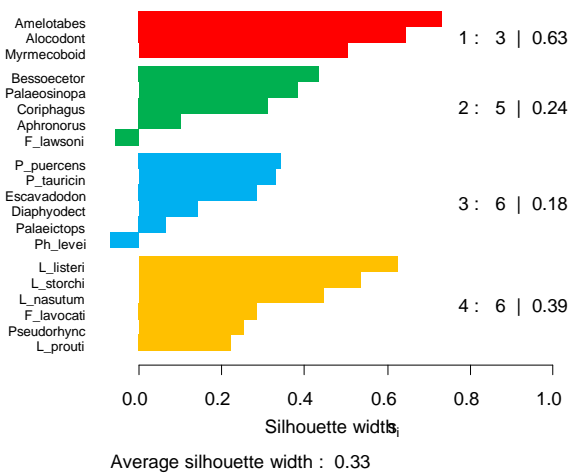
k=2



k=3

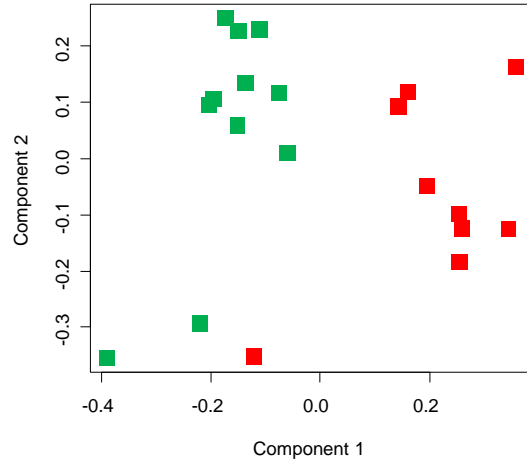
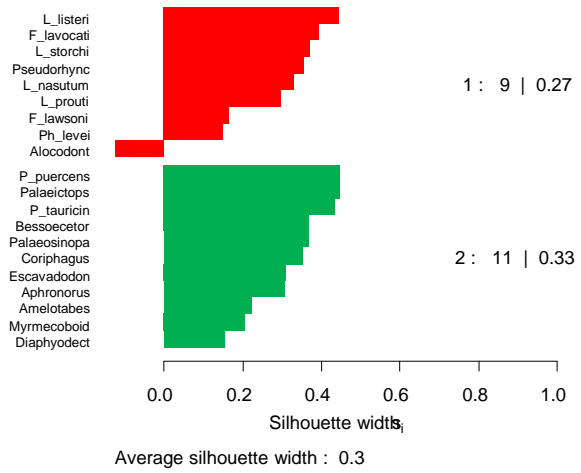


k=4

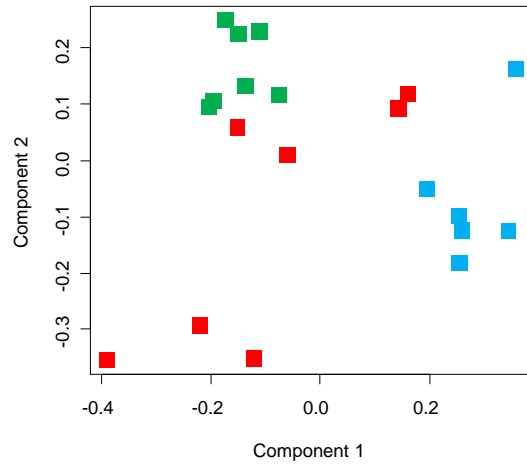
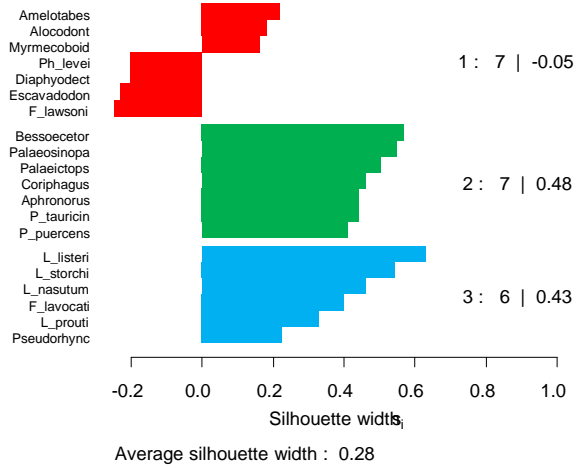


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Ochotonidae

Order Lagomorpha

Fostowicz-Frelik et al. 2010

Pearson BDC

Negative: 17

Positive: 49

Clusters: 4

Clusterability

Hopkins Statistic: 0.684

Dip test: 0.04

Dip test p-value: 0.015

Spearman BDC

Negative: 24

Positive: 60

Clusters: 3

Spearman BDC reveals an additional eleven significant, positive correlations and seven significant, negative correlations as compared to the Pearson BDC. These new correlations result in the addition of a singleton cluster from the Pearson BDC results to a larger cluster of taxa in the Spearman BDC results. The average silhouette width for the four Pearson clusters was 0.23 and for the three Spearman clusters was 0.26. The cluster membership difference for the Pearson and Spearman BDC was 5%.

The three-cluster medoid partition has an average silhouette width of 0.23, with three taxa having negative silhouette widths. None of the clusters exactly match those observed in the Spearman BDC. For $k=4$, medoid partition had an average silhouette width of 0.26, with one taxon having a negative silhouette width. Again, none of the medoid clusters exactly matched any clusters from the Pearson BDC. The cluster membership difference between the Pearson BDC and the medoid partition was 0.43. Fuzzy analysis failed for these distances.

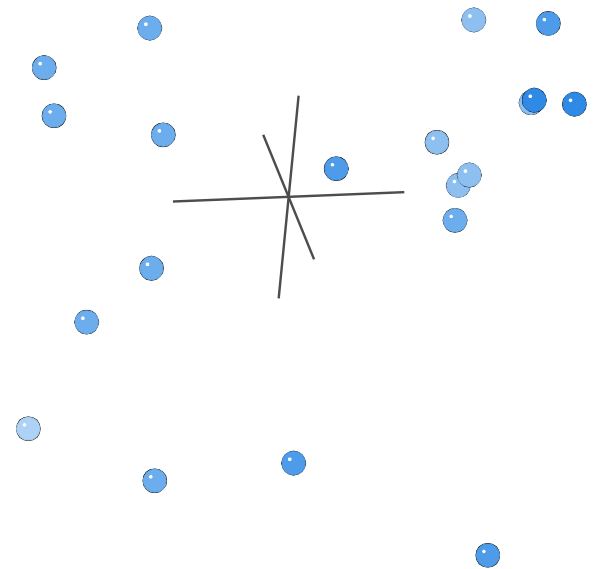
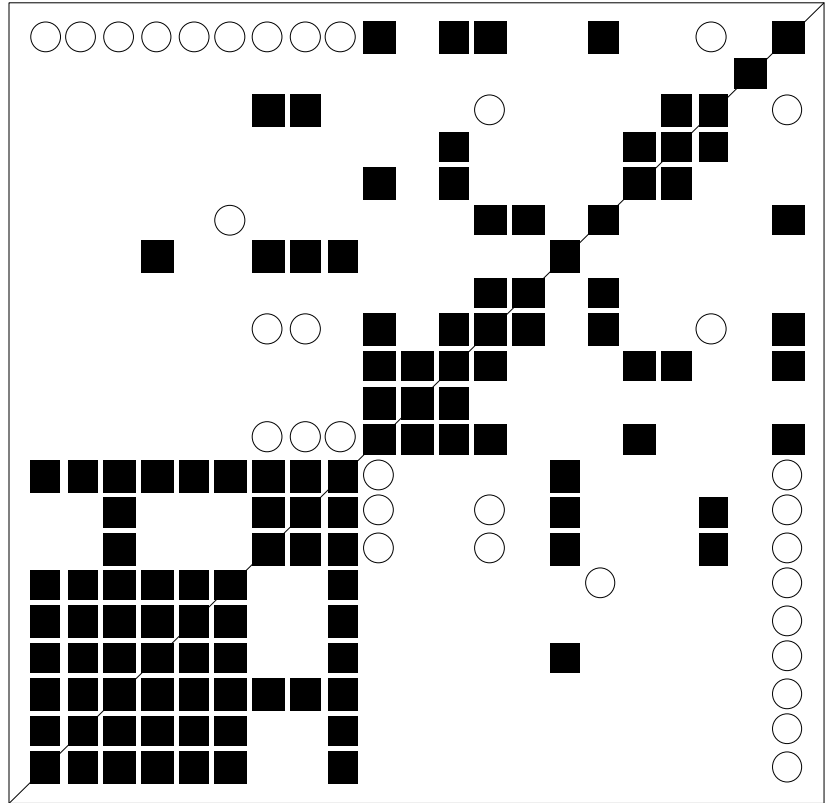
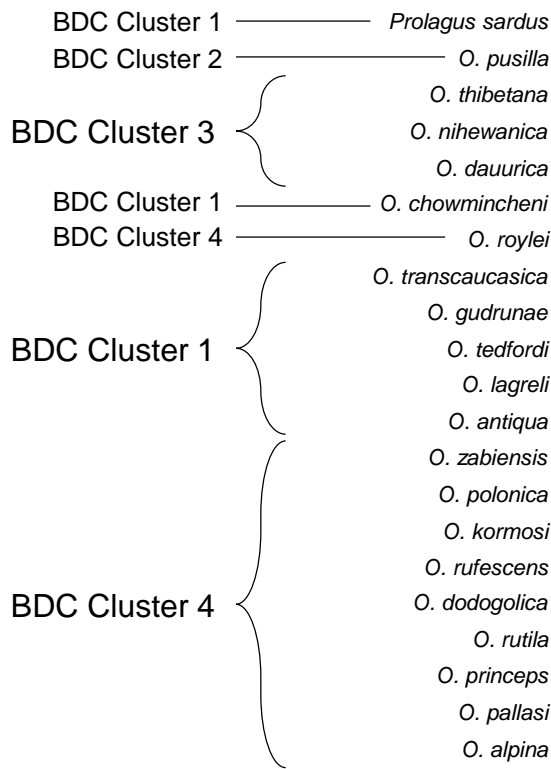
Again, we find that the Spearman BDC differs only slightly from the Pearson BDC, despite additional instances of significant correlation. The medoid partition only serves to emphasize what was already apparent in the BDC results: There is no clear clustering evident in these taxa based on these characters and distances. Again, we conclude only that the results are inconclusive for the presence of discontinuity or a holobaramin.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

Fostowicz-Frelik, Ł., G.J. Frelik, and M. Gasparik. 2010. Morphological phylogeny of pikas (Lagomorpha: Ochotona), with a description of a new species from the Pliocene/Pleistocene transition of Hungary. *Proceedings of the Academy of Natural sciences of Philadelphia* 159:97-118.

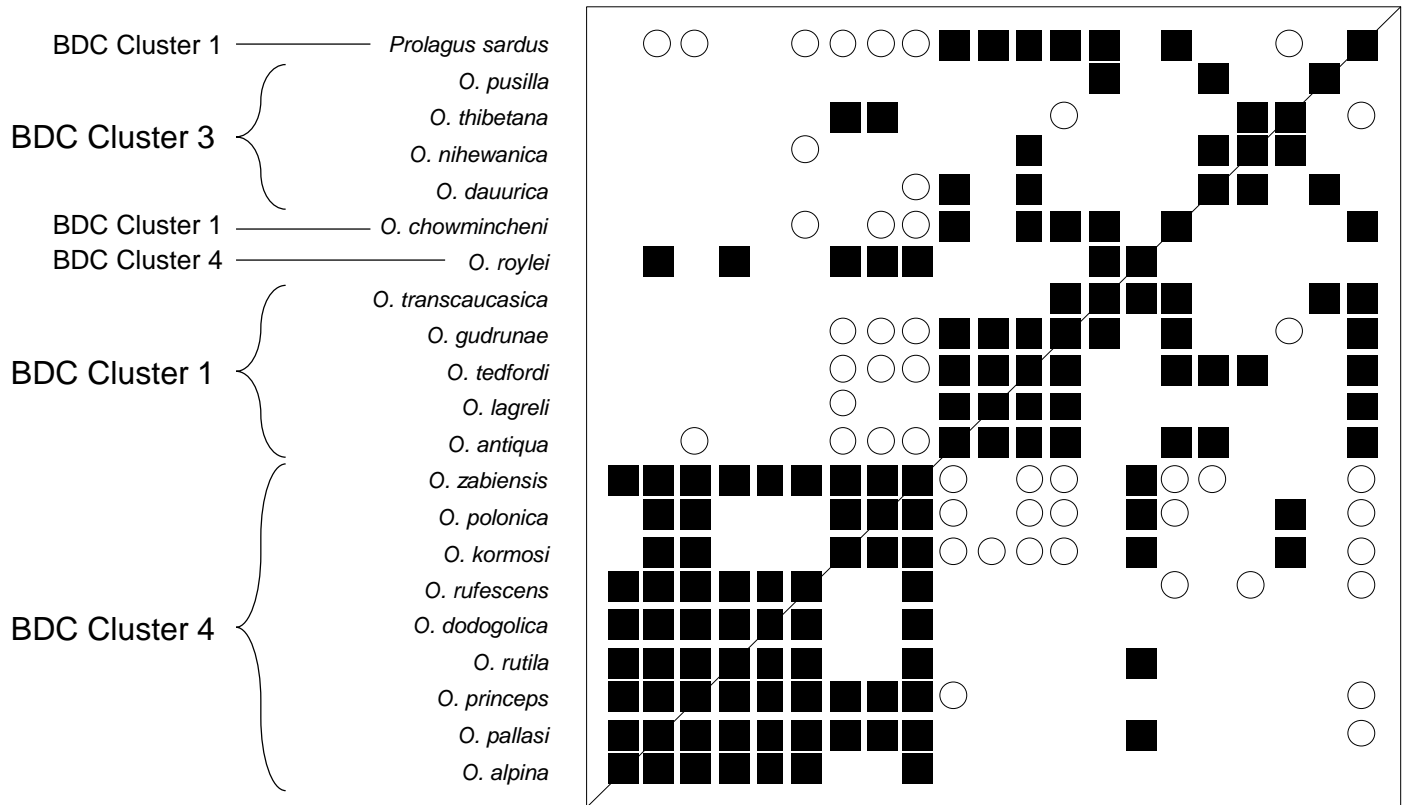
Characters: Craniodental



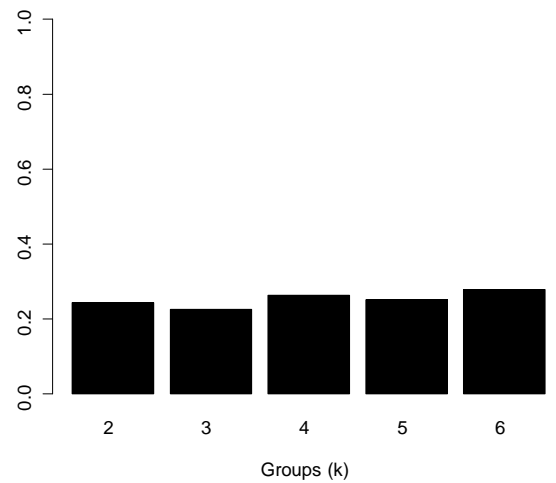
Order Lagomorpha
Family Ochotonidae

Published taxa	21
Published characters	38
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	21
Characters used for calculations	24
Median bootstrap value	69
F ₉₀	0.06
Stress of 3D MDS	0.22
k _{min}	6
Conclusion	Inc

Notes: In BDC results, taxic groups are not evident and bootstrap values are very poor. MDS suggests Ochotonidae forms a cluster distinct from the one outgroup taxon.



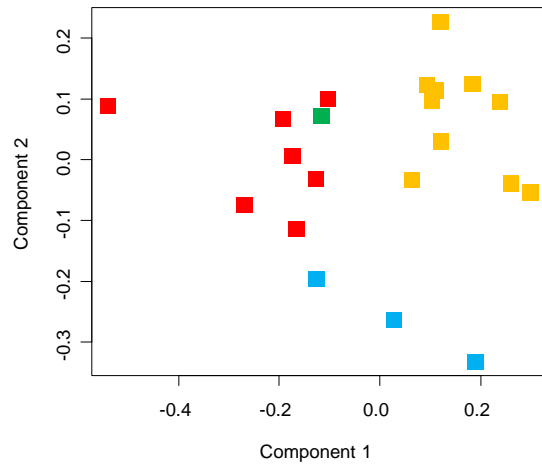
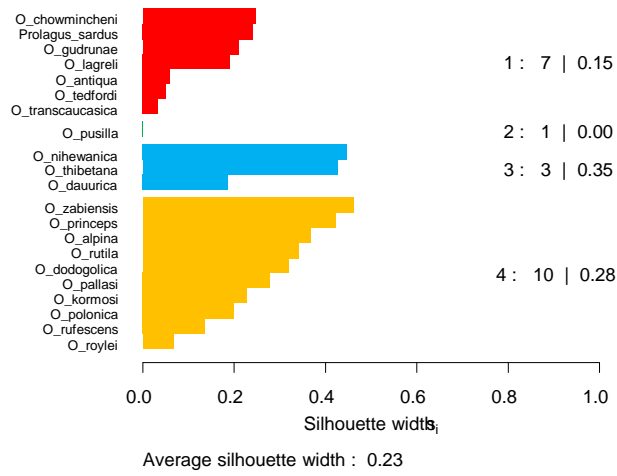
Average Silhouette Widths, Partion Around Medoids



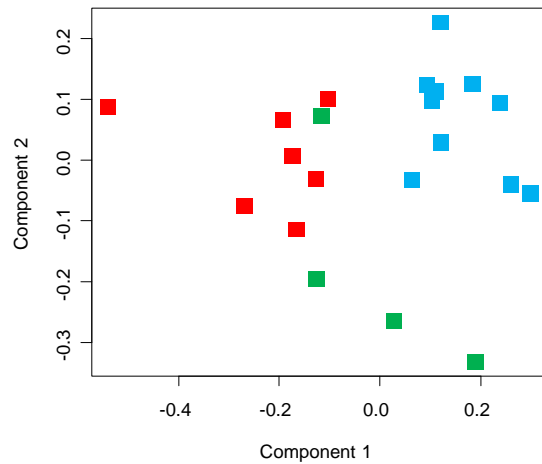
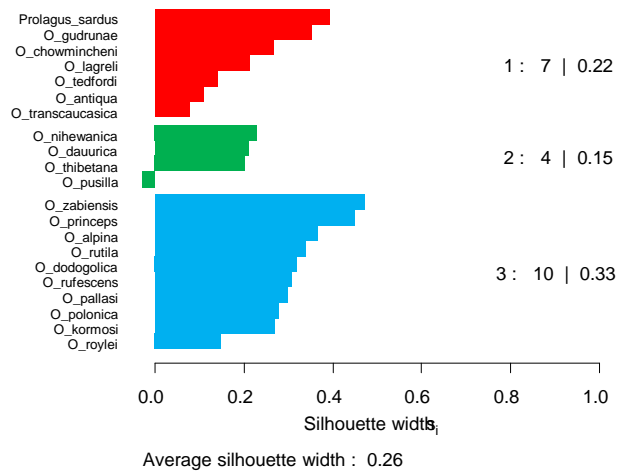
Clade Correspondence: Of the four BDC clusters, only one is a singleton (cluster 2). In figure 4 of Fostowicz-Frelik et al. (2010), only cluster 3 is monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

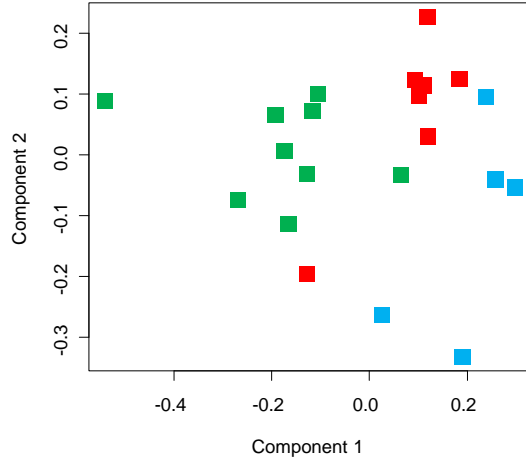
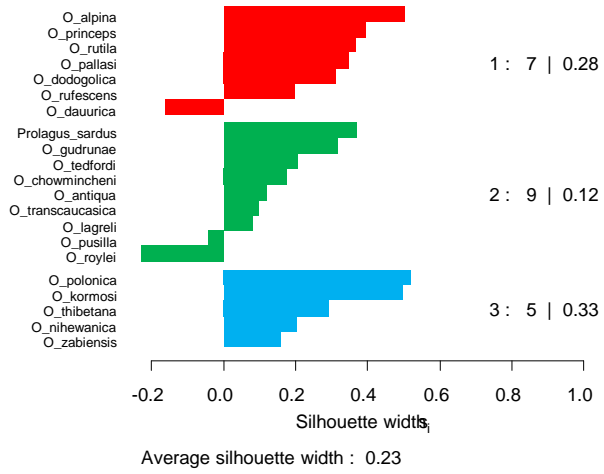


Spearman Correlation

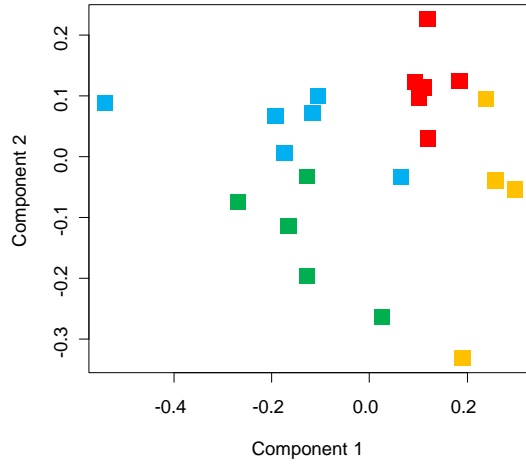
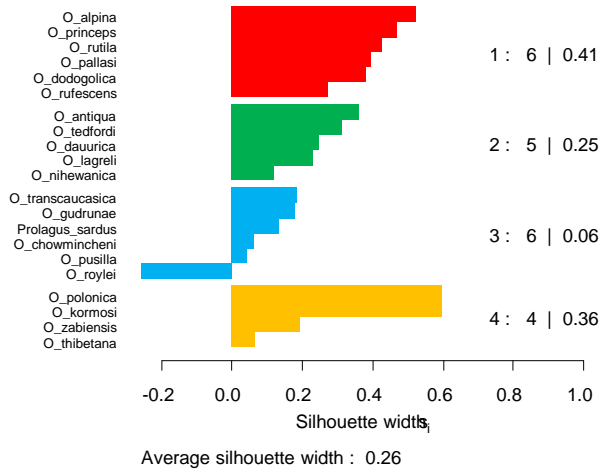


Silhouette plot, Partition Around Medoids

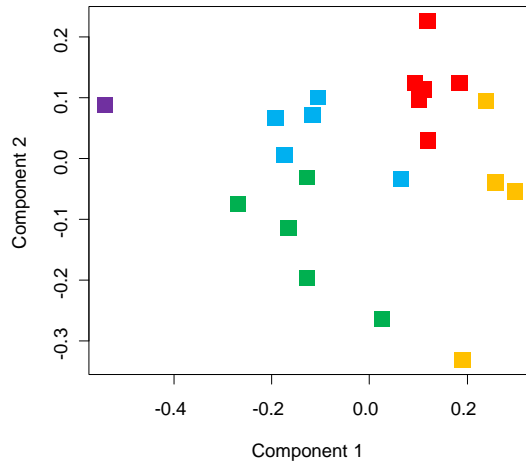
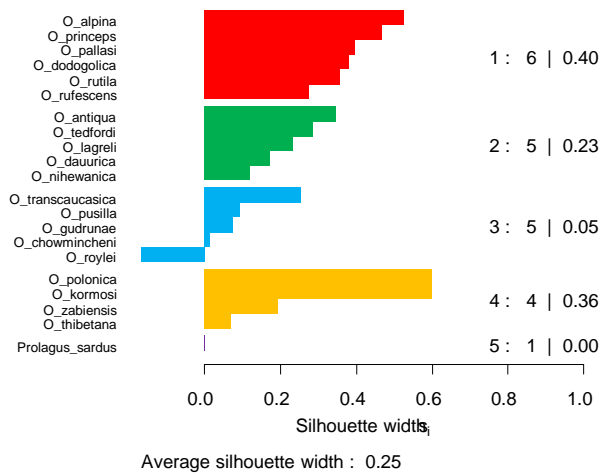
k=3



k=4



k=5



Family Leporidae

Order Lagomorpha

Fostowicz-Frelik 2013

Pearson BDC

Negative: 12

Positive: 9

Clusters: 4

Clusterability

Hopkins Statistic: 0.65

Dip test: 0.045

Dip test p-value: 0.585

Spearman BDC

Negative: 12

Positive: 13

Clusters: 4

Spearman BDC results revealed four additional instances of significant, positive correlation when compared to the Pearson BDC results, but the instances of significant, negative BDC were unchanged. Despite these additional instances of significant, positive correlation, the cluster partition is unchanged. There are four clusters detectable in both Pearson and Spearman BDC. The average silhouette width is 0.3.

Medoid partitioning at $k=4$ also detects the same clusters; however, at $k=3$, the medoid partition was slightly better with a silhouette width of 0.33. Fuzzy analysis at $k=4$ produced an average silhouette width of 0.26, and the cluster membership difference from the Pearson BDC partition was 18%. At $k=3$, however, the fuzzy partition was identical to the three-cluster medoid partition.

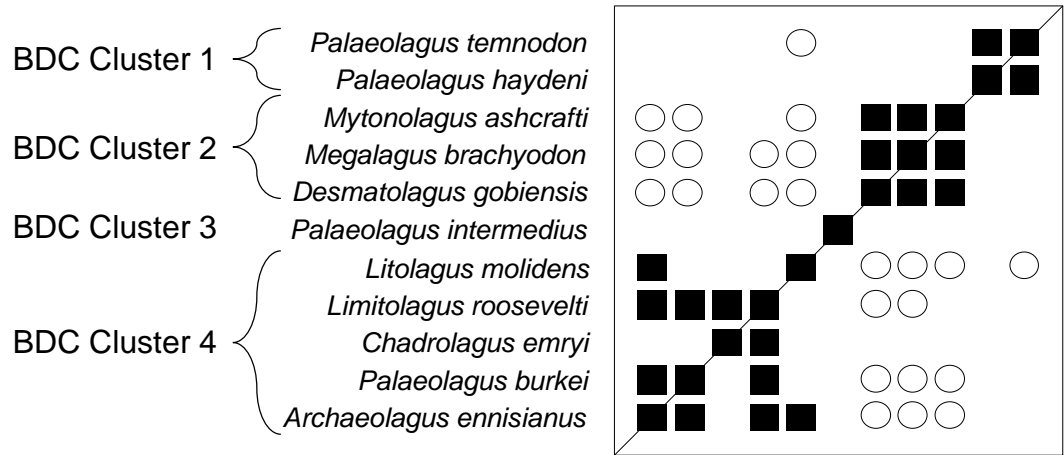
The original analysis cited poor bootstrap values as the reason for judging these results inconclusive. We might add here that the genus *Palaeolagus* is divided into three different clusters, which are separated by significant, negative BDC. Even the three-cluster partition supported by medoid partitioning and fuzzy analysis splits *Palaeolagus* into separate groups. These results reinforce the original conclusion.

Original conclusion: Inconclusive

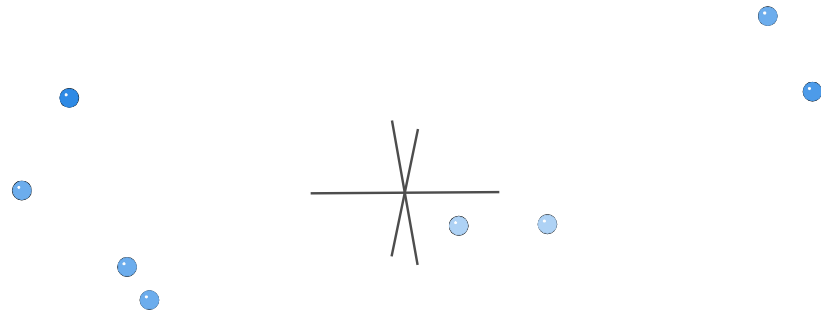
Updated conclusion: Inconclusive

Fostowicz-Frelik, Ł. 2013. Reassessment of *Chadrolagus* and *Litolagus* (Mammalia: Lagomorpha) and a new genus of North American Eocene lagomorph from Wyoming. *American Museum Novitates* 3773:1-76.

Characters: Craniodental



Palaeolagus intermedius ●



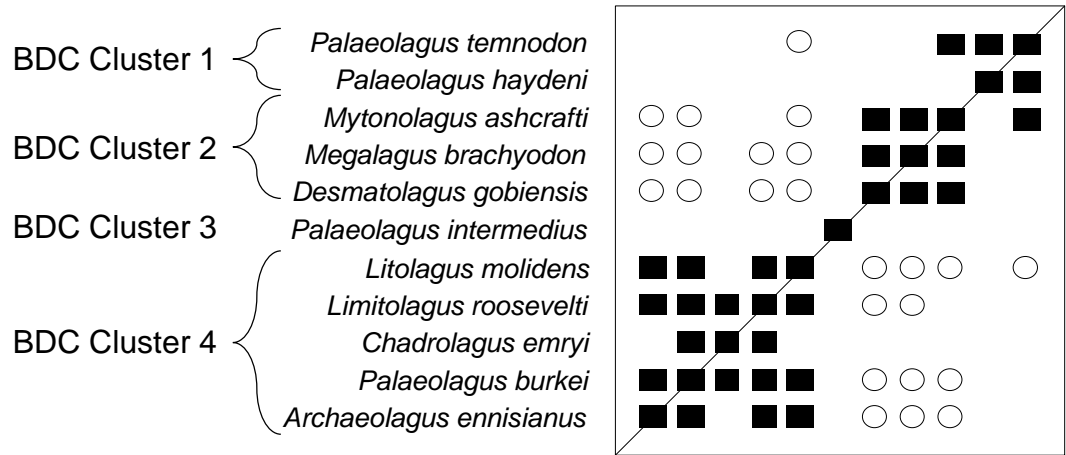
Chadrolagus emryi ●

Mytonolagus ashcrafti ●

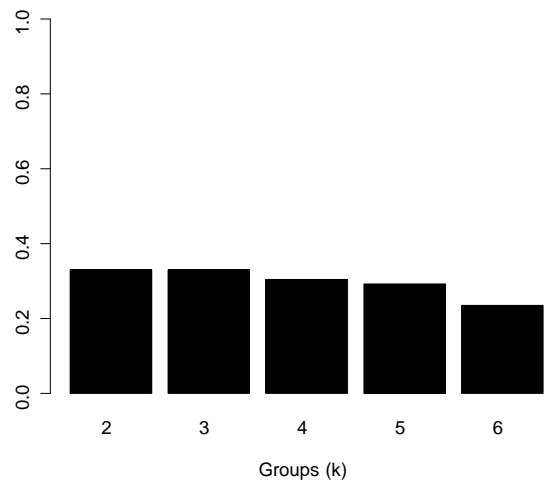
Order Lagomorpha
Family Leporidae

Published taxa	11
Published characters	44
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	11
Characters used for calculations	34
Median bootstrap value	89
F ₉₀	0.49
Stress of 3D MDS	0.11
k _{min}	6
Conclusion	Inc

Notes: BDC results have poor bootstrap values, and MDS results indicate a highly diffuse cloud of taxa.



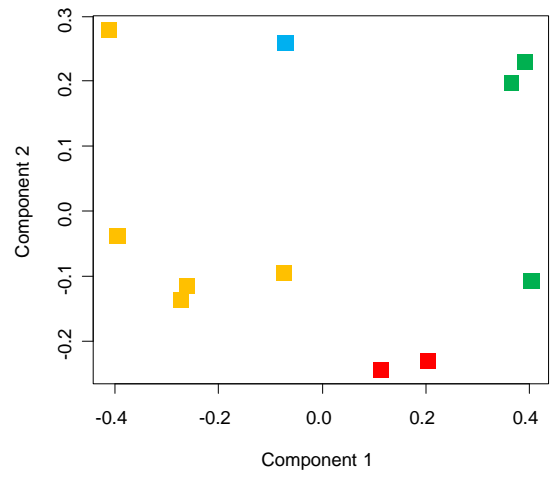
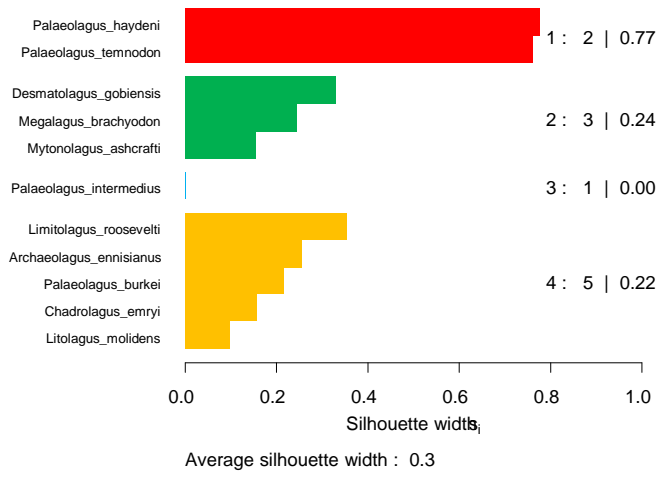
Average Silhouette Widths, Partion Around Medoids



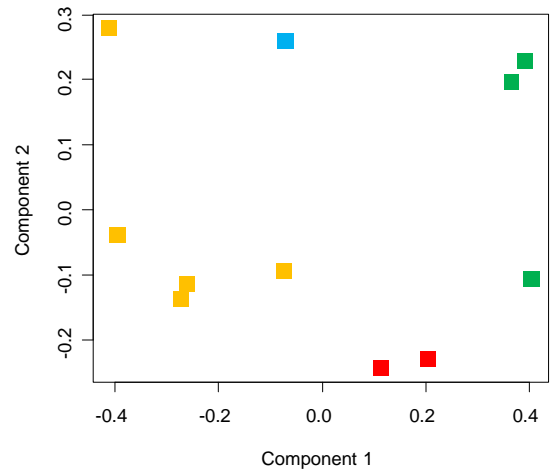
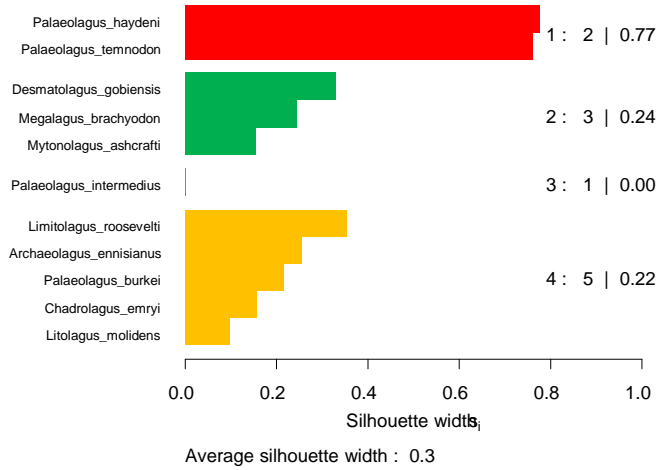
Clade Correspondence: Of the four BDC clusters, three contain more than one taxon. All three clusters are monophyletic in the phylogeny in figure 33 of Fostowicz-Frelik (2013) if the phylogeny were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

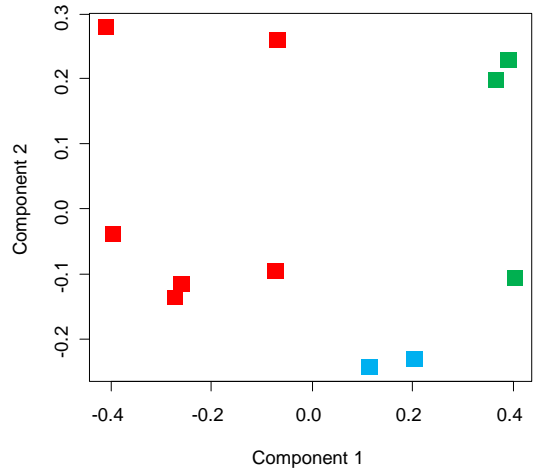
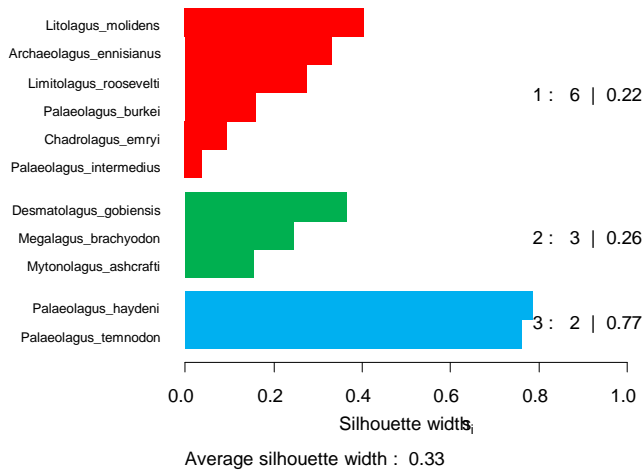


Spearman Correlation

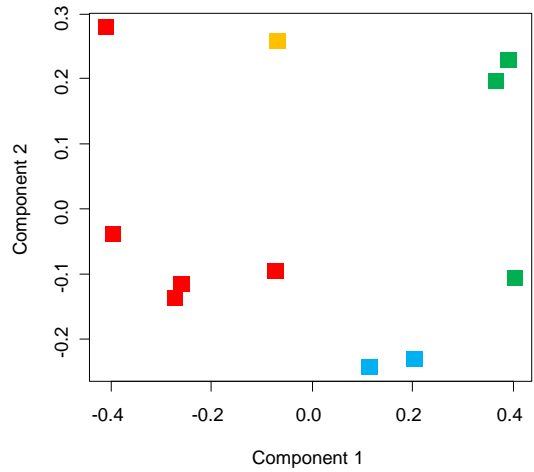
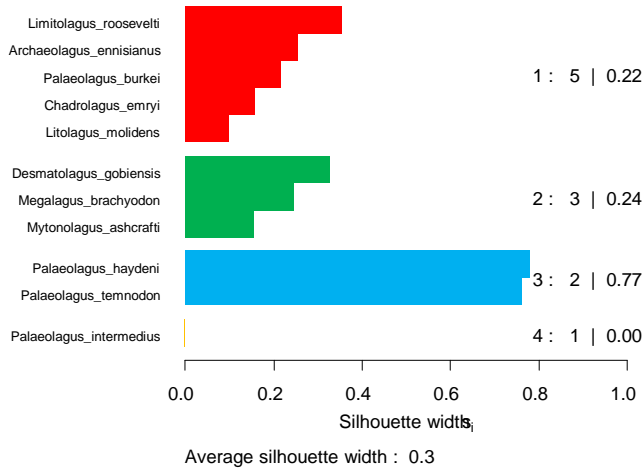


Silhouette plot, Partition Around Medoids

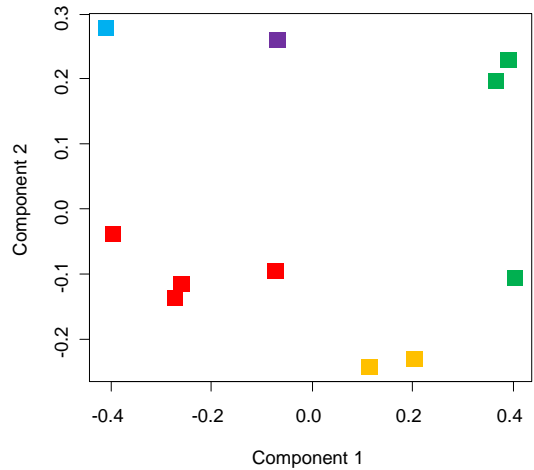
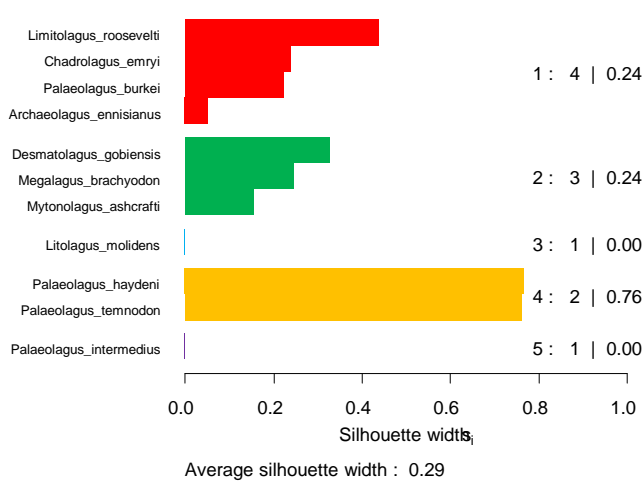
k=3



k=4

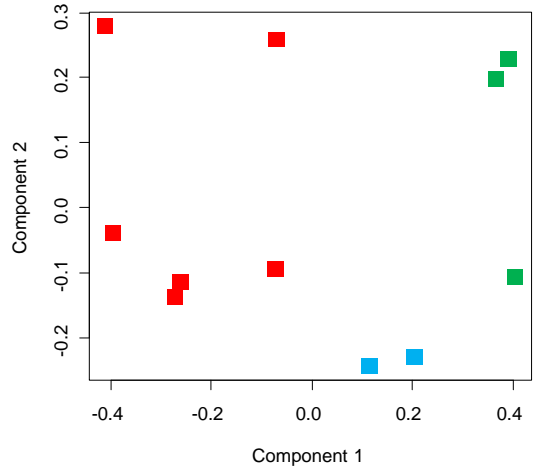
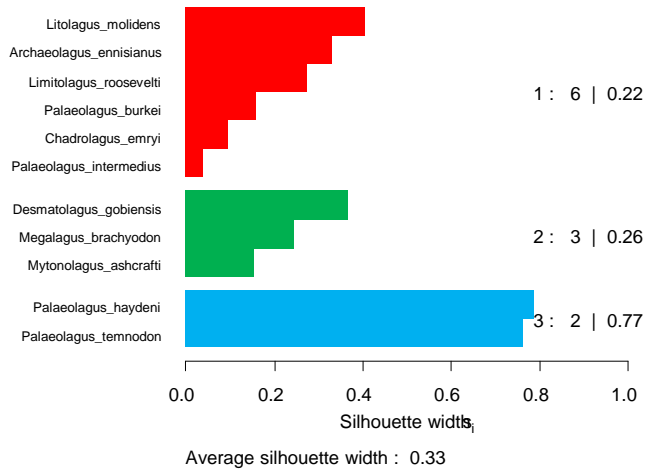


k=5

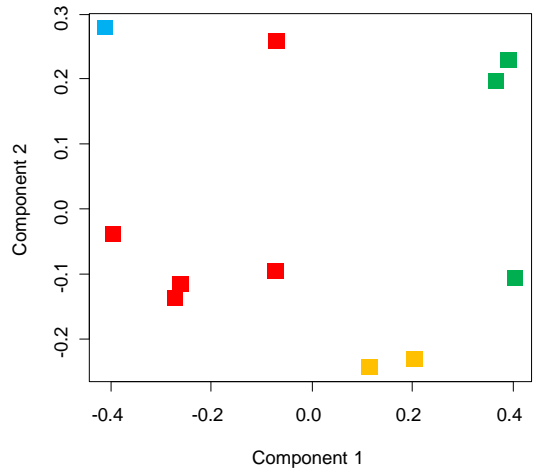
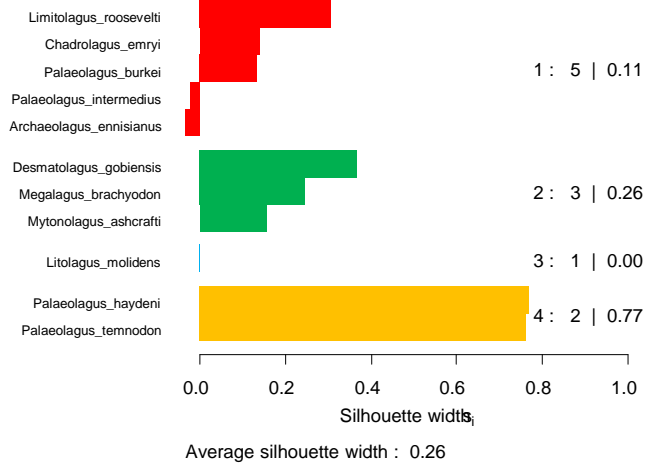


Silhouette plot, Fuzzy Analysis

k=3



k=4



Family Aplodontidae

Order Rodentia

Hopkins 2008

Pearson BDC

Negative: 1206

Positive: 1476

Clusters: 2

Clusterability

Hopkins Statistic: 0.864

Dip test: 0.0057

Dip test p-value: 0.664

Spearman BDC

Negative: 1220

Positive: 1759

Clusters: 2

The Spearman BDC results increased instances of significant, positive BDC by 19%, but the instances of significant, negative BDC increased by only 0.3%. Despite this substantial increase in significant, positive BDC, the Spearman BDC clusters were the same as the Pearson BDC clusters. This two-cluster partition rendered an average silhouette width of 0.38.

The medoid partition at k=2 did not produce the same clusters as the BDC results but they were very similar. The cluster membership difference was only 5%, and the average silhouette width for the two-cluster medoid partition was 0.39. The medoid partition at k=4 had a much better average silhouette width of 0.47, but the number of taxa with negative silhouette widths increased from two in the two-cluster medoid partition to five in the four-cluster medoid partition.

Fuzzy analysis at k=2 also generated a partition very similar to the BDC clusters, with a cluster membership difference of only 5%. The average silhouette width for the two-cluster fuzzy analysis was 0.4. At k=4, the fuzzy analysis generated a partition with an average silhouette width of 0.48 and only one taxon with a negative silhouette width.

The original results were judged inconclusive because of the frequent occurrence of significant, positive BDC between the two clusters. The MDS results appear to show two families and a set of outgroup taxa that have no obvious discontinuity. Here, the medoid and fuzzy partition also support the recognition of two groups of taxa very similar to the BDC result, but neither agreed on their precise membership. Likewise, based on the average silhouette widths, a four-cluster partition seemed to generate better results in both medoid partitioning and fuzzy analysis, however the BDC as reported here do not support recognizing four different clusters. It is possible that subdividing the taxon set to adjacent subsets visible in the MDS results might yield better recognition of discontinuity. Given the present results, however, these characters and distances are judged inconclusive.

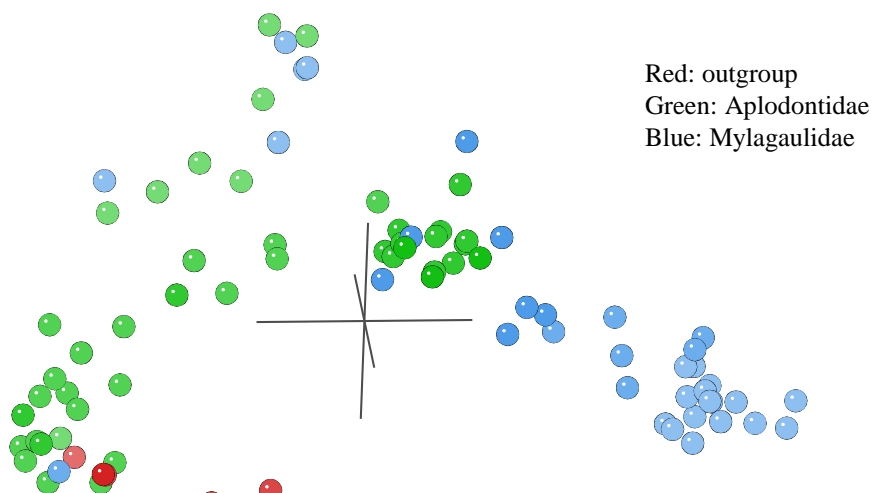
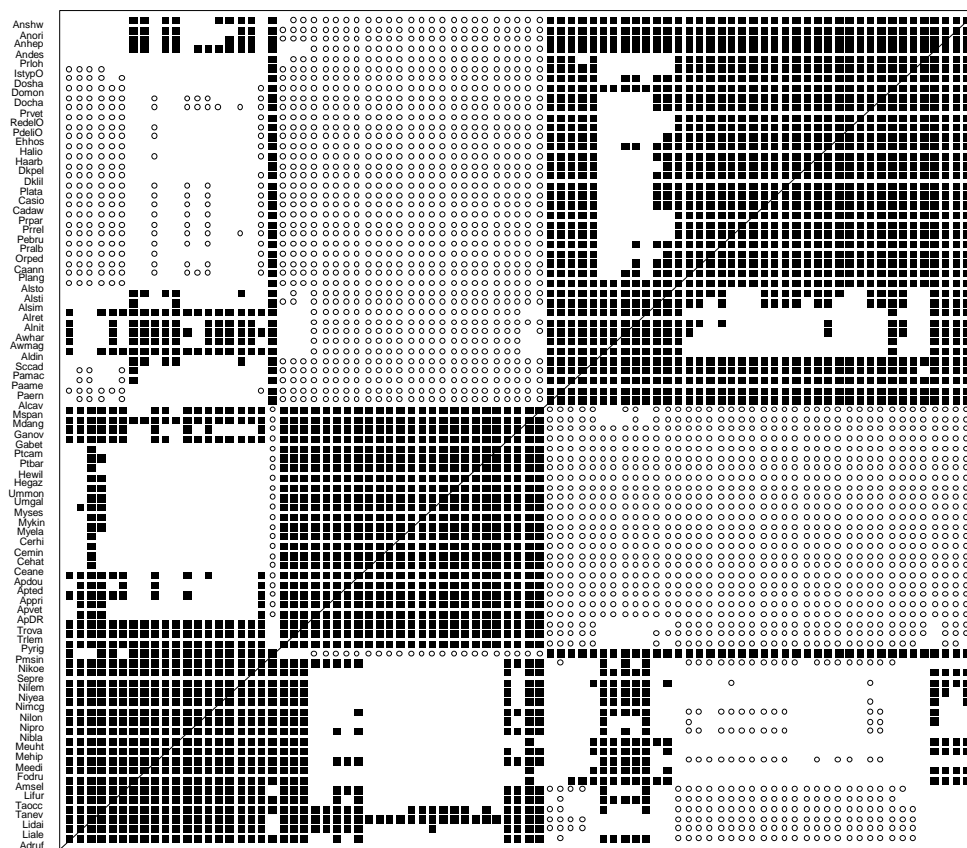
Original conclusion: Inconclusive

Updated conclusion: Inconclusive

Characters: Craniodental

BDC Cluster 1

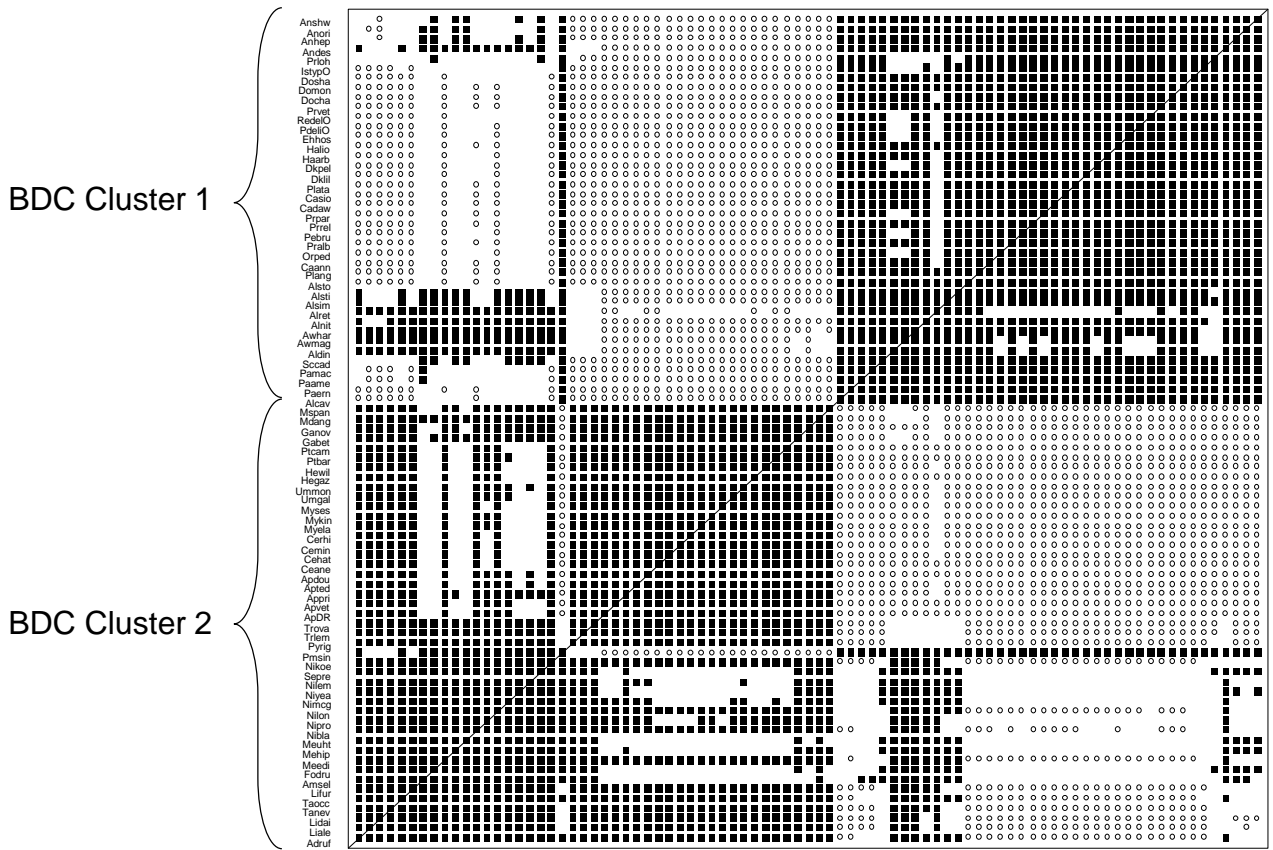
BDC Cluster 2



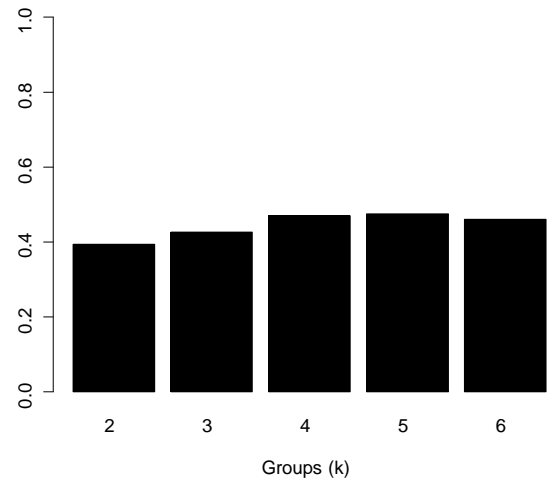
Order Rodentia
Family Aplodontidae

Published taxa	107
Published characters	249
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	85
Characters used for calculations	145
Median bootstrap value	95
F ₉₀	0.54
Stress of 3D MDS	0.15
k _{min}	7
Conclusion	Inc

Notes: No evidence of discontinuity within superfamily Aplodontioidea. MDS reveals a cluster of taxa with families blending into one another.



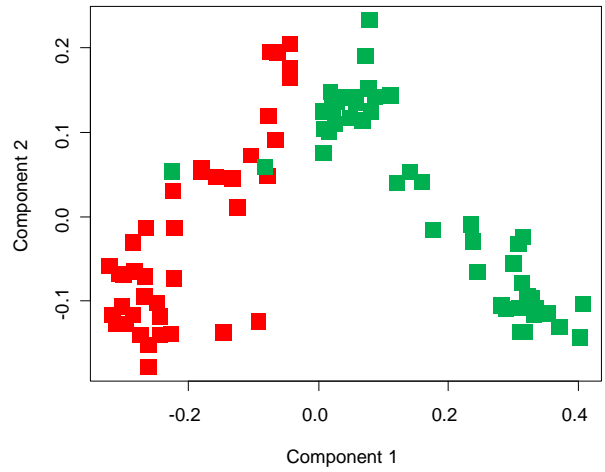
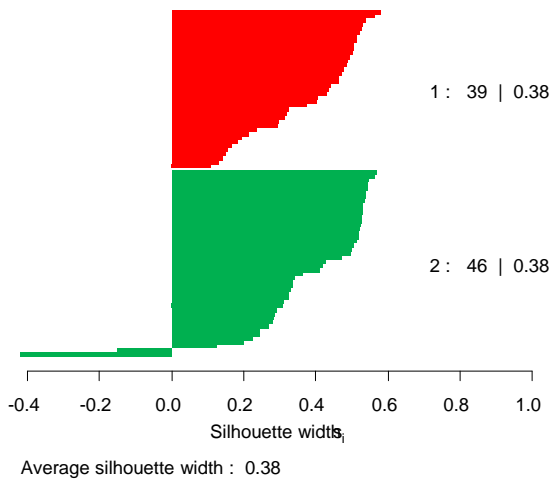
Average Silhouette Widths, Partion Around Medoids



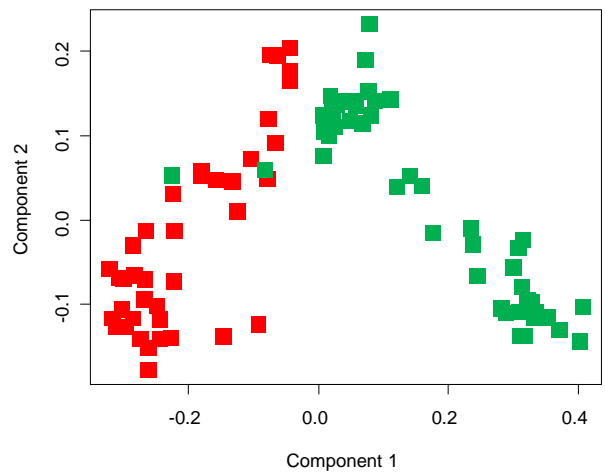
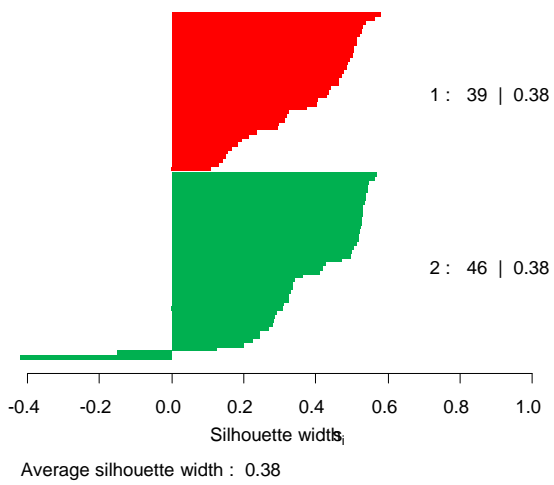
Clade Correspondence: Two large clusters are evident in the BDC results. They are both monophyletic in the phylogeny shown in Figure 2 of Hopkins (2008).

Silhouette plot, BDC partitions

Pearson Correlation

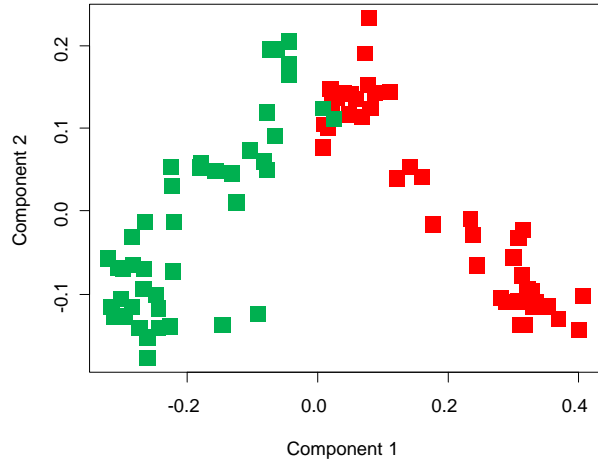
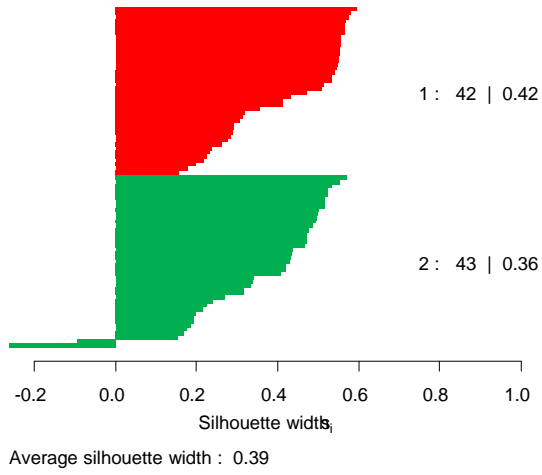


Spearman Correlation

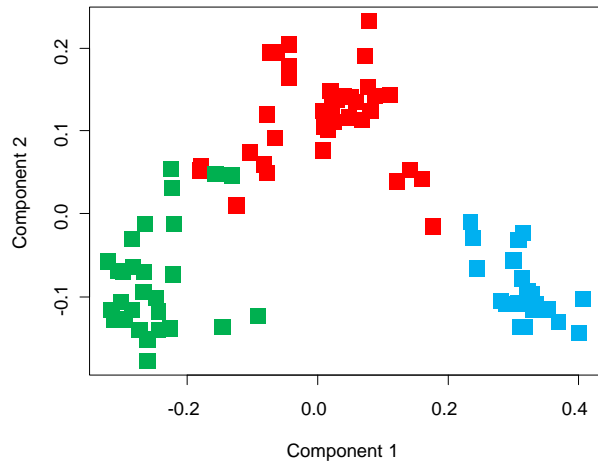
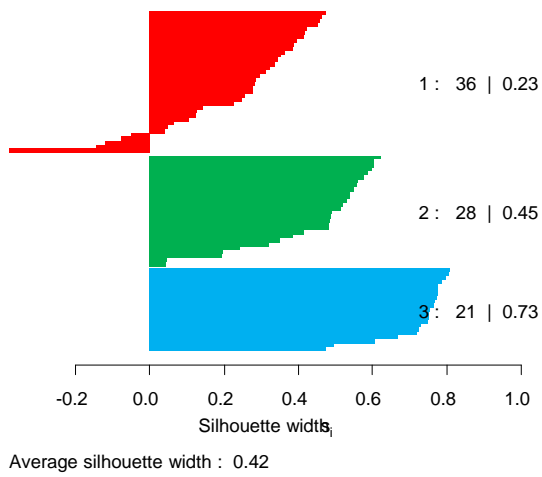


Silhouette plot, Partition Around Medoids

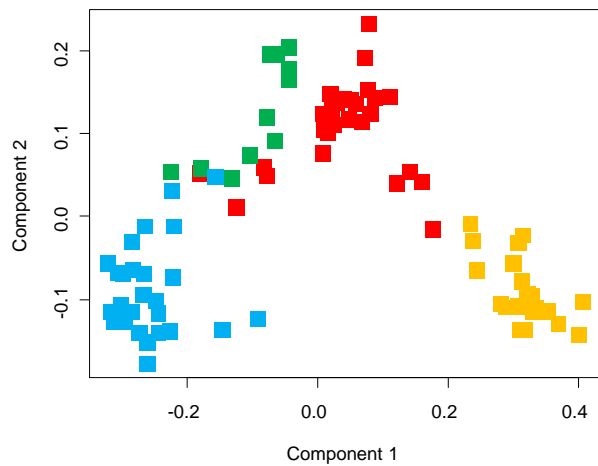
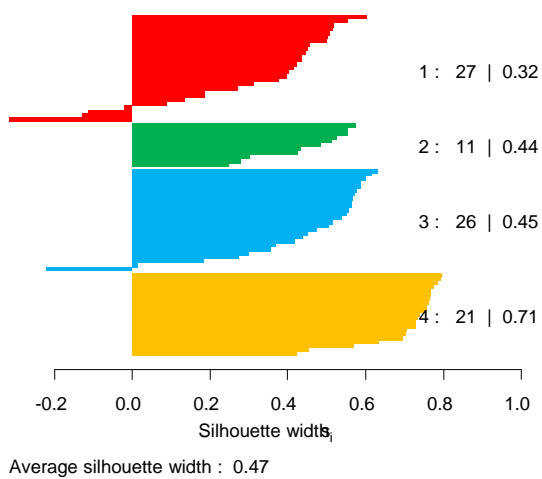
k=2



k=3

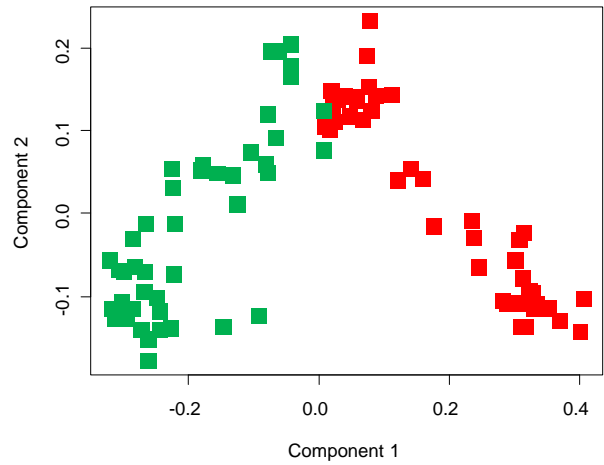
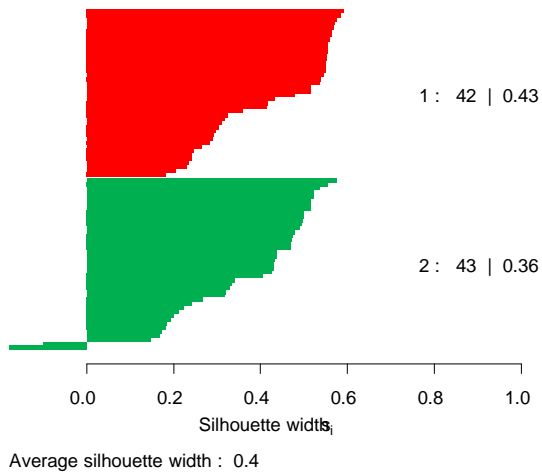


k=4

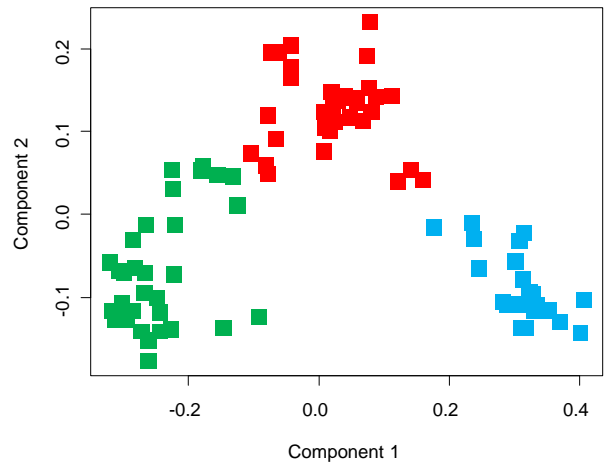
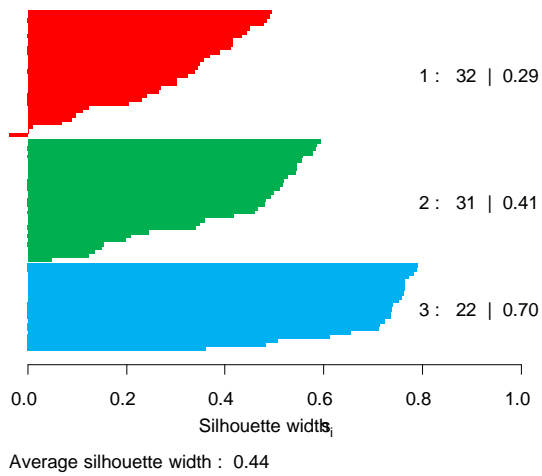


Silhouette plot, Fuzzy Analysis

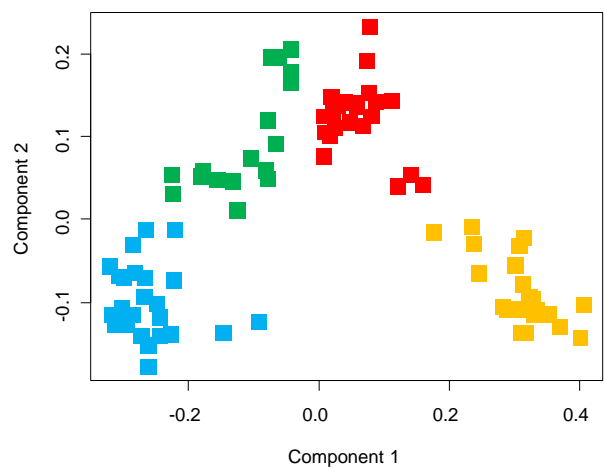
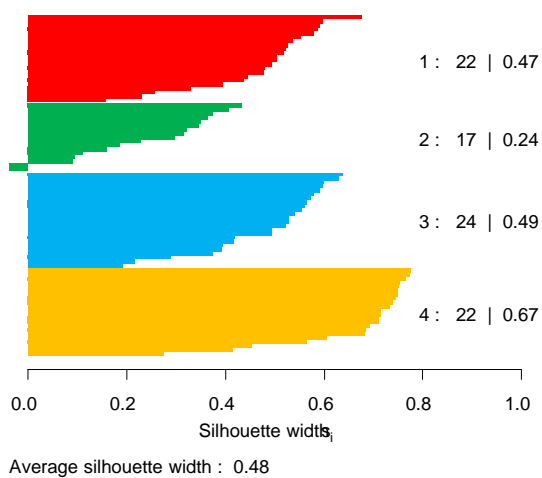
k=2



k=3



k=4



Family Castoridae

Order Rodentia
Rybczynski 2007

Pearson BDC
Negative: 35
Positive: 109
Clusters: 3

Clusterability
Hopkins Statistic: 0.761
Dip test: 0.029
Dip test p-value: 0.103

Spearman BDC
Negative: 13
Positive: 113
Clusters: 2

The Spearman BDC results generated an additional four instances of significant, positive correlation, which united a singleton cluster from the Pearson BDC results to a larger cluster of taxa. Nevertheless, the membership of the largest cluster remains the same in the Pearson and Spearman BDC results, and the cluster membership difference was 4%. The average silhouette width for the three-cluster Pearson BDC was 0.22, with three taxa having negative silhouette widths. The average silhouette width for the two-cluster Spearman BDC was substantially better at 0.36, with only one taxon having a negative silhouette width.

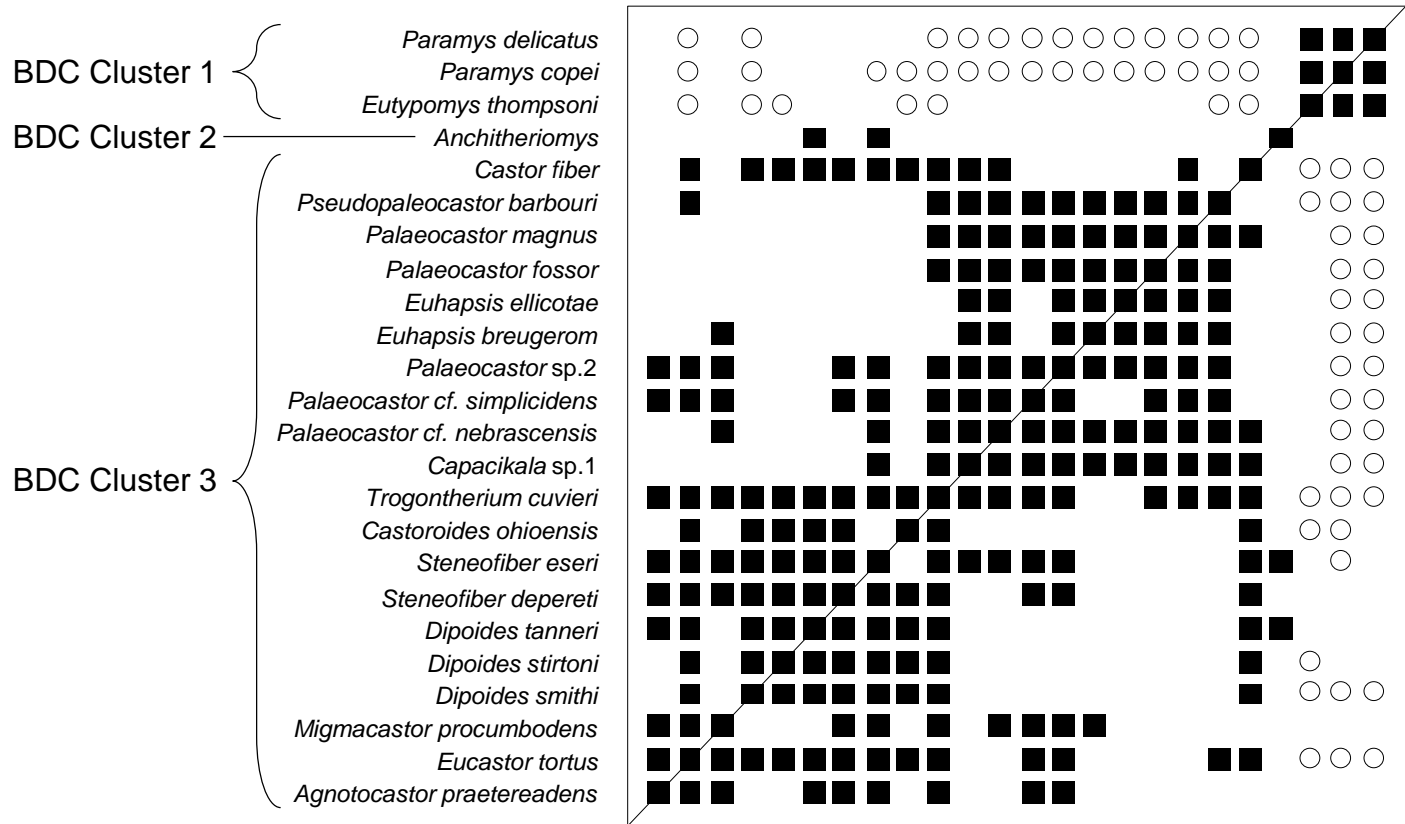
The medoid partition at $k=3$ does not agree with the Pearson BDC results. The average silhouette width for the three-cluster medoid partition was 0.29, with only one taxon having a negative silhouette width. The cluster membership difference for the Pearson BDC and medoid partition was 38%. The medoid partition at $k=2$ was substantially worse, with an average silhouette width of only 0.18.

Fuzzy analysis only produced results for the two-cluster partition, which had an average silhouette width of 0.19.

The original conclusions noted the clean division between the ingroup and outgroup taxa as evident in both the BDC and MDS results. Here we find little support for that division in either the Spearman BDC (which groups one of the castorids with the outgroup taxa), the medoid partition, or the fuzzy analysis. This makes the original conclusion more uncertain. We may here conclude that this holobaramin is uncertain and might exclude the castorid *Anchitheriomys*.

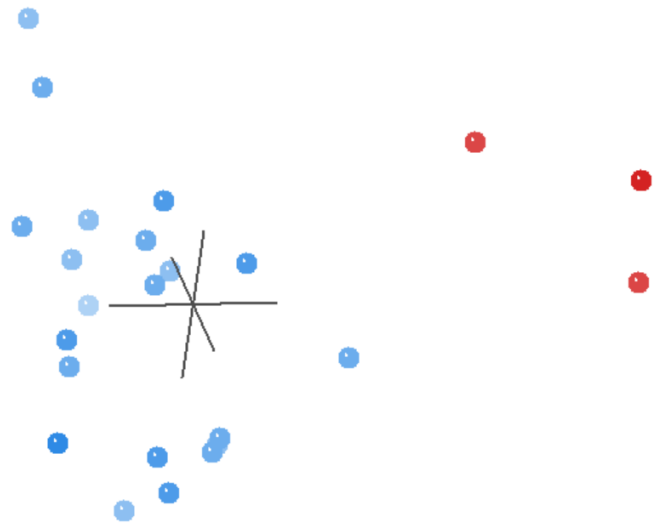
Original conclusion: HB?
Updated conclusion: HB

Characters: Cranial and postcranial



Order Rodentia
Family Castoridae

Published taxa	39
Published characters	88
Character relevance	0.75
Taxic relevance	0.5
Taxa used for calculations	24
Characters used for calculations	41
Median bootstrap value	78
F ₉₀	0.16
Stress of 3D MDS	0.21
k _{min}	6
Conclusion	HB



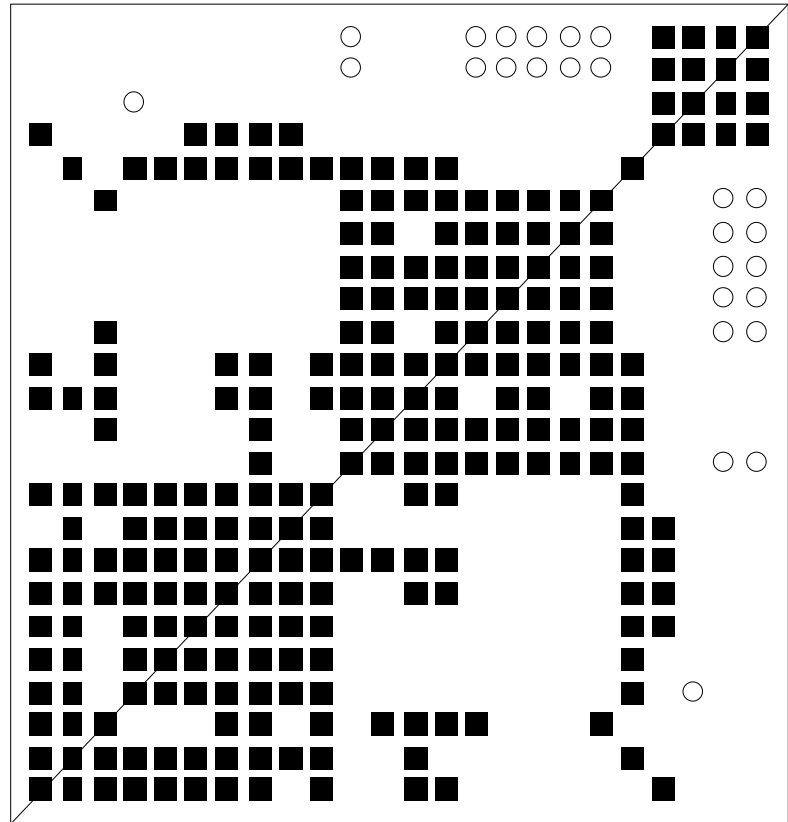
Notes: Castorid taxa are well separated from the outgroup in both BDC and MDS results. Castoridae appears to be a holobaramin.

BDC Cluster 1

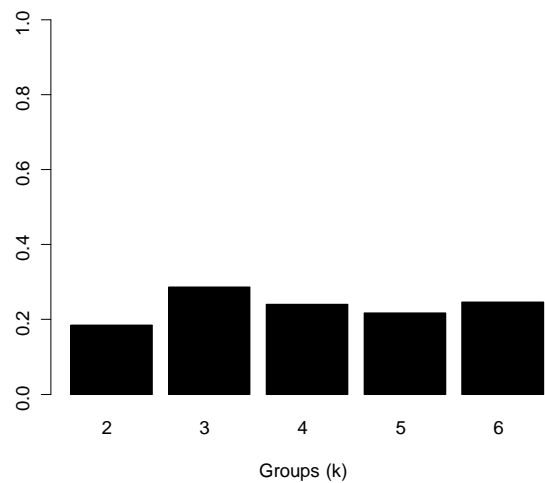
- Paramys delicatus*
- Paramys copei*
- Eutypomys thompsoni*
- Anchitheriomys*
- Castor fiber*
- Pseudopaleocastor barbouri*
- Palaeocastor magnus*
- Palaeocastor fossor*
- Euhapsis ellicotae*
- Euhapsis breugerom*
- Palaeocastor sp.2*
- Palaeocastor cf. simplicidens*
- Palaeocastor cf. nebrascensis*

BDC Cluster 3

- Capacikala sp.1*
- Trogontherium cuvieri*
- Castoroides ohioensis*
- Steneofiber eseri*
- Steneofiber depereti*
- Dipoides tanneri*
- Dipoides stirtoni*
- Dipoides smithi*
- Migmacastor procumbodens*
- Eucastor tortus*
- Agnotocastor praetereadens*



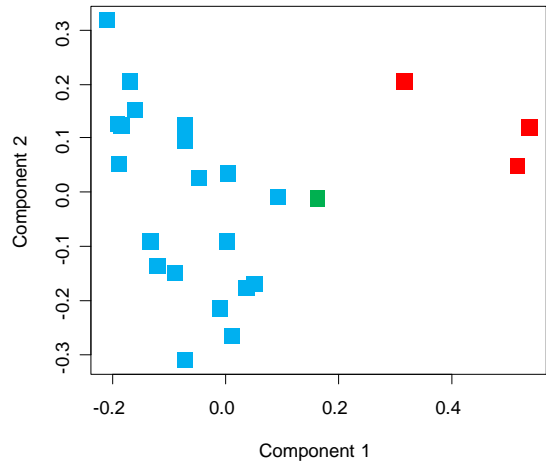
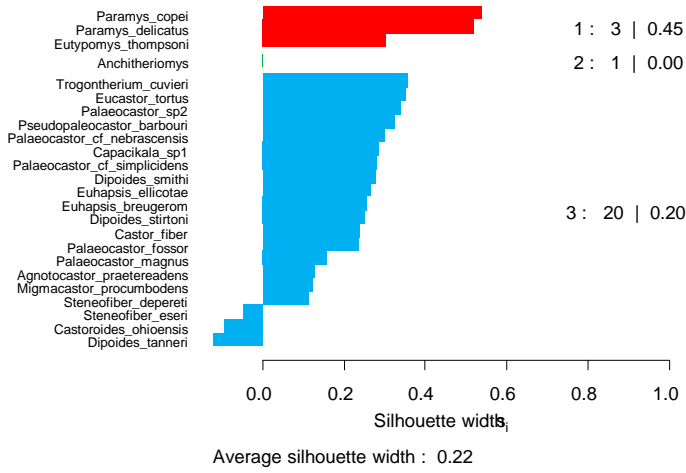
Average Silhouette Widths, Partion Around Medoids



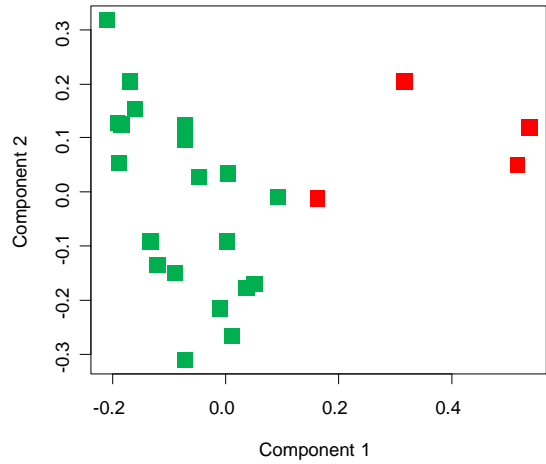
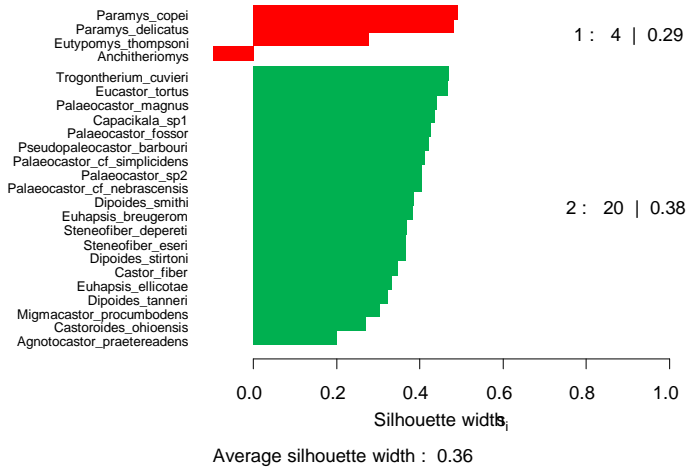
Clade Correspondence: There are two BDC clusters and one singleton. The smaller cluster is monophyletic in Figure 3 of Rybczynski (2007), but the larger cluster is not.

Silhouette plot, BDC partitions

Pearson Correlation

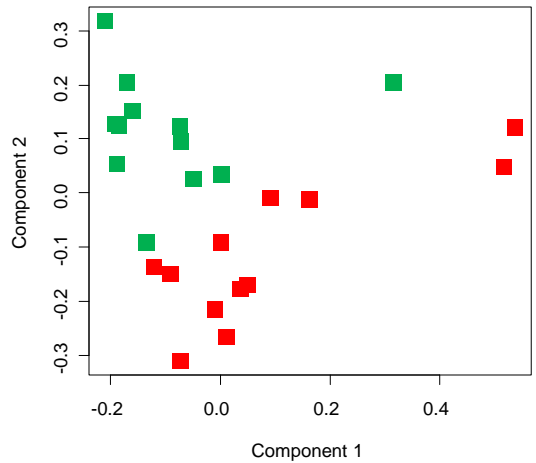
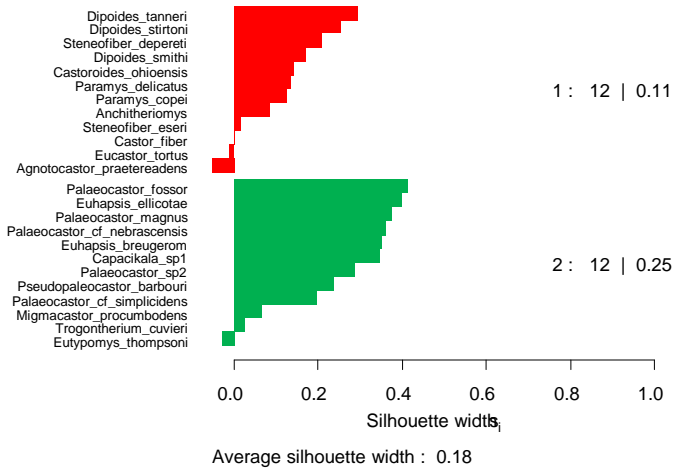


Spearman Correlation

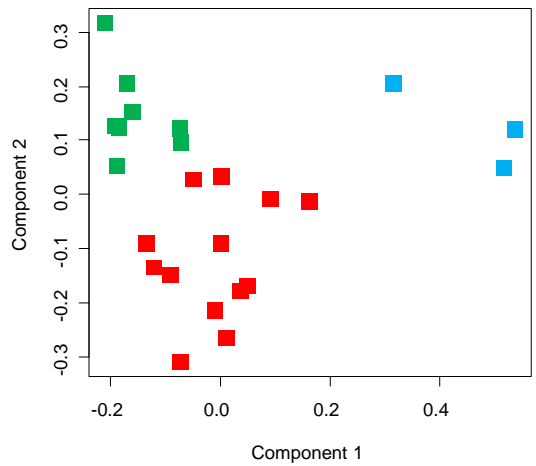
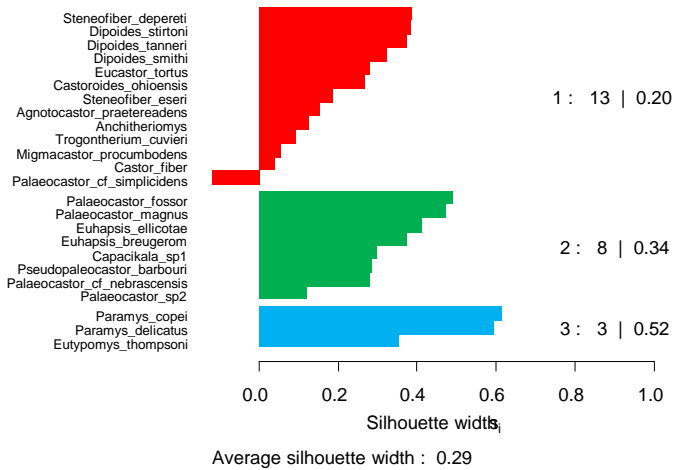


Silhouette plot, Partition Around Medoids

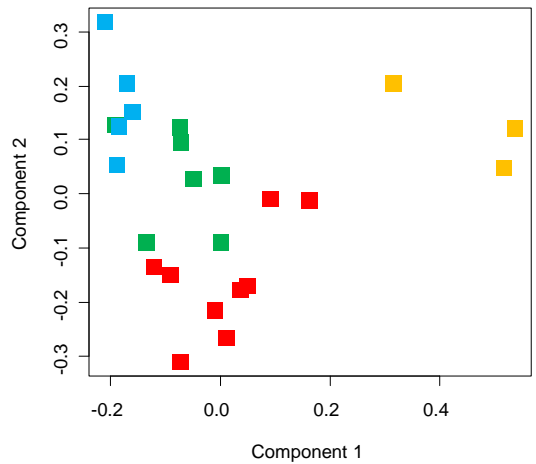
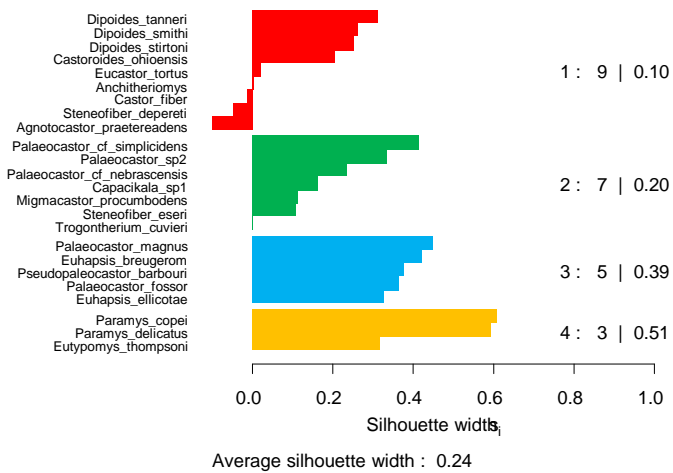
k=2



k=3

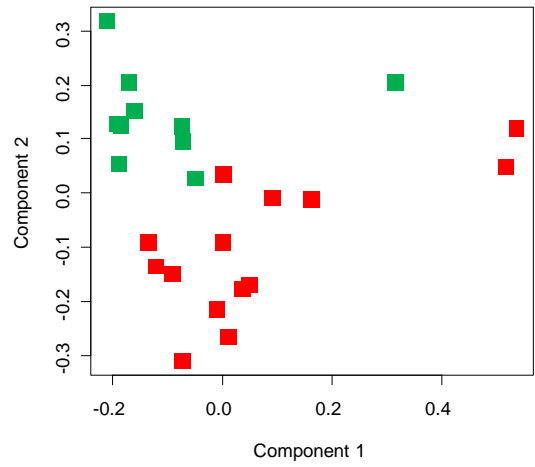
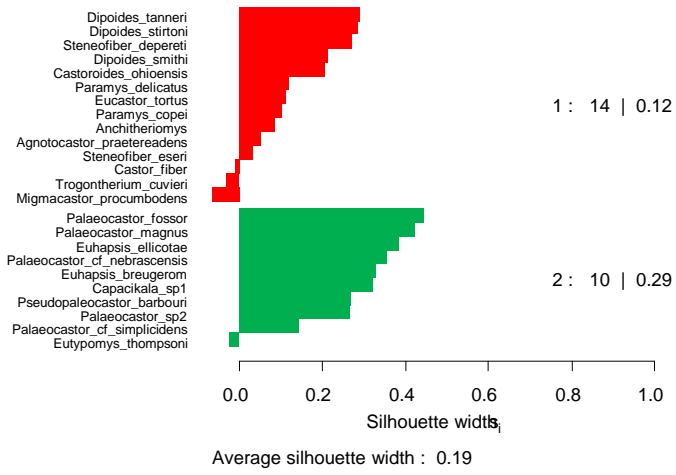


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Cricetidae

Order Rodentia

Maridet and Ni 2013

Pearson BDC

Negative: 49

Positive: 337

Clusters: 3

Clusterability

Hopkins Statistic: 0.843

Dip test: 0.011

Dip test p-value: 0.881

Spearman BDC

Negative: 37

Positive: 367

Clusters: 2

Three clusters are discernible in the Pearson BDC results, with an average silhouette width of 0.39. Spearman BDC reveals an addition 30 instances of significant, positive correlation and twelve fewer instances of significant, negative BDC. These changes in BDC produce a partition of only two clusters, with a cluster membership difference of 8% and an average silhouette width of 0.37.

The medoid partition at $k=3$ differs from the Pearson BDC results. None of the exact clusters are retained, and the cluster membership difference is 22%. The three-cluster medoid partition has an average silhouette value of 0.37. The two-cluster medoid partition also differs from the Spearman BDC clustering. The average silhouette width for the two-cluster medoid partition is 0.35. The best average silhouette width for medoid partitioning is 0.44 at $k=4$.

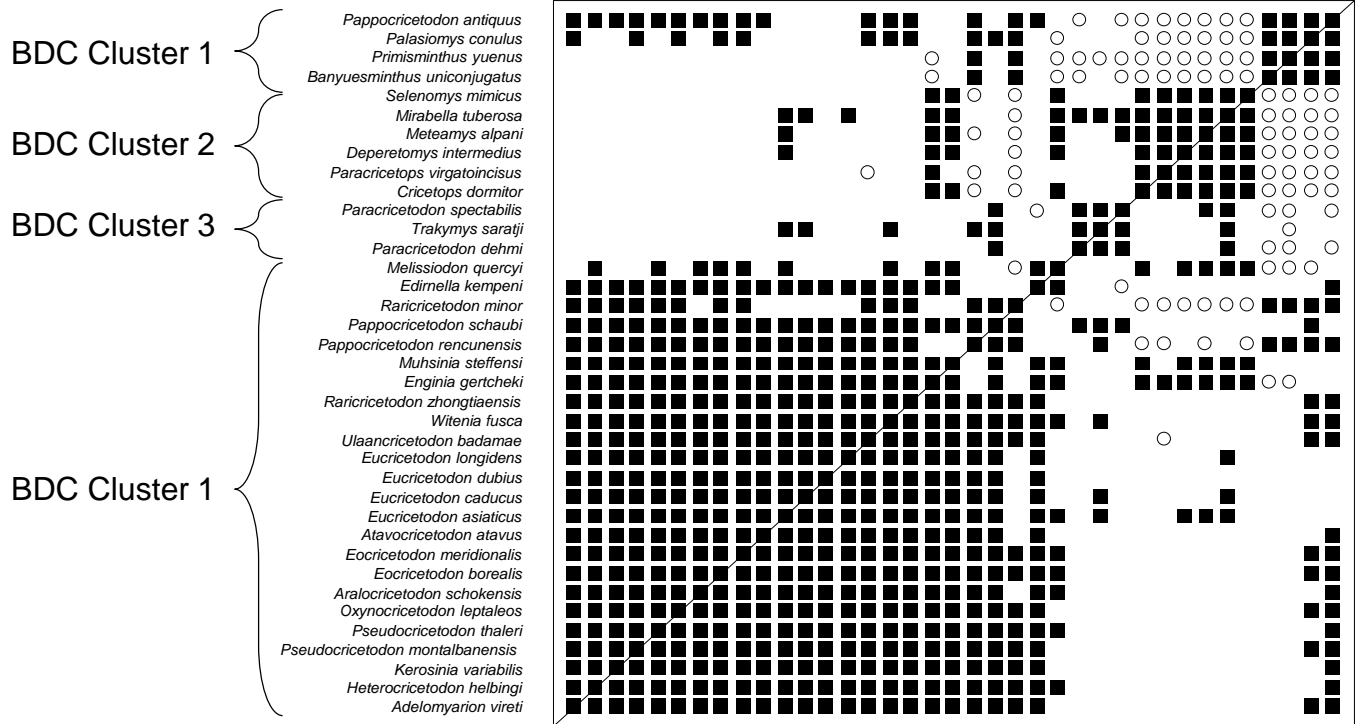
Fuzzy analysis only generated results for a two-cluster partition, but it was substantially worse than any other partition generated, with an average silhouette width of 0.27.

The original analysis noted the lack of evidence of clear discontinuity in the BDC and MDS results. The results here confirm that.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

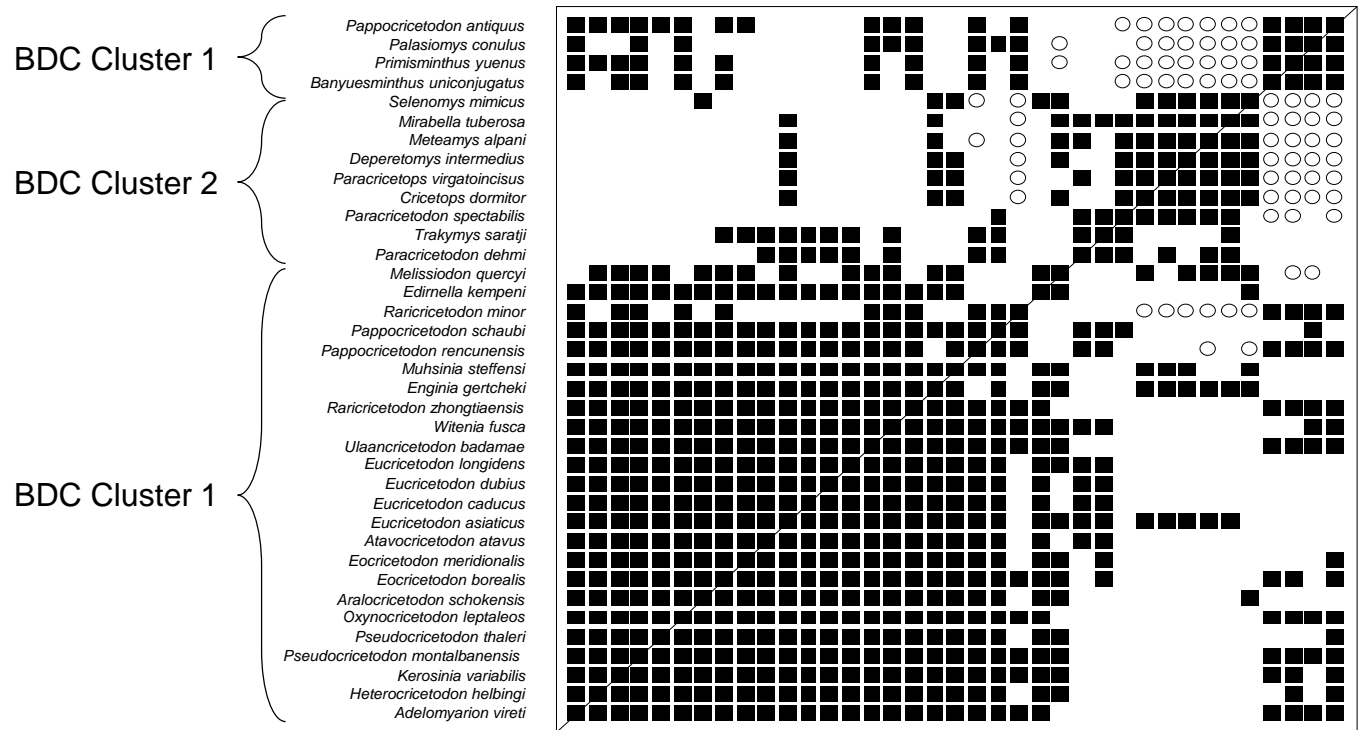
Characters: Craniodental



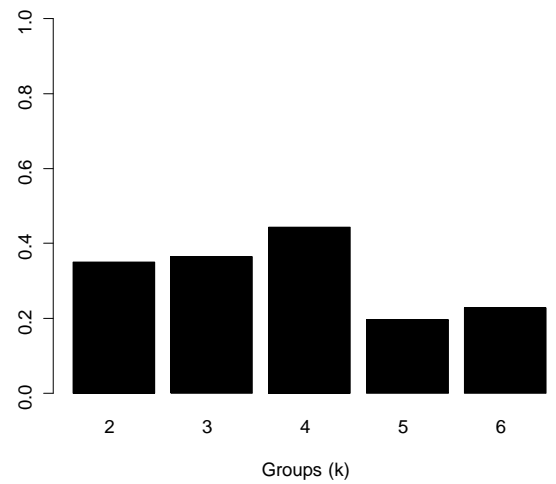
Order Rodentia
Family Cricetidae

Published taxa	37
Published characters	67
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	37
Characters used for calculations	50
Median bootstrap value	73
F ₉₀	0.34
Stress of 3D MDS	0.18
k _{min}	5
Conclusion	Inc

Notes: No evidence of discontinuity in BDC or MDS results.



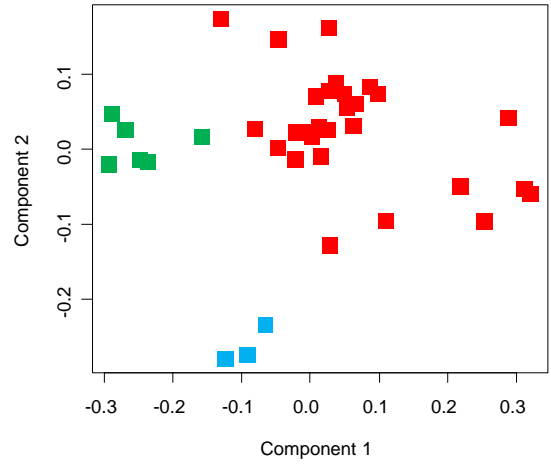
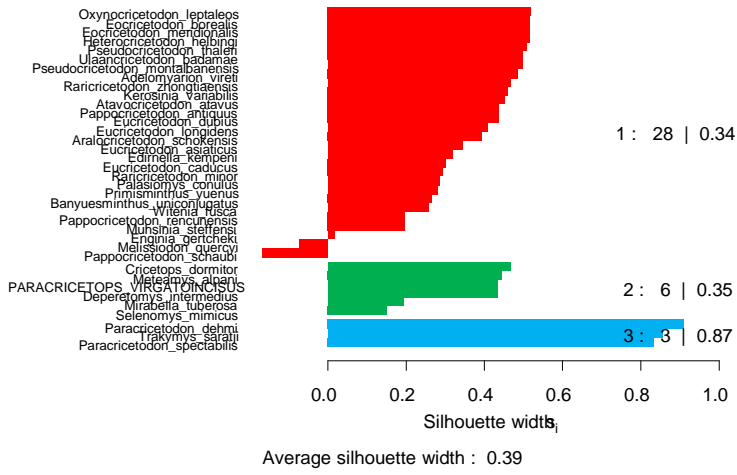
Average Silhouette Widths, Partion Around Medoids



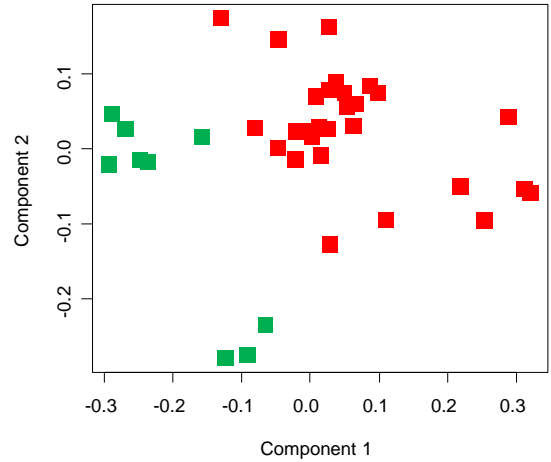
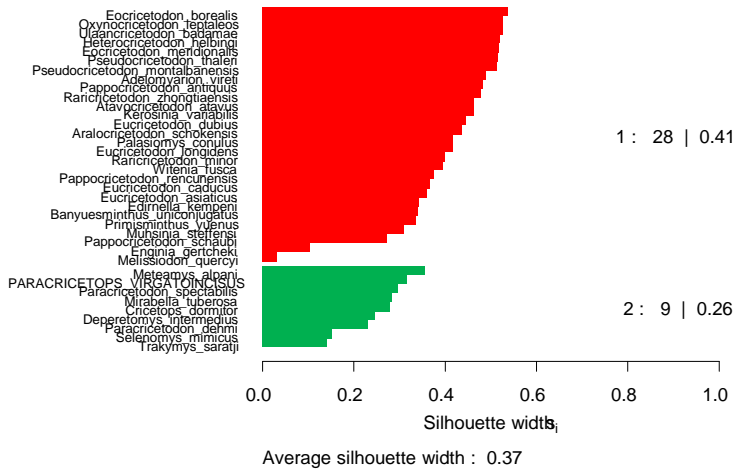
Clade Correspondence: All three BDC clusters contain more than one taxon. Only cluster 3 is monophyletic in figure 5 of Maridet and Ni (2013).

Silhouette plot, BDC partitions

Pearson Correlation

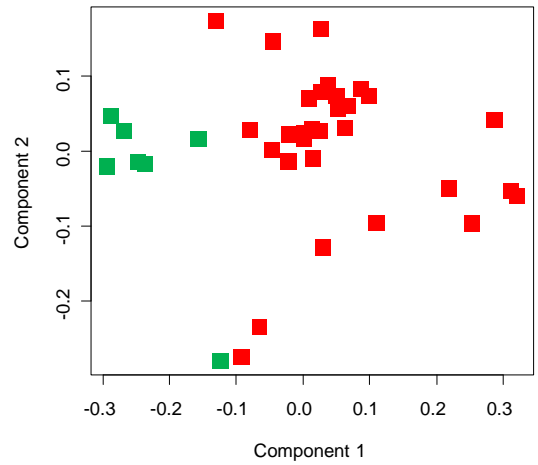
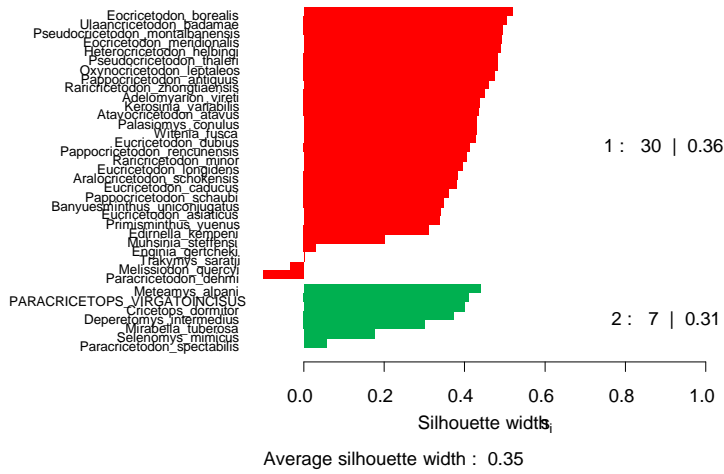


Spearman Correlation

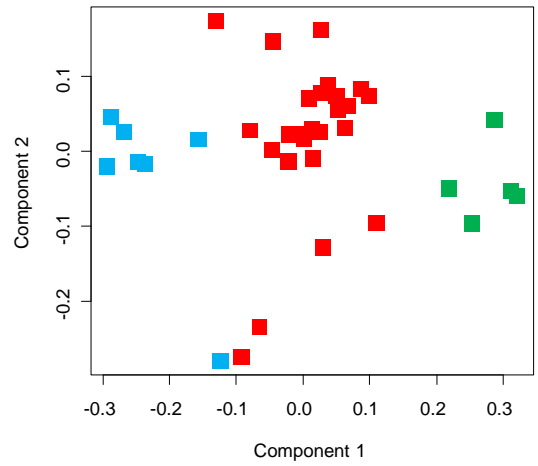
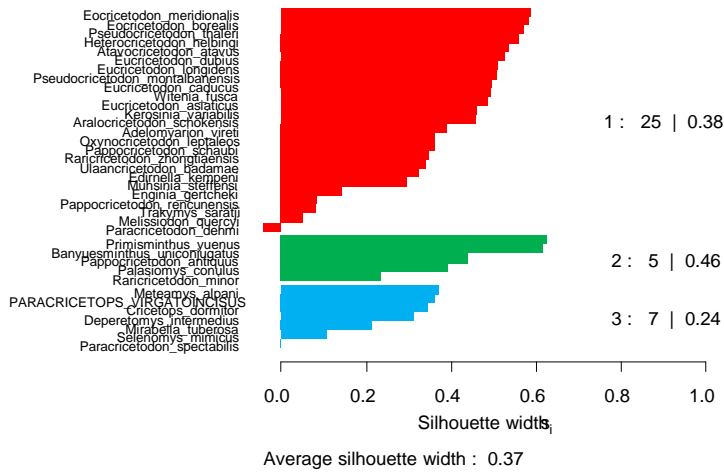


Silhouette plot, Partition Around Medoids

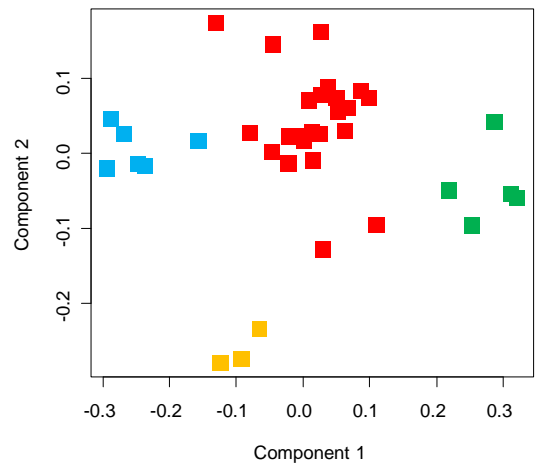
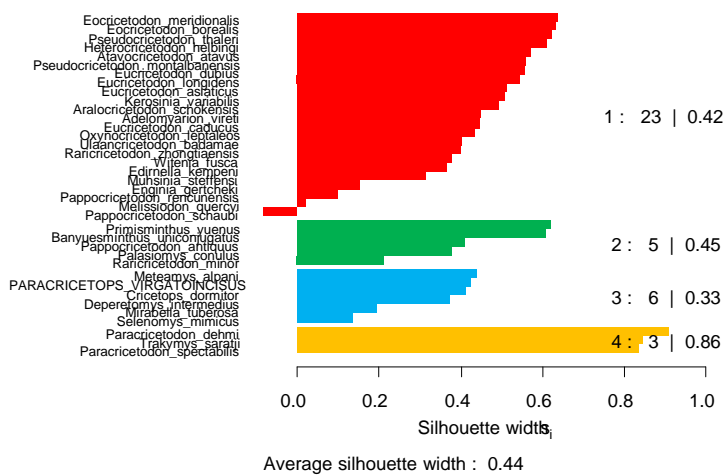
k=2



k=3

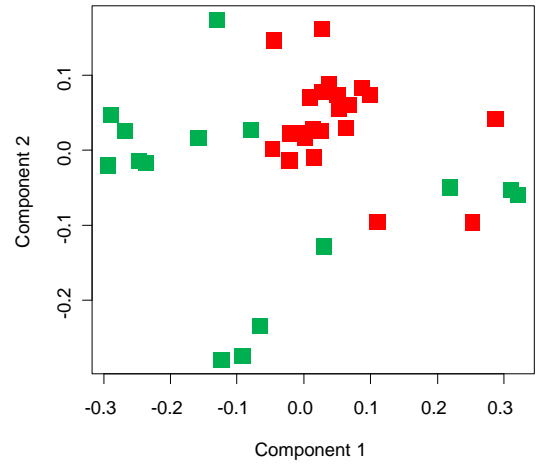
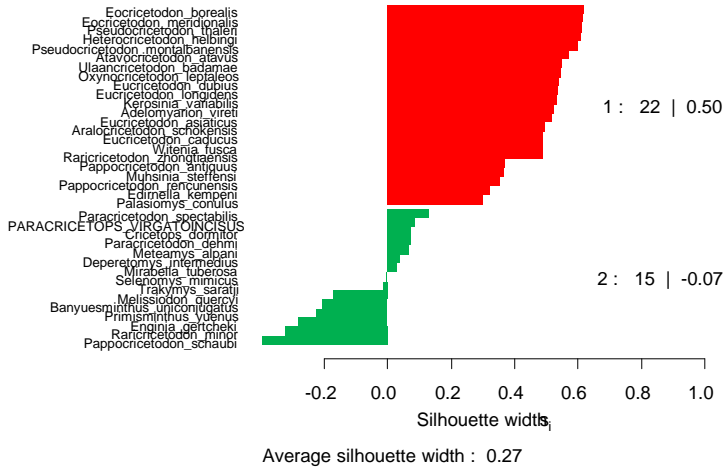


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Anomaluridae

Order Rodentia

Sallam et al. 2010

Pearson BDC

Negative: 49

Positive: 51

Clusters: 3

Clusterability

Hopkins Statistic: 0.788

Dip test: 0.025

Dip test p-value: 0.782

Spearman BDC

Negative: 60

Positive: 61

Clusters: 2

The Spearman BDC adds ten instances of significant, positive correlation and eleven instances of significant, negative correlation. This results in the reduction of clusters from three in the Pearson BDC results to two in the Spearman BDC results. The cluster membership difference is 11%. The family Anomaluridae forms a cluster in both Pearson and Spearman BDC, and it is divided from the other taxa by significant, negative BDC. The average silhouette widths for the three-cluster Pearson BDC partition is 0.42 and for the two-cluster Spearman BDC partition is 0.41.

The medoid partition at k=3 is identical to the Pearson BDC clustering, and the medoid partition at k=2 is identical to the Spearman BDC clustering. The fuzzy analysis at k=2 produces a partition identical to the Spearman BDC clustering, but the fuzzy partition at k=3 produces clusters slightly different from the Pearson BDC (cluster membership difference is 11%). For k=2 and k=3, both fuzzy analysis and medoid partitioning recognize the cluster of anomalurid taxa.

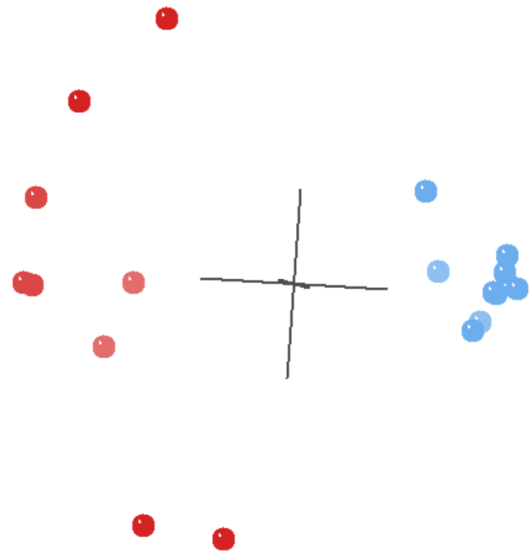
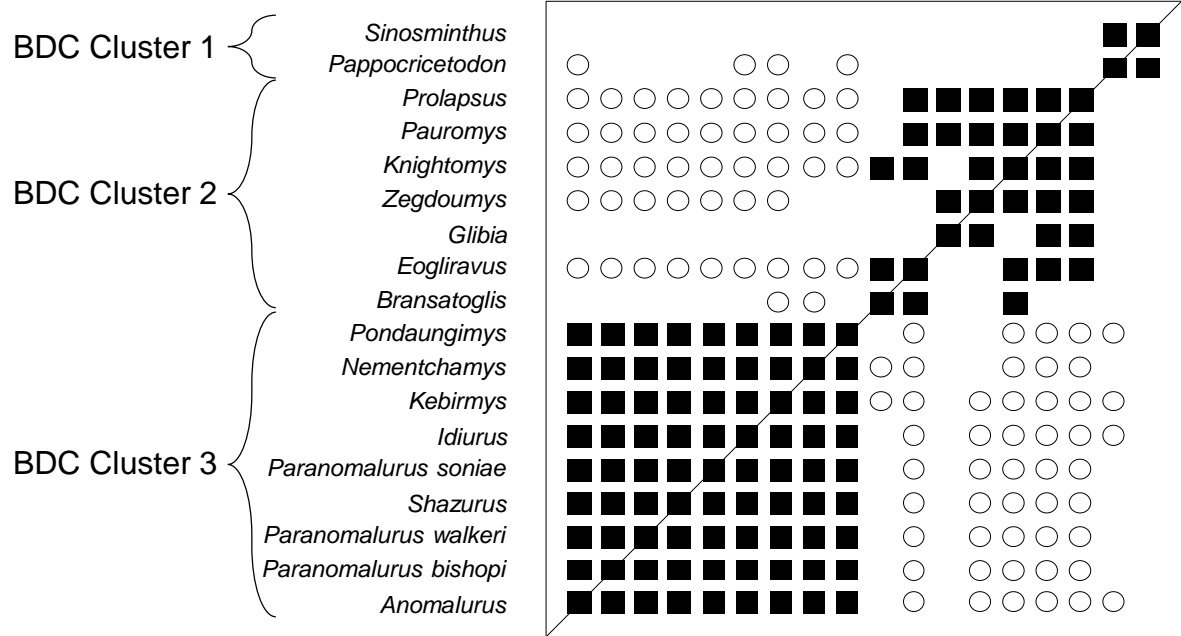
The original analysis concluded that Anomaluridae was probably a holobaramin based on BDC and MDS results. Here the medoid partitioning and fuzzy analysis confirm the original conclusion. The clustering differences are limited to slightly different partitions of the outgroup taxa.

Original conclusion: HB

Updated conclusion: HB

Sallam, H.M., E.R. Seiffert, E.L. Simons, and C. Brindley. 2010. A large-bodied anomaluroid rodent from the earliest late Eocene of Egypt: phylogenetic and biogeographic implications. *Journal of Vertebrate Paleontology* 30:1579-1593.

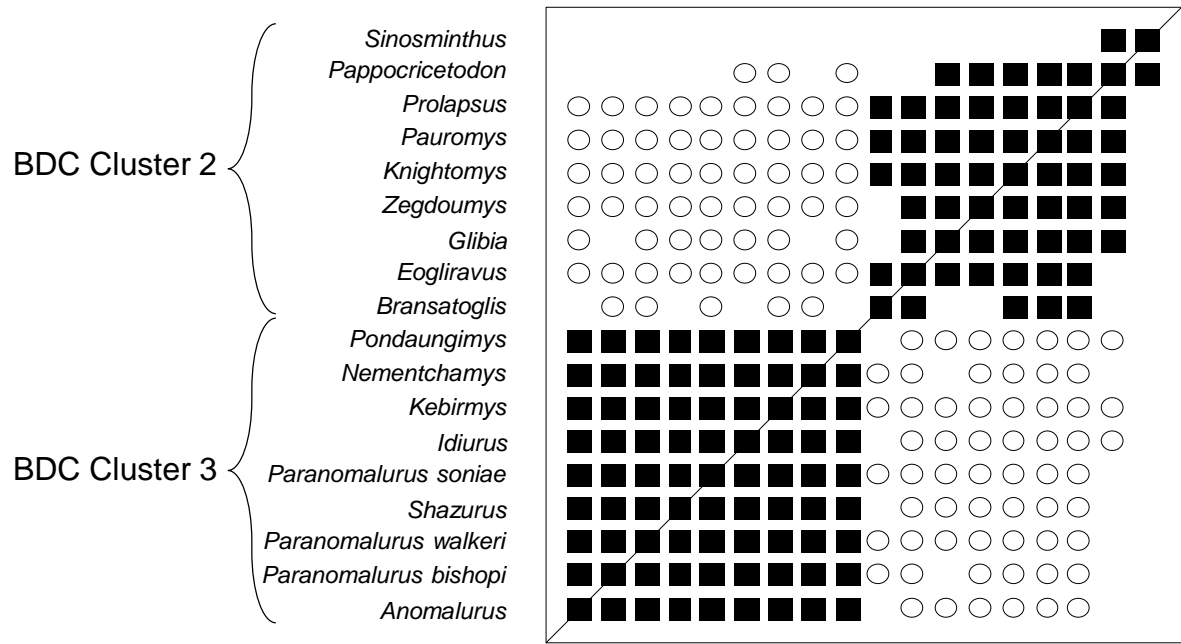
Characters: Craniodental



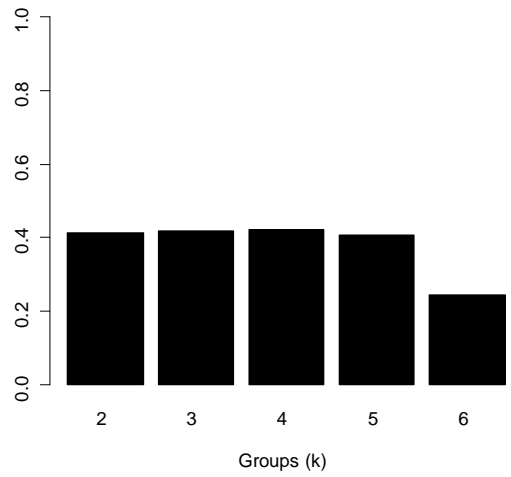
Order Rodentia
Family Anomaluridae

Published taxa	29
Published characters	99
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	18
Characters used for calculations	72
Median bootstrap value	89
F ₉₀	0.48
Stress of 3D MDS	0.18
k _{min}	8
Conclusion	HB

Notes: Anomaluridae form a recognizable cluster in both BDC and MDS results. Anomaluridae is probably a holobaramin.



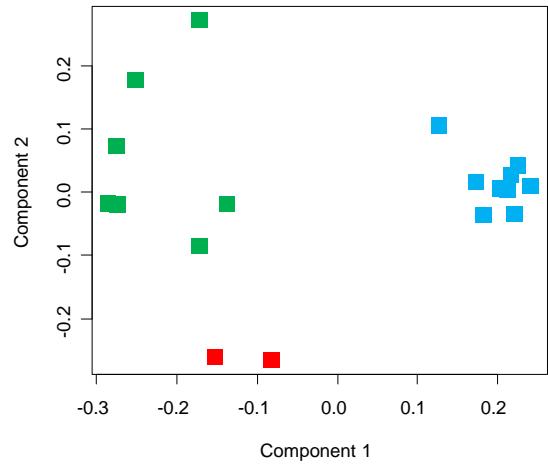
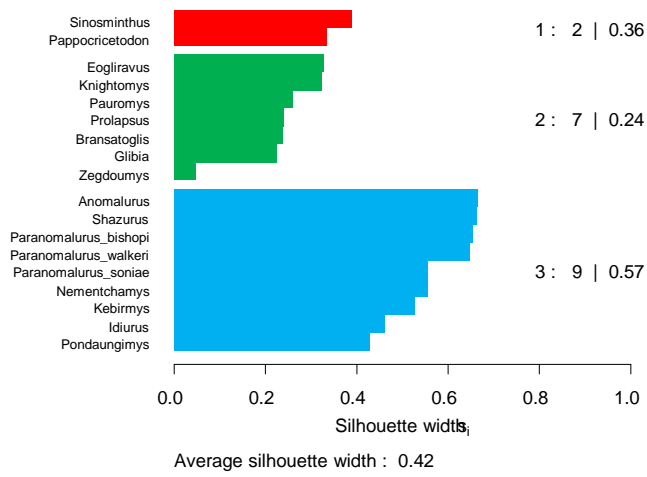
Average Silhouette Widths, Partion Around Medoids



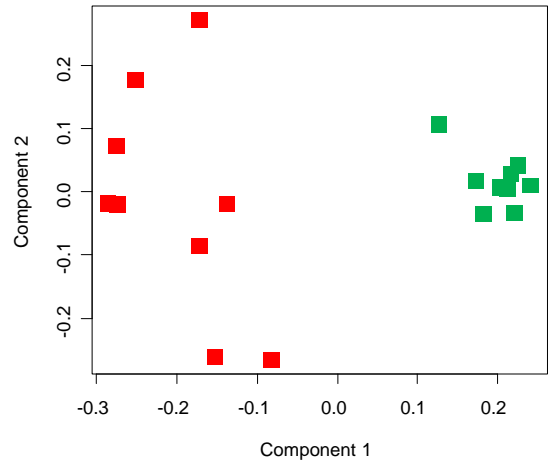
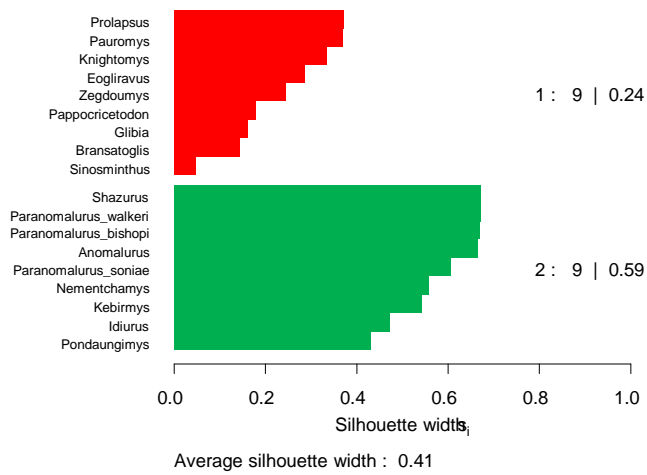
Clade Correspondence: All three BDC clusters contain at least two taxa. Clusters 1 and 3 are monophyletic in Figure 9A of Sallam et al. (2010), but cluster 2 is not.

Silhouette plot, BDC partitions

Pearson Correlation

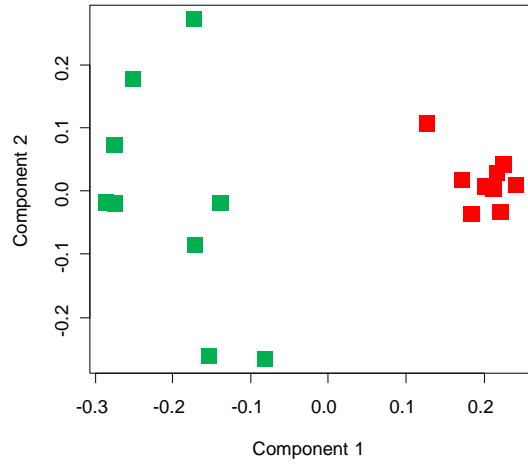
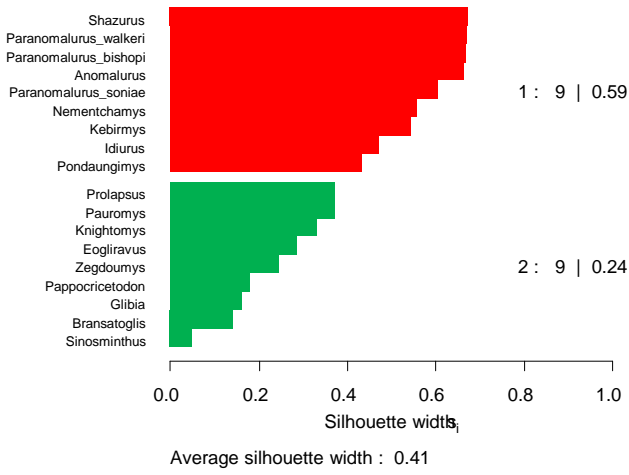


Spearman Correlation

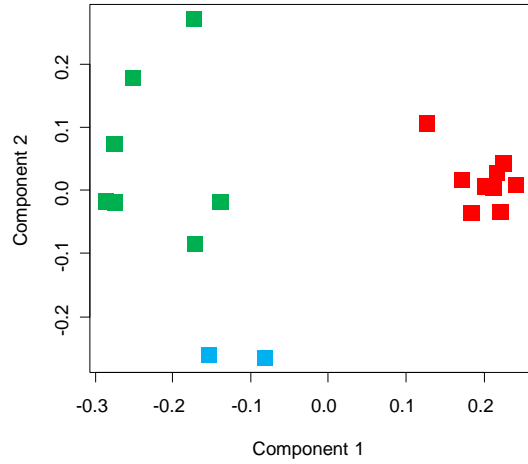
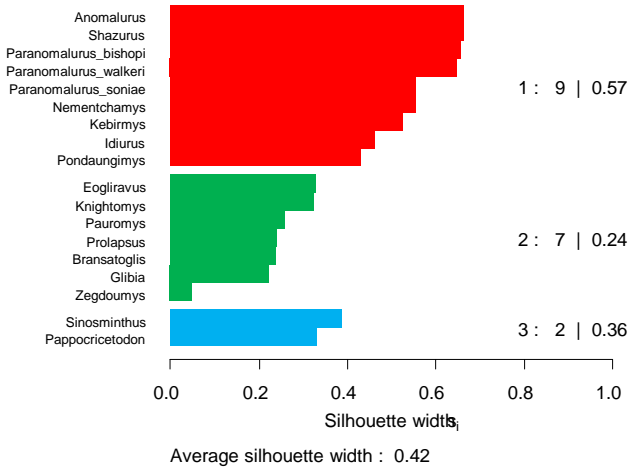


Silhouette plot, Partition Around Medoids

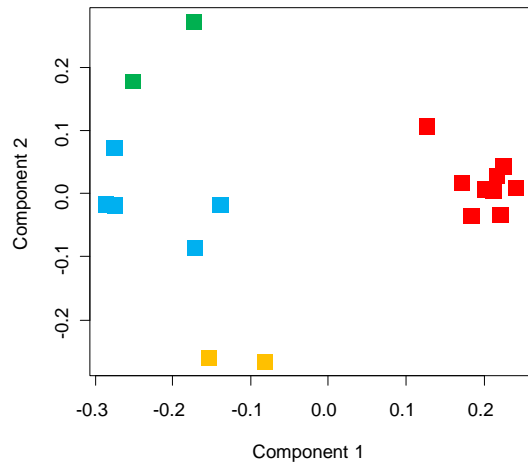
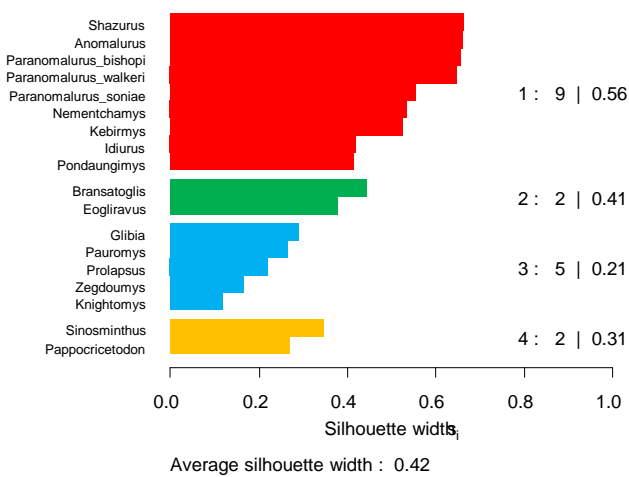
k=2



k=3

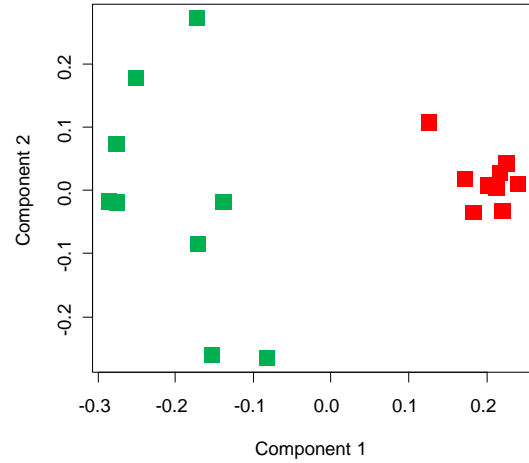
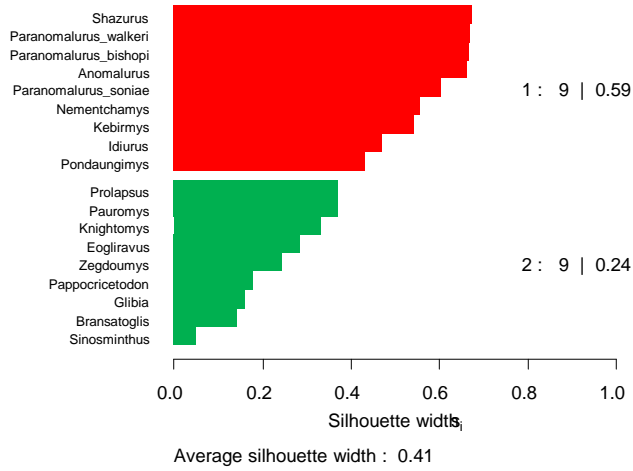


k=4

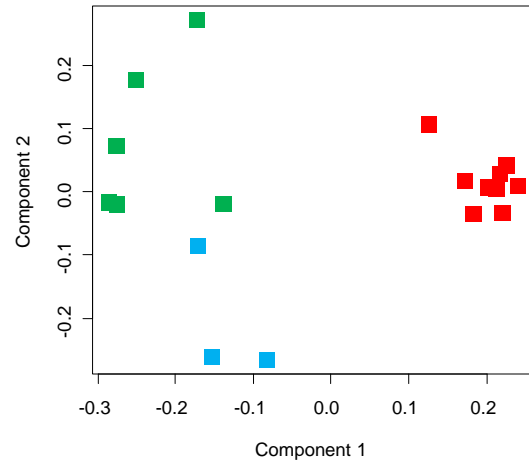
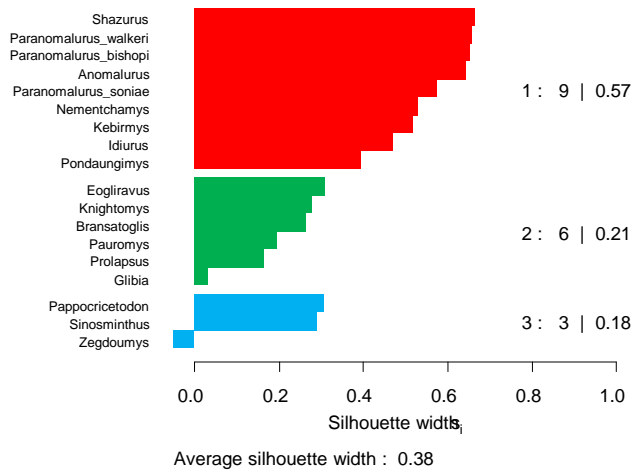


Silhouette plot, Fuzzy Analysis

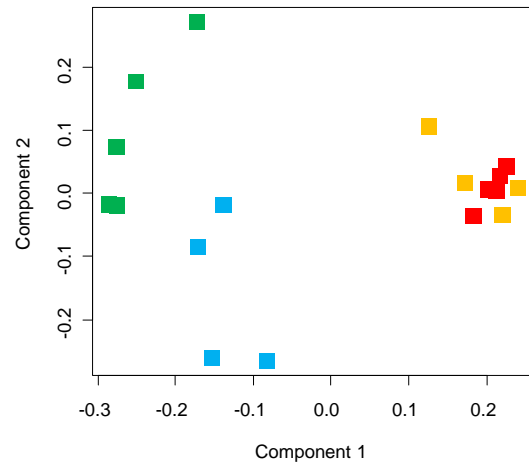
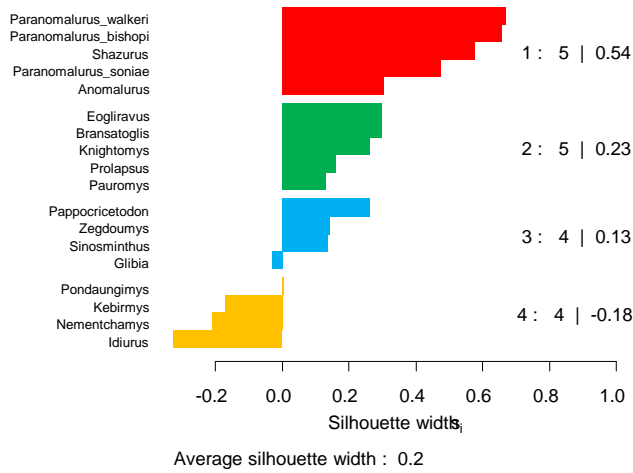
k=2



k=3



k=4



Family Caviidae

Order Rodentia

Pérez and Vucetich 2011

Pearson BDC

Negative: 9

Positive: 23

Clusters: 5

Clusterability

Hopkins Statistic: 0.817

Dip test: 0.044

Dip test p-value: 0.151

Spearman BDC

Negative: 4

Positive: 34

Clusters: 3

The Spearman BDC results reveal an additional eleven instances of significant, positive BDC and five fewer instances of significant, negative BDC. This results in a reduction of clusters from five in the Pearson BDC to three in the Spearman BDC. Two ingroup clusters from the Pearson BDC results are joined in the Spearman BDC, along with a singleton cluster consisting of *Microcavia*. The five-cluster Pearson BDC results have an average silhouette width of 0.31, and the three-cluster Spearman BDC results have an average silhouette width of 0.38. The cluster membership difference is 40%.

The medoid partition at k=5 has a cluster membership difference of 20% when compared to the Pearson BDC partition. The five cluster medoid partition had an average silhouette value of 0.34. The medoid partition at k=3 also had an average silhouette value of 0.34, and the cluster membership difference when compared to the Spearman clusters was 6.7%.

Fuzzy analysis at k=5 differed from both the Pearson BDC and the five-cluster medoid partition. The five-cluster fuzzy partition had an average silhouette width of 0.3. At k=3, the fuzzy partition differed again from both the Spearman BDC and the three-cluster medoid partition. The three-cluster fuzzy partition had an average silhouette width of 0.19.

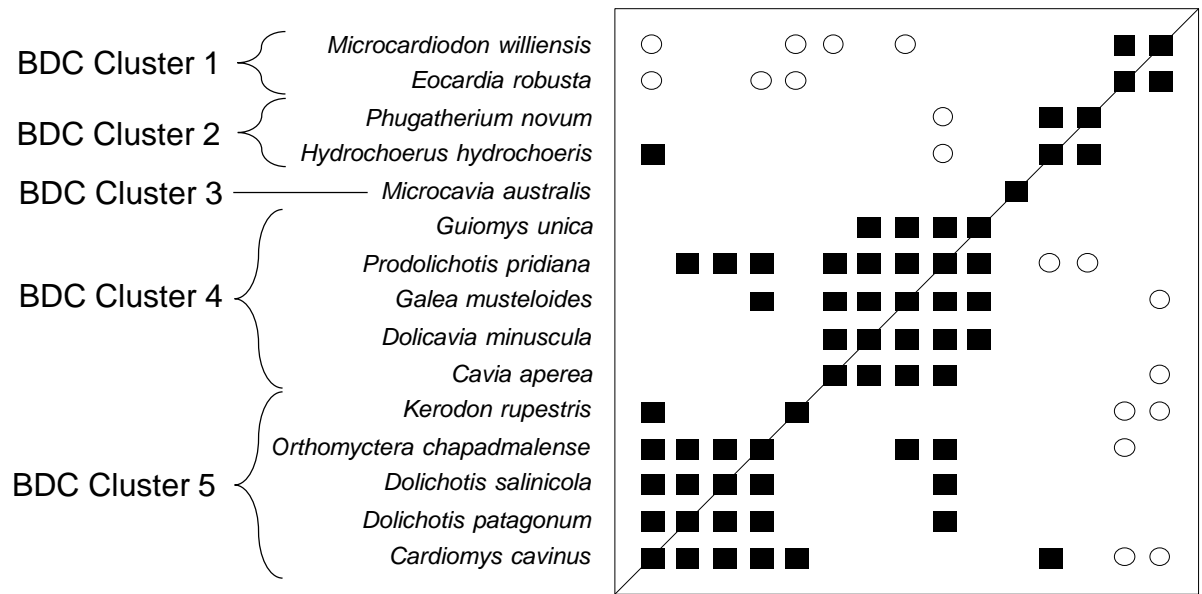
The original analyses were interpreted to be a provisional holobaramin based on sparse instances of significant, negative BDC between ingroup and outgroup taxa and on the MDS results. These results do not confirm this initial conclusion. Here, neither the medoid partitioning nor the fuzzy analysis recovered the same set of ingroup taxa as the Spearman or Pearson BDC in any of the analyses. Hence these new results appear to be inconclusive.

Original conclusion: HB?

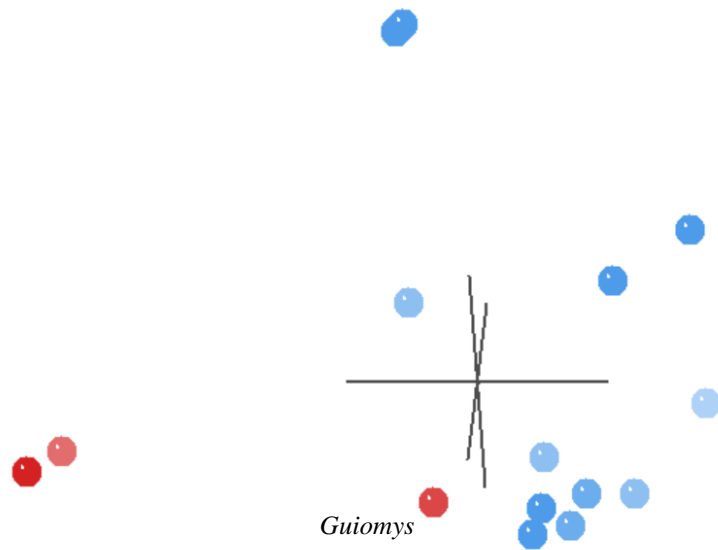
Updated conclusion: Inconclusive

Pérez, M.E. and M.G. Vucetich. 2011. A new extinct genus of Caviioidea (Rodentia, Hystricognathi) from the Miocene of Patagonia (Argentina) and the evolution of cavioid mandibular morphology. *Journal of Mammalian Evolution* 18:163-183.

Characters: Craniodental

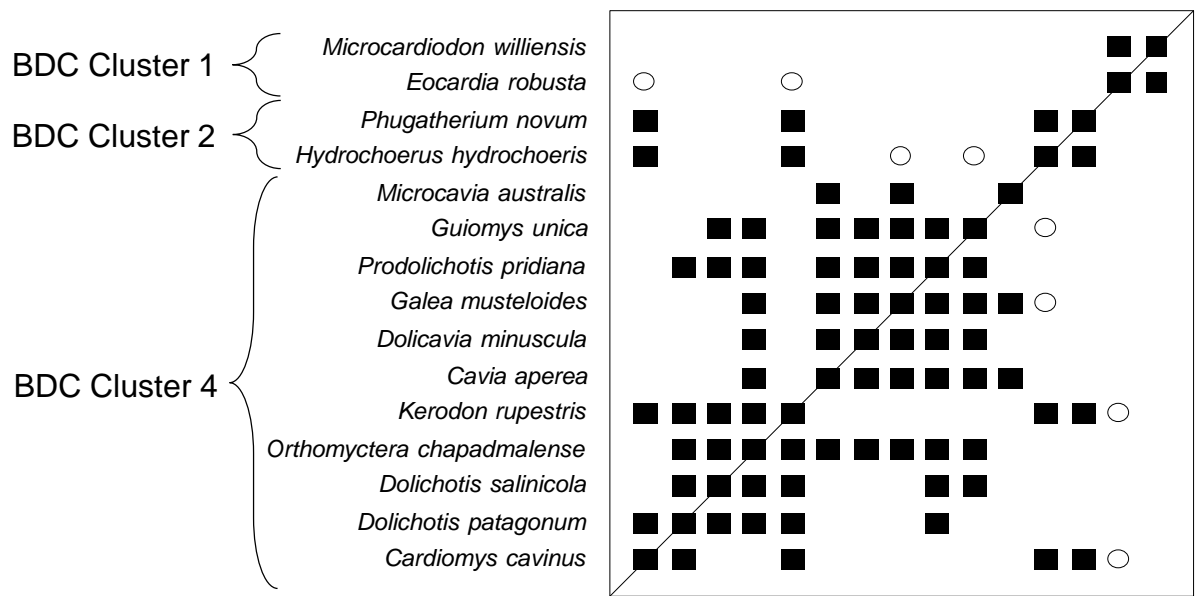


Order Rodentia
Family Caviidae

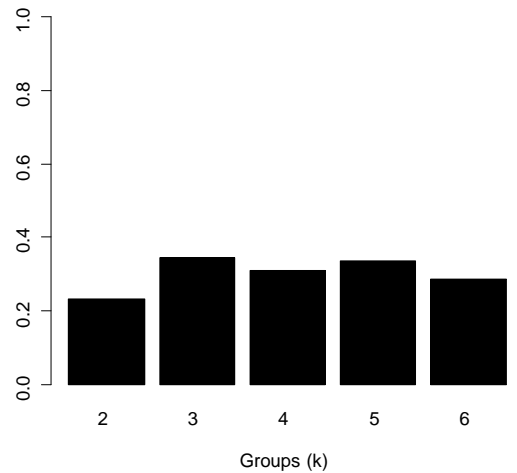


Published taxa	35
Published characters	89
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	15
Characters used for calculations	44
Median bootstrap value	74
F ₉₀	0.1
Stress of 3D MDS	0.13
k _{min}	5
Conclusion	HB?

Notes: Caviidae + *Guiomys* might be a holobaramin. BDC evidence is weak but MDS seems to support a discontinuity.



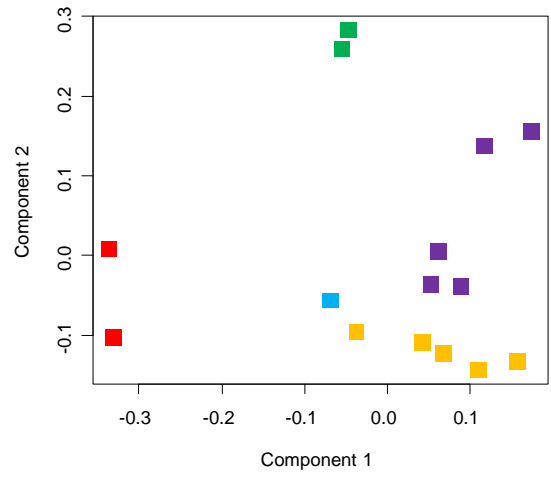
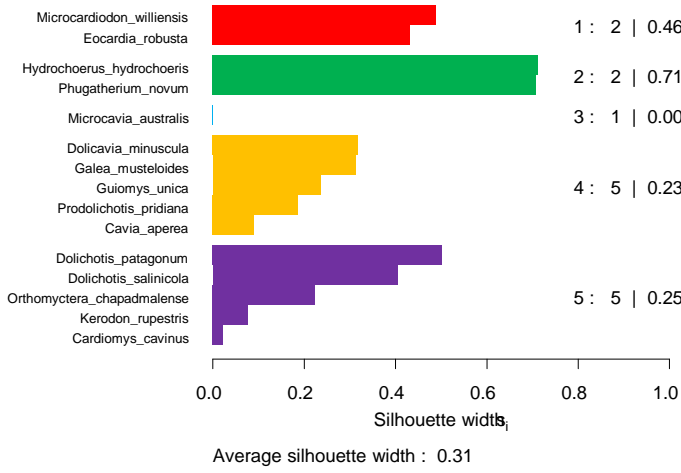
Average Silhouette Widths, Partion Around Medoids



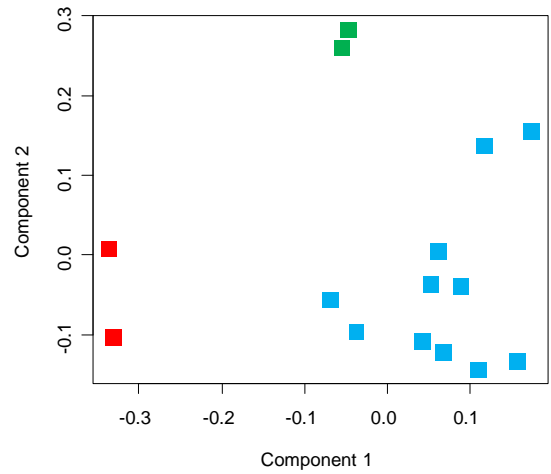
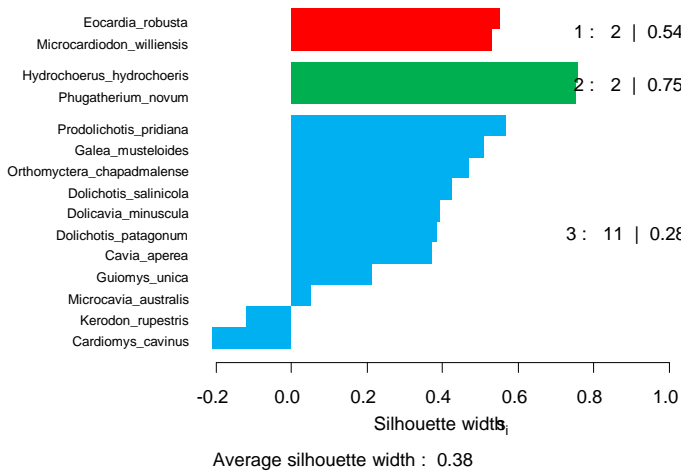
Clade Correspondence: Of the five BDC clusters, only cluster 3 is a singleton. Cluster 1 is the only cluster that corresponds to a clade in the phylogeny of Figure 5 in Perez and Vucetich (2011).

Silhouette plot, BDC partitions

Pearson Correlation

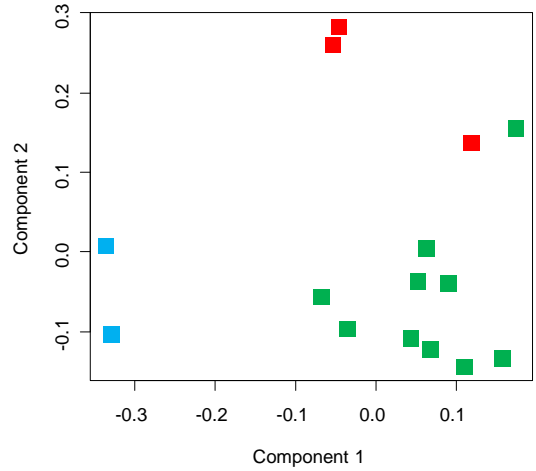
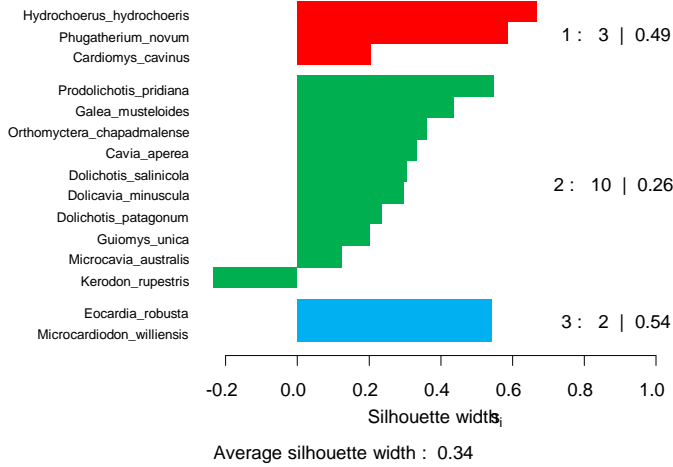


Spearman Correlation

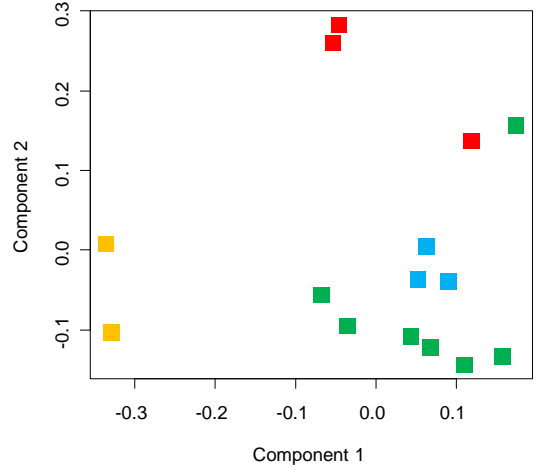
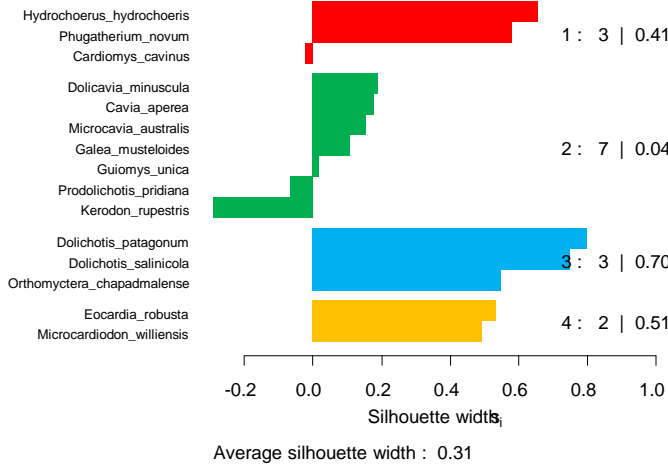


Silhouette plot, Partition Around Medoids

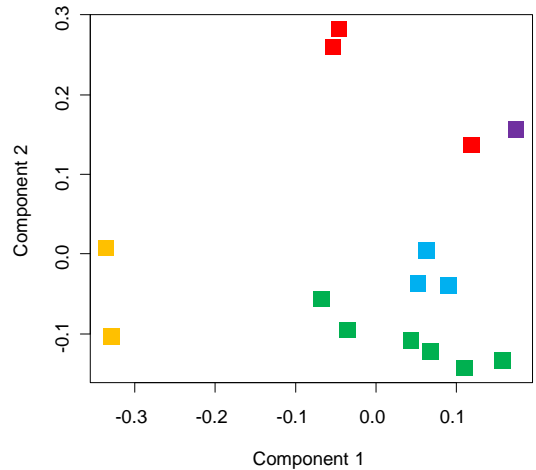
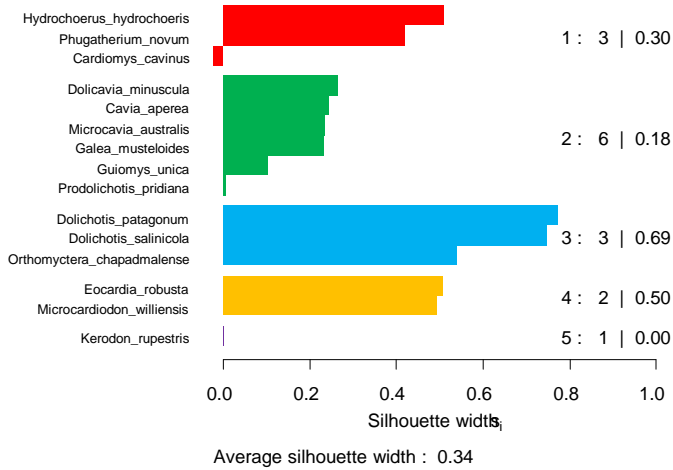
k=3



k=4

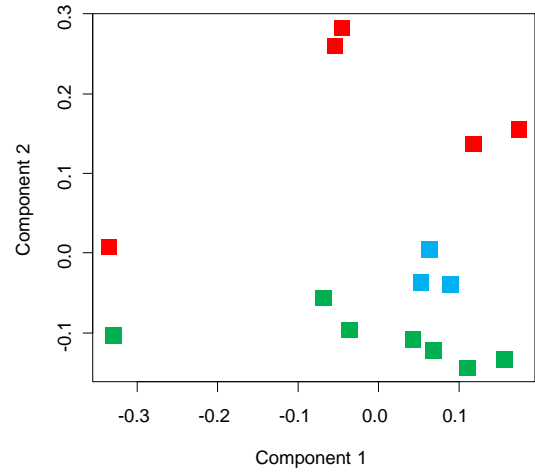
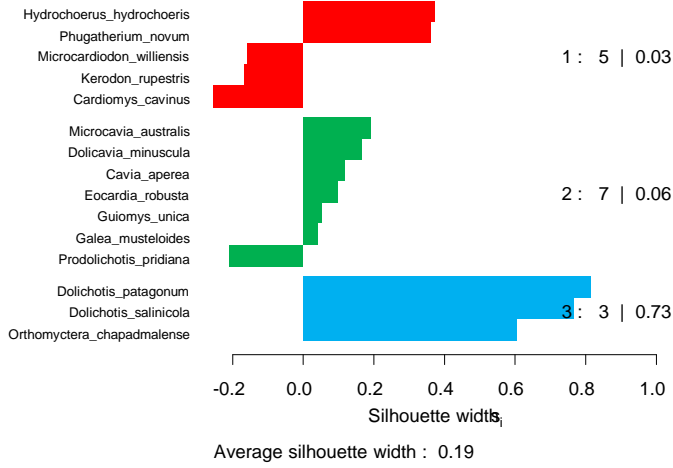


k=5

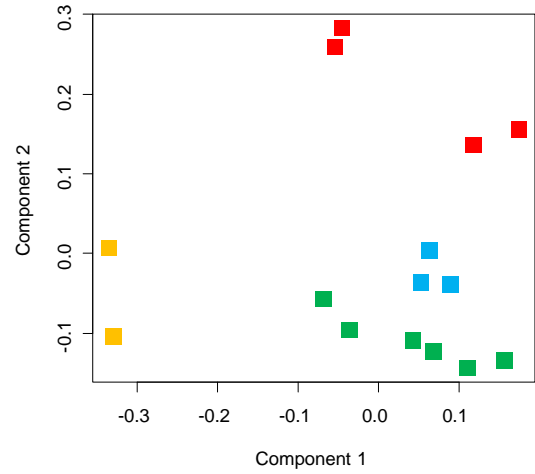
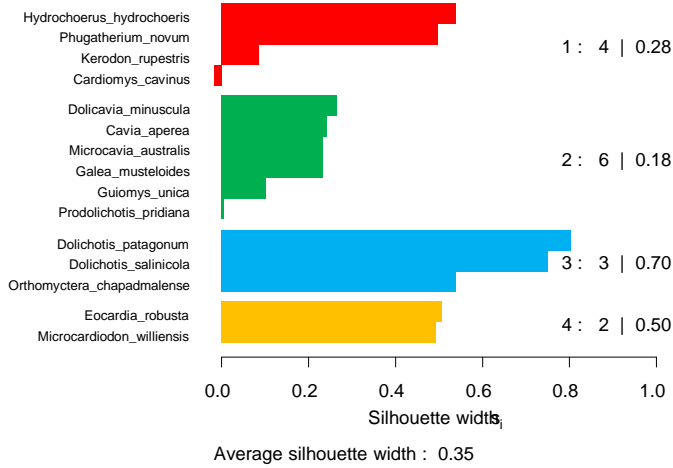


Silhouette plot, Fuzzy Analysis

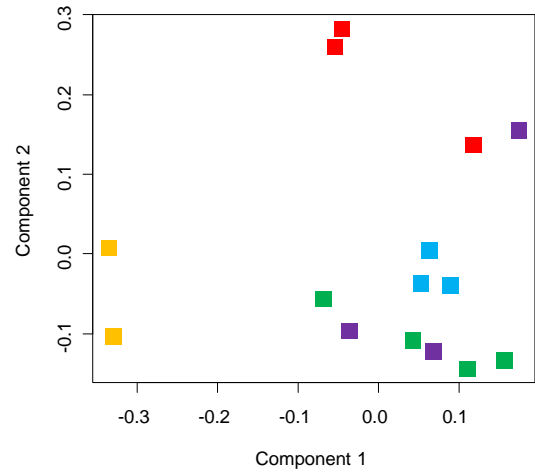
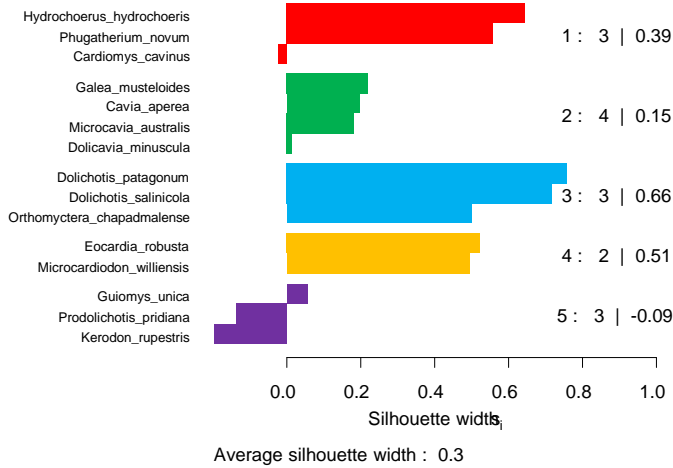
k=3



k=4



k=5



Family Octodontidae

Order Rodentia

Verzi et al. 2013

Pearson BDC

Negative: 148

Positive: 317

Clusters: 2

Clusterability

Hopkins Statistic: 0.837

Dip test: 0.017

Dip test p-value: 0.253

Spearman BDC

Negative: 145

Positive: 318

Clusters: 2

Spearman BDC is very similar to the Pearson BDC, both of which generate an identical two-cluster partition. The average silhouette width of this partition is 0.46.

The two-cluster medoid partition is similar to the Pearson BDC results, with an average silhouette width of 0.38 and a cluster membership difference of 16%. However, as the number of clusters rise, the average silhouette width of the medoid partition substantially improves. At $k=4$, the average silhouette for the medoid partition was 0.52.

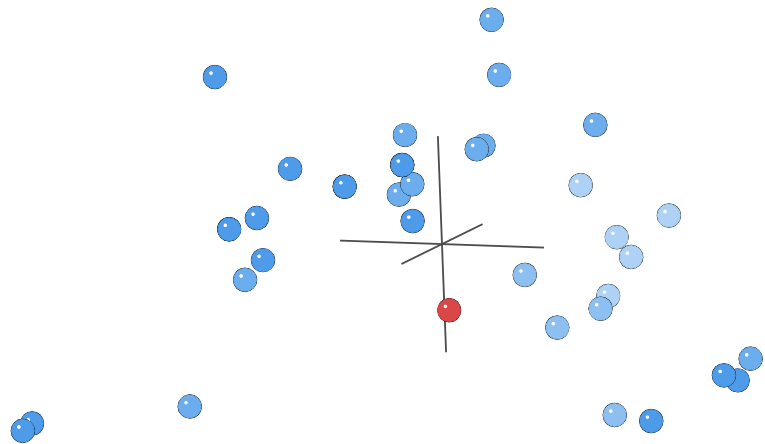
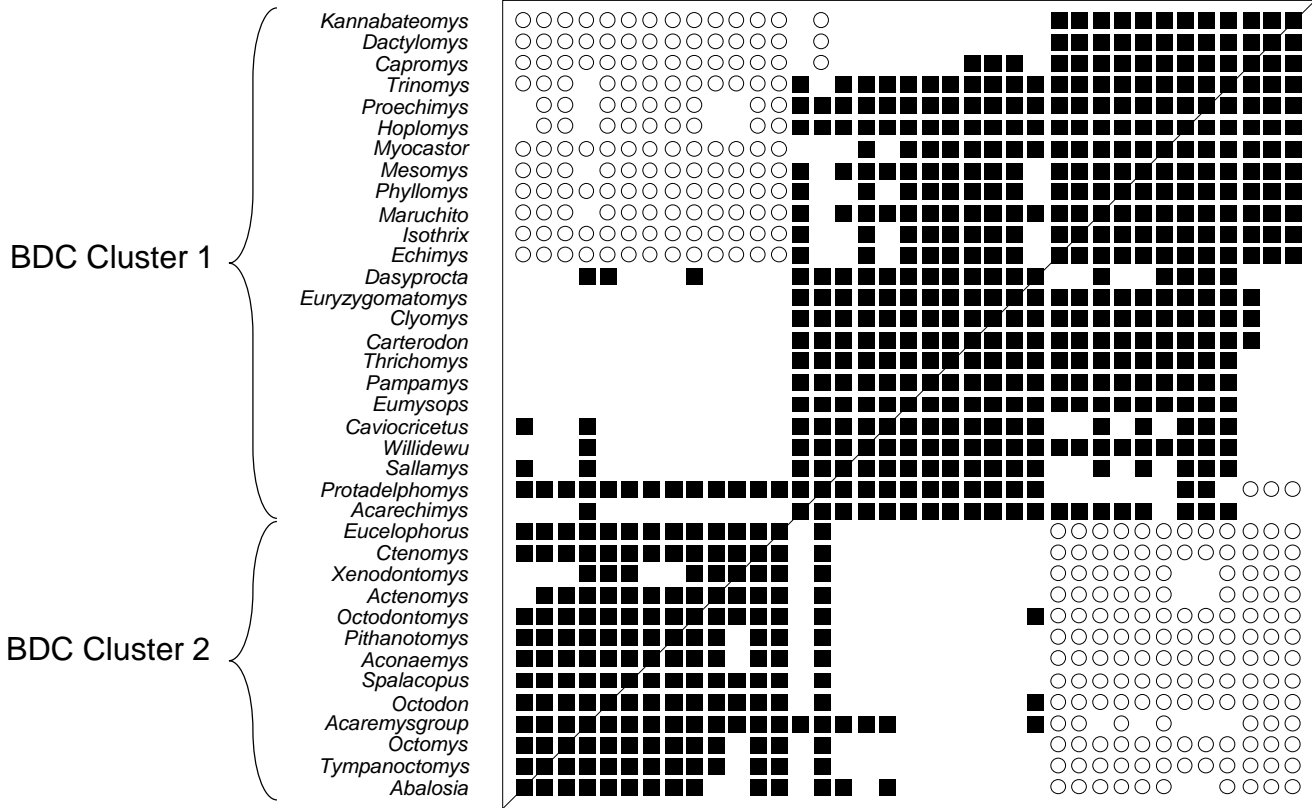
Likewise, the two-cluster fuzzy analysis resembled the Pearson BDC results, with an average silhouette width of 0.44 and a cluster membership difference of 5%. In contrast to the medoid partition, however, fuzzy analysis at larger numbers of clusters reduced the average silhouette width to 0.31 at four clusters.

The original inconclusive judgment was based on a lack of evidence of separate clusters in the MDS results. Instead, the significant, negative correlation observed in the Pearson BDC appears to be caused by an arcuate shape of a continuous cloud of taxa in the MDS. Here, the Spearman BDC results are nearly identical, but the inconsistencies observed in the medoid partitioning and fuzzy analysis reinforce the uncertainty of these results. The original judgment of inconclusive is therefore supported.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

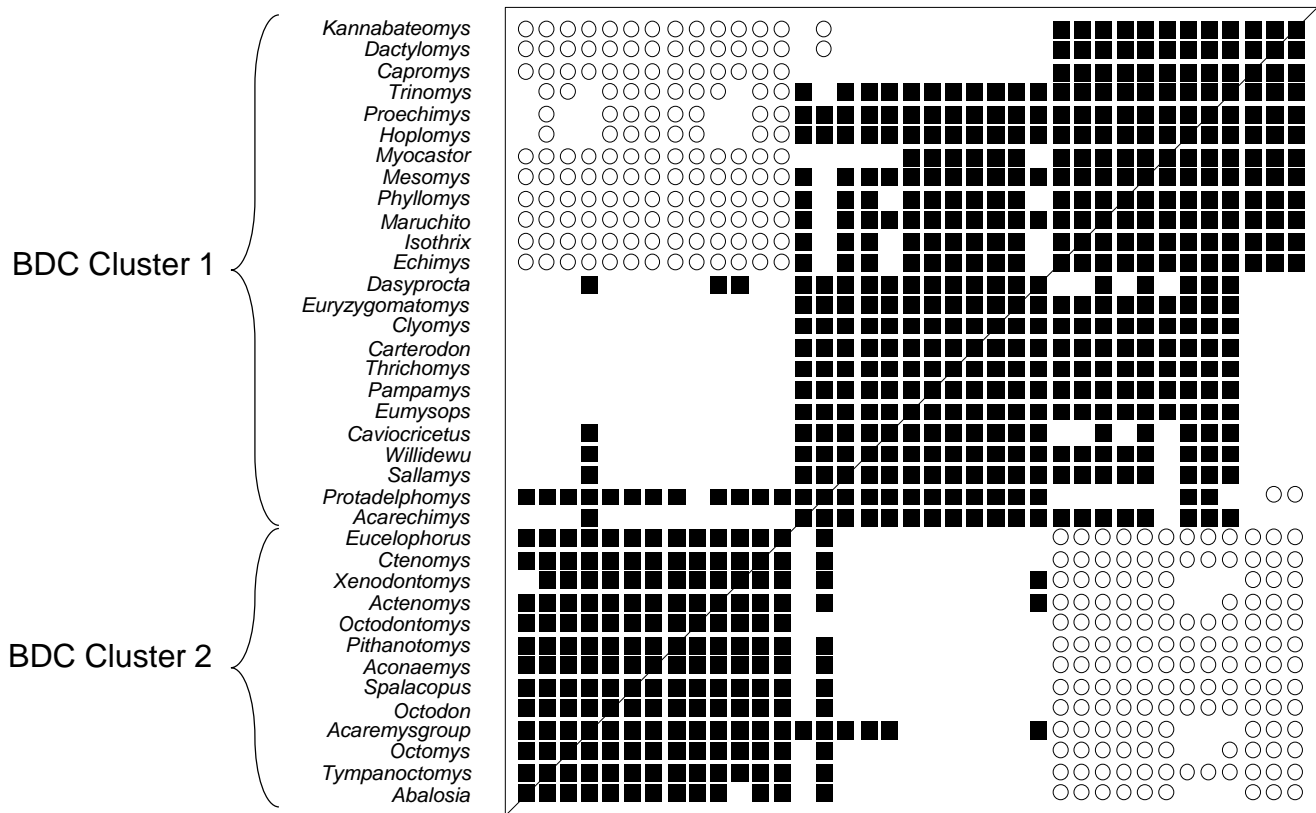
Characters: Craniodental



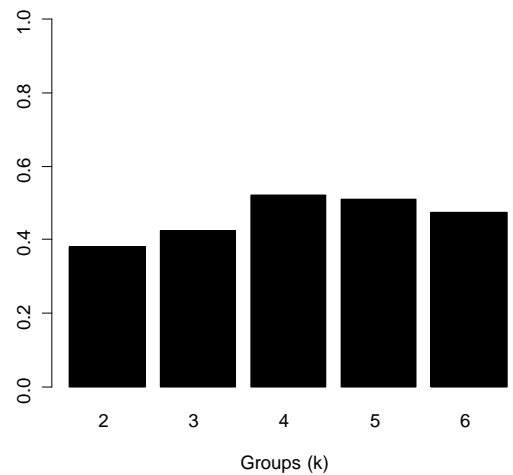
Order Rodentia
Family Octodontidae

Published taxa	54
Published characters	73
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	37
Characters used for calculations	44
Median bootstrap value	76
F ₉₀	0.29
Stress of 3D MDS	0.15
k _{min}	4
Conclusion	Inc

Notes: In BDC, there appear to be two groups, but *Protadelphomys* shares positive BDC with members of both groups. There is no obvious clustering in the MDS results. There is no clear evidence of discontinuity.



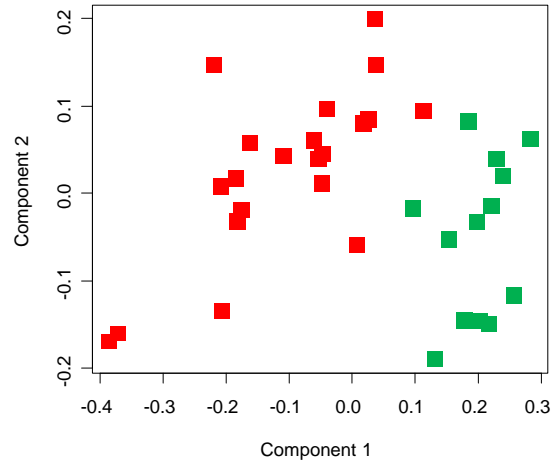
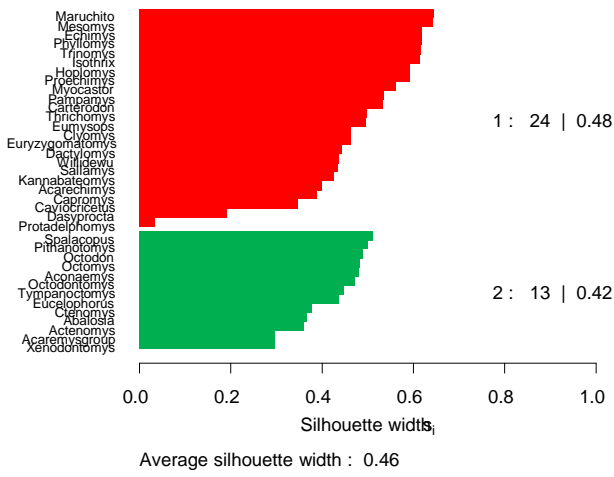
Average Silhouette Widths, Partion Around Medoids



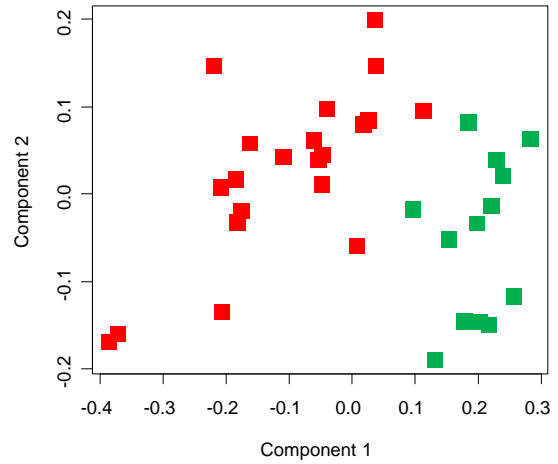
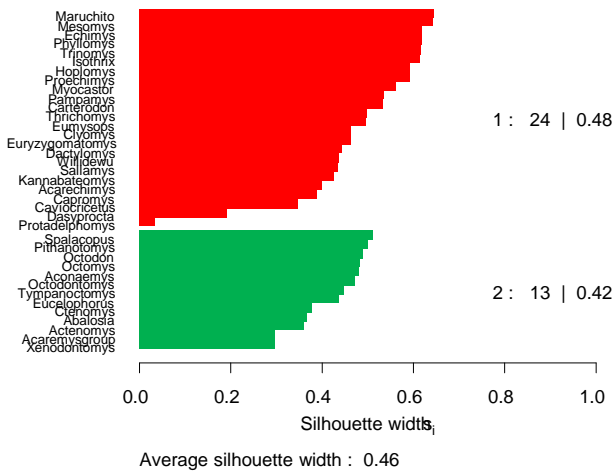
Clade Correspondence: Two large clusters can be seen in the BDC results. The phylogeny published in Figure 1 of Verzi et al. (2013) shows that neither are monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

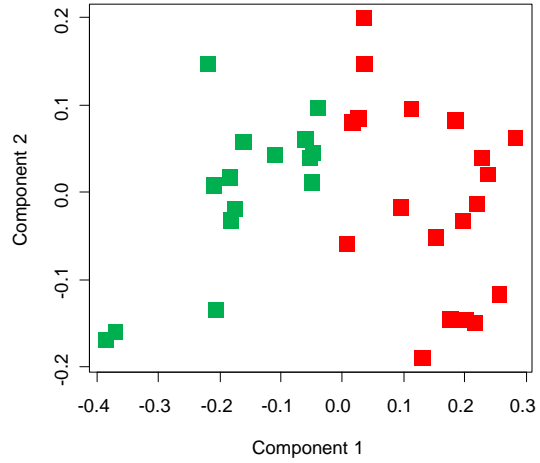
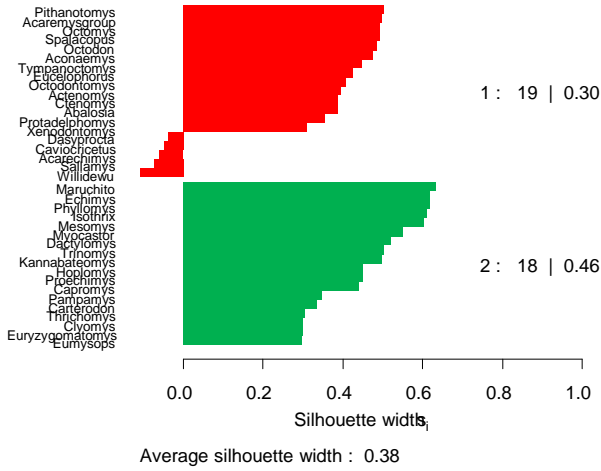


Spearman Correlation

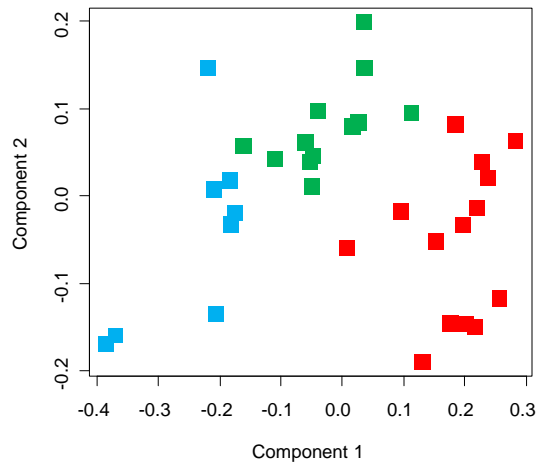
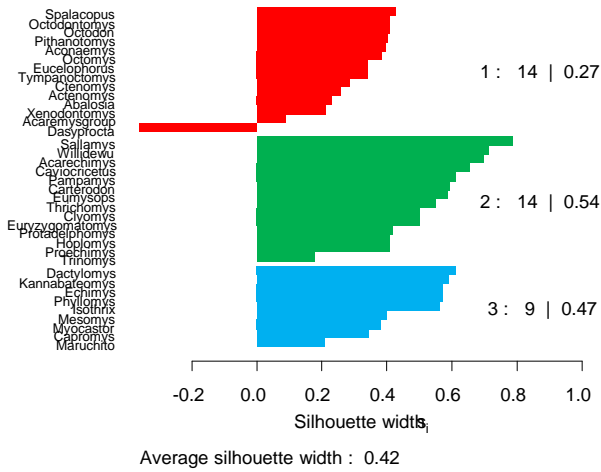


Silhouette plot, Partition Around Medoids

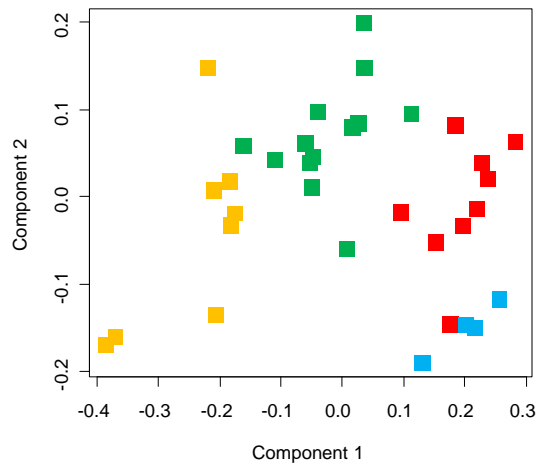
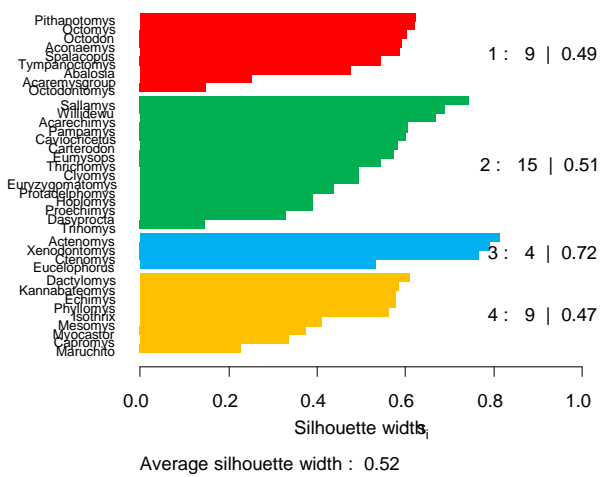
k=2



k=3

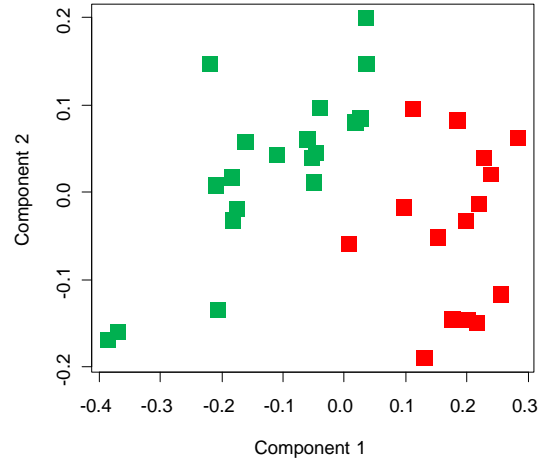
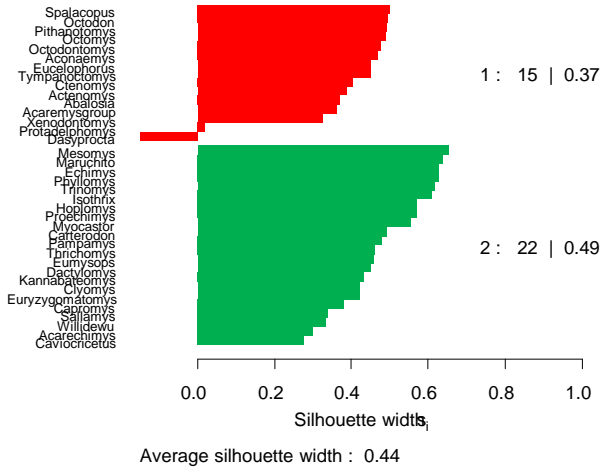


k=4

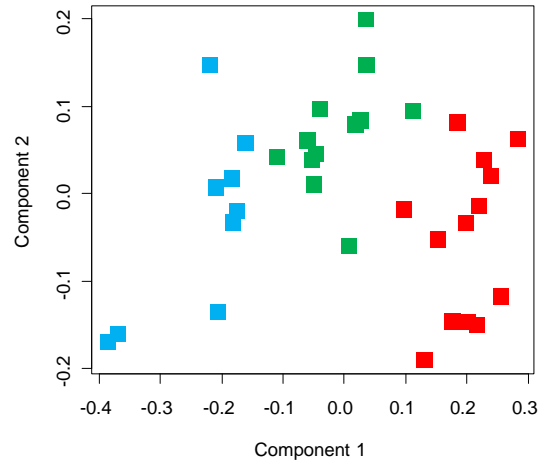
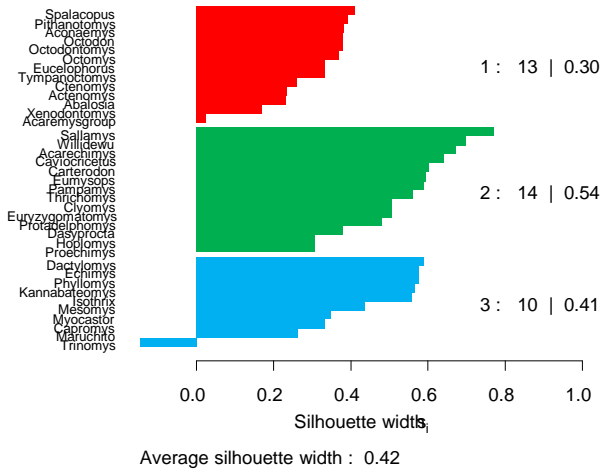


Silhouette plot, Fuzzy Analysis

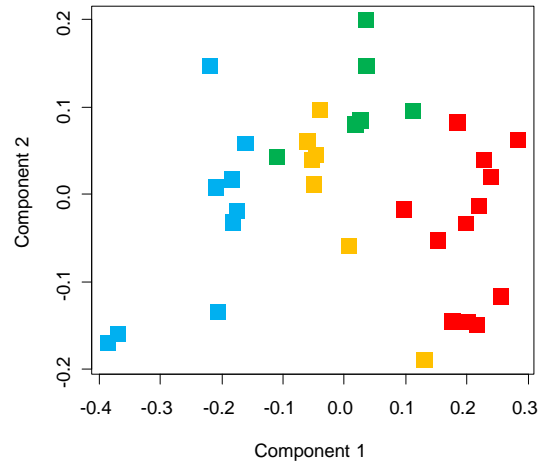
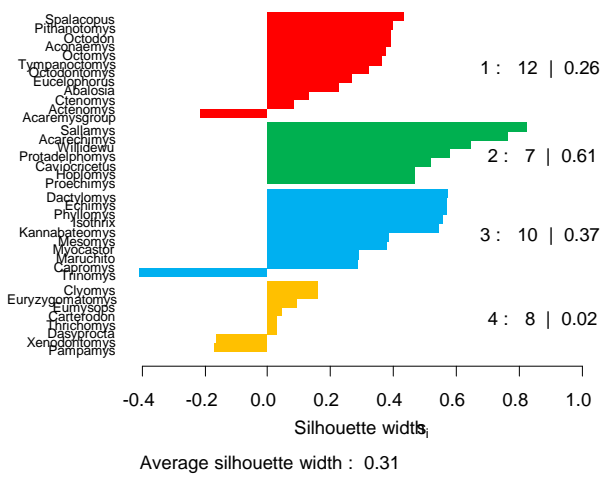
k=2



k=3



k=4



Family Echimyidae

Order Rodentia

Carvalho and Salles 2004

Pearson BDC
Negative: 334
Positive: 611
Clusters: 2

Spearman BDC
Negative: 317
Positive: 590
Clusters: 2

Clusterability

Hopkins Statistic: 0.898
Dip test: 0.012
Dip test p-value: 0.311

The Spearman BDC results differ only slightly from the Pearson BDC and produce identical two-cluster partitions. The average silhouette width for this partition is 0.47.

The two-cluster medoid partitioning is similar to the BDC clustering. The two-cluster medoid partition also has an average silhouette width of 0.47, and the cluster membership difference is 2%. At k=4, the medoid partition also has an average silhouette width of 0.47.

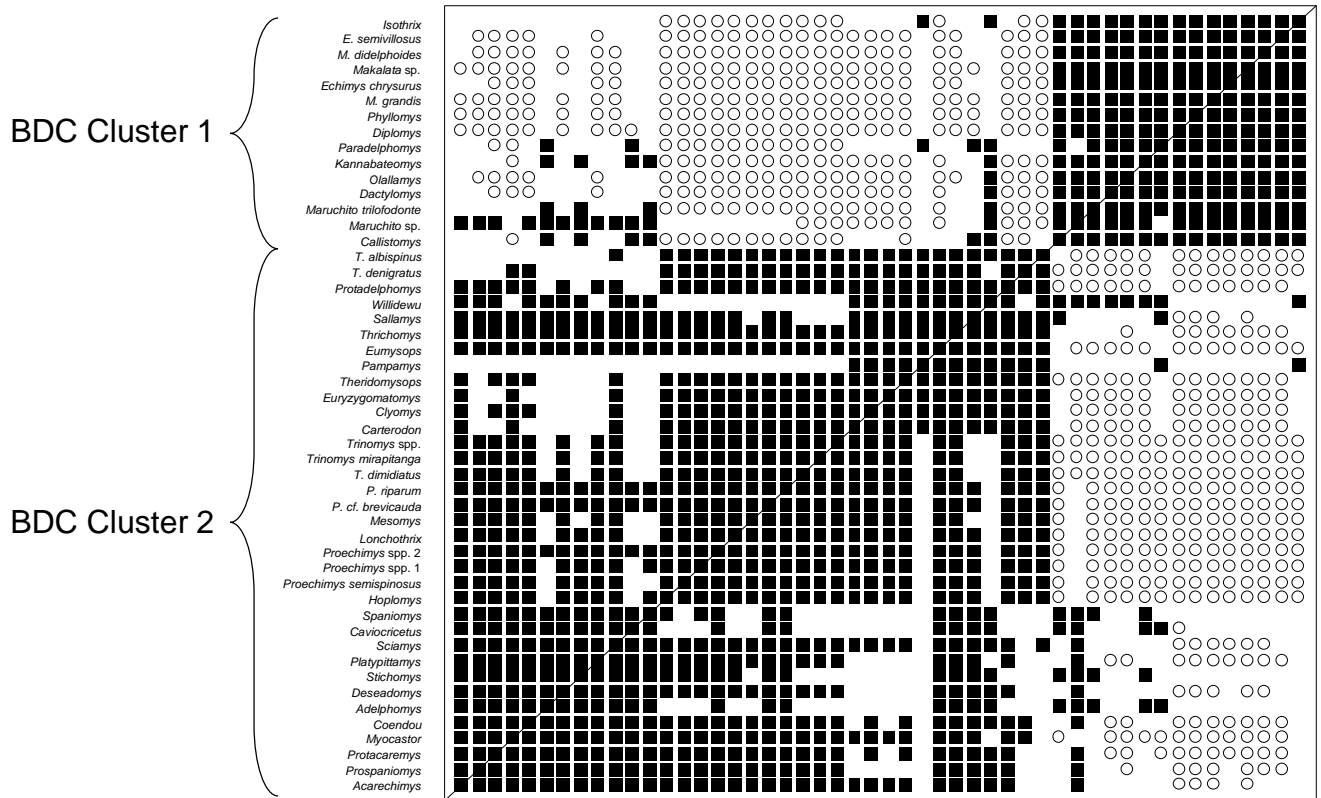
At k=2, the fuzzy analysis generates a partition similar to the BDC clustering, with a cluster membership difference of 4% and an average silhouette width of 0.44. At k=4, however, fuzzy analysis also generates a partition with a average silhouette width of 0.48, as seen in the four-cluster medoid partition. The four-cluster fuzzy analysis and medoid partition are not identical clustering however.

The original results were judged inconclusive because of the occurrence of numerous instances of significant, positive BDC between the observed clusters and because of the MDS results did not show the presence of two obvious clusters. Here again, the medoid partitioning and fuzzy analysis are similar to the clustering observed in the BDC results, but this reinforces the original uncertainty.

Original conclusion: Inconclusive

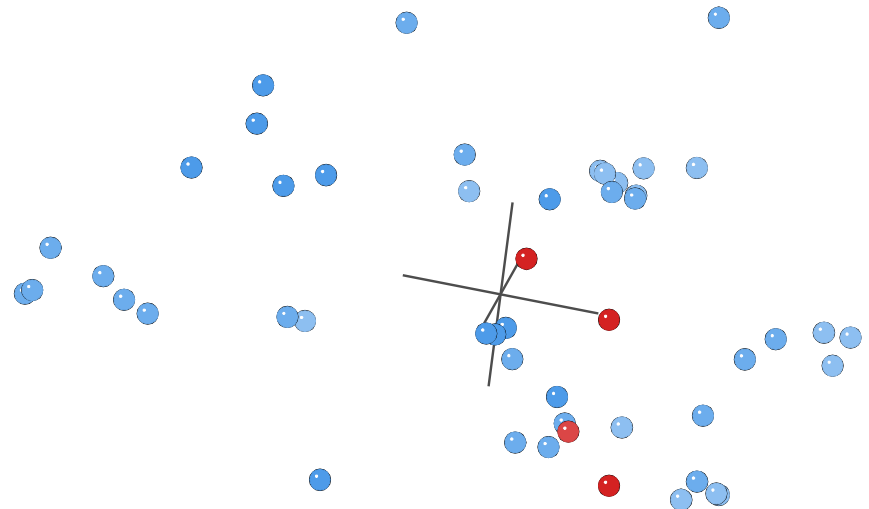
Updated conclusion: Inconclusive

Characters: Craniodental

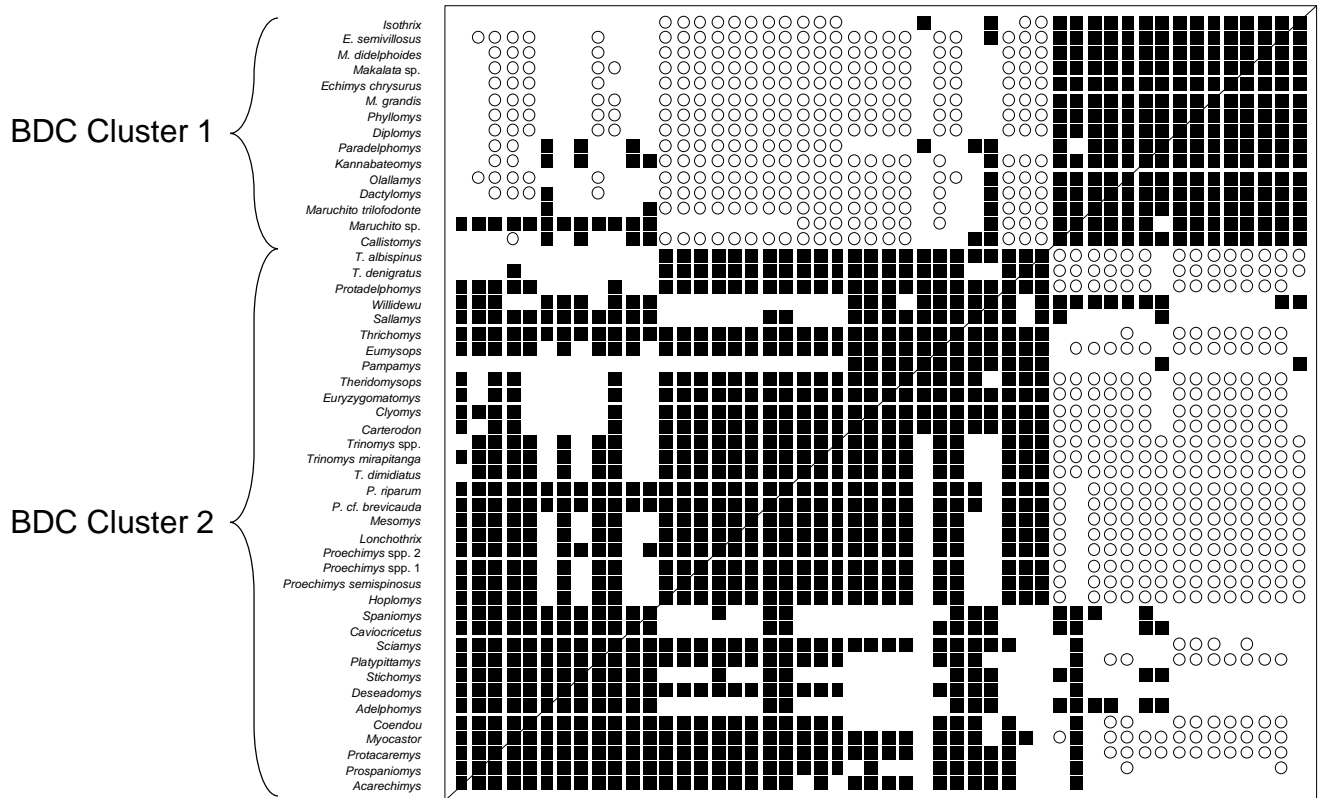


Order Rodentia
Family Echimyidae

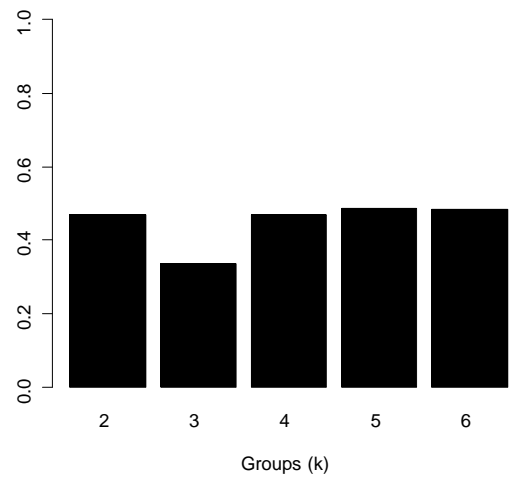
Published taxa	54
Published characters	50
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	50
Characters used for calculations	37
Median bootstrap value	78
F ₉₀	0.34
Stress of 3D MDS	0.13
k _{min}	3
Conclusion	Inc



Notes: Inconclusive; no strong evidence of discontinuity.



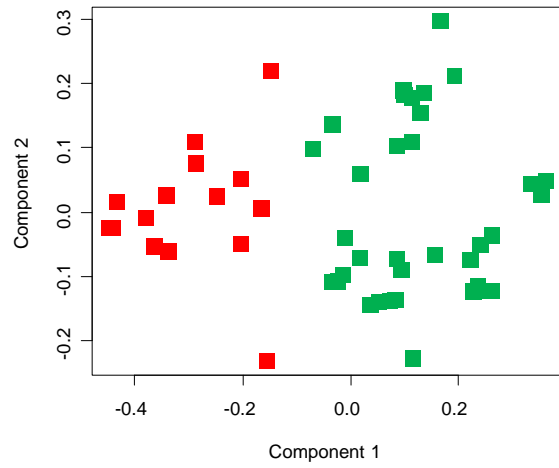
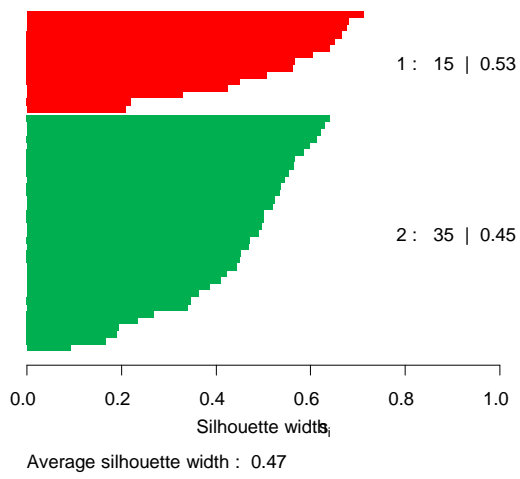
Average Silhouette Widths, Partion Around Medoids



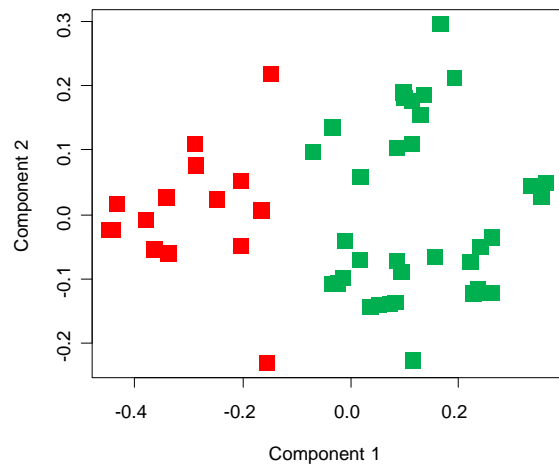
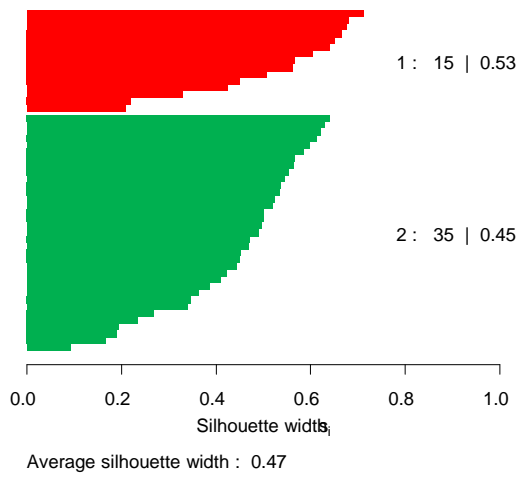
Clade Correspondence: Two large clusters are seen in the BDC results. Both clusters are monophyletic in figure 20 of Carvalho and Salles (2004), if the phylogeny were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

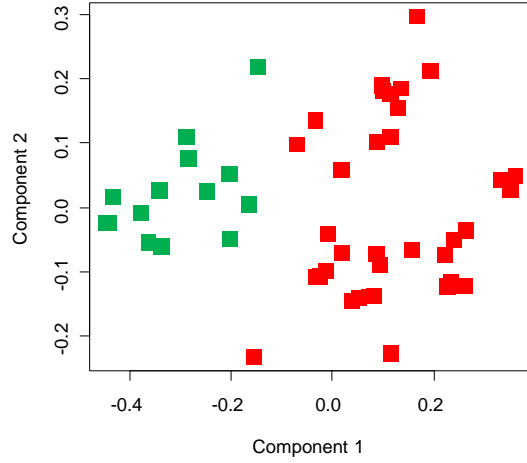
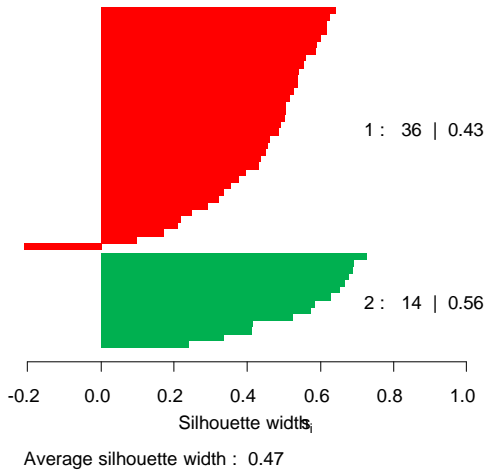


Spearman Correlation

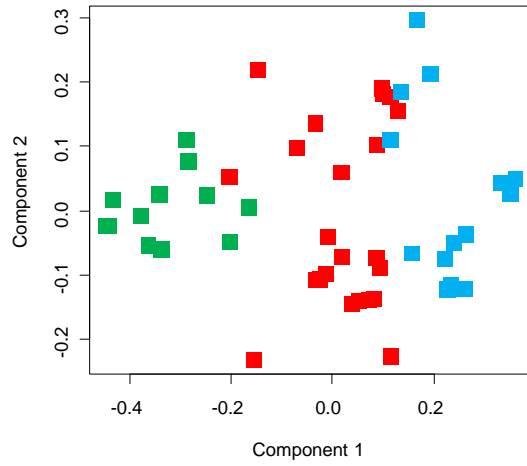
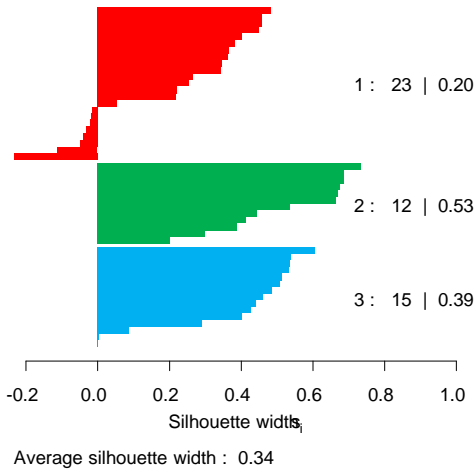


Silhouette plot, Partition Around Medoids

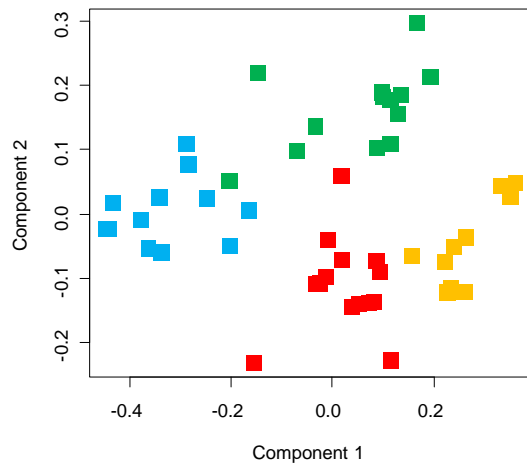
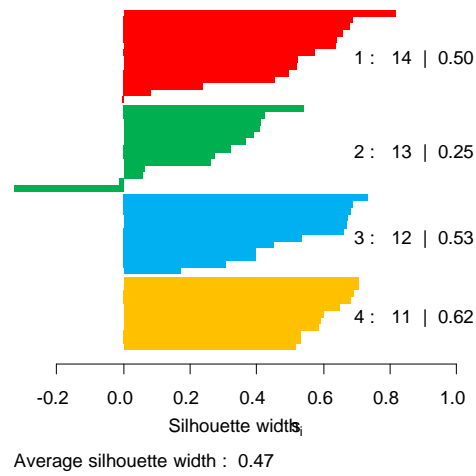
k=2



k=3

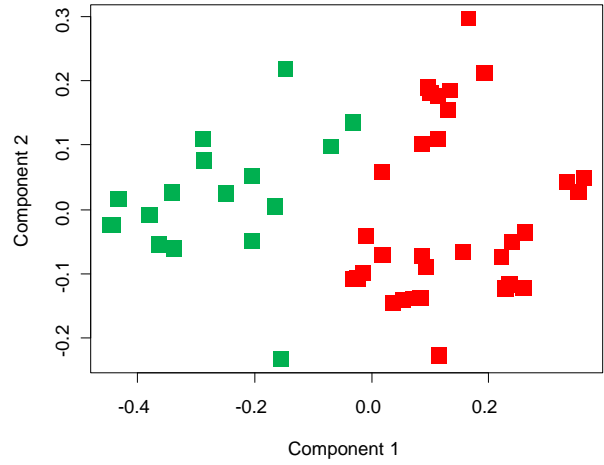
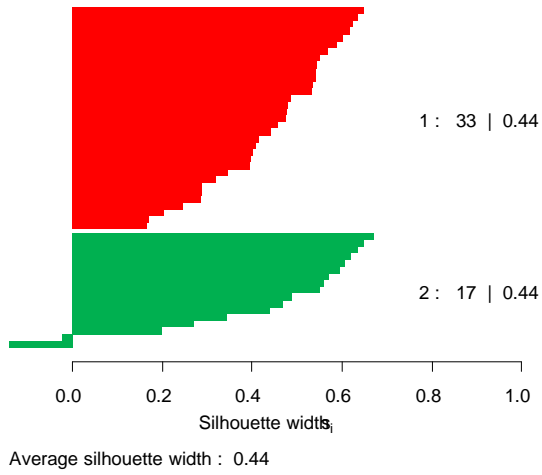


k=4

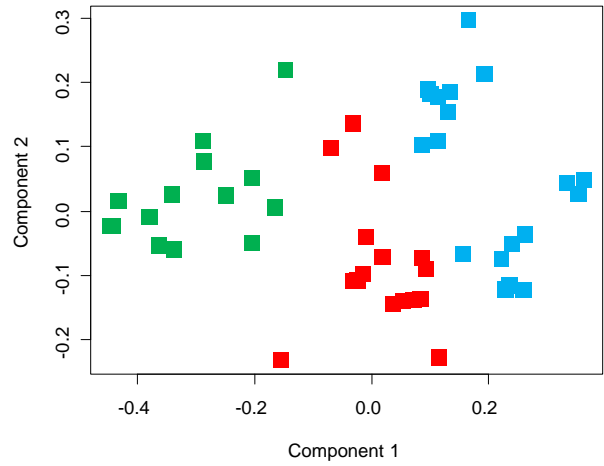
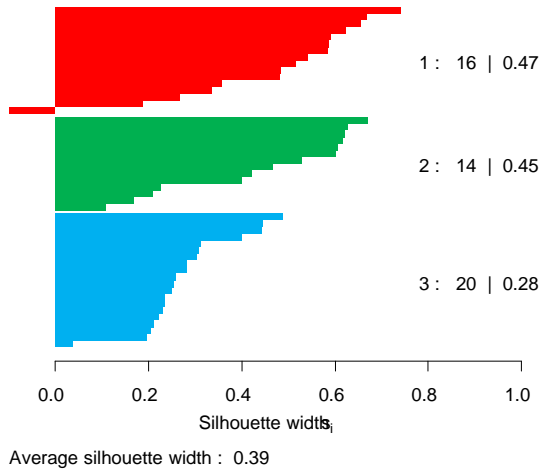


Silhouette plot, Fuzzy Analysis

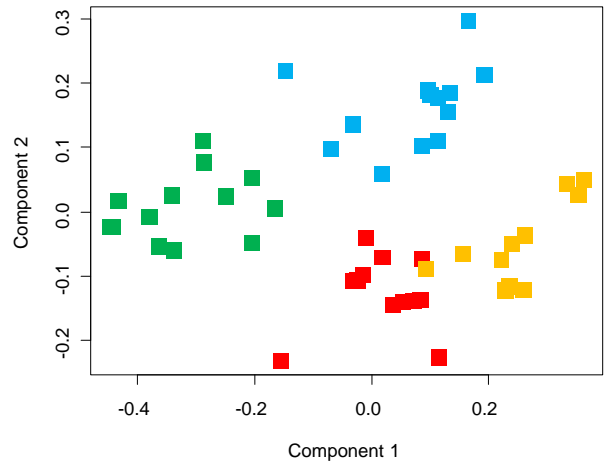
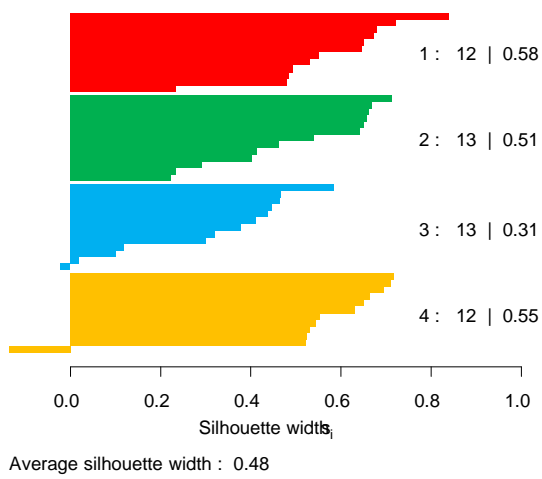
k=2



k=3



k=4



Family Palaeoryctidae

Order Insectivora

Rankin and Holroyd 2014

Pearson BDC

Negative: 3

Positive: 10

Clusters: 4

Clusterability

Hopkins Statistic: 0.74

Dip test: 0.057

Dip test p-value: 0.318

Spearman BDC

Negative: 2

Positive: 10

Clusters: 3

The number of taxon pairs exhibiting significant, positive BDC did not change between the Pearson and Spearman BDC results, but which pairs exhibited these correlations did. That change caused three clusters in the Pearson results to be redistributed, thus reducing the number of clusters from four to three. The cluster membership difference is 40%. The average silhouette width for the four Pearson BDC clusters was 0.28 and for the three Spearman BDC clusters was 0.32.

Medoid partitioning at k=3 partially confirmed the Pearson BDC clustering, with a cluster membership difference of 30% and an average silhouette width of 0.37. At k=3, the medoid partition was identical to the Spearman BDC clustering.

Fuzzy analysis at k=4 agreed exactly with the medoid partitioning, but at k=3, the fuzzy partition differed substantially from the Spearman BDC clusters. The three-cluster fuzzy analysis had an average silhouette width of only 0.17.

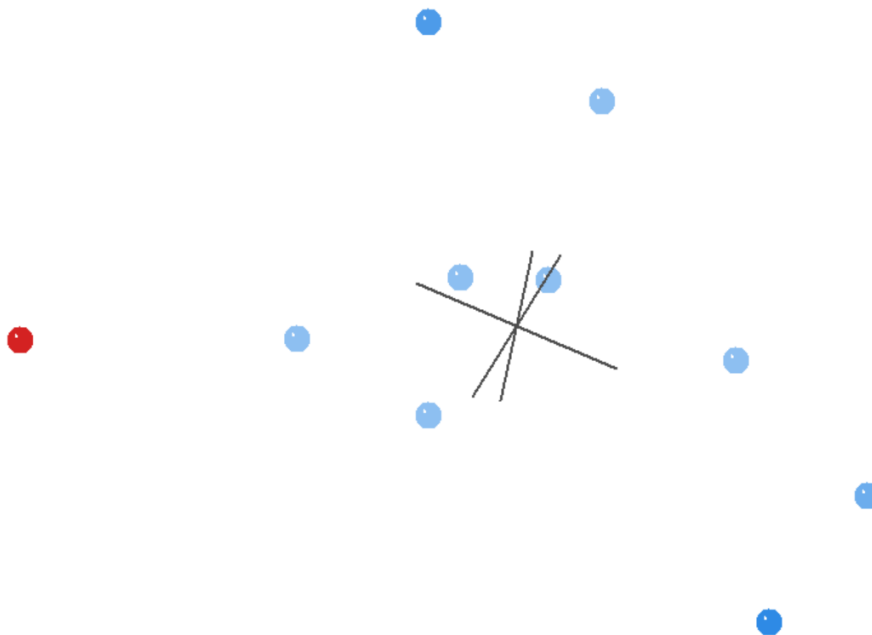
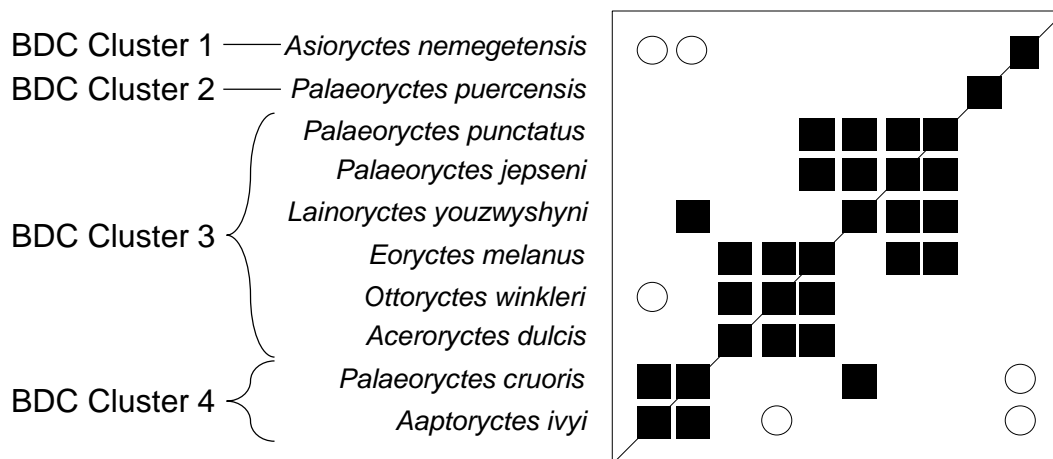
The original conclusion was based on a lack of significant, negative BDC and a sparse distribution of taxa in the MDS results. Here we find little support for the four-cluster Pearson BDC partition. Although the medoid partition confirms the three-cluster Spearman BDC, the fuzzy analysis does not. If anything, the common four-cluster results of the medoid partition and fuzzy analysis would seem to provide a consistent taxonomic clustering, but the clusters separate the species of genus *Palaeoryctes* into different clusters. The lack of consistency warrants uncertainty.

Original conclusion: inconclusive

Updated conclusion: inconclusive

Rankin, B.D. and P.A. Holroyd. 2014. *Aceroryctes dulcis*, a new palaeoryctid (Mammalia, Eutheria) from the early Eocene of the Wasatch Formation of southwestern Wyoming, USA. *Canadian Journal of Earth Sciences* 51:919-926.

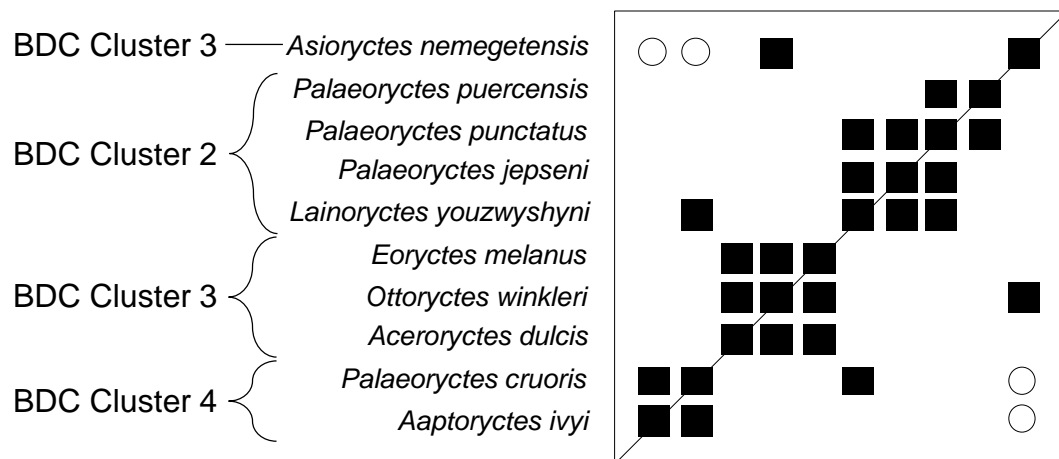
Characters: Dental



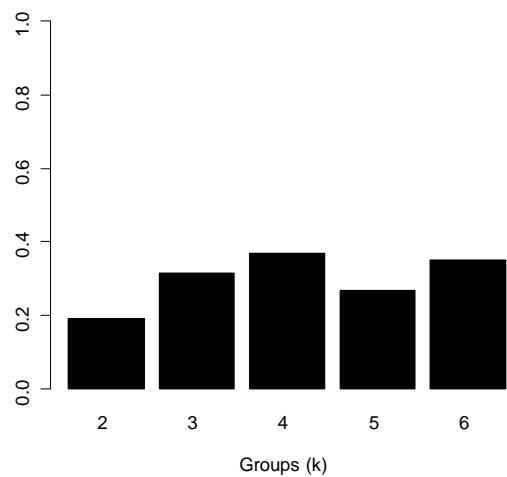
Order Insectivora
Family Palaeoryctidae

Published taxa	10
Published characters	32
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	10
Characters used for calculations	18
Median bootstrap value	78
F ₉₀	0.09
Stress of 3D MDS	0.17
k _{min}	4
Conclusion	Inc

Notes: The outgroup taxon *Asioryctes* is moderately separated from the ingroup taxa, but not sufficiently to warrant inferring discontinuity.



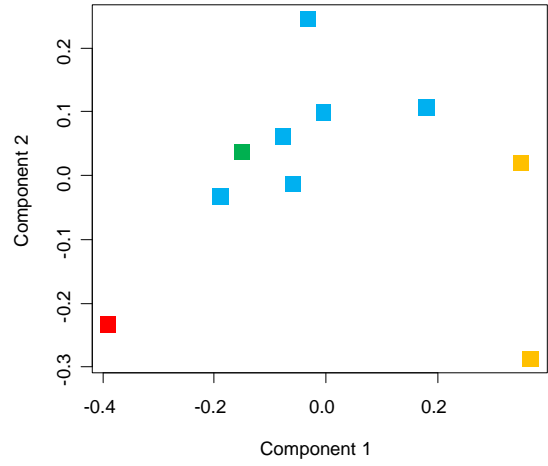
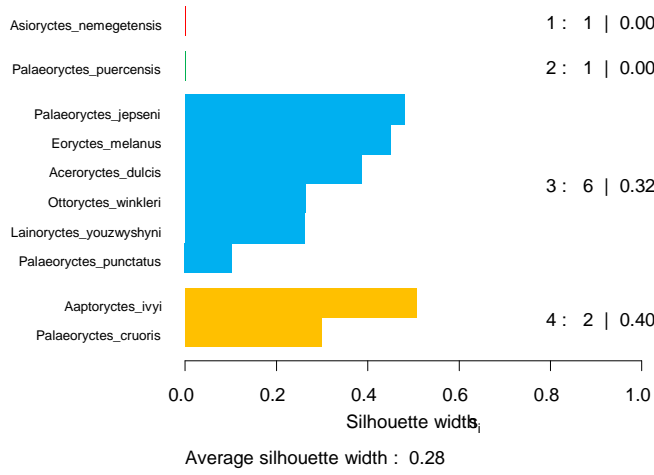
Average Silhouette Widths, Partion Around Medoids



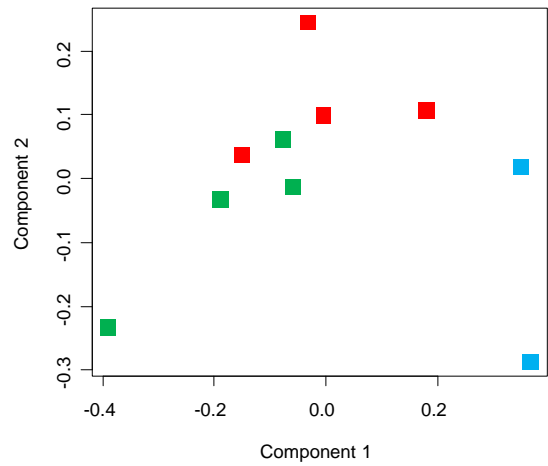
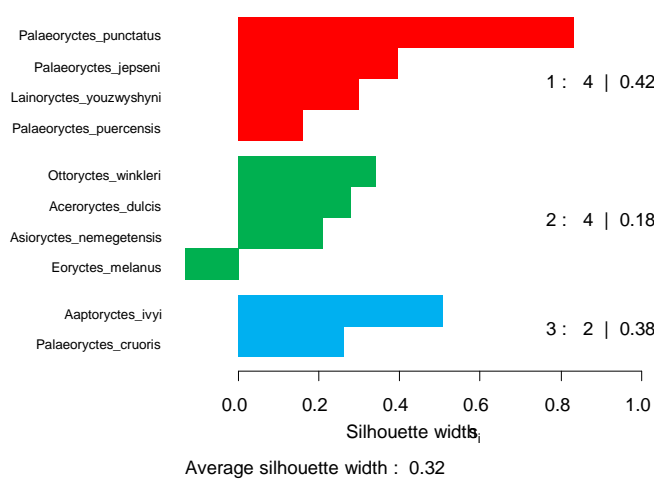
Clade Correspondence: BDC clusters 3 and 4 contain six and two taxa respectively. The published phylogeny in Figure 4c of Rankin and Holroyd (2014) shows only cluster 4 as monophyletic. The taxa of cluster 3 form an unresolved polytomy in the phylogeny.

Silhouette plot, BDC partitions

Pearson Correlation

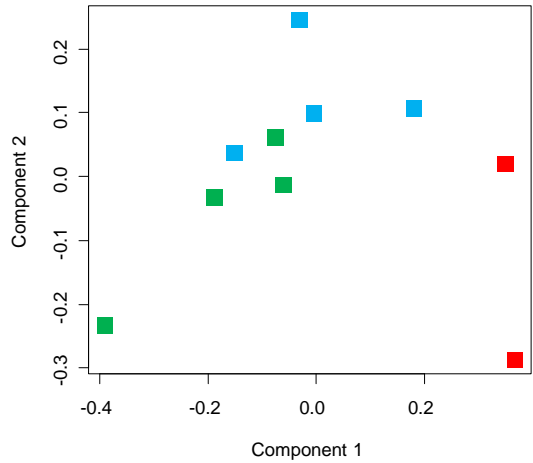
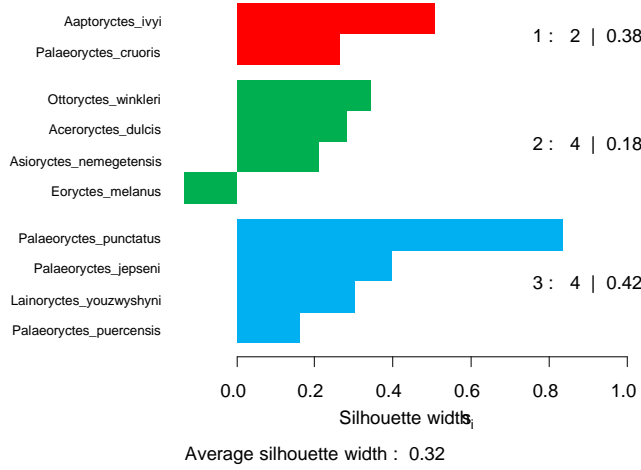


Spearman Correlation

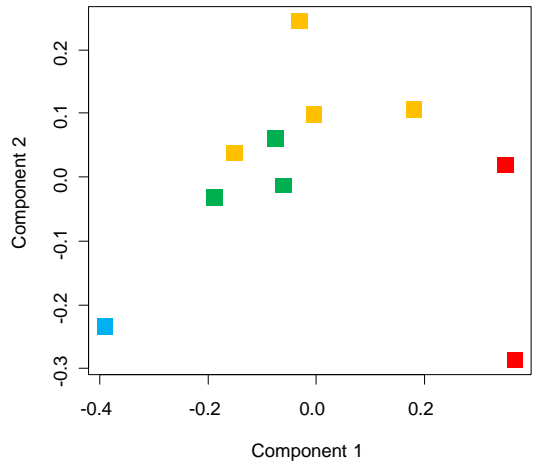
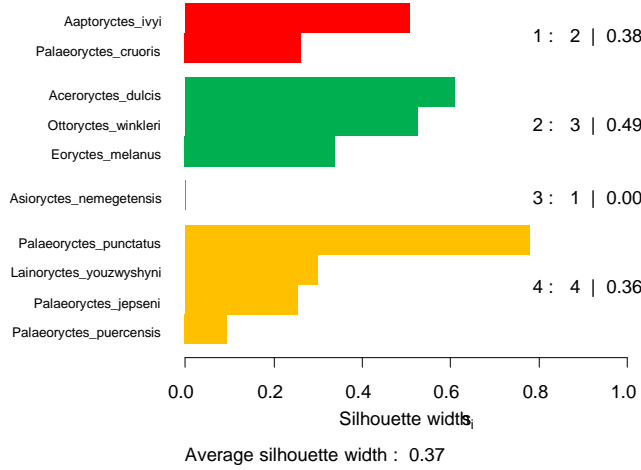


Silhouette plot, Partition Around Medoids

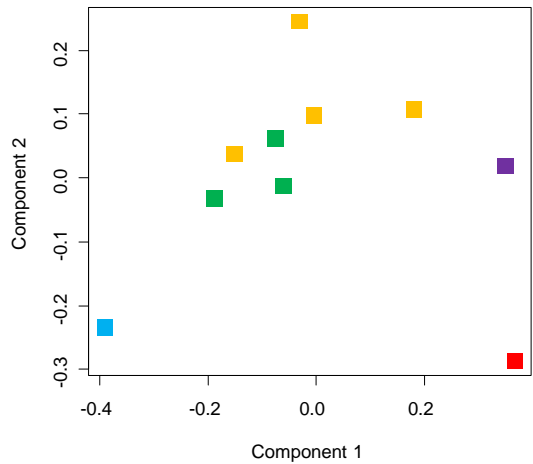
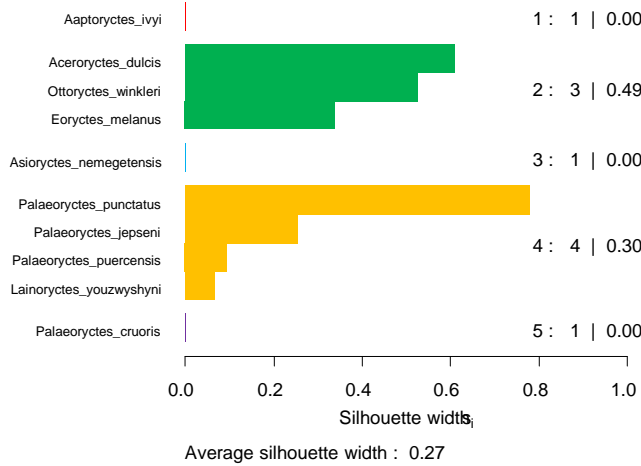
k=3



k=4

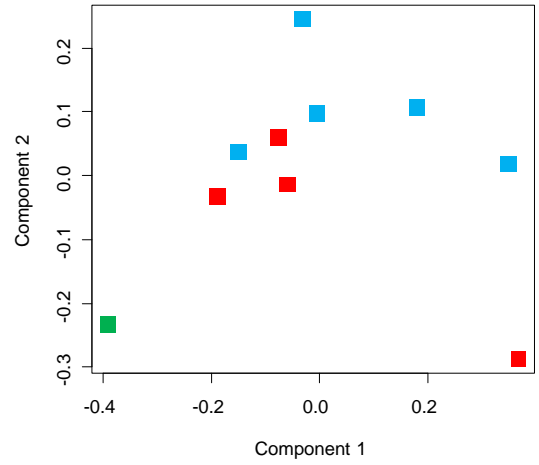
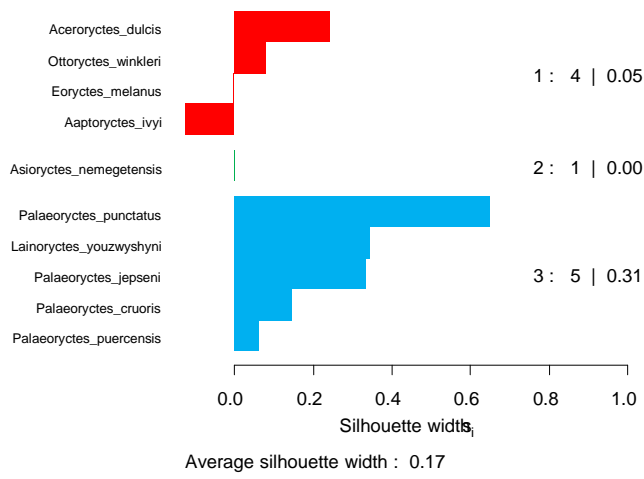


k=5

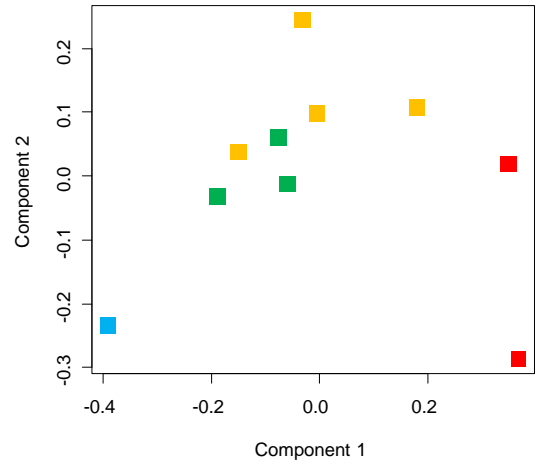
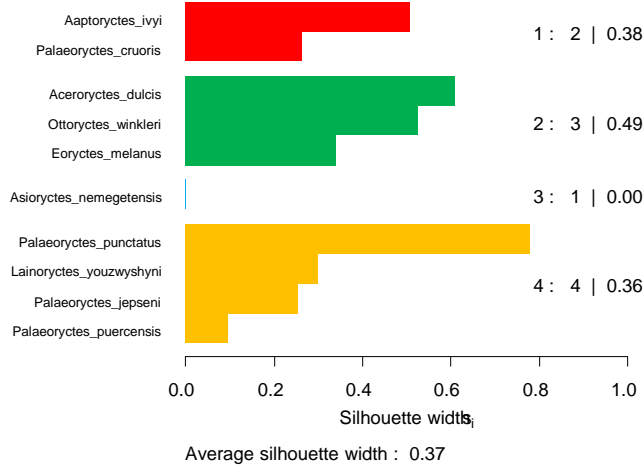


Silhouette plot, Fuzzy Analysis

k=3



k=4



Family Manidae

Order Pholidota

Kondrashov and Agadjanian 2012

Pearson BDC

Negative: 68

Positive: 57

Clusters: 3

Clusterability

Hopkins Statistic: 0.738

Dip test: 0.026

Dip test p-value: 0.7

Spearman BDC

Negative: 70

Positive: 68

Clusters: 2

The Spearman BDC adds instances of significant positive and negative correlation that reinforces the obvious division evident in the Pearson BDC. The number of clusters is reduced from three in the Pearson BDC to two in the Spearman BDC. The three-cluster Pearson BDC partition has an average silhouette width of 0.4, and the average silhouette width for the two-cluster Spearman BDC partition is 0.46. Neither partition had any taxa with negative silhouette values. The cluster membership difference was 17%.

At $k=3$, the medoid partition exactly matched the Pearson BDC clusters. At $k=2$, the medoid partition has a silhouette value of 0.42. It closely matches the Spearman BDC clusters, except that it transfers *Necromanis* to the other cluster.

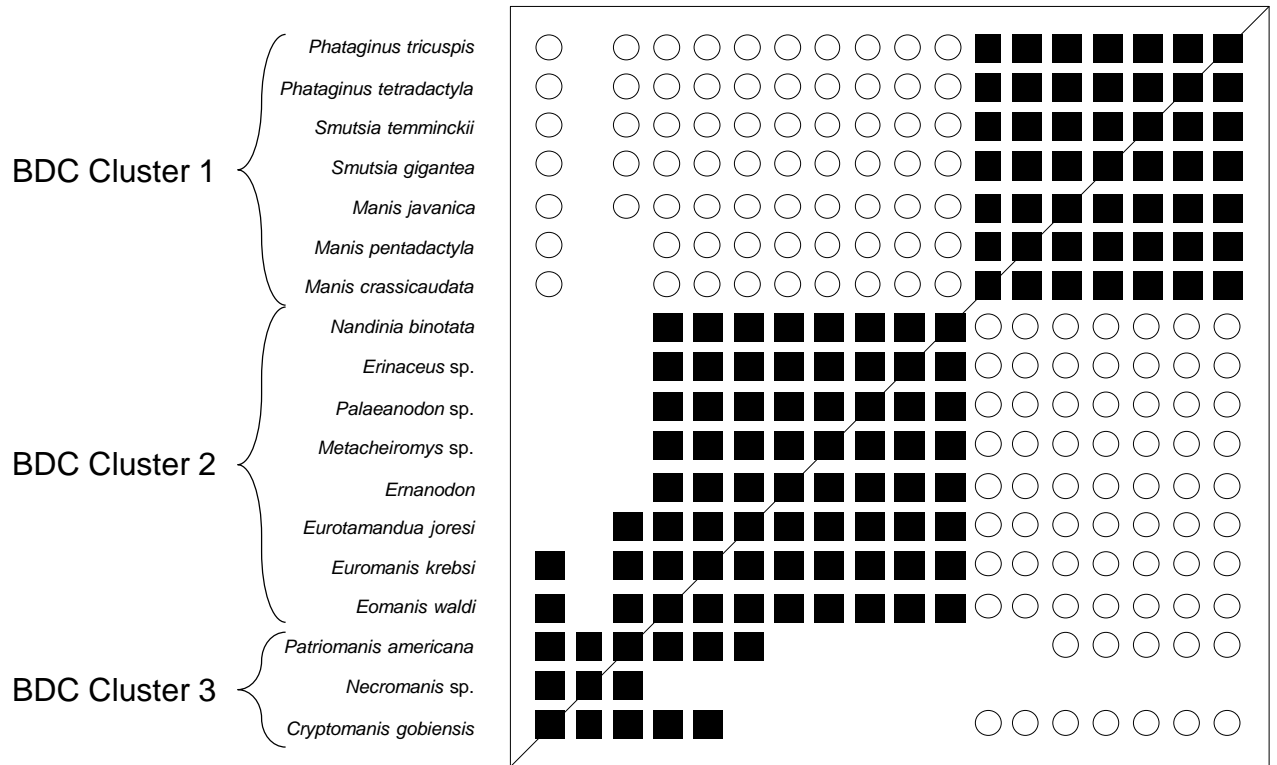
Fuzzy analysis agreed exactly with the Pearson BDC clusters at $k=3$ and with the Spearman BDC clusters at $k=2$.

In combining clusters from three to two, the Spearman BDC results and the fuzzy analysis reinforce the original conclusion that Manidae is a holobaramin.

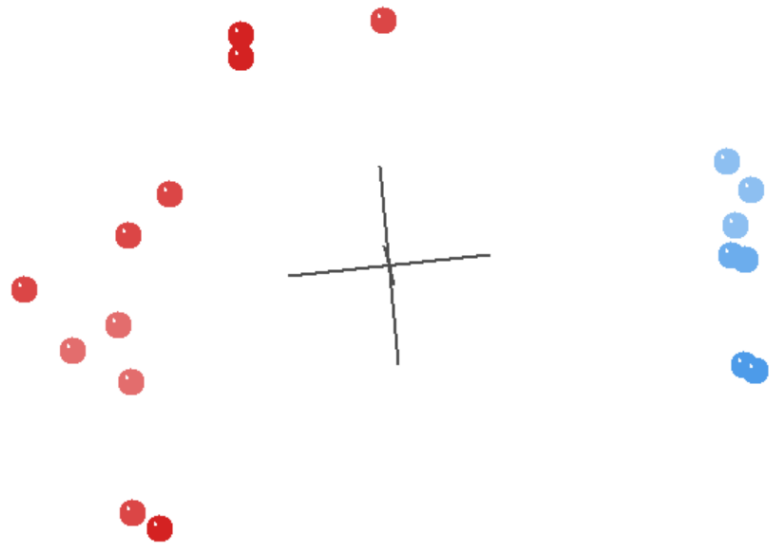
Original conclusion: HB

Updated conclusion: HB

Characters: Cranial and postcranial

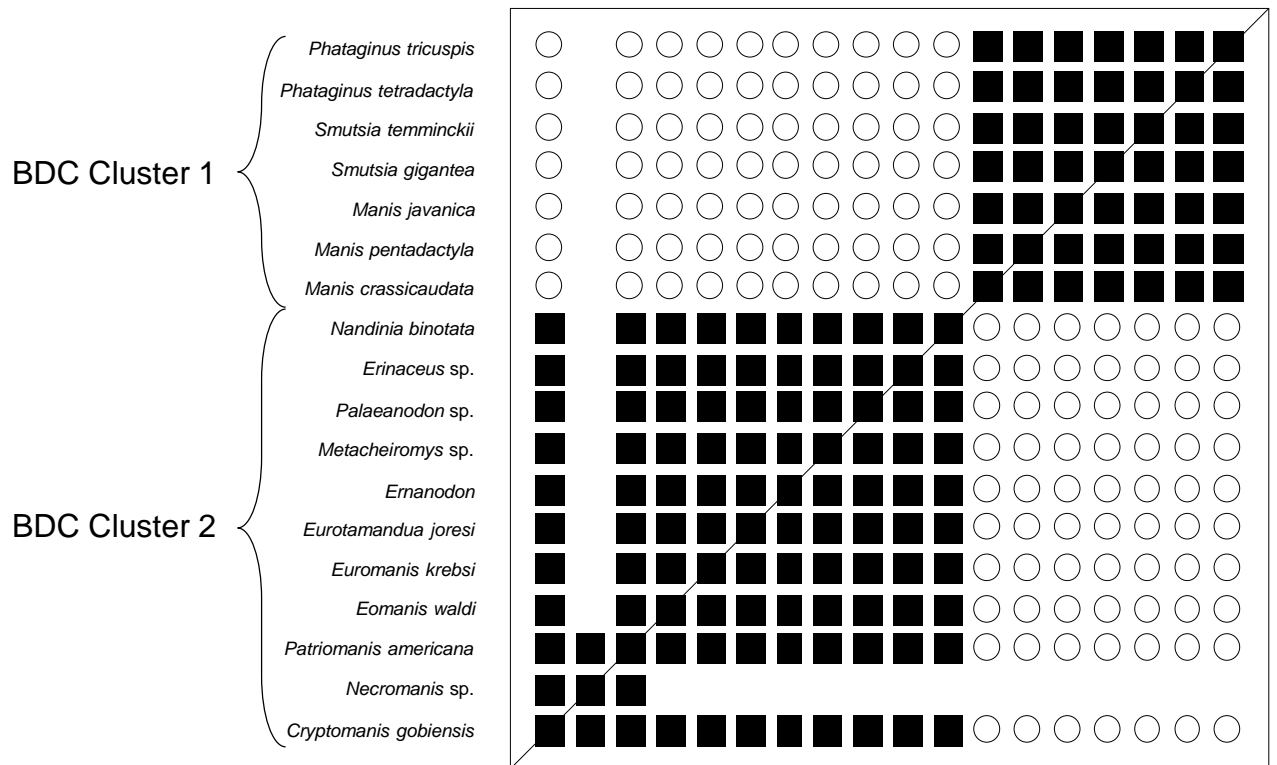


Order Pholidota
Family Manidae

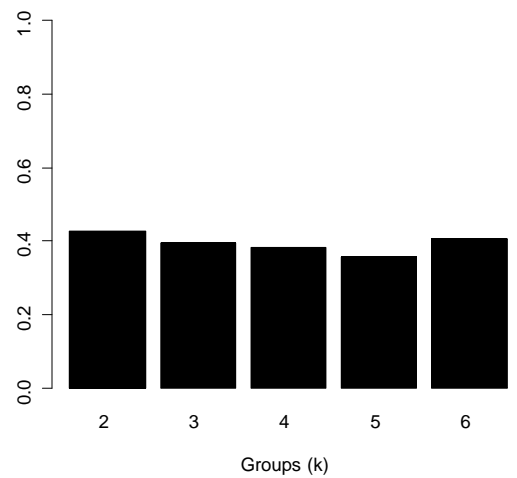


Published taxa	18
Published characters	395
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	18
Characters used for calculations	209
Median bootstrap value	100
F ₉₀	0.77
Stress of 3D MDS	0.16
k _{min}	9
Conclusion	HB

Notes: Manidae is well-separated in both BDC and MDS results. Manidae is probably a holobaramin.



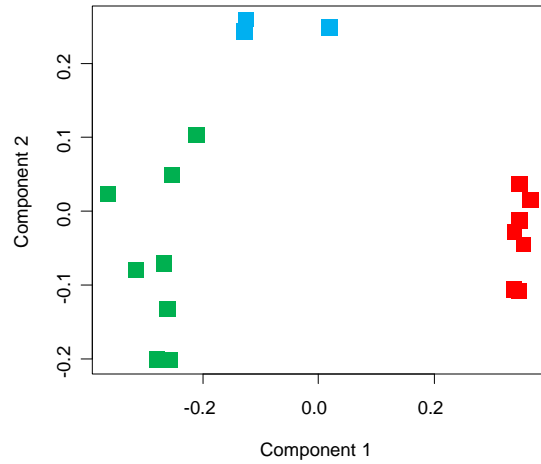
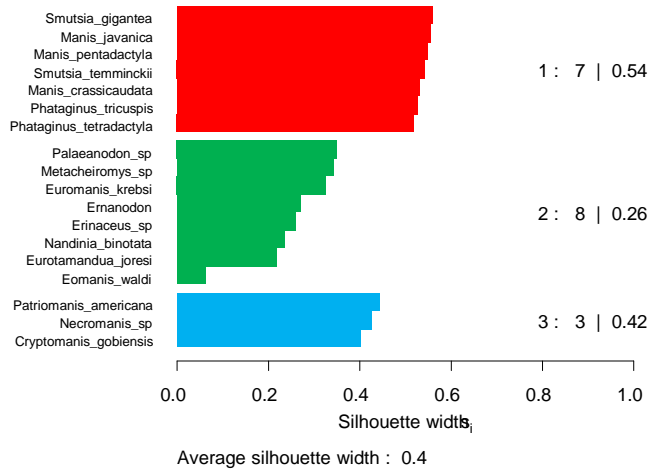
Average Silhouette Widths, Partion Around Medoids



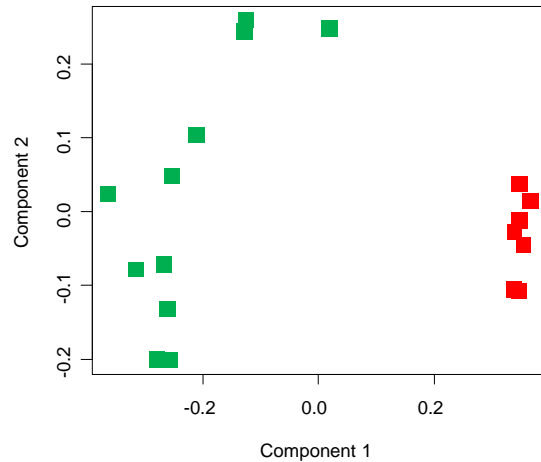
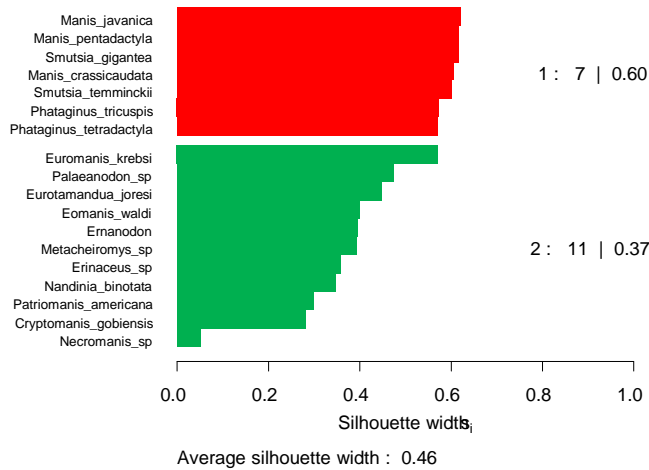
Clade Correspondence: There are three BDC clusters of two or more taxa each. The phylogeny of figure 12 in Kondrashov and Agadjanian (2012) reveals all three are monophyletic, if the phylogeny were drawn as unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

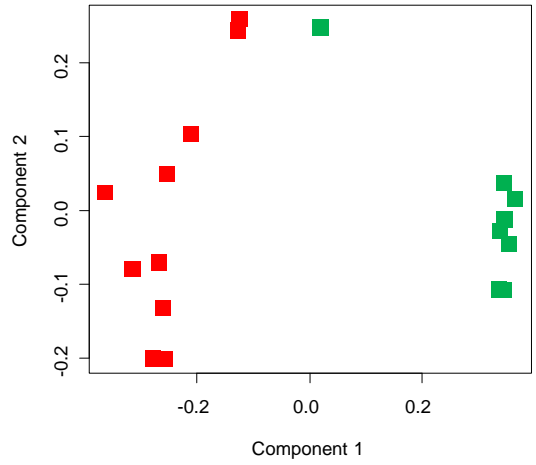
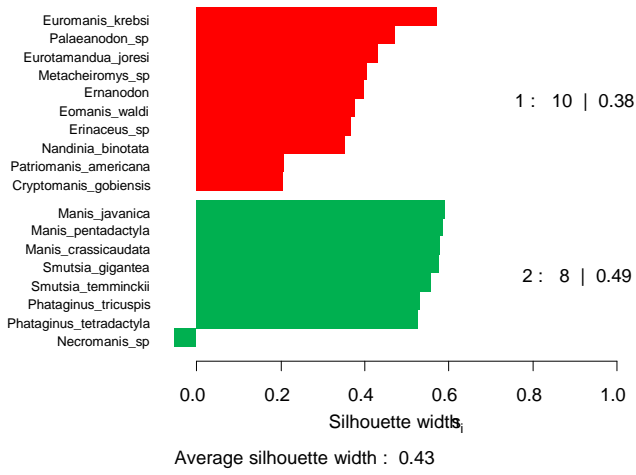


Spearman Correlation

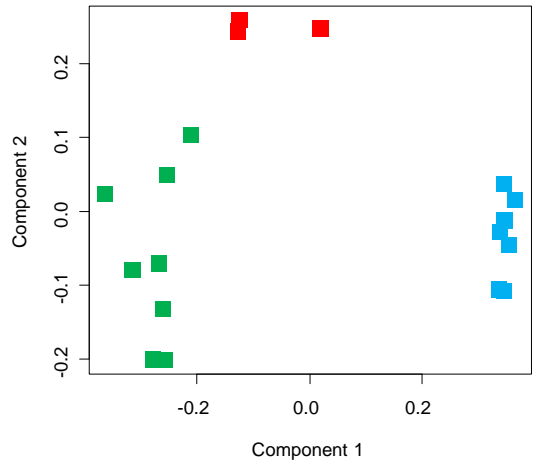
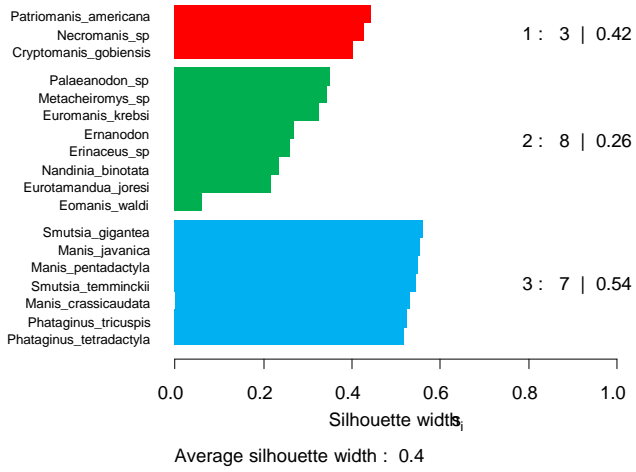


Silhouette plot, Partition Around Medoids

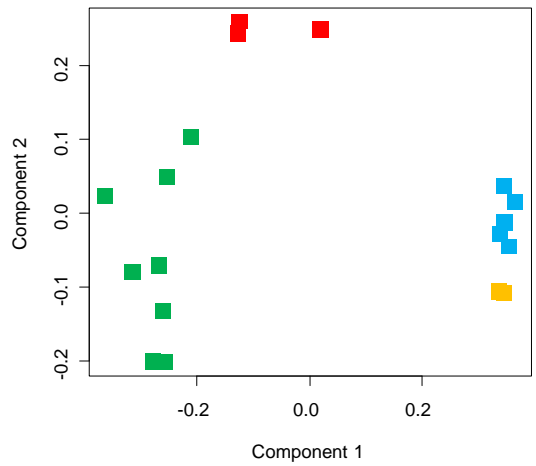
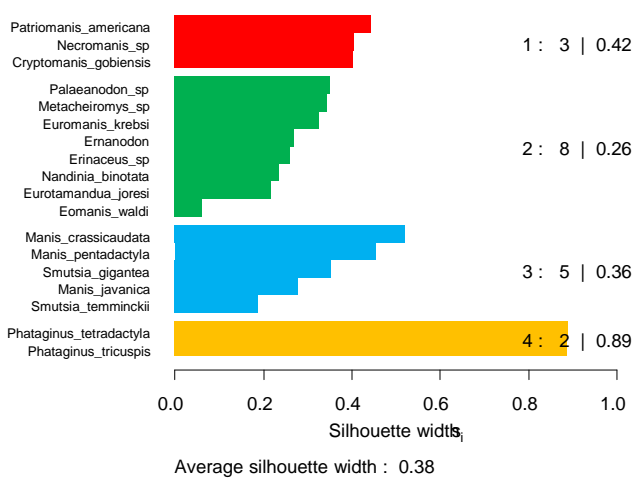
k=2



k=3

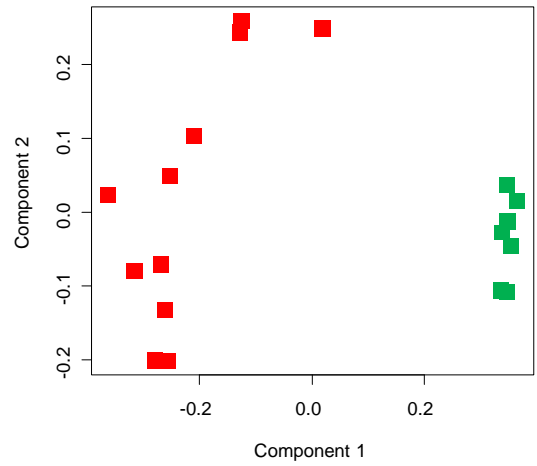
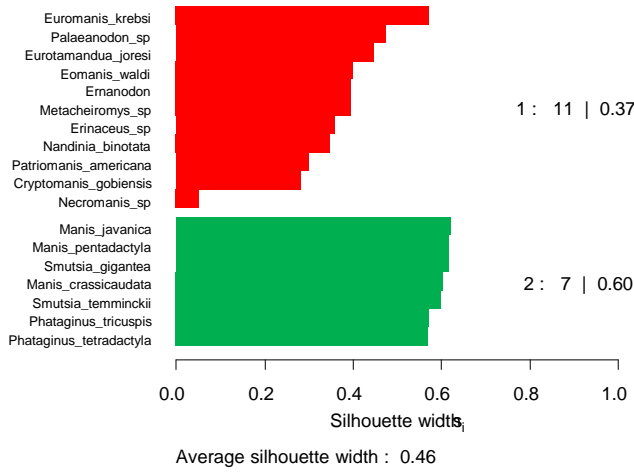


k=4

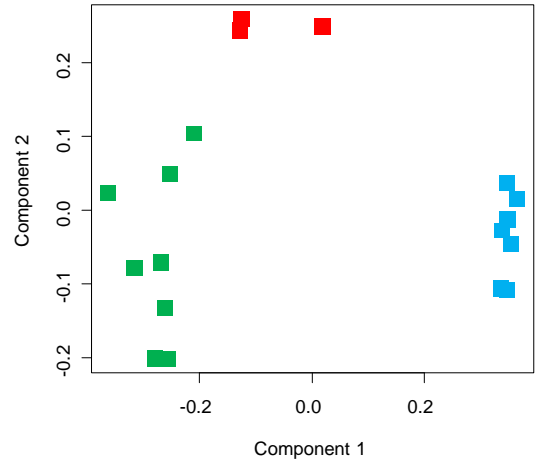
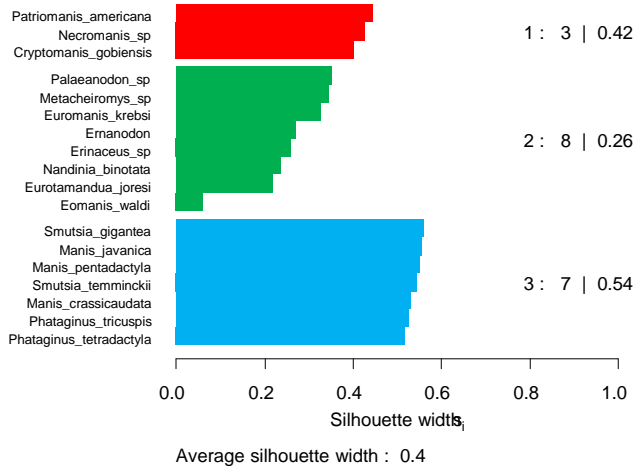


Silhouette plot, Fuzzy Analysis

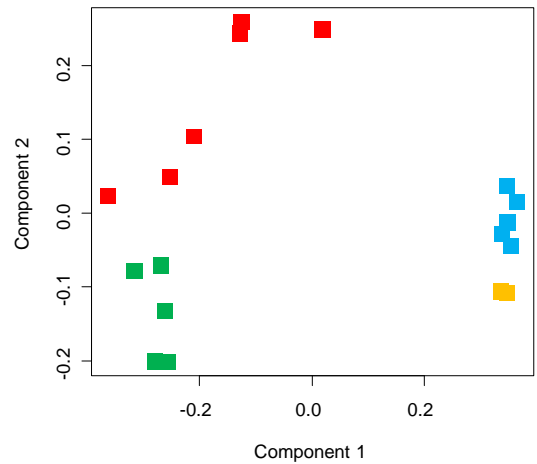
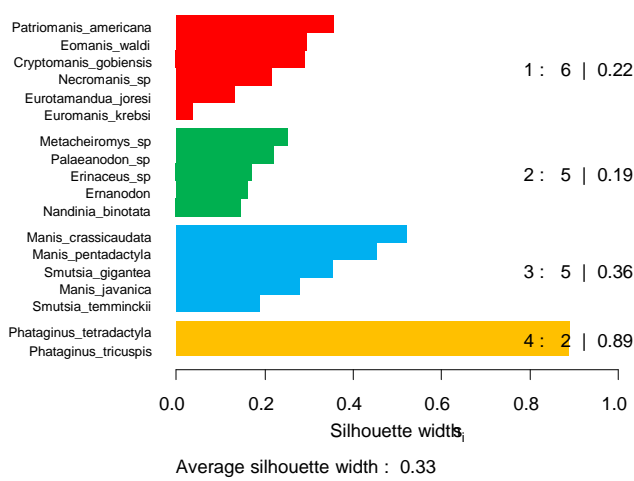
k=2



k=3



k=4



Family Hyaenodontidae

Order Carnivora

Polly 1996

Pearson BDC

Negative: 22

Positive: 27

Clusters: 4

Clusterability

Hopkins Statistic: 0.773

Dip test: 0.038

Dip test p-value: 0.252

Spearman BDC

Negative: 15

Positive: 39

Clusters: 3

Twelve additional instances of significant, positive correlation in the Spearman BDC results reduce the number of clusters from four in the Pearson BDC to three in the Spearman BDC. The four-cluster Pearson BDC partition has an average silhouette width of 0.44, and the three-cluster Spearman BDC partition has an average silhouette width of 0.38. The cluster membership difference was 19%.

At $k=4$, medoid partitioning produces clusters identical to the Pearson BDC results. At $k=3$, the medoid partition is identical to the Spearman BDC clustering.

Fuzzy analysis at $k=4$ closely matches the Pearson BDC results, with *Propterodon* transferred to a different cluster. The average silhouette width for the four-cluster fuzzy analysis is 0.48, and the cluster membership difference between the four-cluster fuzzy analysis and Pearson BDC partition is 6%. At $k=3$, fuzzy analysis returned a partition substantially different from the Spearman BDC clustering and the three-cluster medoid partition. The average silhouette width for the fuzzy partition at $k=3$ is 0.34.

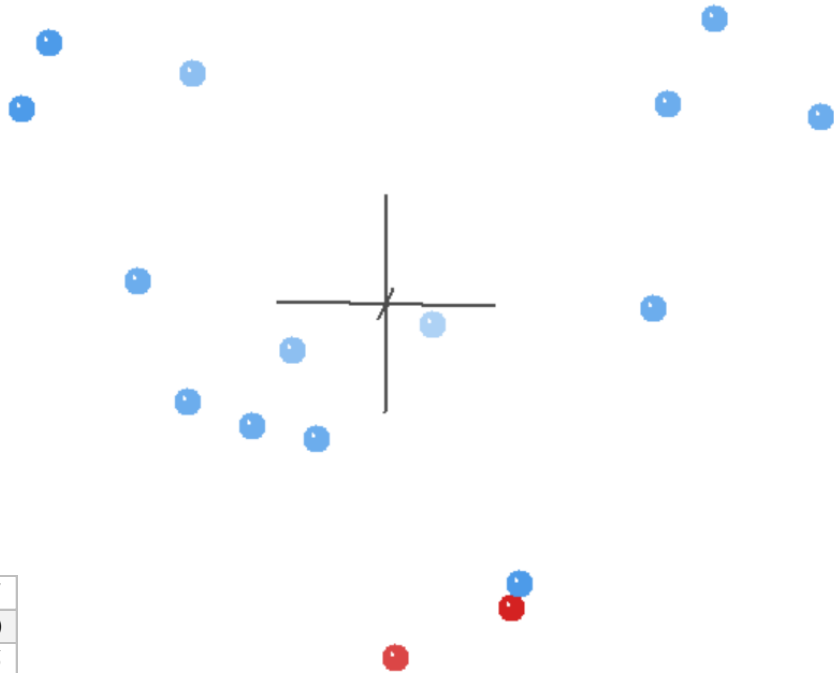
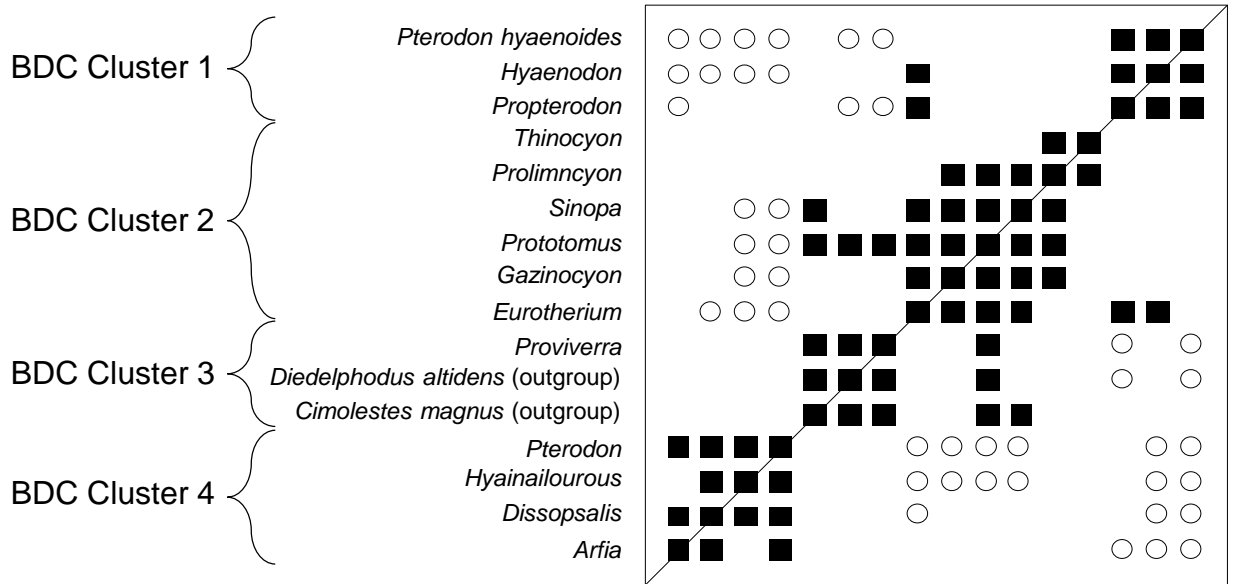
The original conclusion that the results were inconclusive was based on poor bootstrap values in the Pearson BDC, and a lack of obvious discontinuity in the MDS. Here the consistency of the four-cluster medoid partitioning and fuzzy analysis with the Pearson BDC clusters suggests that the Pearson results are more reliable than originally judged. At the very least, a cluster consisting of four taxa (*Arfia*, *Dissopsalis*, *Pterodon*, and *Hyainalouros*) appears in the Pearson BDC, Spearman BDC, medoid partition ($k=3$ and $k=4$), and fuzzy analysis ($k=3$ and $k=4$). This group corresponds to a clade that contains Polly's Pterodontinae. The evidence of discontinuity is poor (sparse instances of significant, negative correlation in the Pearson and Spearman BDC results); however, there is no significant, positive BDC between this clade and any other taxa in the set. Given its consistent appearance in fuzzy analysis, medoid partition, and BDC, we may tentatively conclude that this is an uncertain holobaramin.

Original conclusion: Inconclusive

Updated conclusion: HB?

Polly, P.D. 1996. The skeleton of *Gazinocyon vulpeculus* gen. et comb. nov. and the cladistic relationships of Hyaenodontidae (Eutheria, Mammalia). *Journal of Vertebrate Paleontology* 16:303-319.

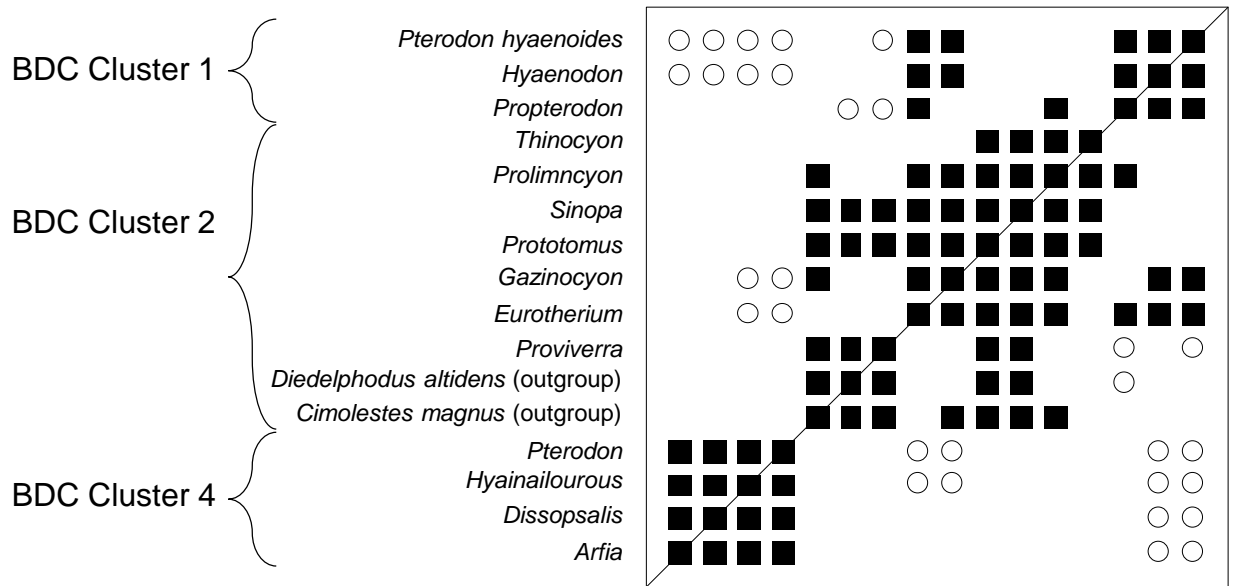
Characters: Craniodental and postcranial



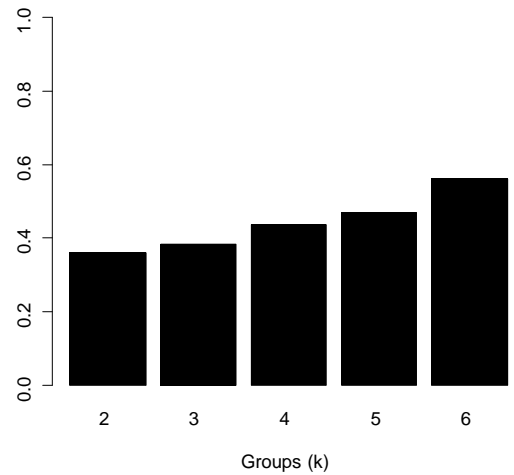
Order Carnivora
Family Hyaenodontidae

Published taxa	17
Published characters	60
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	16
Characters used for calculations	32
Median bootstrap value	75
F ₉₀	0.12
Stress of 3D MDS	0.12
k _{min}	5
Conclusion	Inc

Notes: The BDC results mostly have poor bootstrap values, and there is no discontinuity evident in the MDS.



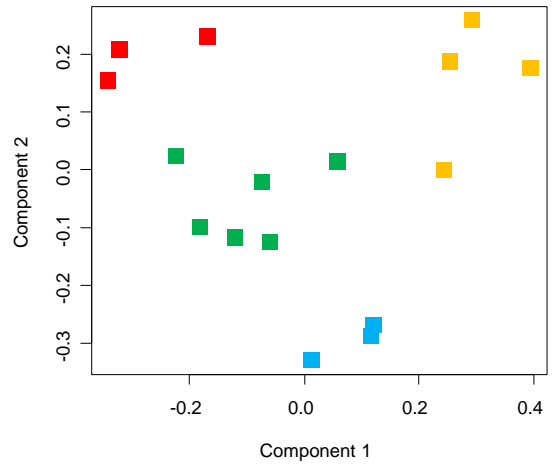
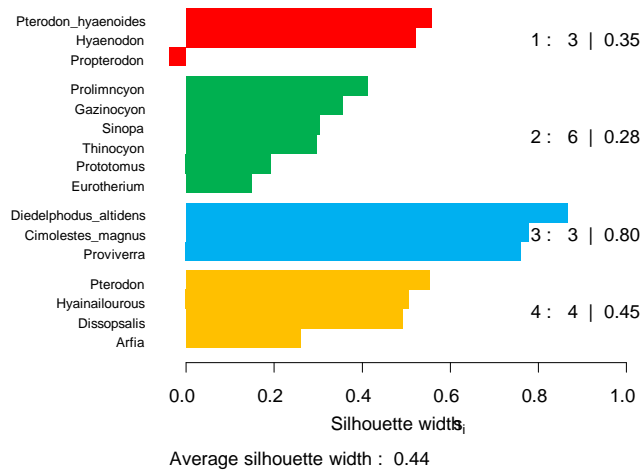
Average Silhouette Widths, Partion Around Medoids



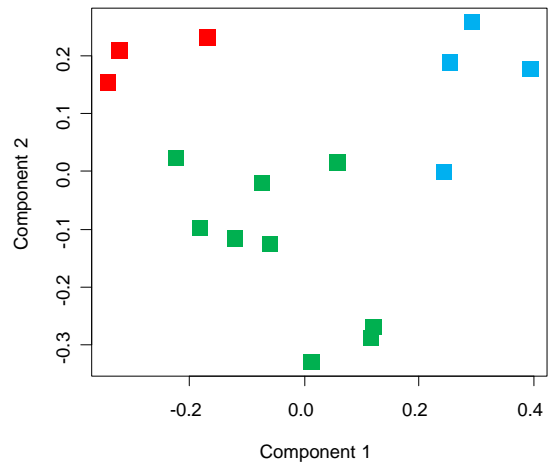
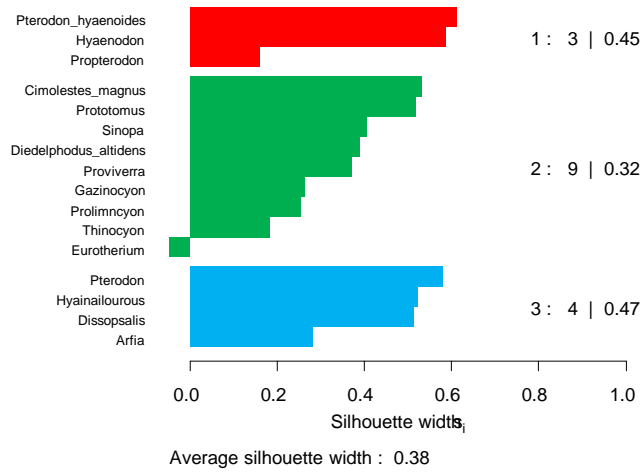
Clade Correspondence: All four BDC clusters contain more than one taxon each. Three of these clusters correspond to clades in the published phylogeny, if it were drawn unrooted (Figure 10, Polly 1996). The largest cluster in the BDC analysis, cluster 2, is paraphyletic in the published phylogeny.

Silhouette plot, BDC partitions

Pearson Correlation

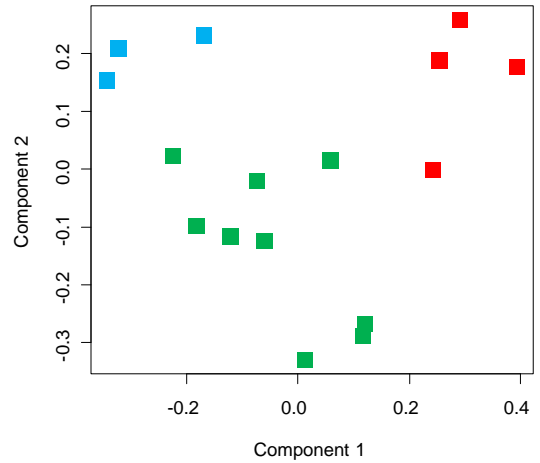
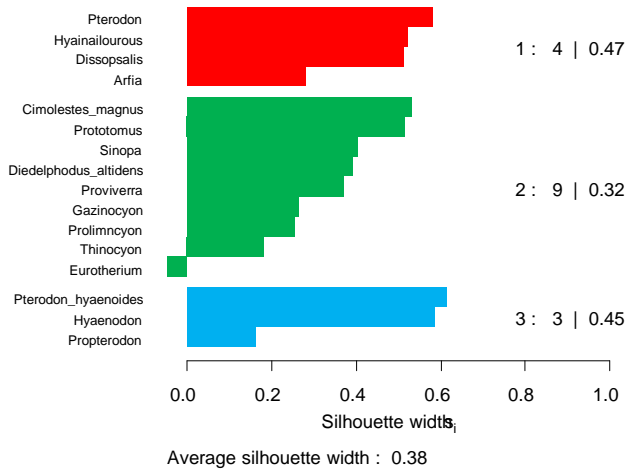


Spearman Correlation

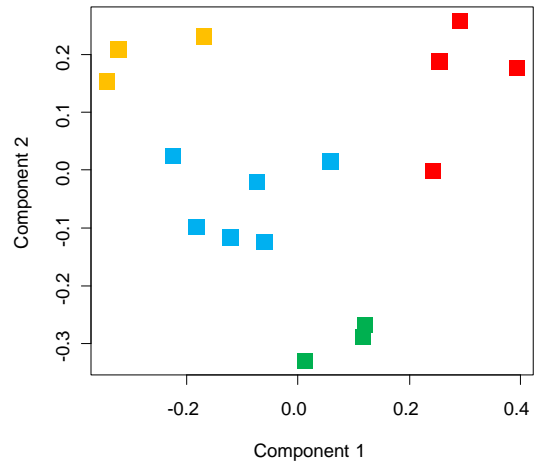
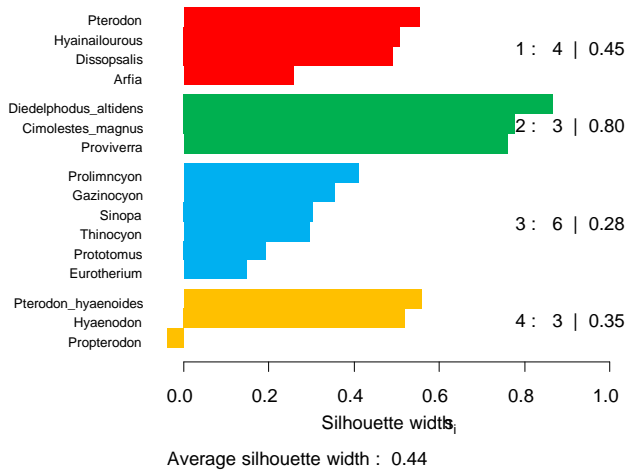


Silhouette plot, Partition Around Medoids

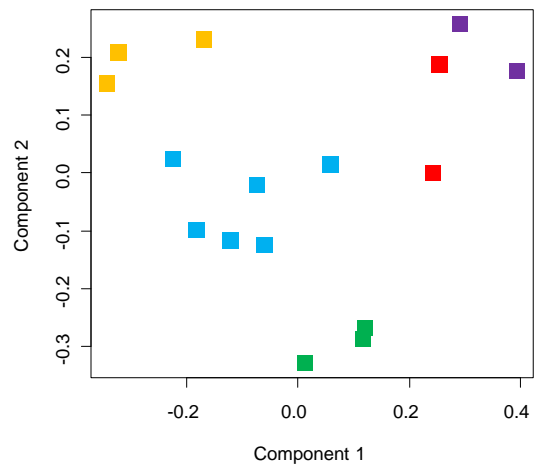
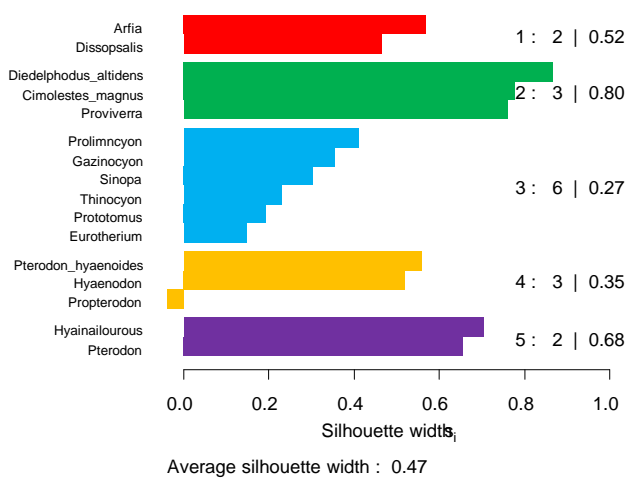
k=3



k=4

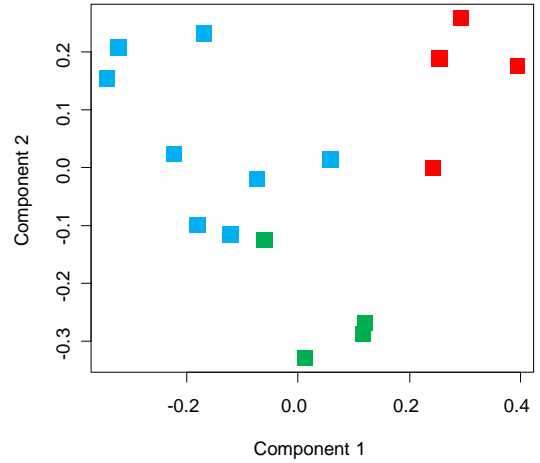
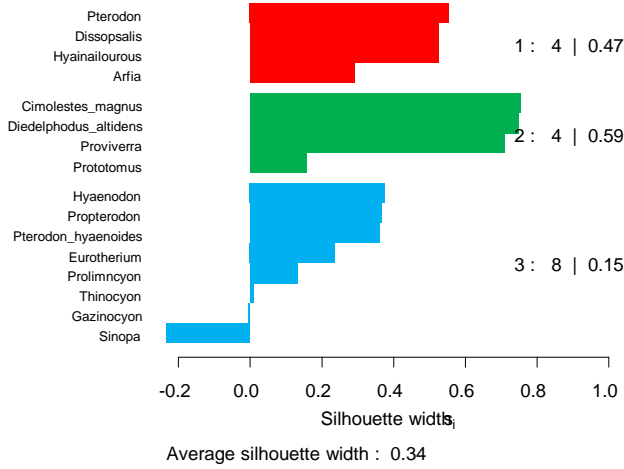


k=5

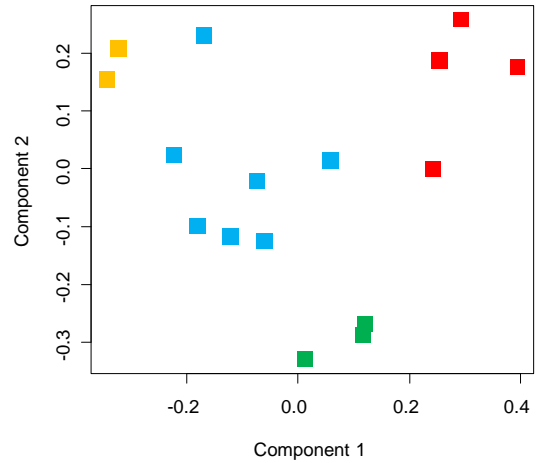
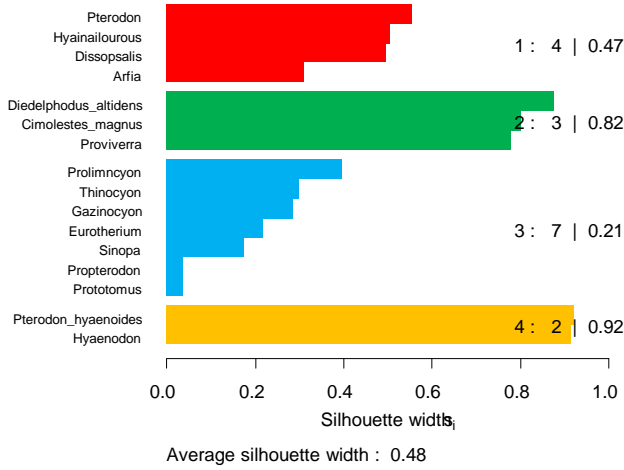


Silhouette plot, Fuzzy Analysis

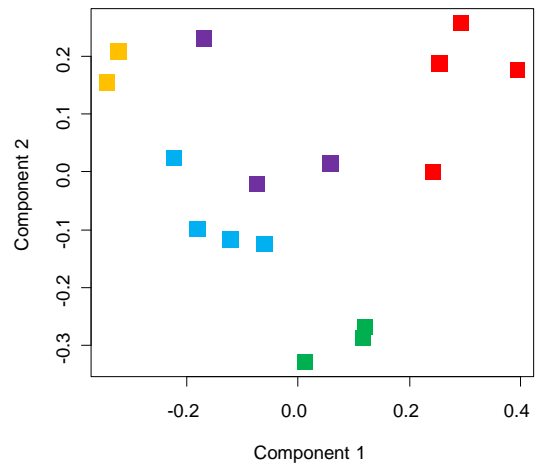
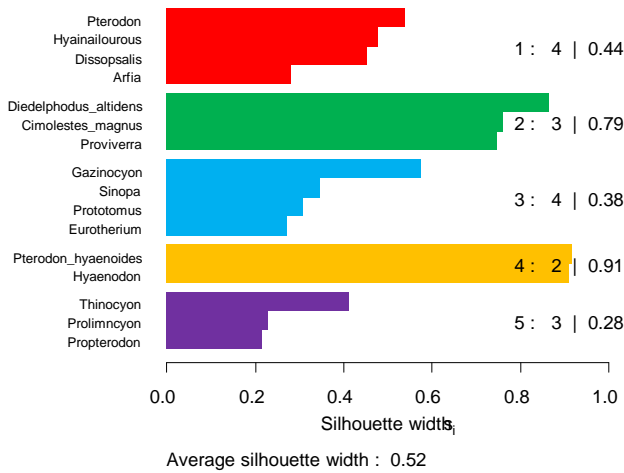
k=3



k=4



k=5



Family Felidae

Order Carnivora

Holliday 2007

Pearson BDC

Negative: 274

Positive: 693

Clusters: 2

Clusterability

Hopkins Statistic: 0.77

Dip test: 0.009

Dip test p-value: 0.829

Spearman BDC

Negative: 140

Positive: 668

Clusters: 2

The Spearman BDC results show 25 fewer instances of significant, positive correlation and 134 fewer instances of significant, negative correlation. Despite these dramatic differences, the clustering partition is the same, with two clearly separated clusters that have an average silhouette width of 0.37.

Medoid partitioning does not support the two-cluster partition revealed by the BDC results; however, the two cluster medoid partition is of poor quality. The average silhouette width is 0.13, and there are seventeen taxa with negative silhouette widths. The cluster membership difference for the two-cluster medoid partition and the BDC clusters is 58%. Medoid partitioning at $k=3$ and $k=4$ was similarly poor, with average silhouette widths of 0.15 and 0.14 respectively.

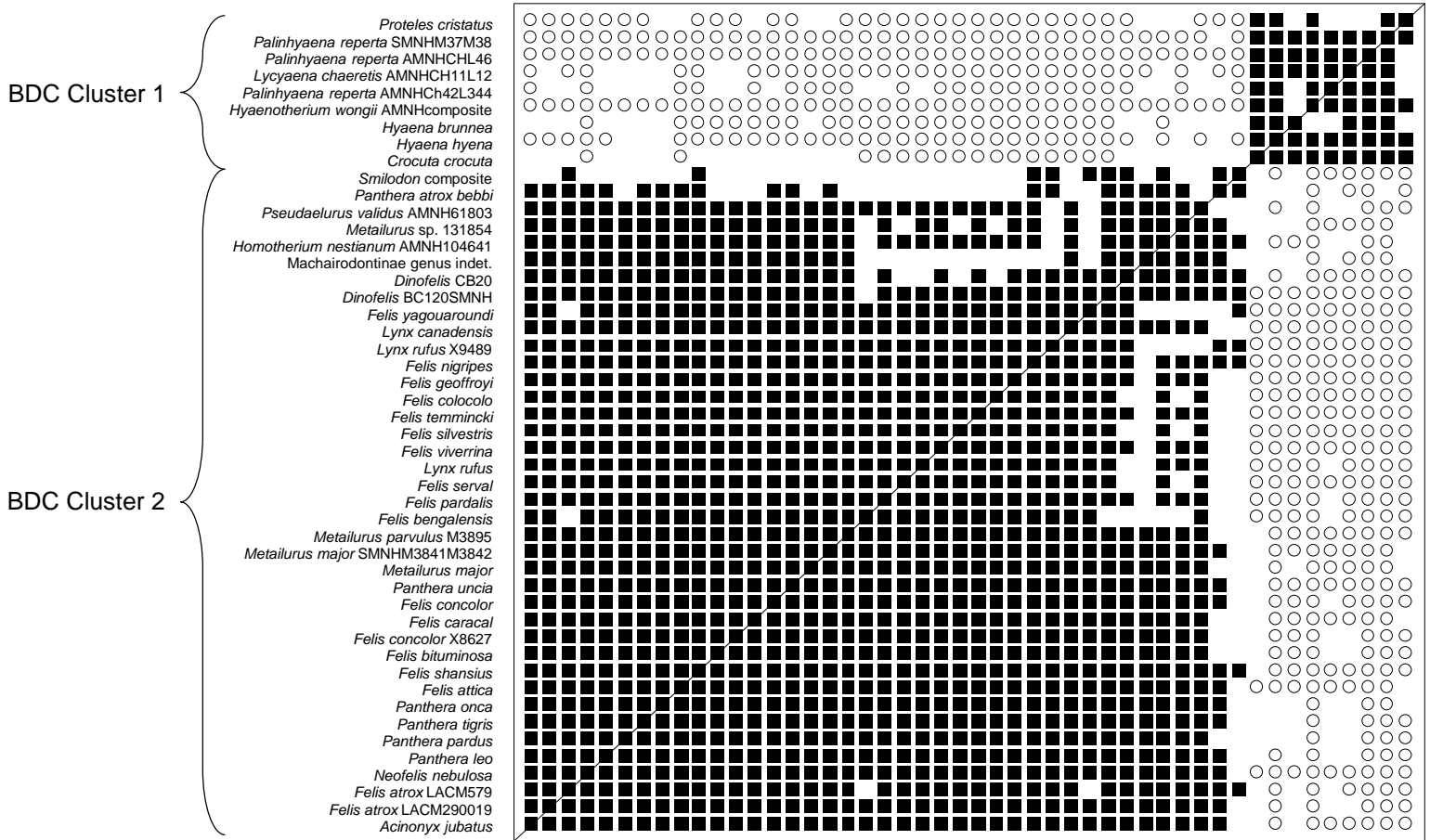
Two-cluster fuzzy analysis produced a partition slightly better than the medoid partition but still not consistent with the BDC results. The average silhouette width was 0.23, and the cluster membership difference between the BDC results and the two-cluster fuzzy analysis was 23%.

Given the consistency between the Spearman and Pearson BDC results, we may reinforce the original conclusion that the felids are a holobaramin. The lack of consistency with the medoid partition or fuzzy analysis is a concern; however, since these results are poor quality, we may reasonably discount them. It is possible that the elongated, nonglobular shape of these clusters prevent effective detection by medoid partition or fuzzy analysis.

Original conclusion: HB

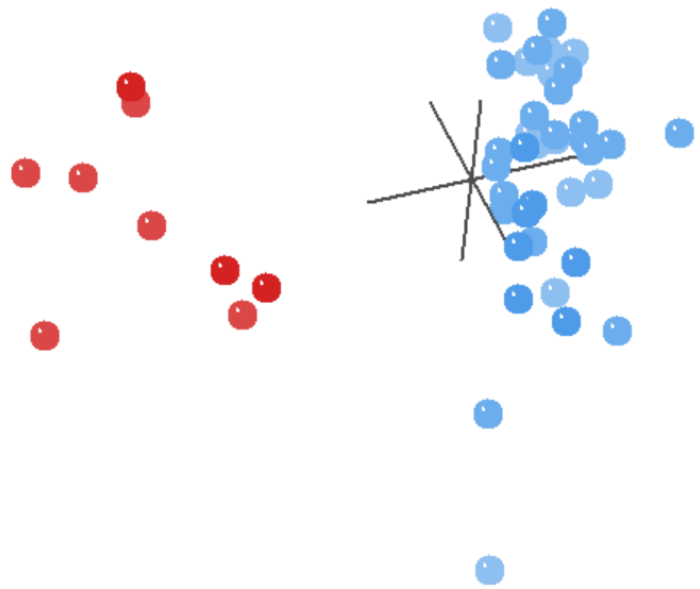
Updated conclusion: HB

Characters: Craniodental



Order Carnivora
Family Felidae

Published taxa	168
Published characters	154
Character relevance	0.75
Taxic relevance	0.5
Taxa used for calculations	48
Characters used for calculations	103
Median bootstrap value	87
F ₉₀	0.46
Stress of 3D MDS	0.32
k _{min}	11
Conclusion	HB



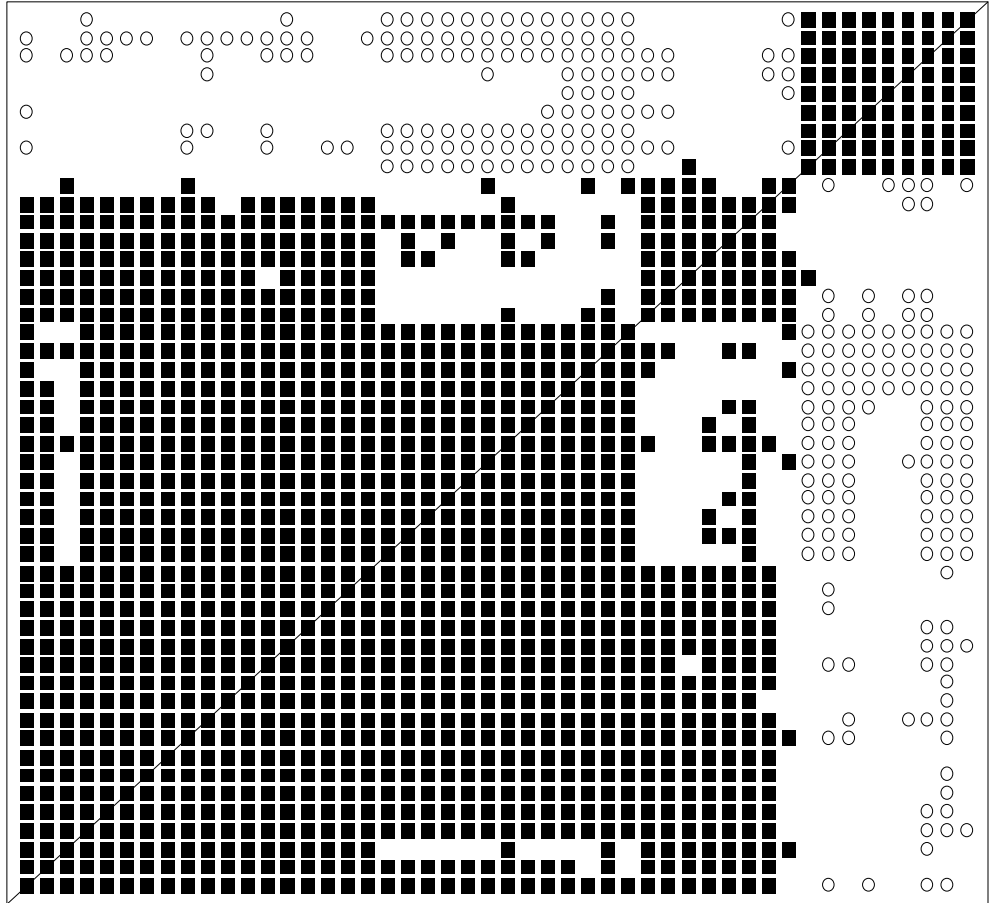
Notes: The published dataset was trimmed to include just the Felidae and Hyaenidae as in Robinson and Cavanaugh's original analysis (1998. Evidence for a holobaraminic origin of the cats. *CRSQ* 35:2-14). BDC and MDS support a discontinuity between the two families. Felidae is likely a holobaramin.

BDC Cluster 1

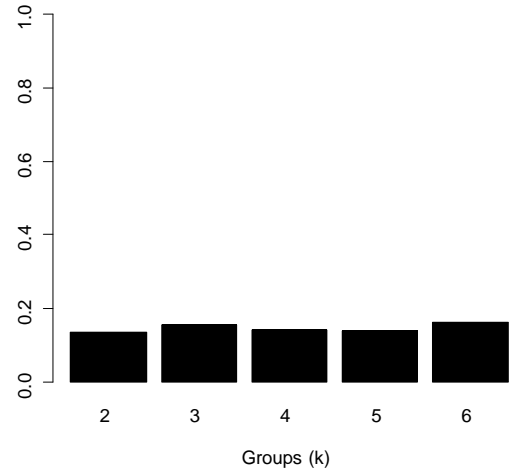
- Proteles cristatus*
- Palinhyena reperta* SMNHM37M38
- Palinhyena reperta* AMNHCHL46
- Lycyaena chaeretic* AMNHCH11L12
- Palinhyena reperta* AMNHCh42L344
- Hyaenotherium wongii* AMNHComposite
- Hyaena brunnea*
- Hyaena hyena*
- Crocuta crocuta*

BDC Cluster 2

- Smilodon compositus*
- Panthera atrox bebbi*
- Pseudaelurus validus* AMNH61803
- Metailurus* sp. 131854
- Homotherium nestianum* AMNH104641
- Machairodontinae* genus indet.
- Dinofelis* CB20
- Dinofelis* BC120SMNH
- Felis yagouaroundi*
- Lynx canadensis*
- Lynx rufus* X9489
- Felis nigripes*
- Felis geoffroyi*
- Felis colocolo*
- Felis temmincki*
- Felis silvestris*
- Felis viverrina*
- Lynx rufus*
- Felis serval*
- Felis pardalis*
- Felis bengalensis*
- Metailurus parvulus* M3895
- Metailurus major* SMNHM3841M3842
- Metailurus major*
- Panthera uncia*
- Felis concolor*
- Felis caracal*
- Felis concolor* X8627
- Felis bituminosa*
- Felis shansius*
- Felis attica*
- Panthera onca*
- Panthera tigris*
- Panthera pardus*
- Panthera leo*
- Neofelis nebulosa*
- Felis atrox* LACM579
- Felis atrox* LACM290019
- Acinonyx jubatus*



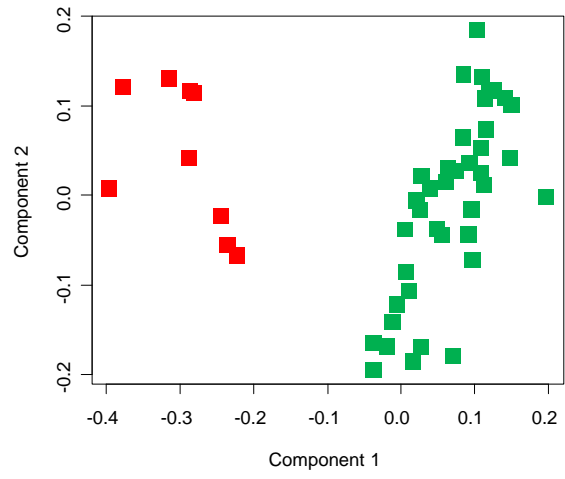
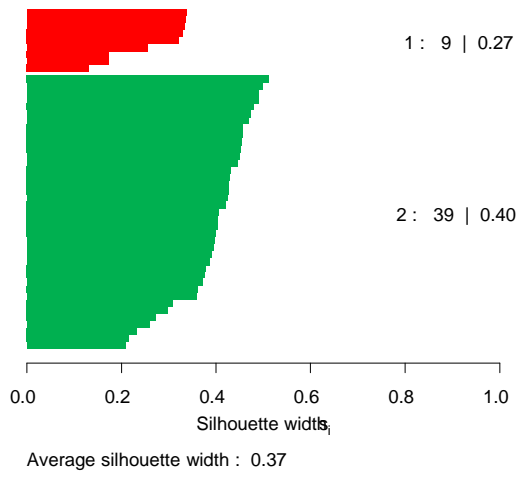
Average Silhouette Widths, Partion Around Medoids



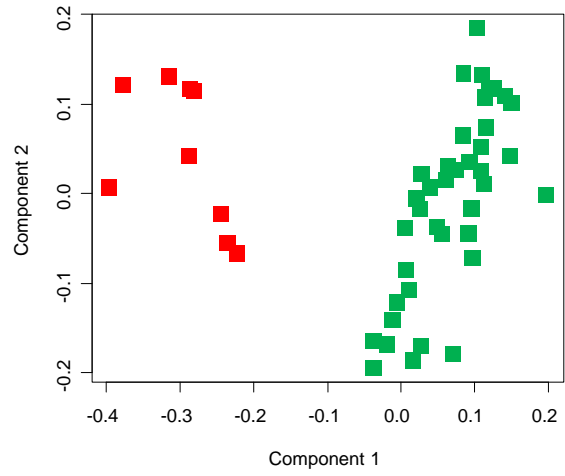
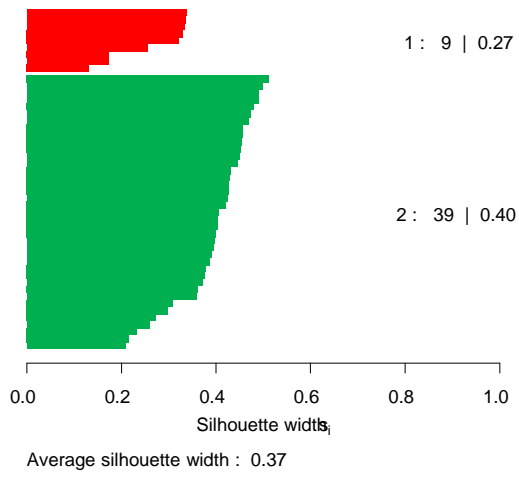
Clade Correspondence: Both BDC clusters contain well more than one taxon. Allowing for the taxonomic sampling difference (taxa were removed from the BDC analysis), both clusters appear as clades in the published phylogeny on p. 82, Figure 13 of Holliday (2007).

Silhouette plot, BDC partitions

Pearson Correlation

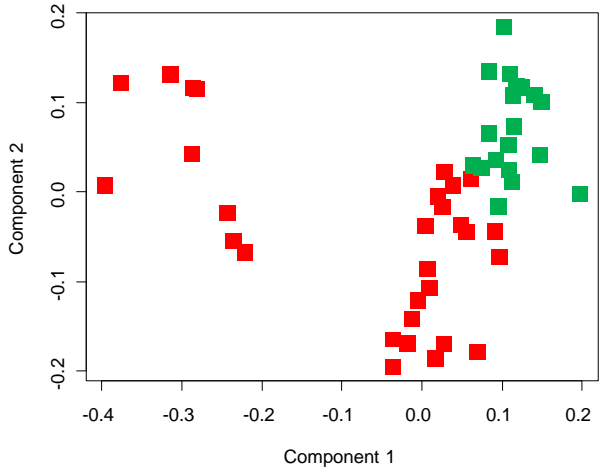
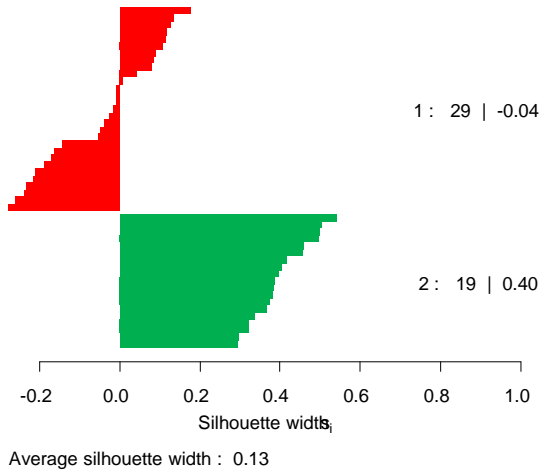


Spearman Correlation

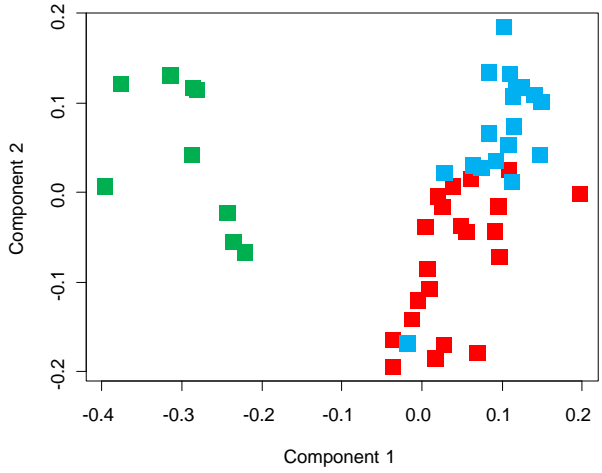
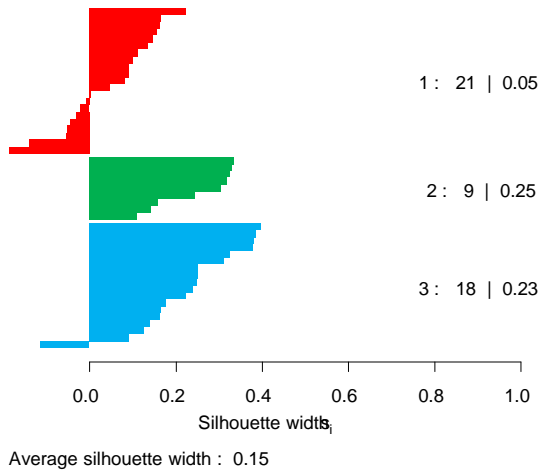


Silhouette plot, Partition Around Medoids

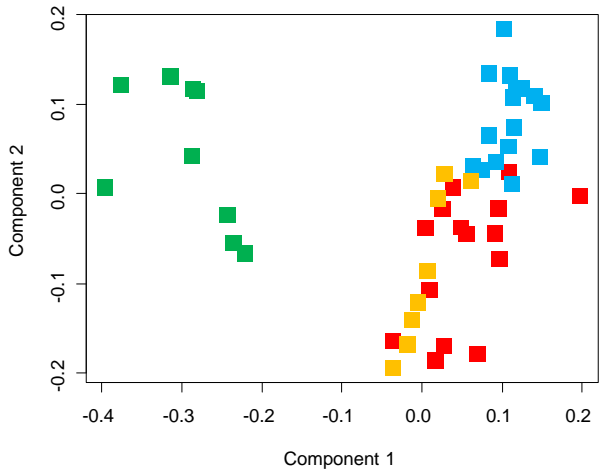
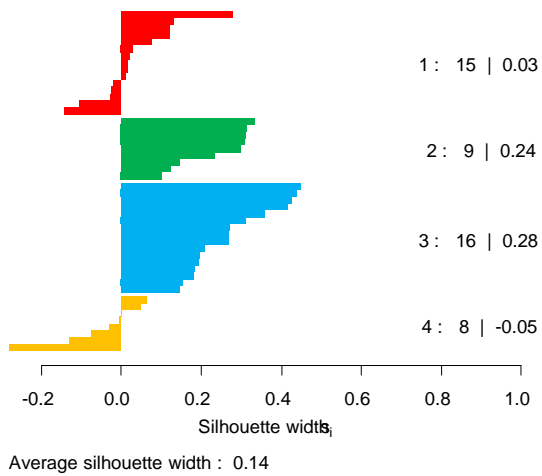
k=2



k=3

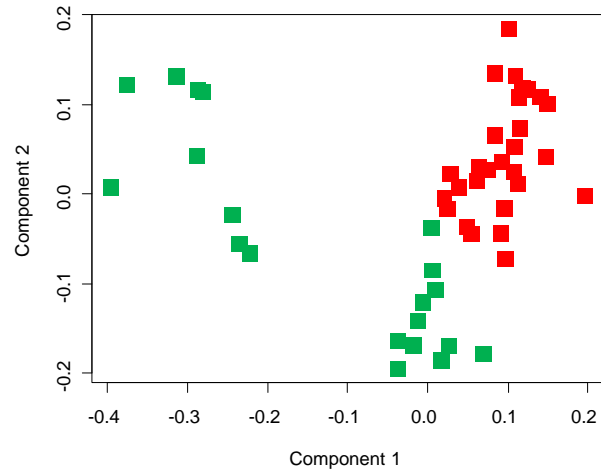
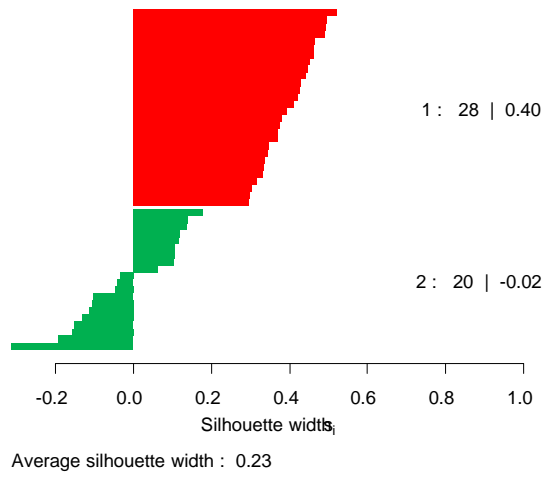


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Felidae

Order Carnivora
Christiansen 2013

Pearson BDC

Negative: 31
Positive: 89
Clusters: 3

Spearman BDC

Negative: 49
Positive: 97
Clusters: 2

Clusterability

Hopkins Statistic: 0.827
Dip test: 0.027
Dip test p-value: 0.263

The Spearman BDC adds eight instances of significant, positive correlation and eighteen instances of significant, negative correlation to the results of the Pearson BDC. These changes merge two clusters from the Pearson BDC into a single cluster in the Spearman BDC. The three-cluster Pearson BDC partition has an average silhouette width of 0.52, and the two-cluster Spearman BDC partition has an average silhouette width of 0.48. The cluster membership difference is 14%.

At $k=2$, the medoid partition agrees exactly with the Spearman BDC clusters, but at $k=3$, medoid partitioning differs from the Pearson BDC clusters. The three-cluster medoid partition has an average silhouette width of 0.49, and the cluster membership difference between the three-cluster medoid partition and the Pearson BDC clusters is 9%. The three-cluster medoid partition actually more closely resembles the Spearman BDC clusters. They differ only by the separation of *Canis lupus* into a separate group.

At $k=2$, fuzzy analysis generates a partition identical to the Spearman BDC clusters, but at $k=3$, fuzzy analysis differs from the Pearson BDC clusters and from the three-cluster medoid partition. When compared to the Pearson BDC clusters, the three-cluster fuzzy analysis had a cluster membership difference of 5%. The three-cluster fuzzy analysis has an average silhouette width of 0.48, and one taxon (*Pseudaelurus*) with a strongly negative silhouette width.

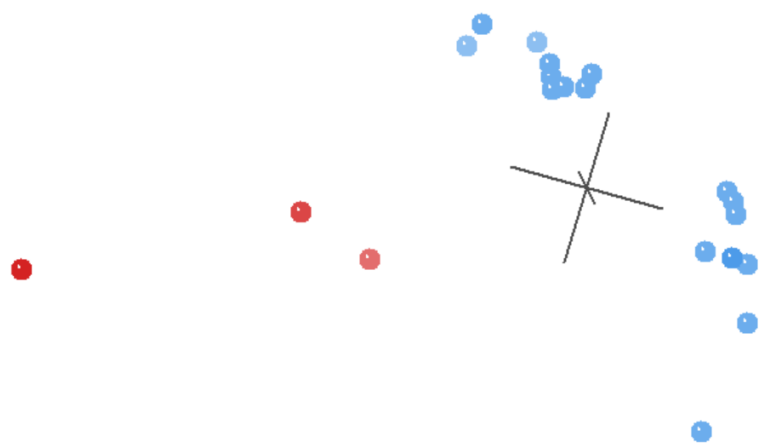
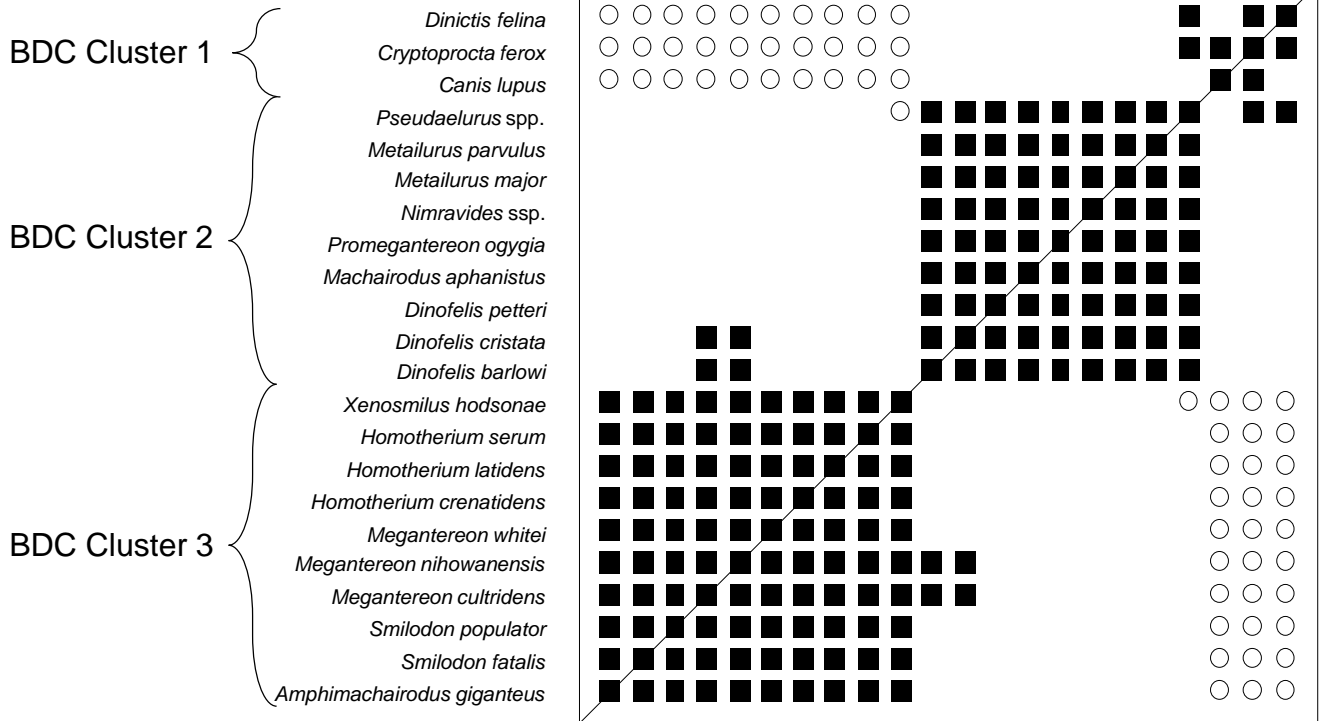
The original results prompted the judgment that Felidae, including the Machairodontinae, constituted a holobaramin. This was based on significant, negative correlation observed between the outgroup taxa and the crown Machairodontinae and significant, positive correlation observed between two species of *Dinofelis* and two species of *Megantereon*, which connected two evident subgroups of the Felidae. In the Spearman BDC, these correlation patterns have substantially changed. Thirteen taxon pairs involving members of the outgroup and ingroup now exhibit significant, positive BDC. The significant, positive correlation connecting the two subgroups of Felidae have disappeared, and in their place, there are eighteen additional instances of significant, negative correlation between these felid subgroups. The agreement of the medoid partition and fuzzy analysis with the Spearman but not the Pearson BDC reinforces the legitimacy of the Spearman clusters.

Nevertheless, the MDS appears to show four clusters, two of ingroup taxa and two of outgroup taxa. Grouping the ingroup and outgroup taxa together seems to create an artificially spread out cluster. It is possible if the outgroup were reduced by eliminating the outlying *Canis lupus* that the results of Spearman BDC, medoid partition, and fuzzy analysis could support the original conclusion. Currently, these results support either recognizing the Machairodontinae as a holobaramin or simply judging these data as inconclusive.

Original conclusion: HB

Updated conclusion: Inconclusive

Characters: Craniodental



Order Carnivora
Family Felidae

Published taxa	22
Published characters	50
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	22
Characters used for calculations	50
Median bootstrap value	85
F ₉₀	0.41
Stress of 3D MDS	0.12
k _{min}	6
Conclusion	HB

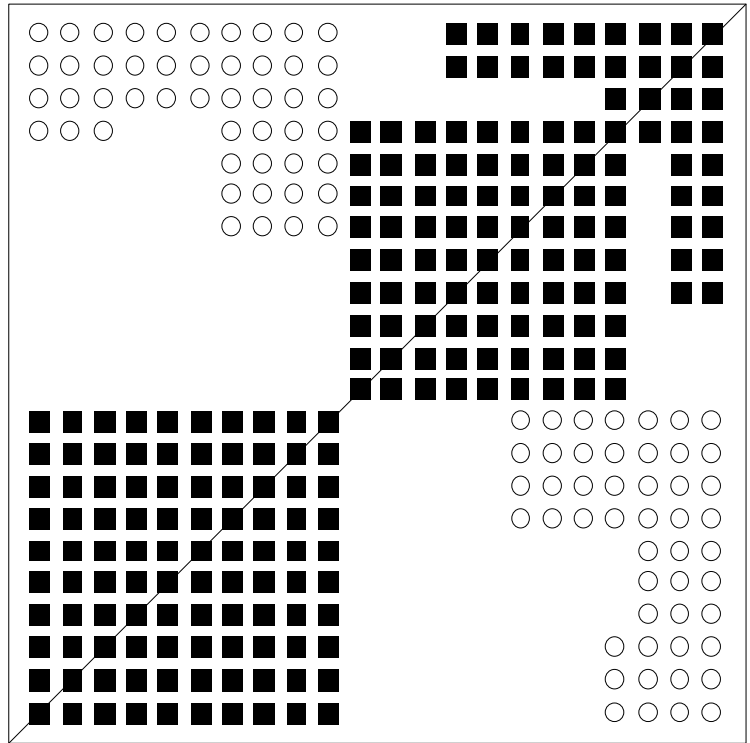
Notes: Machairodontinae is the focus of this character set, but there are four extinct genera recognized as Felinae by McKenna and Bell (1997): *Pseudaelurus*, *Metailurus*, *Nimravides*, and *Dinofelis*. Results show the felids well-separated from outgroup taxa in MDS and BDC results. BDC indicates two groups of felids with positive BDC between them (but with poor bootstrap values between them). Felidae is likely a holobaramin.

BDC Cluster 2

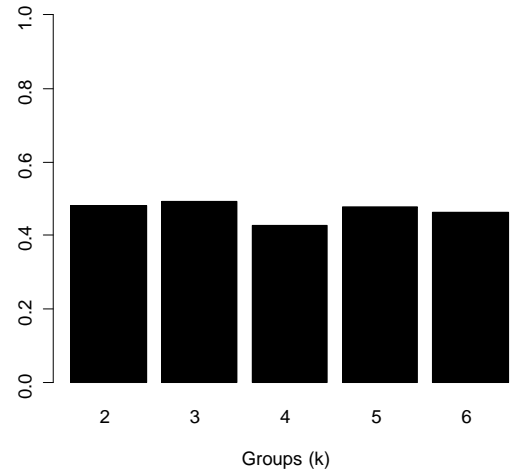
- Dinictis felina*
- Cryptoprocta ferox*
- Canis lupus*
- Pseudaelurus spp.*
- Metailurus parvulus*
- Metailurus major*
- Nimravides ssp.*
- Promegantereon ogygia*
- Machairodus aphanistus*
- Dinofelis petteri*
- Dinofelis cristata*
- Dinofelis barlowi*

BDC Cluster 3

- Xenosmilus hodsonae*
- Homotherium serum*
- Homotherium latidens*
- Homotherium crenatidens*
- Megantereon whitei*
- Megantereon nihowanensis*
- Megantereon cultridens*
- Smilodon populator*
- Smilodon fatalis*
- Amphimachairodus giganteus*



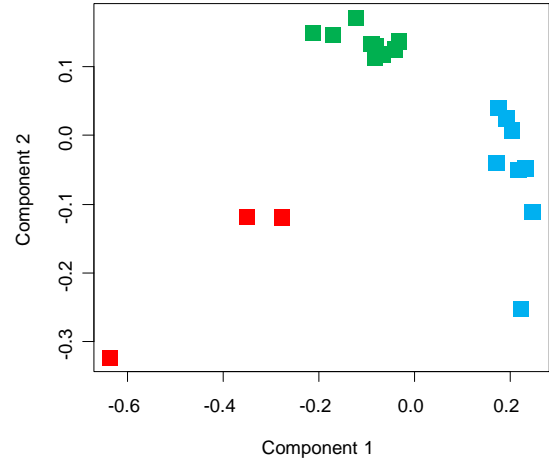
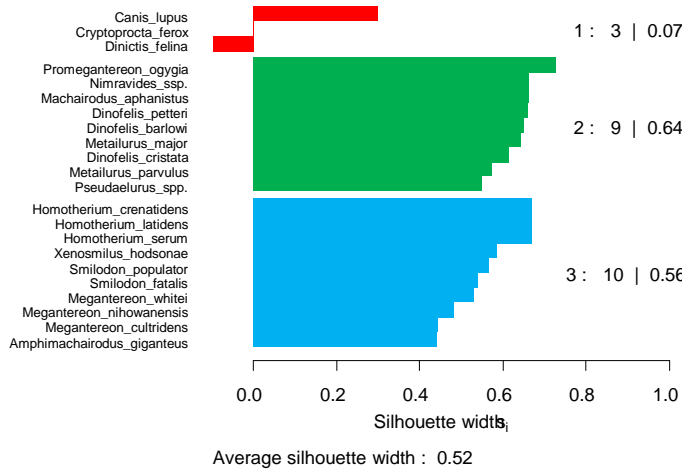
Average Silhouette Widths, Partion Around Medoids



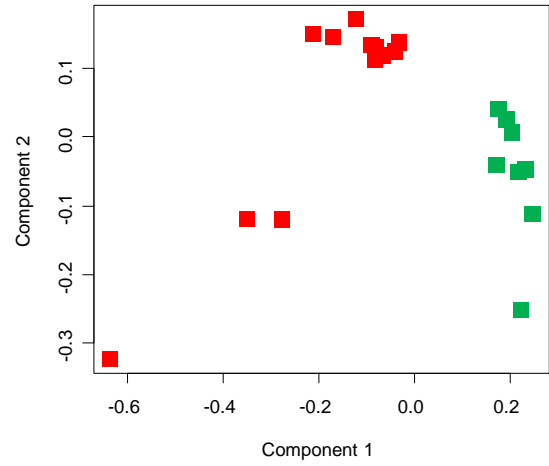
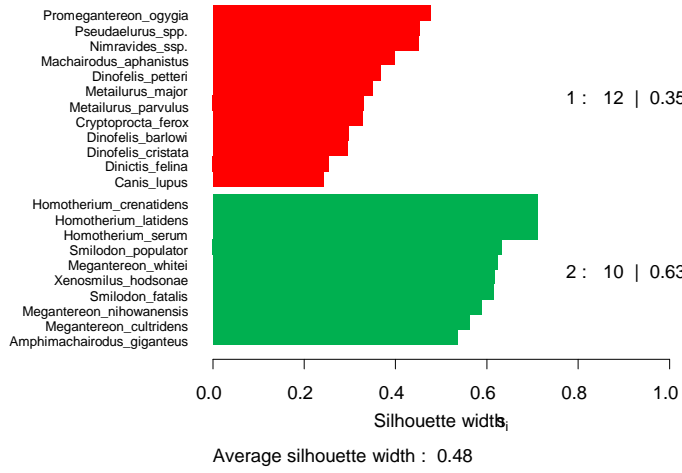
Clade Correspondence: All three BDC clusters contain more than one taxon. Clusters 1 and 3 are clades in the phylogeny in Figure 2 of Christiansen (2013). Cluster 2 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

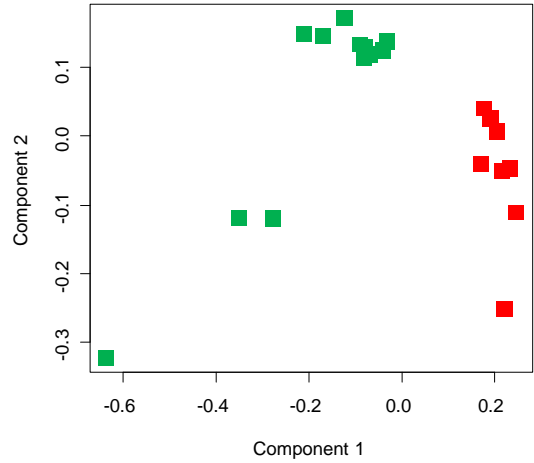
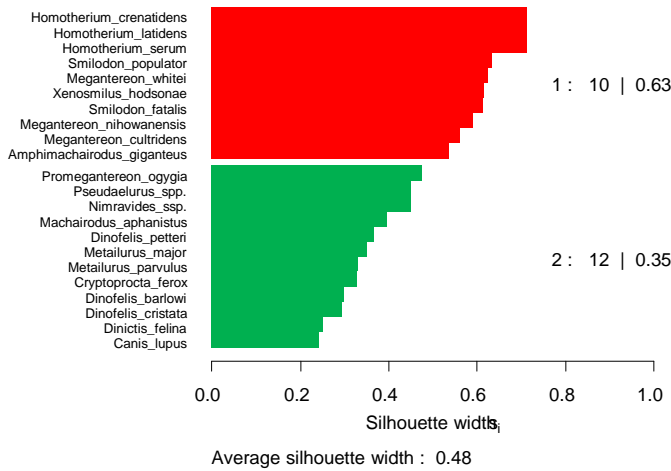


Spearman Correlation

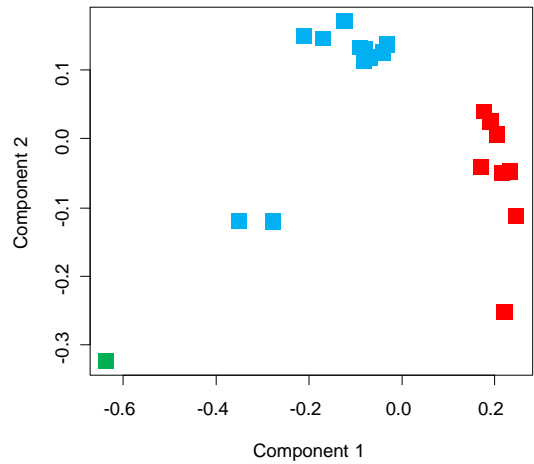
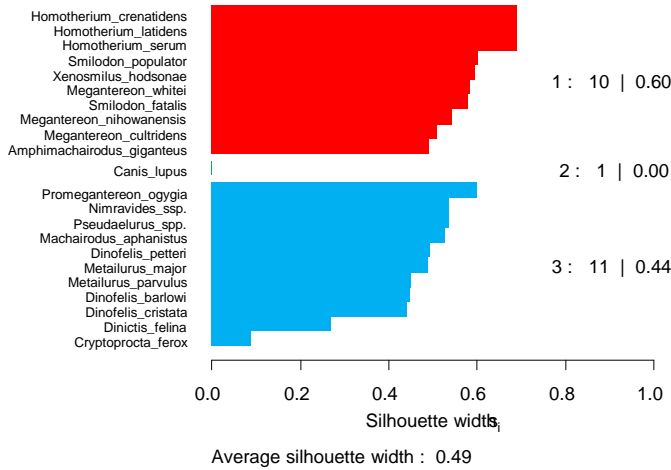


Silhouette plot, Partition Around Medoids

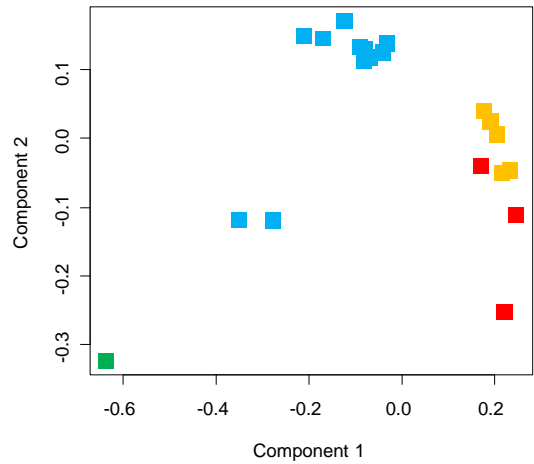
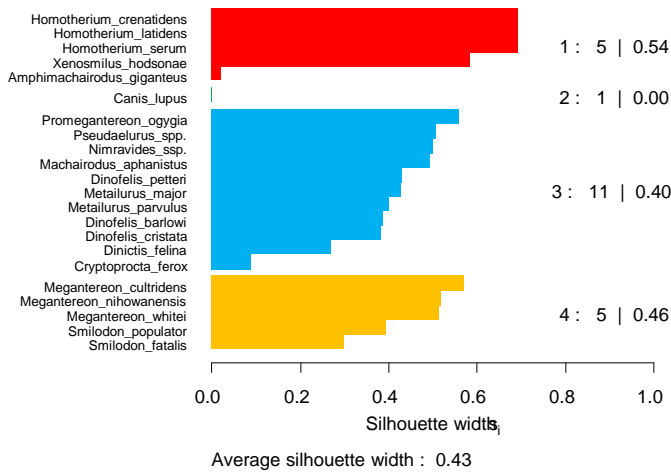
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k=3

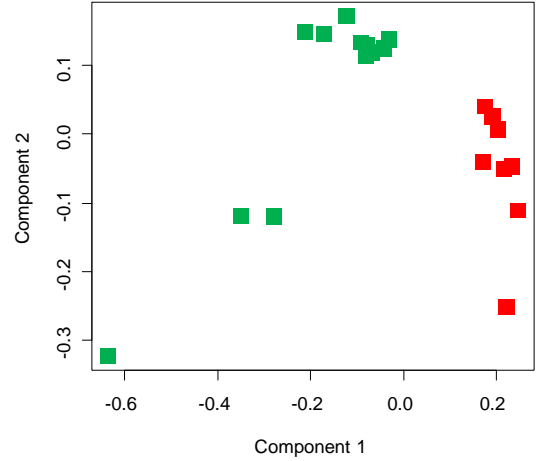
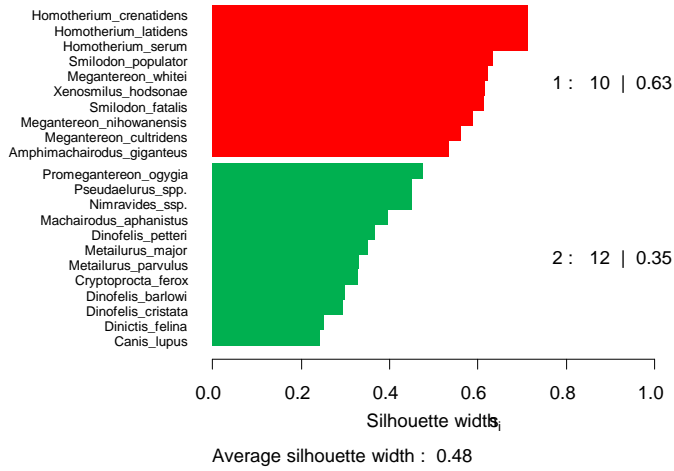


k=4

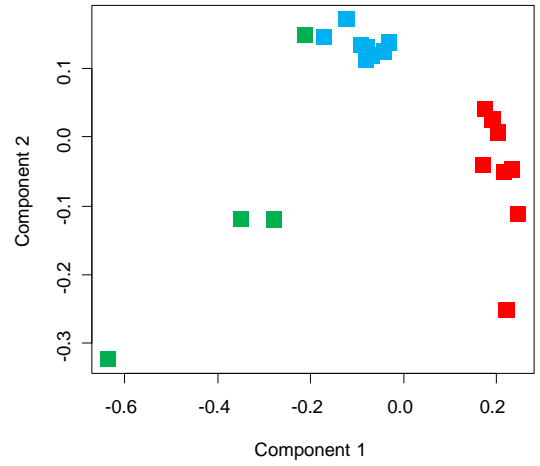
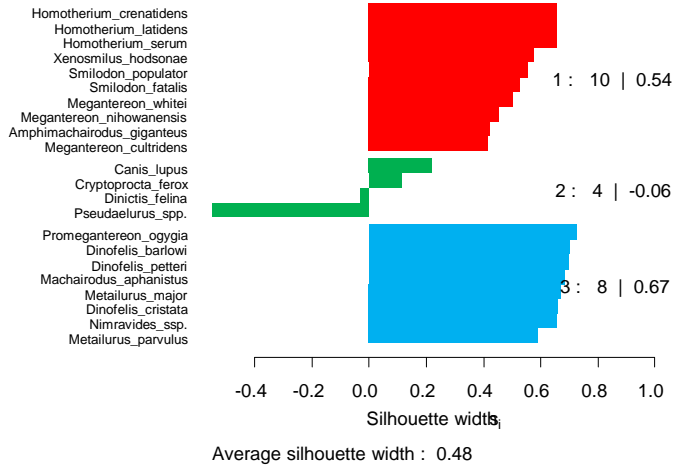


Silhouette plot, Fuzzy Analysis

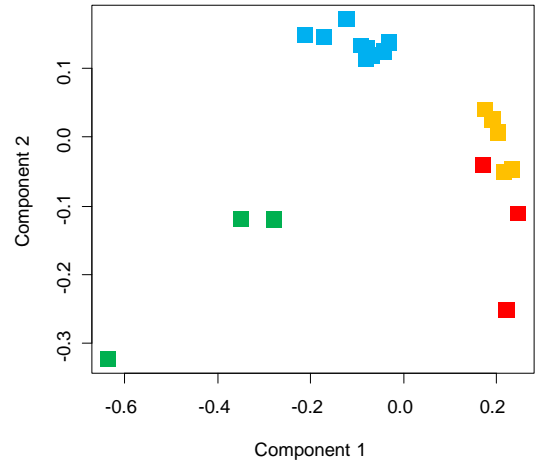
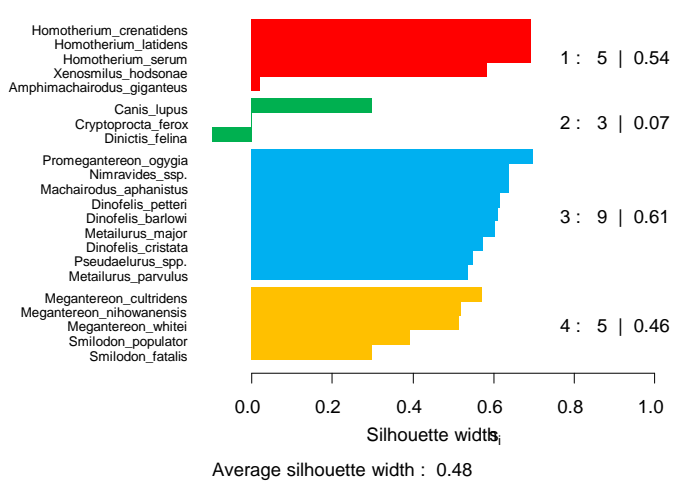
k=2



k=3



k=4



Subfamily Barbuorofelinae

Order Carnivora
Morlo et al. 2004

Pearson BDC
Negative: 18
Positive: 8
Clusters: 3

Clusterability
Hopkins Statistic: 0.729
Dip test: 0.052
Dip test p-value: 0.476

Spearman BDC
Negative: 16
Positive: 14
Clusters: 2

The Spearman BDC results add six instances of significant, positive BDC that reduces the number of clusters from three in the Pearson BDC to two in the Spearman BDC. The average silhouette width for the three-cluster Pearson BDC results was 0.5 and for the two-cluster Spearman BDC results was 0.49. The cluster membership difference between these two partitions was 20%.

Medoid partitioning at k=3 agrees exactly with the Pearson BDC clusters. At k=2, the medoid partition differs by a single taxon from the Spearman BDC clusters. Moving *Prosansanosmilus eggeri* to the other cluster results in a strongly negative silhouette width for *Prosansanosmilus* and an average silhouette width of 0.4.

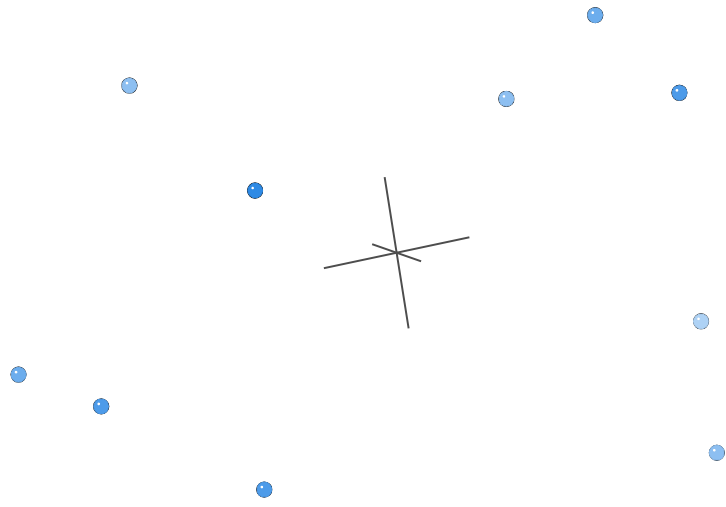
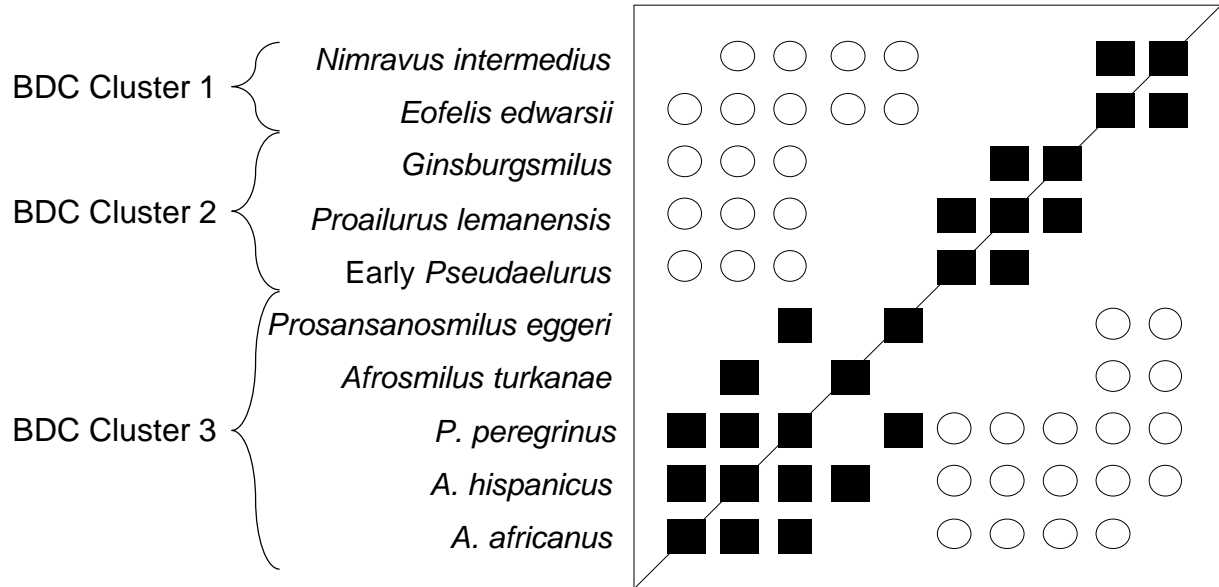
At k=3, the fuzzy analysis also agrees exactly with the Pearson BDC clusters. At k=2, the fuzzy partition is the same as the Spearman BDC.

The original conclusion cited poor bootstrap values and a lack of obvious discontinuity to reserve judgment on these results. Here, we find good agreement with the Pearson BDC clusters, and the fuzzy analysis also supports the Spearman BDC clustering. Further, the two-cluster medoid partition also supports the Spearman BDC clustering by showing the poor fit that results from moving *Prosansanosmilus* to the other cluster. Taken together, these analyses support recognizing one or two holobaramins in these taxa. One group consists of *Nimravus*, *Eofelis*, *Proailurus*, early *Pseudaelurus*, and the other group consists of two species of *Prosansanosmilus* and three species of *Afrosmilus*. The wide dispersal of the taxa in the MDS results suggests that these clusters may be artificial, but the present results support recognizing a provisional discontinuity between these groups.

Original conclusion: Inconclusive
Updated conclusion: HB?

Morlo, M., S. Peigne, and D. Nagel. 2004. A new species of *Prosansanosmilus*: implications for the systematic relationships of the family Barbourfelidae new rank (Carnivora, Mammalia). *Zoological Journal of the Linnean Society* 140:43-61.

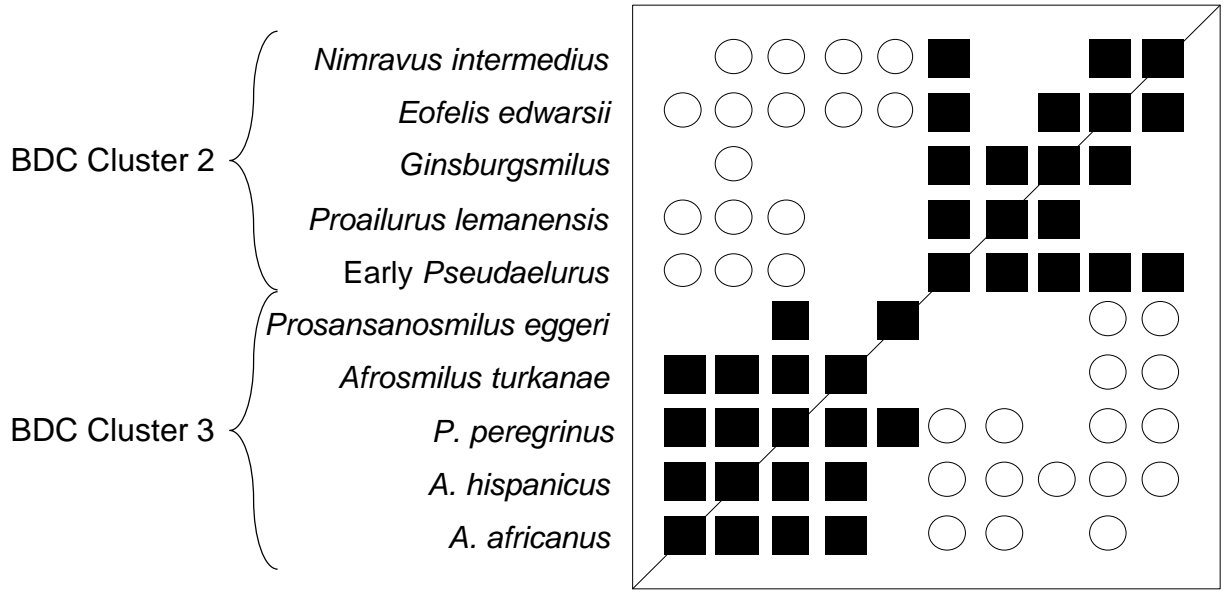
Characters: Dental



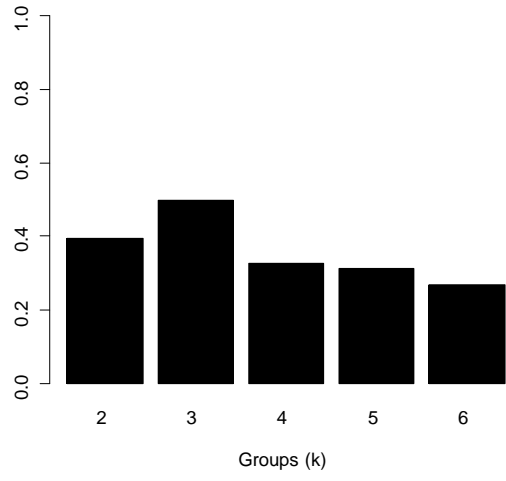
Order Carnivora
Subfamily Barbourfelinae

Published taxa	11
Published characters	22
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	10
Characters used for calculations	16
Median bootstrap value	71
F ₉₀	0.11
Stress of 3D MDS	0.1
k _{min}	3
Conclusion	Inc

Notes: The BDC results have poor bootstrap values, and the MDS reveals a diffuse distribution of taxa. There is no evidence of discontinuity.



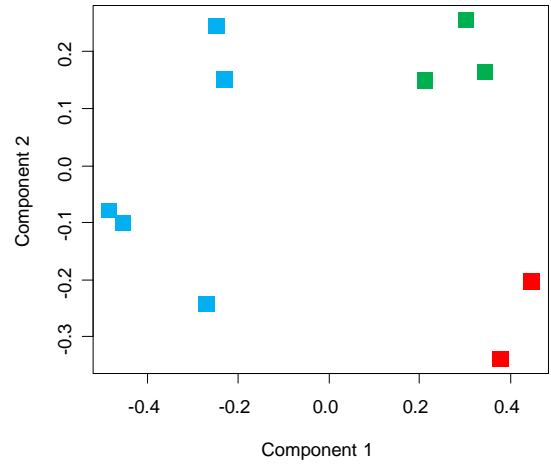
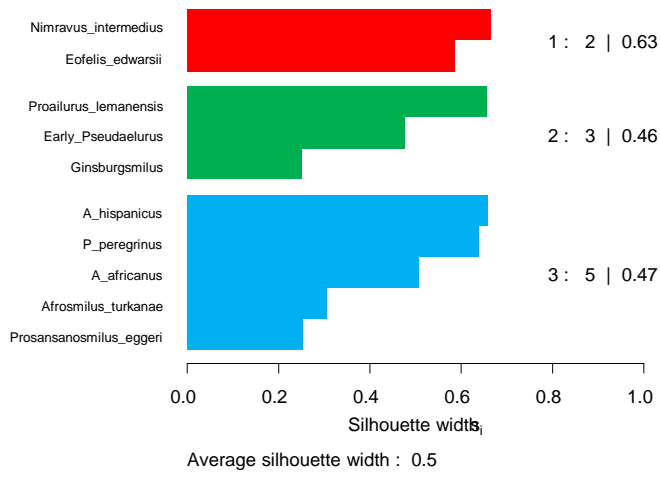
Average Silhouette Widths, Partion Around Medoids



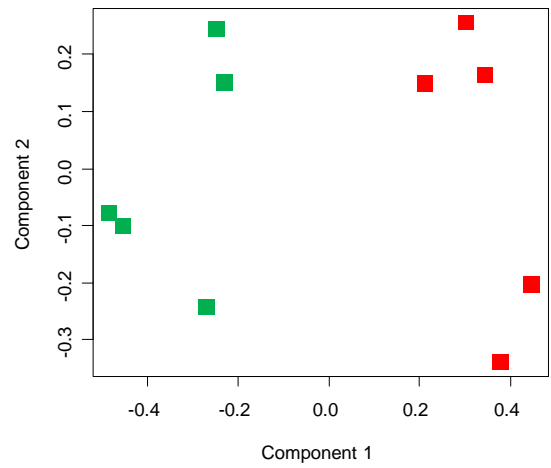
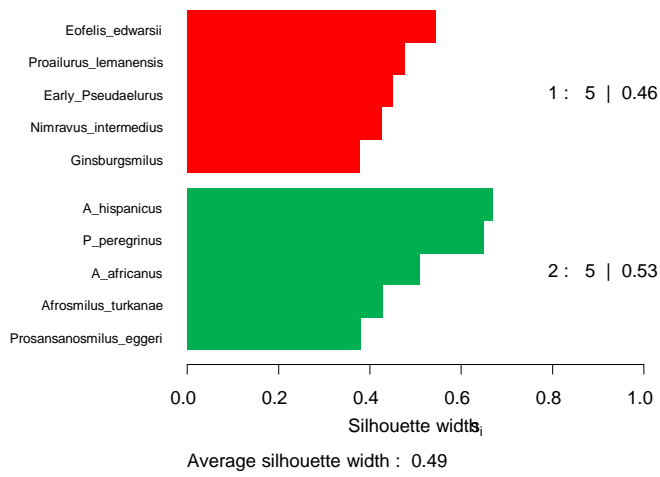
Clade Correspondence: All three BDC clusters contain two or more taxa. Clusters 1 and 3 are monophyletic in Figure 4 of Morlo et al. (2004), but cluster 2 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

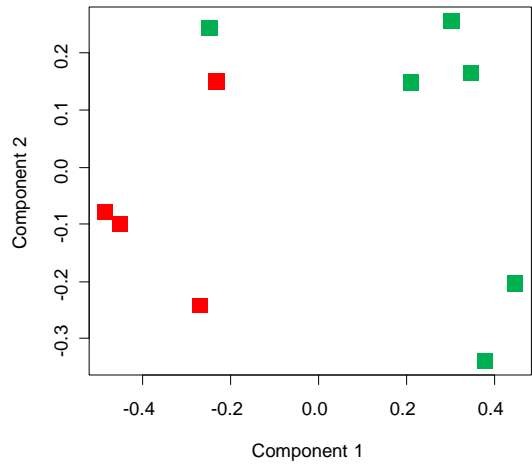
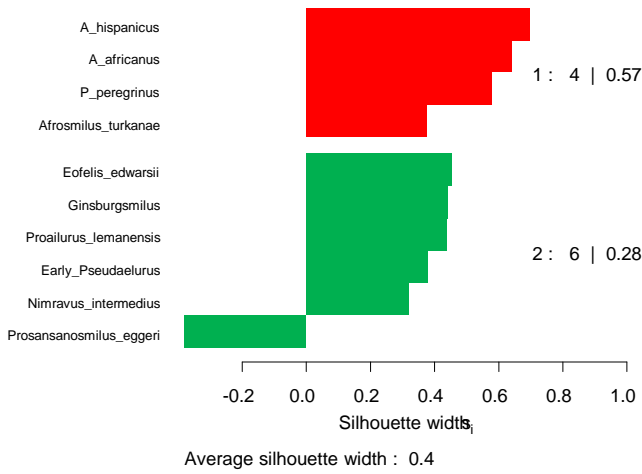


Spearman Correlation

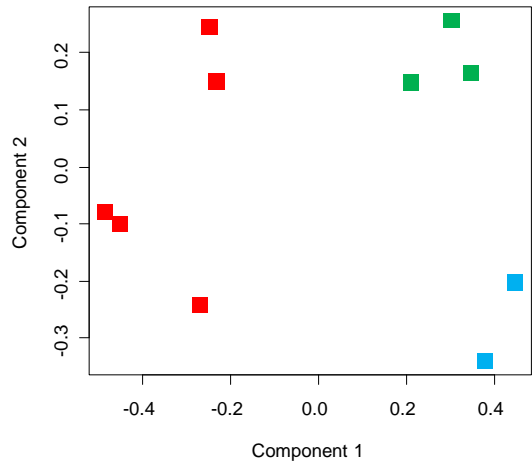
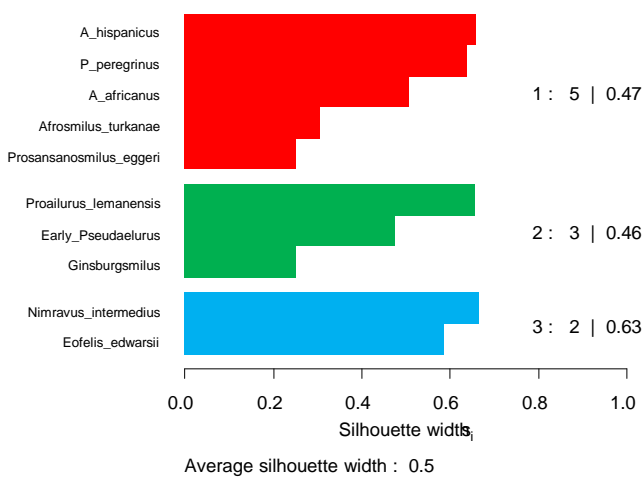


Silhouette plot, Partition Around Medoids

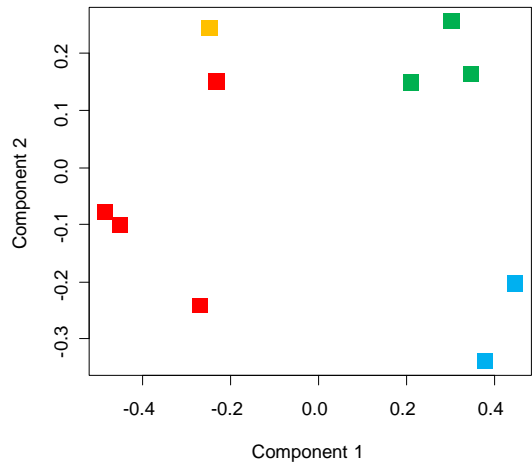
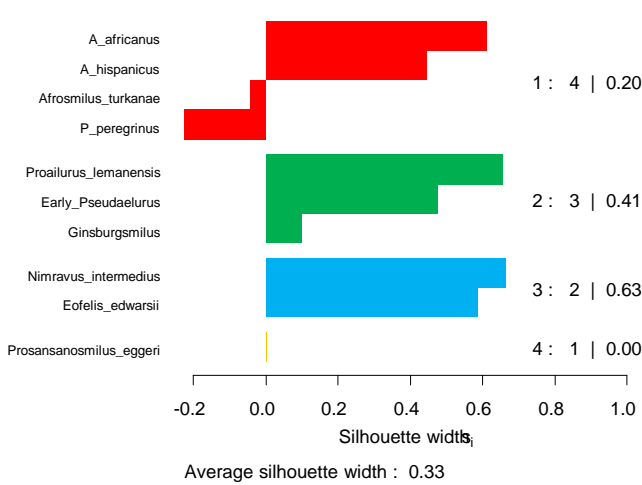
k=2



k=3

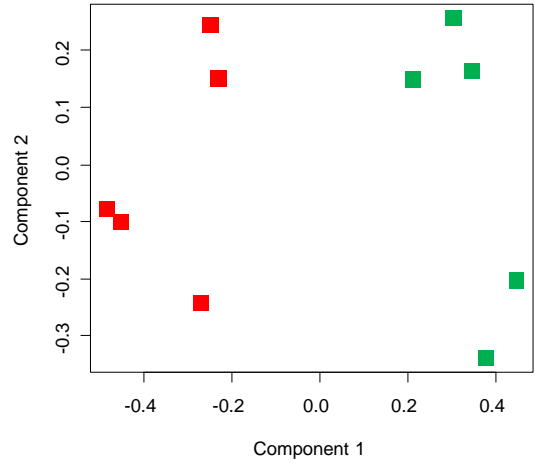
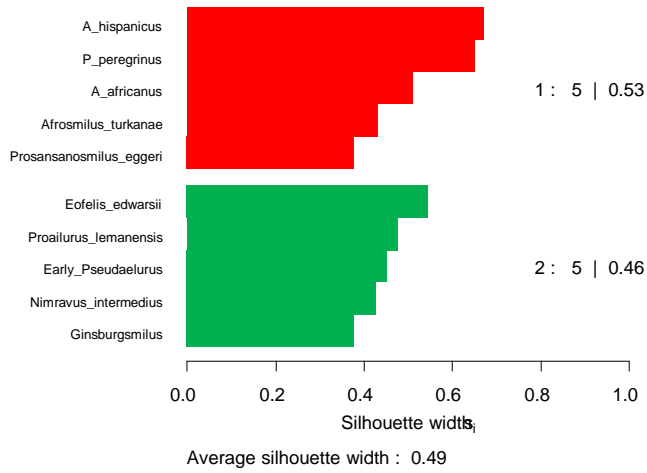


k=4

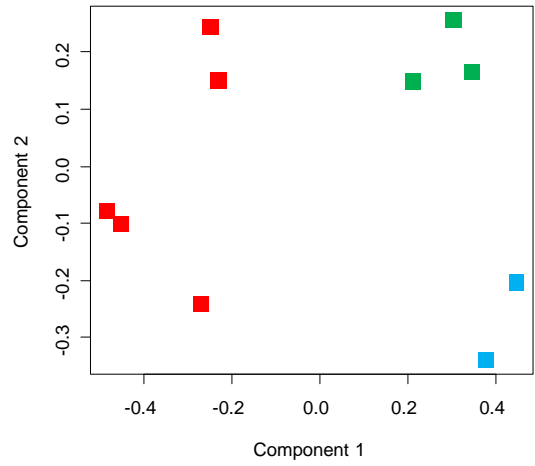
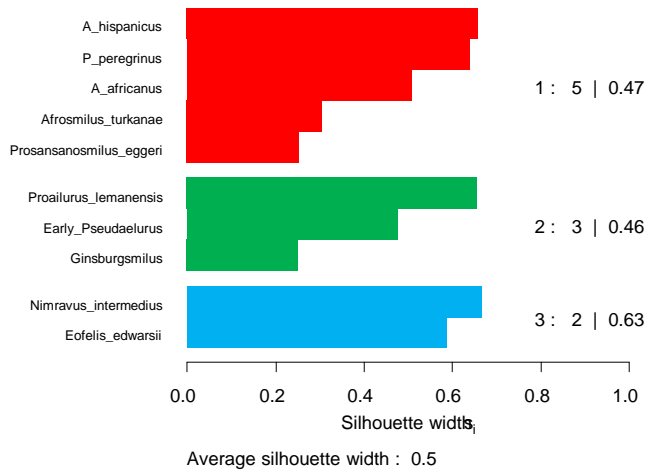


Silhouette plot, Fuzzy Analysis

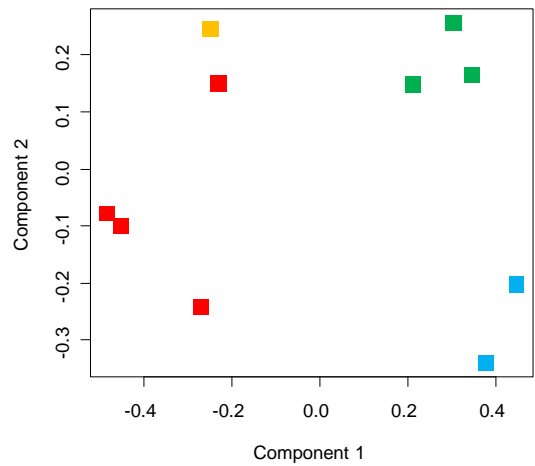
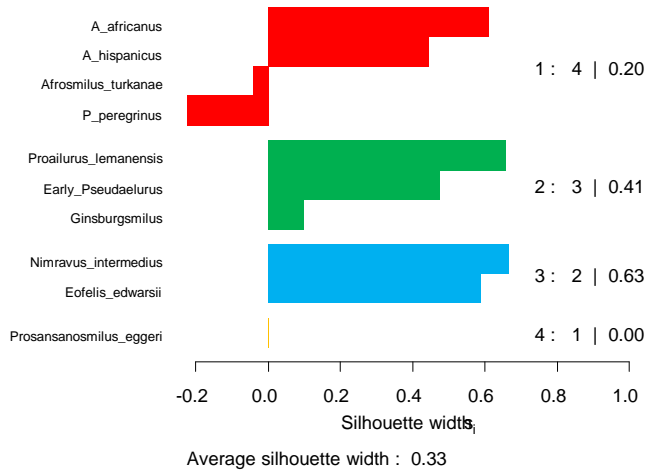
k=2



k=3



k=4



Family Ursidae

Order Carnivora

Abella 2012

Pearson BDC

Negative: 19

Positive: 65

Clusters: 3

Clusterability

Hopkins Statistic: 0.778

Dip test: 0.023

Dip test p-value: 0.803

Spearman BDC

Negative: 19

Positive: 77

Clusters: 3

Three different clusters can be recognized in the original Pearson BDC results. The Spearman BDC results add twelve instances of significant, positive correlation but the cluster partition is the same. The average silhouette width for this partition is 0.42.

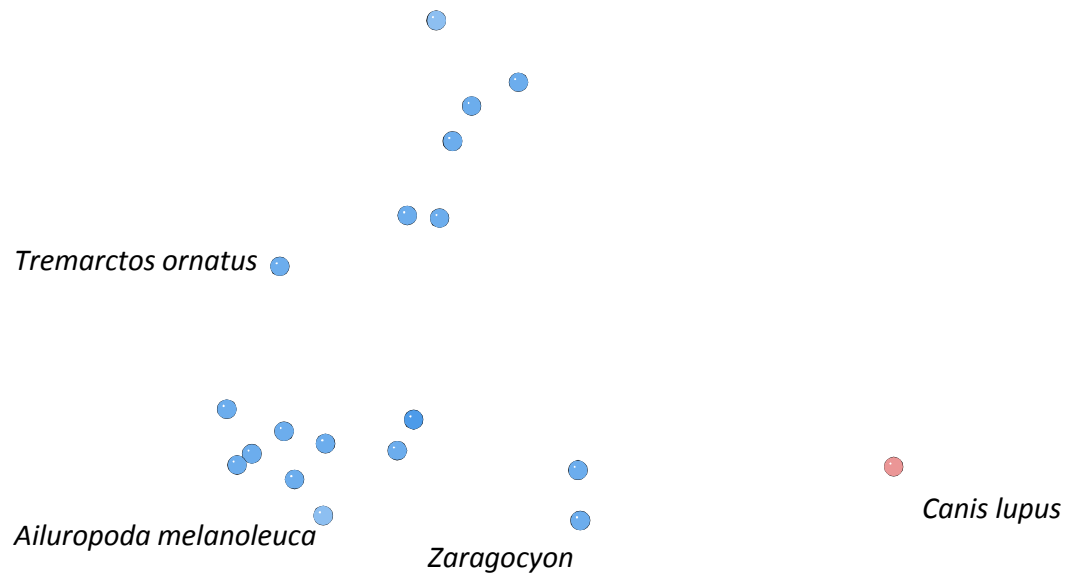
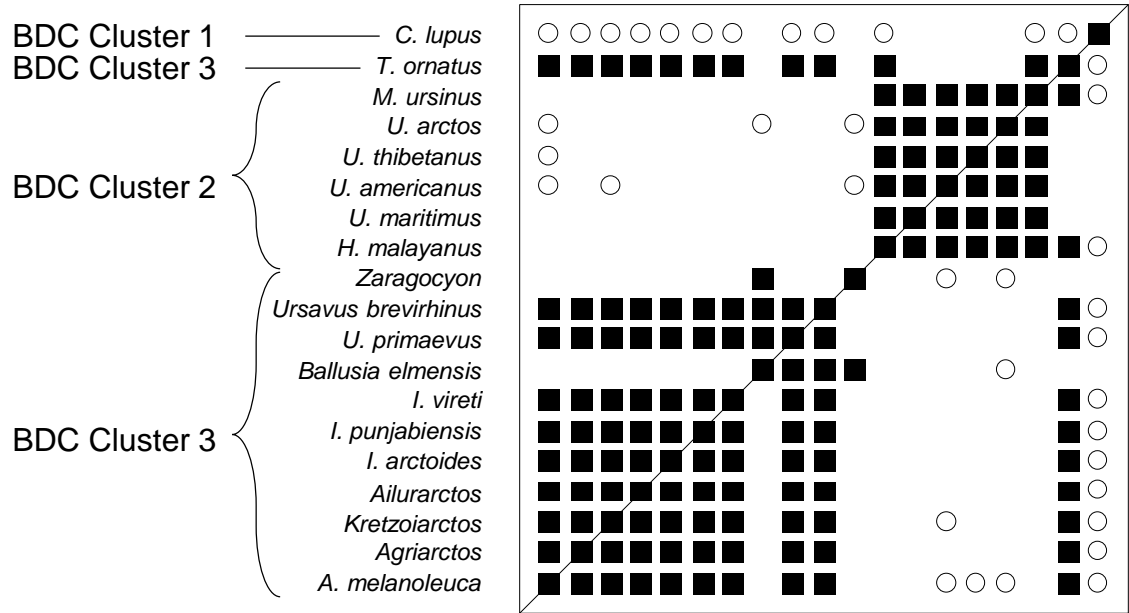
At k=3, medoid partitioning resembles the BDC results (20% cluster membership difference), but places four ursids in the same cluster with the outgroup *Canis lupus*. The average silhouette width for the three-cluster medoid partition is 0.4. Fuzzy analysis at k=3 agrees exactly with the medoid partition.

The original judgment of Ursidae as a tentative holobaramin was based significant, negative BDC between *Canis lupus* and twelve ursids and on the position of *Tremarctos* as a sort of intermediate between the two clusters of ursids. *Tremarctos* shared significant, positive BDC with members of both clusters. In the Spearman BDC results, the number of significant, negative correlations between *Canis* and ursids is reduced to eight. With the medoid partition and fuzzy analysis consistently grouping *Canis* in the same cluster with four ursids, we may downgrade the uncertain holobaraminic status of Ursidae to simply inconclusive.

Original conclusion: HB?

Updated conclusion: Inconclusive

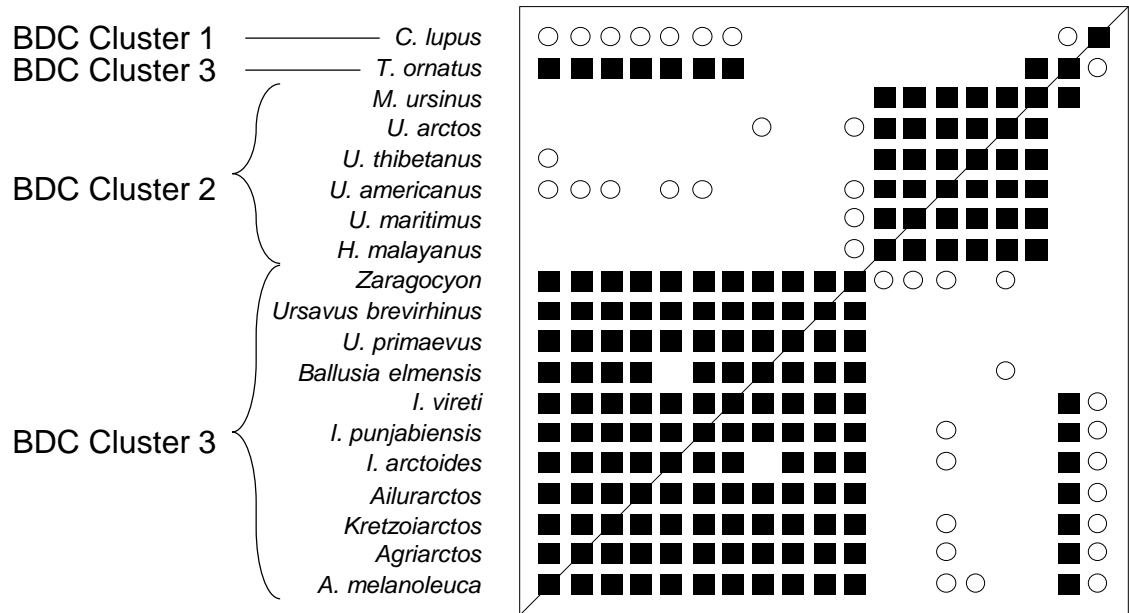
Characters: Craniodental



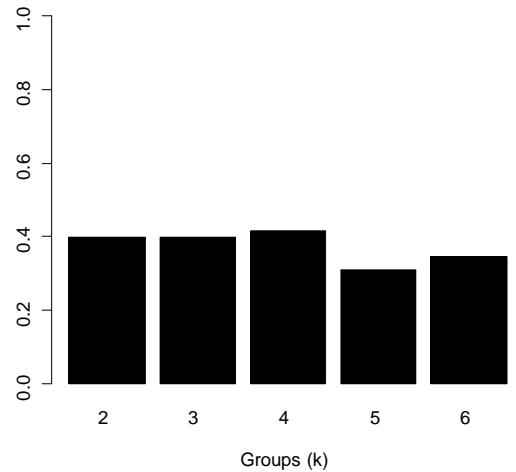
Order Carnivora
Family Ursidae

Published taxa	19
Published characters	82
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	19
Characters used for calculations	53
Median bootstrap value	82
F ₉₀	0.23
Stress of 3D MDS	0.14
k _{min}	5
Conclusion	HB?

Notes: Ursidae is well-separated from the outgroup taxon *Canis lupus* in both BDC and MDS results. Within the group, ursids form two groups that are connected only by the spectacled bear *Tremarctos ornatus*, which also appears in an intermediate position in the MDS results. Ursidae appears to be a holobaramin.



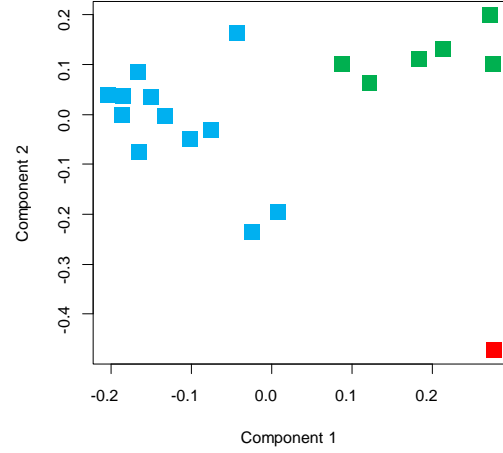
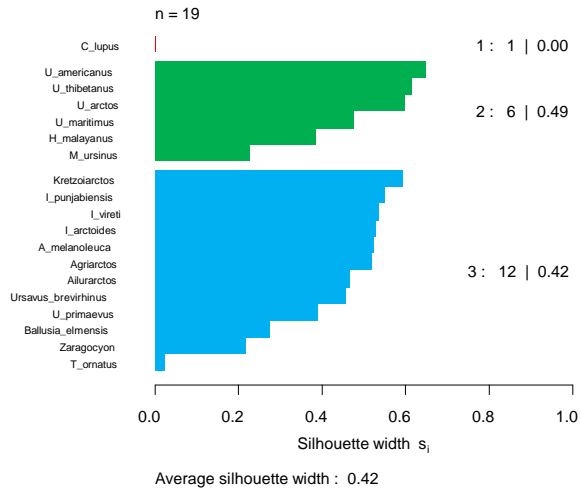
Average Silhouette Widths, Partion Around Medoids



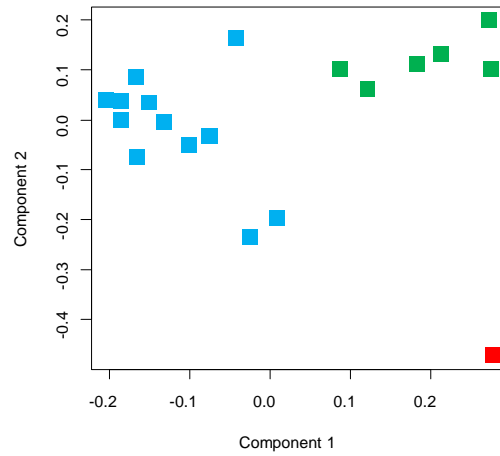
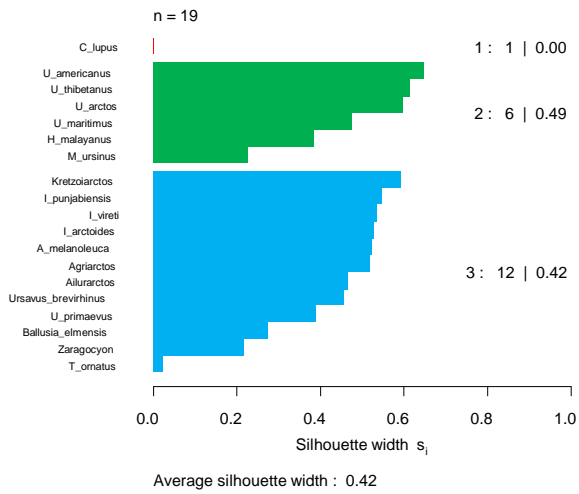
Clade Correspondence: Two of the three BDC clusters contain more than one taxon each. Only cluster 3 appears as a clade in the phylogeny of Figure 3 (Abella et al. 2012). The other cluster is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

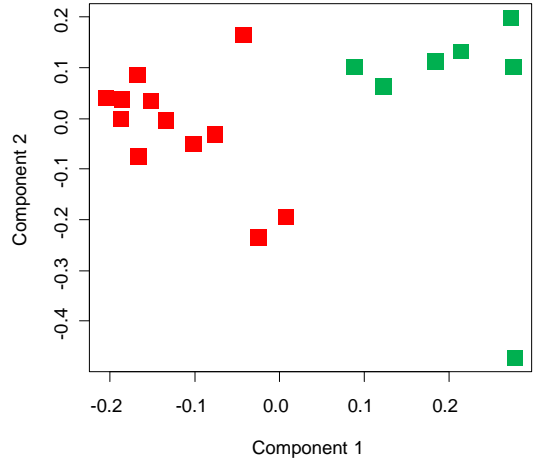
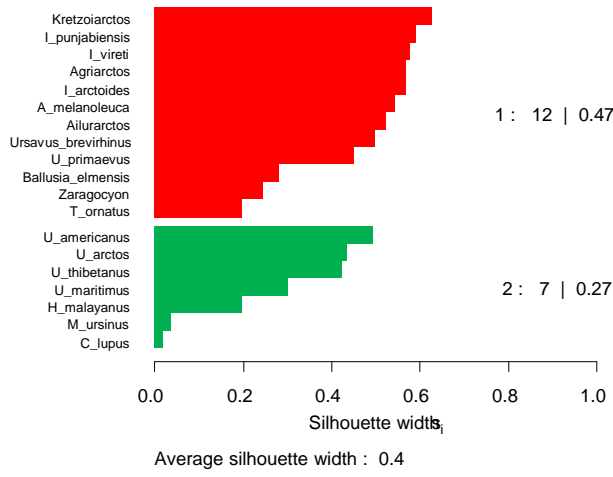


Spearman Correlation

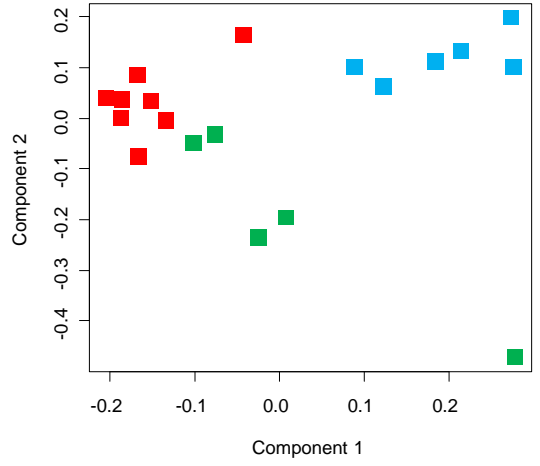
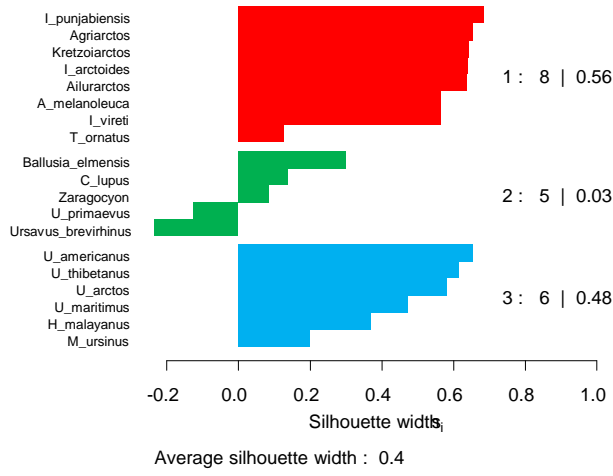


Silhouette plot, Partition Around Medoids

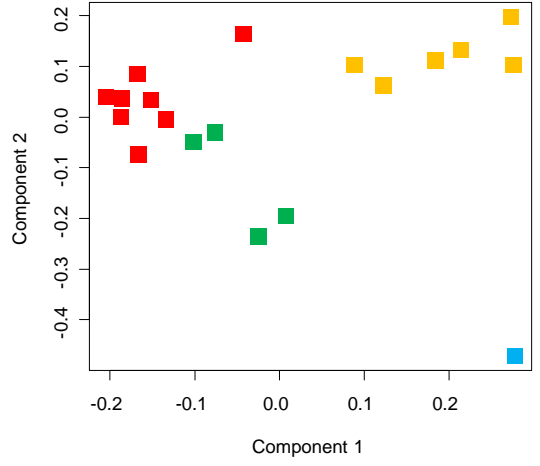
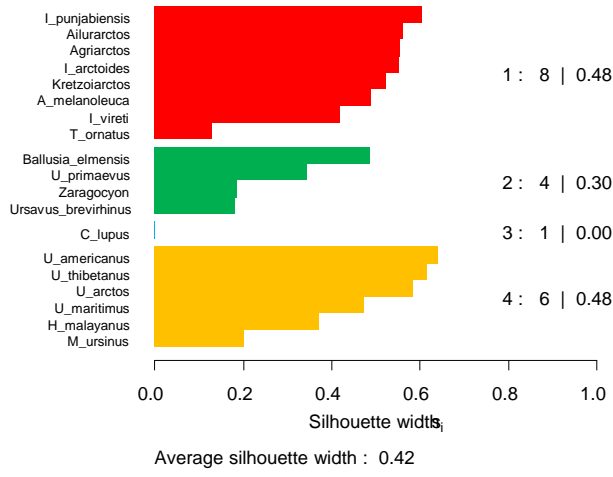
k=2



k=3

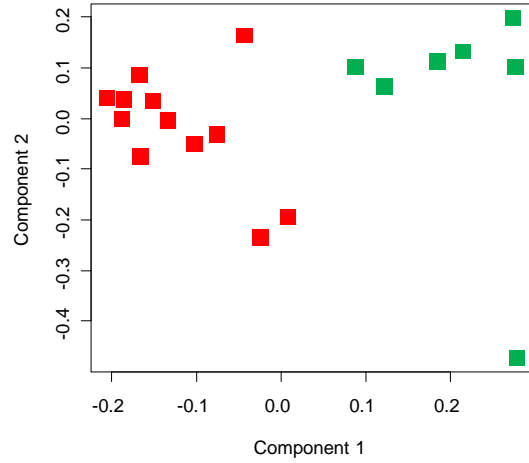
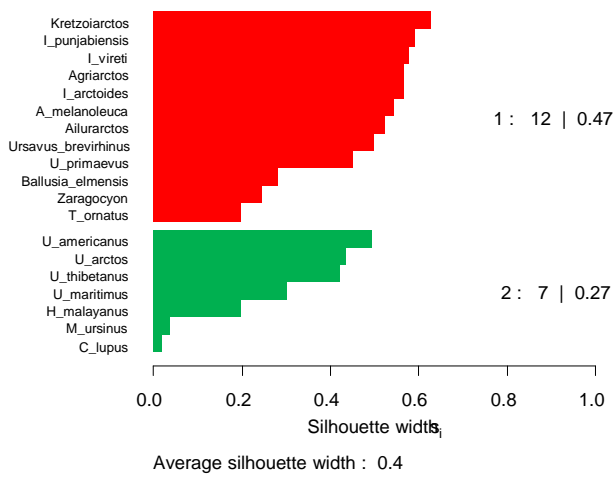


k=4

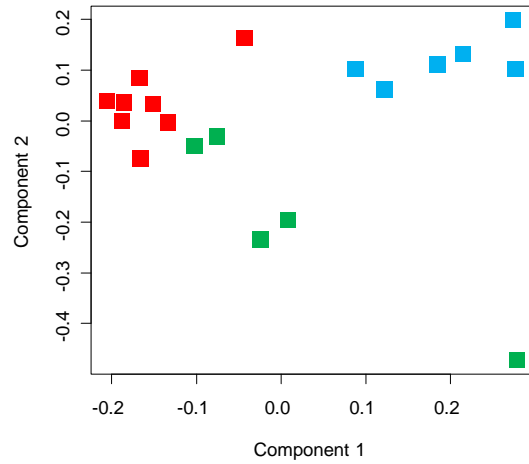
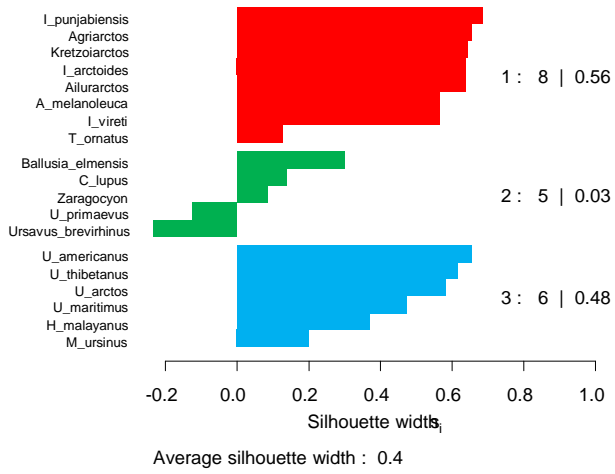


Silhouette plot, Fuzzy Analysis

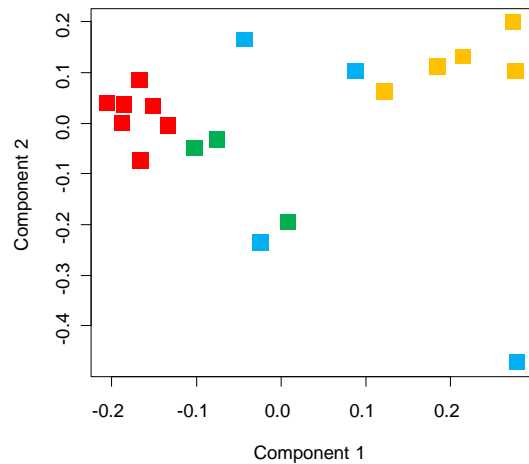
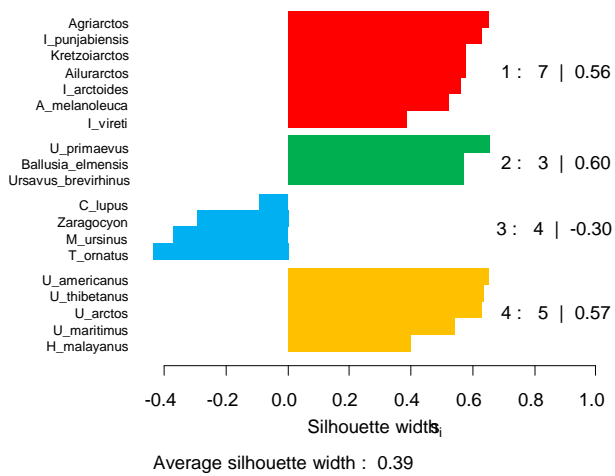
k=2



k=3



k=4



Family Otariidae

Order Carnivora
Churchill et al. 2014

Pearson BDC
Negative: 32
Positive: 144
Clusters: 3

Clusterability
Hopkins Statistic: 0.77
Dip test: 0.022
Dip test p-value: 0.428

Spearman BDC
Negative: 26
Positive: 144
Clusters: 2

Spearman BDC has the same number of instances of significant, positive correlation as the Pearson BDC, but the distribution of these correlations is different. Now, seven new correlations not seen in the Pearson BDC reduce the number of clusters from three to two. The Pearson BDC clusters have an average silhouette width of 0.28, and the Spearman BDC clusters have an average silhouette width of 0.29. The cluster membership difference is 8%.

The three-cluster medoid partition has an average silhouette width of 0.17 and does not support the Pearson BDC clusters. The three-cluster medoid partition and the Pearson BDC clusters have a cluster membership difference of 40%. At $k=2$, the medoid partition has an average silhouette width of 0.15 and is also inconsistent with the Spearman BDC clusters.

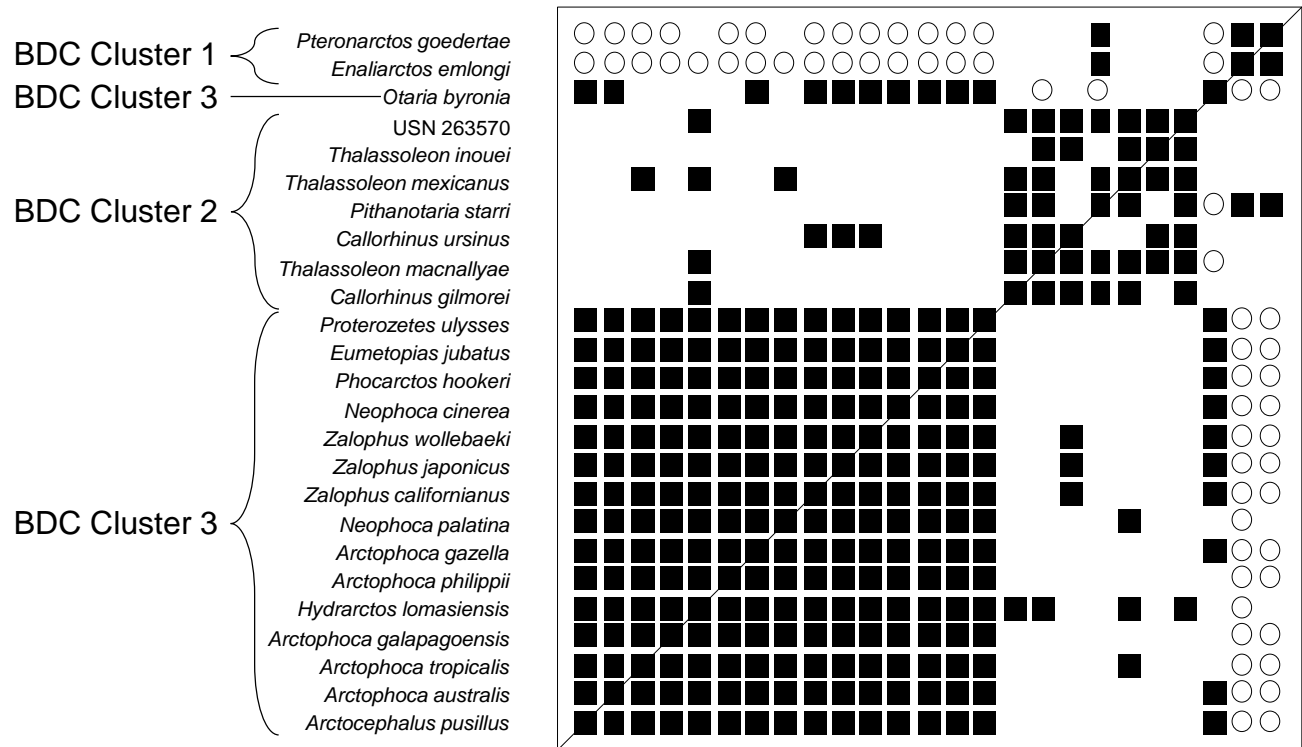
Three-cluster fuzzy analysis could not be calculated, but the two-cluster fuzzy partition was exactly the same as the Spearman BDC clusters.

The original analysis noted the gap between the ingroup and two outgroup taxa in the MDS and the significant, negative correlation between the ingroup and outgroup taxa as evidence of an Otariidae holobaramin. Here, the Spearman BDC results do not support that separation but instead include the outgroup taxa with the ingroup. The lack of confirmation from the medoid partition and fuzzy analysis also warrants caution in interpreting these results. These results are inconclusive.

Original conclusion: HB
Updated conclusion: Inconclusive

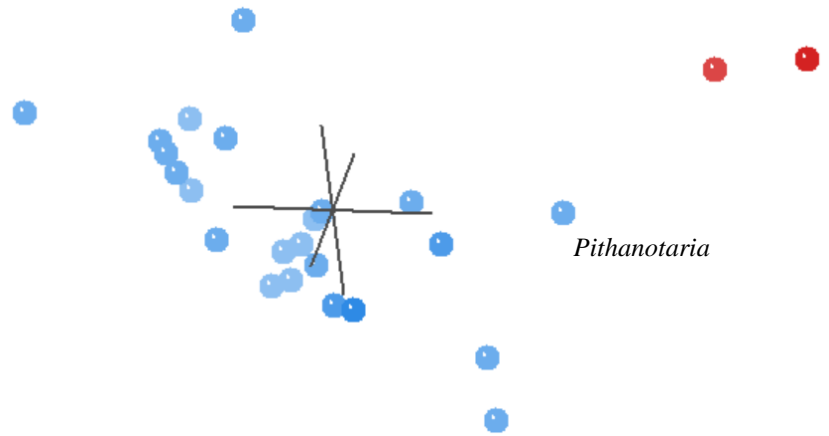
Churchill, M., R.W. Boessenecker, and M.T. Clementz. 2014. Colonization of the southern hemisphere by fur seals and sea lions (Carnivora: Otariidae) revealed by combined evidence phylogenetic and Bayesian biogeographical analysis. *Zoological Journal of the Linnean Society* 172:200-225.

Characters: Craniodental, postcranial, behavioral

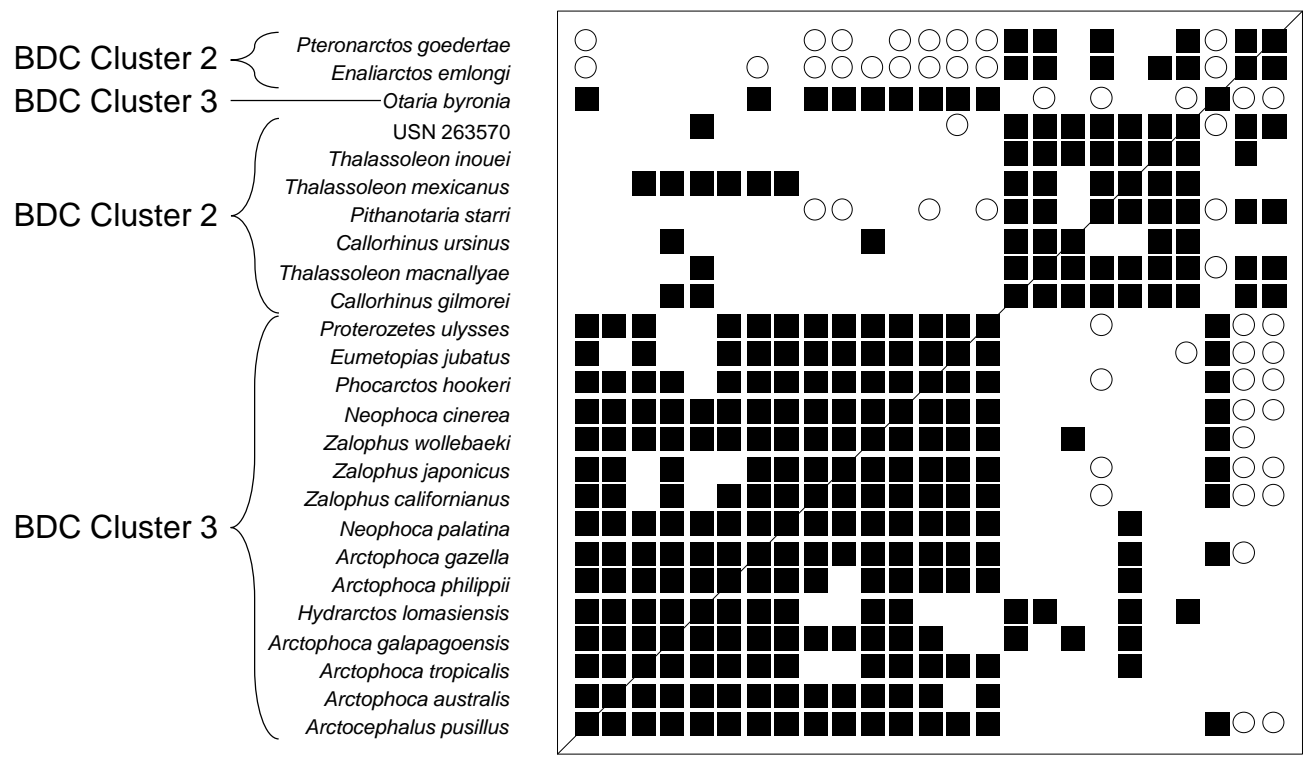


Order Carnivora
Family Otariidae

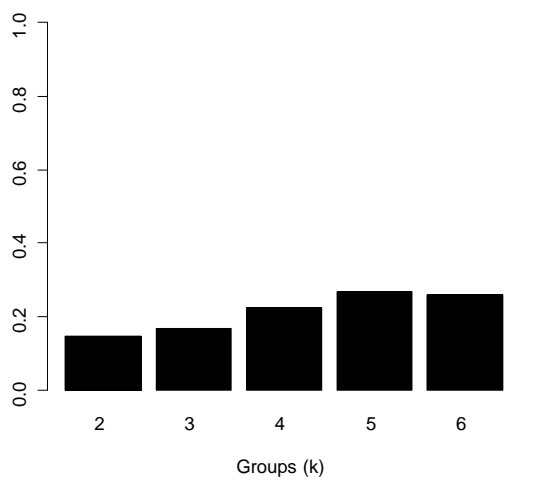
Published taxa	25
Published characters	107
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	25
Characters used for calculations	84
Median bootstrap value	80
F ₉₀	0.24
Stress of 3D MDS	0.26
k _{min}	10
Conclusion	HB



Notes: Otariidae is well-separated from the outgroup taxa in both BDC and MDS results. BDC reveals positive correlation between the outgroup taxa and *Pithanotaria*, but their proximity is not evident in the MDS results. Otariidae is likely a holobaramin.



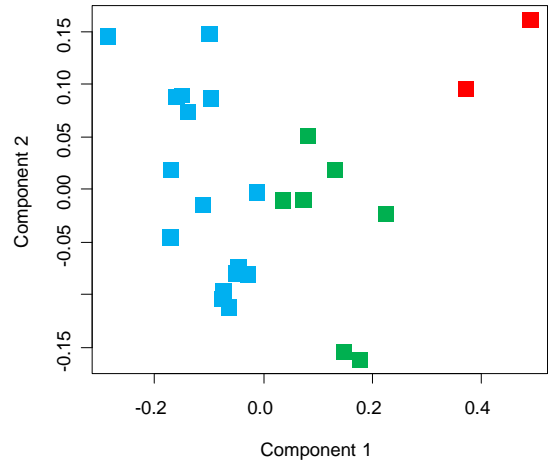
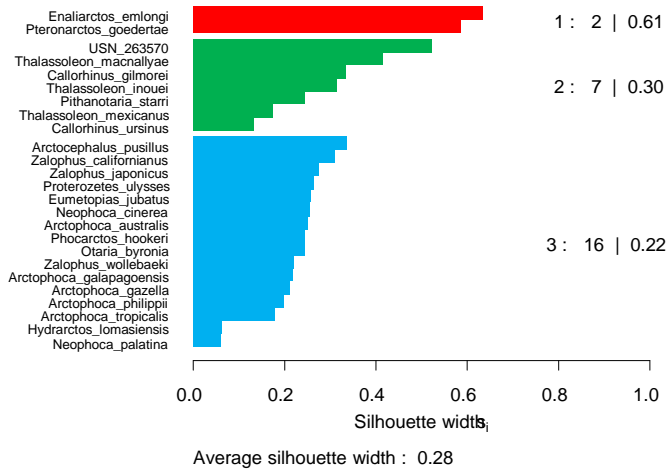
Average Silhouette Widths, Partion Around Medoids



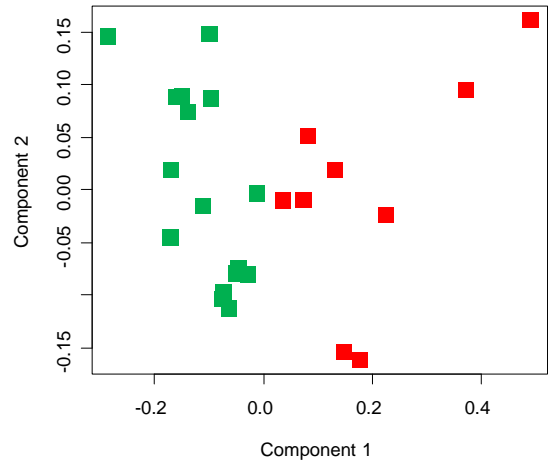
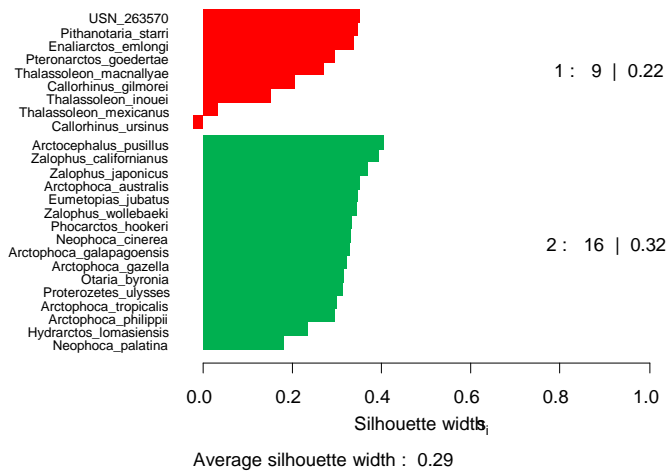
Clade Correspondence: All three clusters evident in the BDC results contain more than one taxon each. Only the outgroup cluster (#1) appeared as a clade in the published phylogeny (Figure 3A, Churchill et al. (2014)).

Silhouette plot, BDC partitions

Pearson Correlation

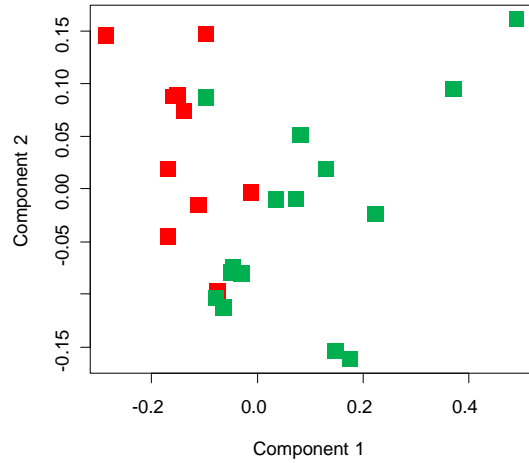
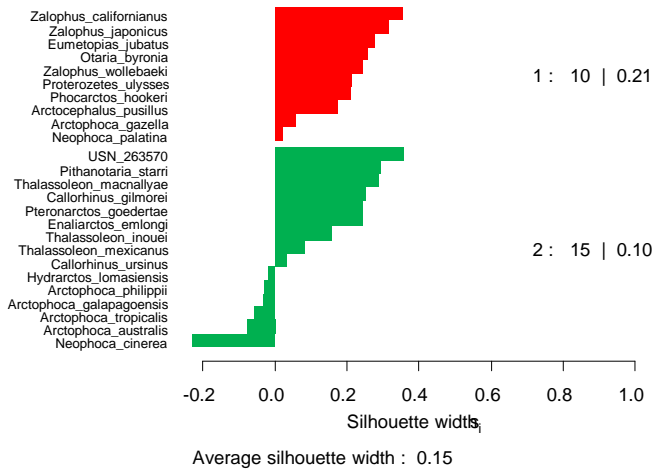


Spearman Correlation

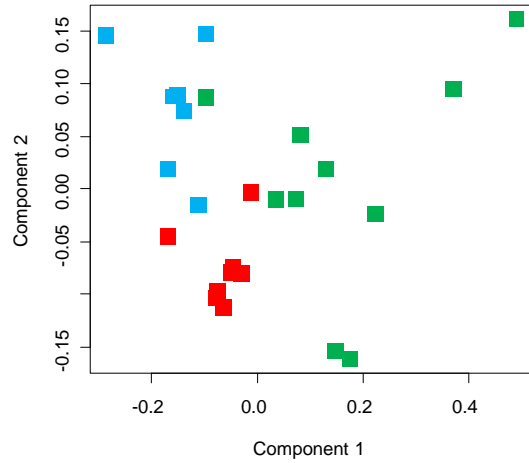
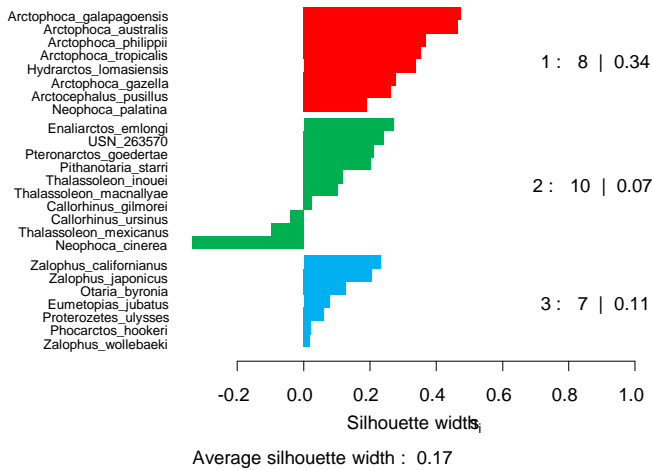


Silhouette plot, Partition Around Medoids

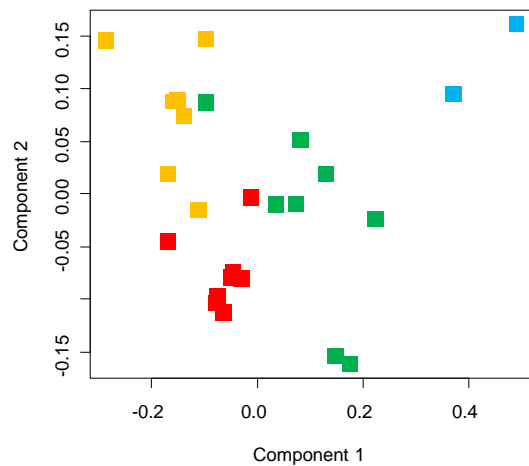
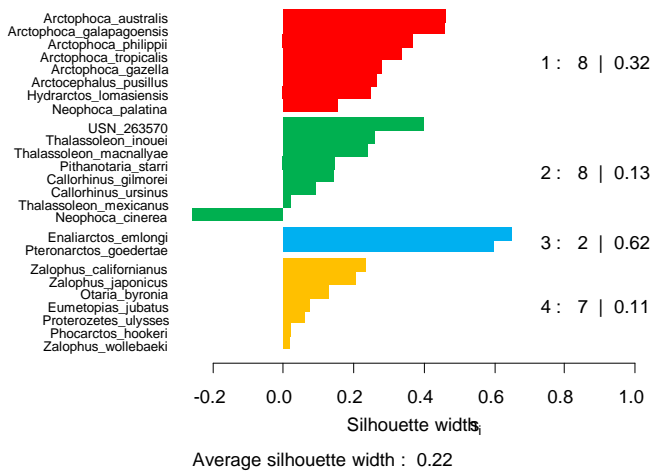
k=2



k=3

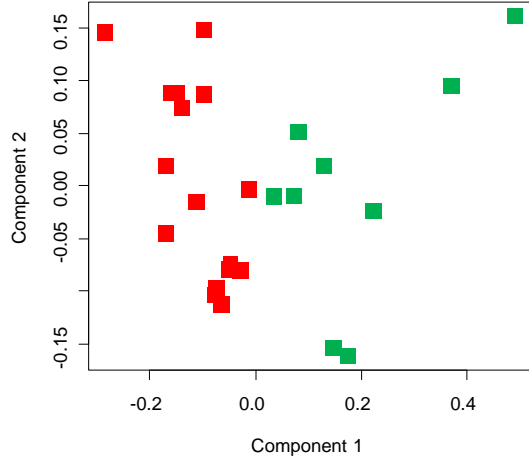
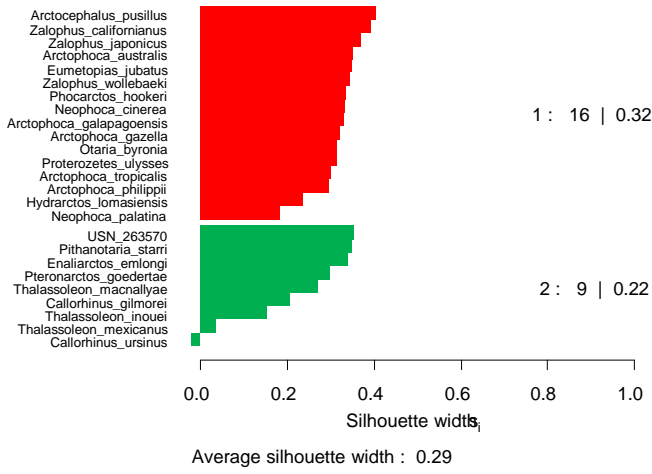


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Odobenidae

Order Carnivora

Boessenecker and Churchill 2013

Pearson BDC

Negative: 52

Positive: 57

Clusters: 2

Clusterability

Hopkins Statistic: 0.729

Dip test: 0.028

Dip test p-value: 0.447

Spearman BDC

Negative: 56

Positive: 64

Clusters: 2

Additional instances of significant, positive correlation can be observed in the Spearman BDC results when compared to the Pearson BDC results, but the clusters are the same. The average silhouette width for this partition is 0.37.

The two-cluster medoid partition generally agrees with the BDC clusters, except it moves one taxon (*Pontolis magnus*) from one cluster to the other. The cluster membership difference is 5%. The two-cluster medoid partition has an average silhouette width of 0.38.

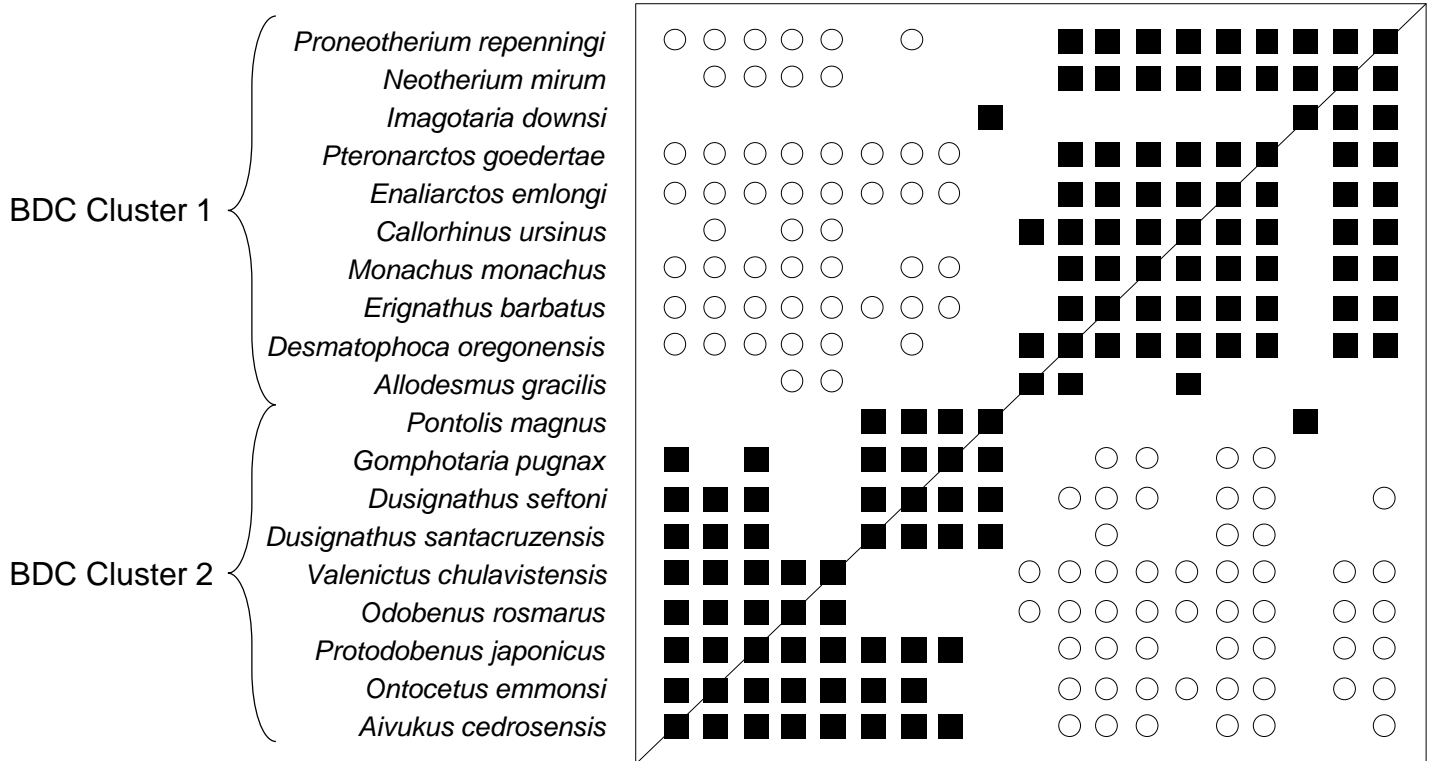
The two-cluster fuzzy analysis agrees exactly with the BDC partition.

These results reinforce the original conclusion. Odobenidae is probably a holobaramin.

Original conclusion: HB?

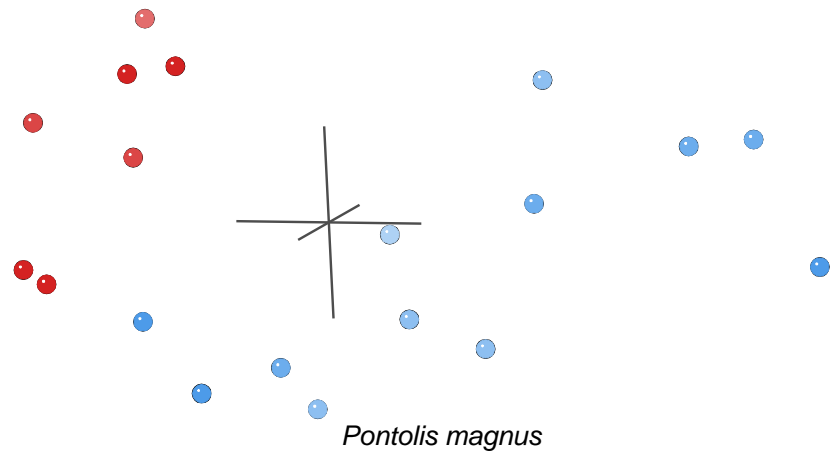
Updated conclusion: HB?

Characters: Craniodental and postcranial

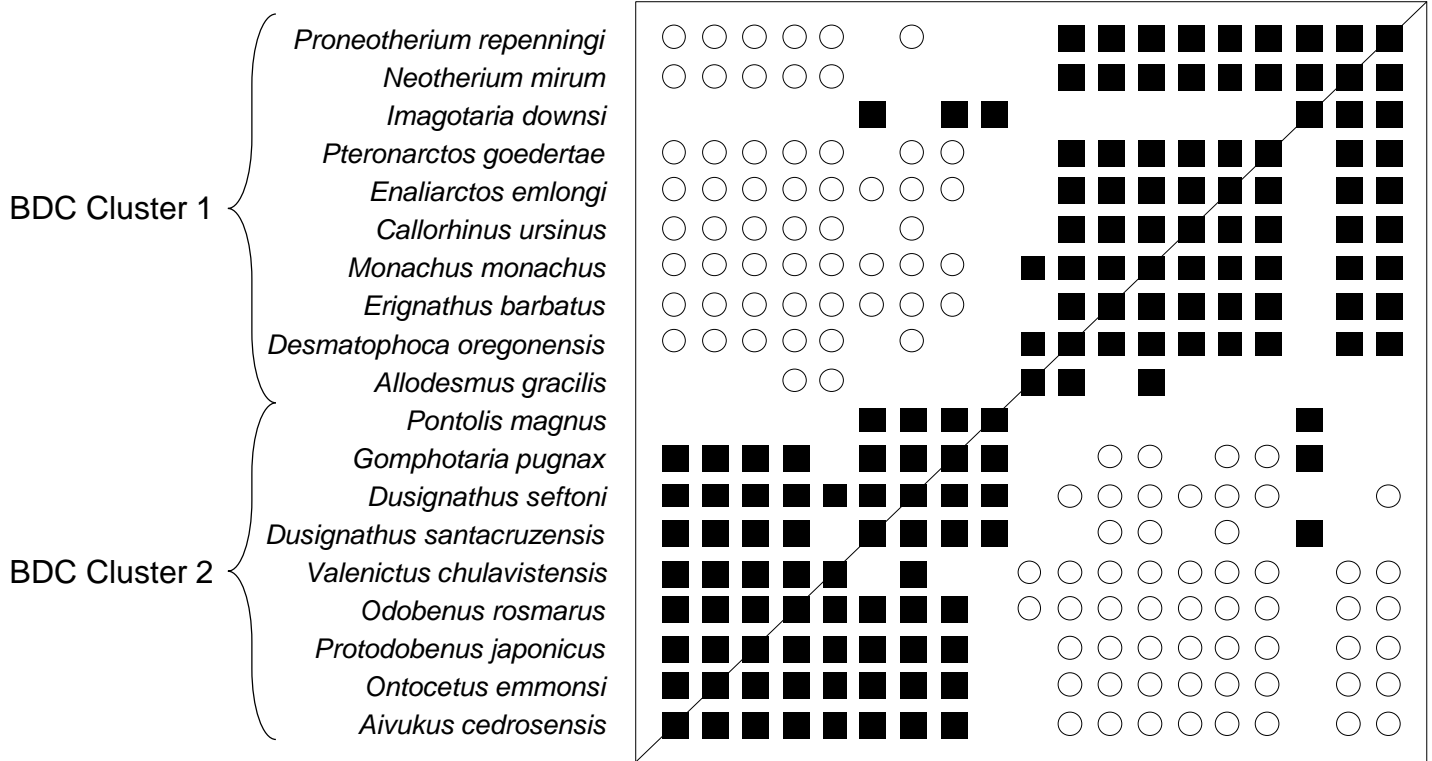


Order Carnivora
Family Odobenidae

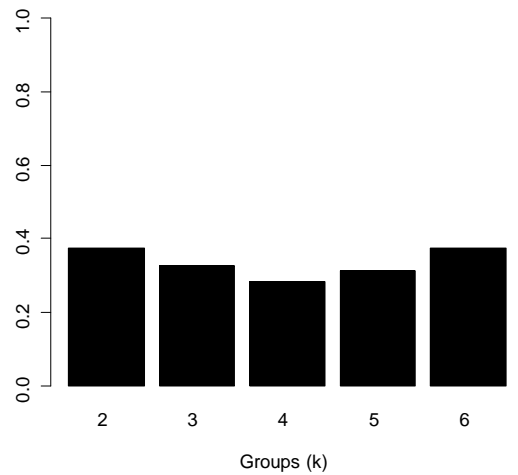
Published taxa	23
Published characters	90
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	19
Characters used for calculations	82
Median bootstrap value	89
F ₉₀	0.48
Stress of 3D MDS	0.14
k _{min}	7
Conclusion	HB?



Notes: Odobenidae is well separated from the outgroup taxa in the BDC results, with the exception of *Pontolis*, which is positively correlated with members of the ingroup and outgroup. The MDS results do not reveal a clear distinction between the two groups, although *Pontolis* does not appear to be closely associated with the outgroup taxa. Odobenidae might be a holobaramin.



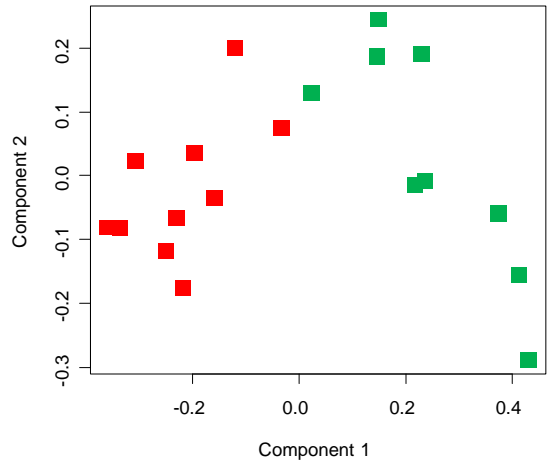
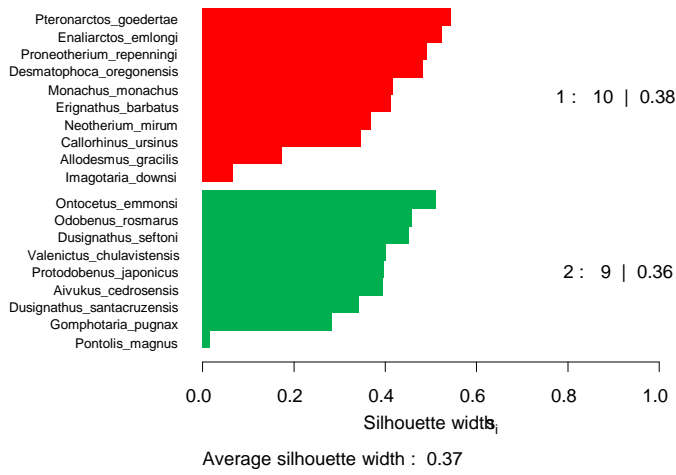
Average Silhouette Widths, Partion Around Medoids



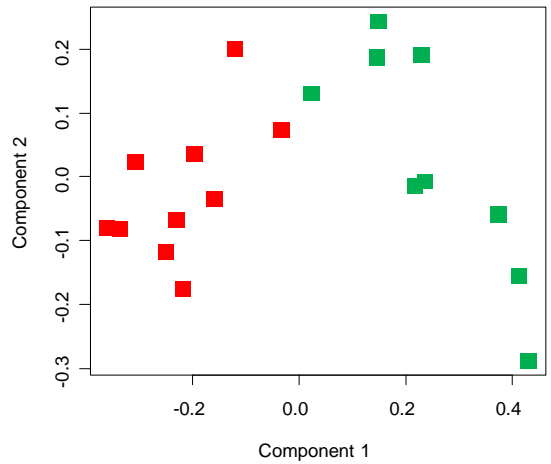
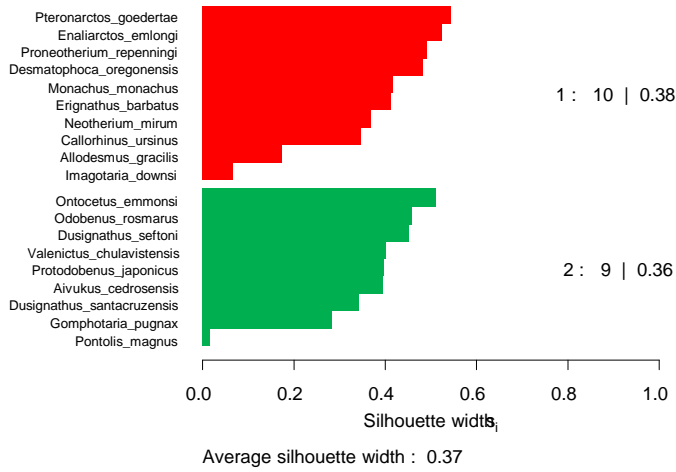
Clade Correspondence: There are two clusters of >1 taxa identifiable in the BDC results. Both are monophyletic in the phylogeny of Figure 8 in Boessenecker et al. (2013), if the phylogeny were unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

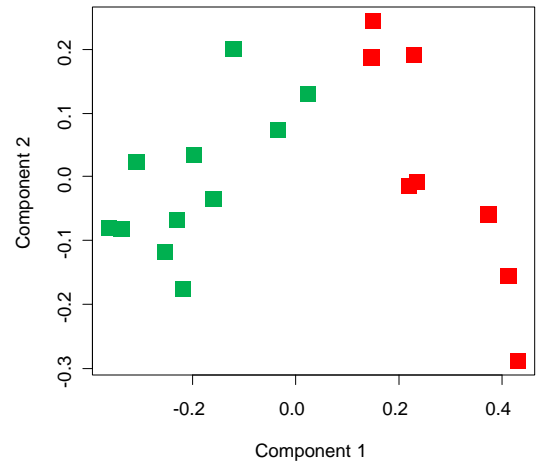
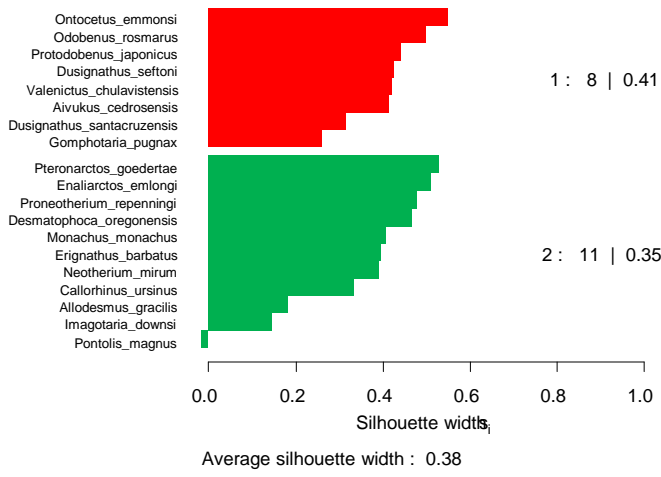


Spearman Correlation

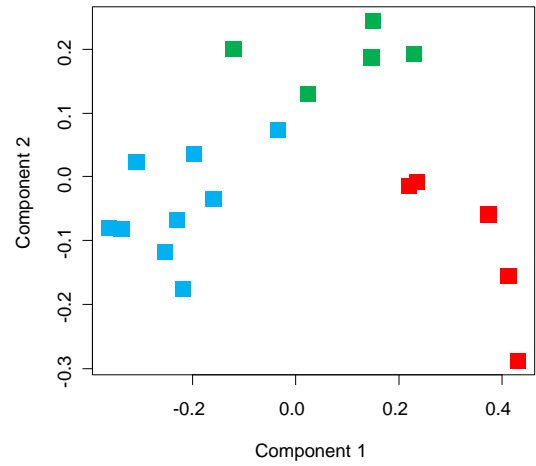
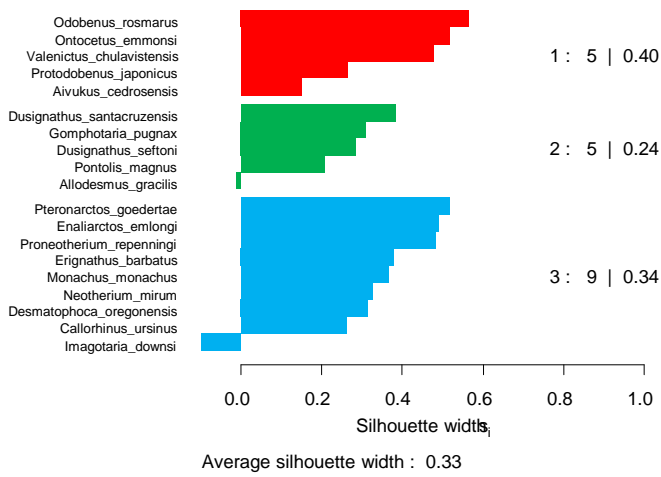


Silhouette plot, Partition Around Medoids

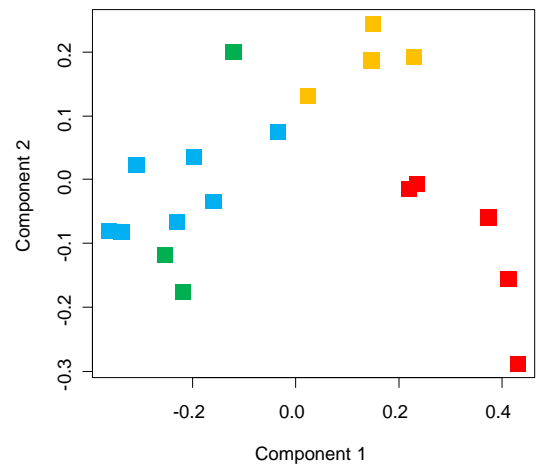
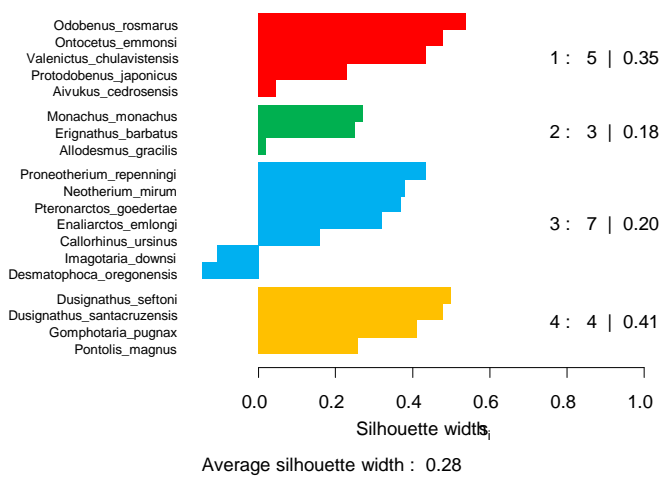
k=2



k=3

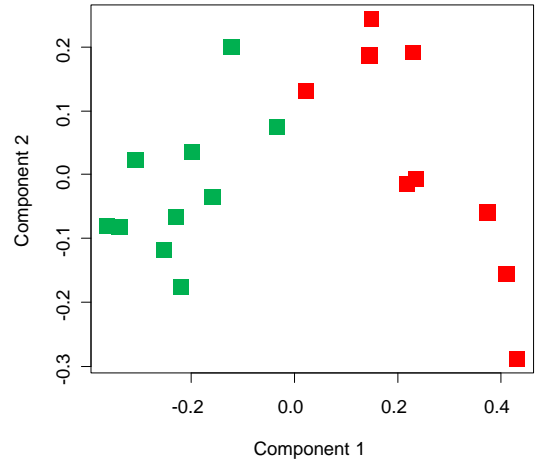
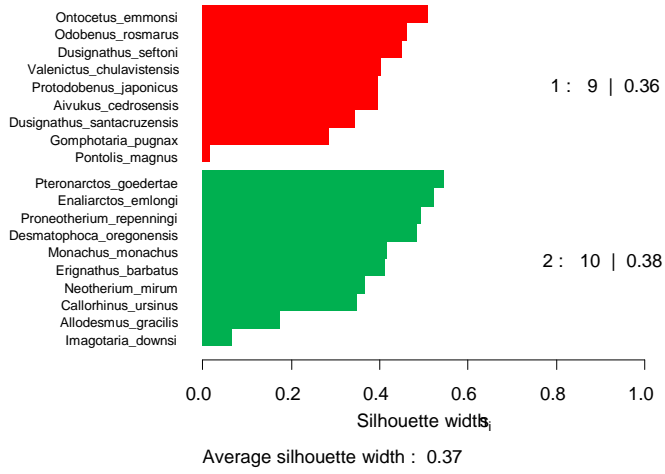


k=4

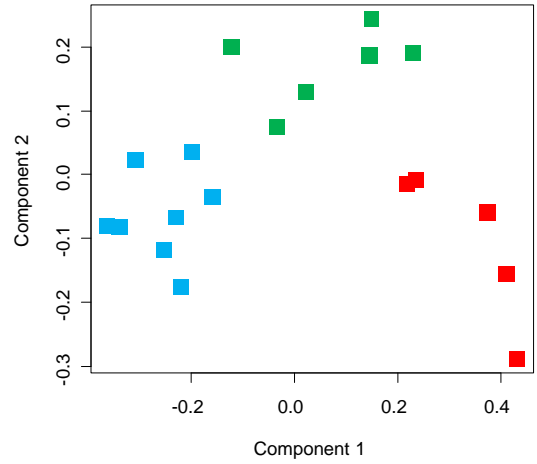
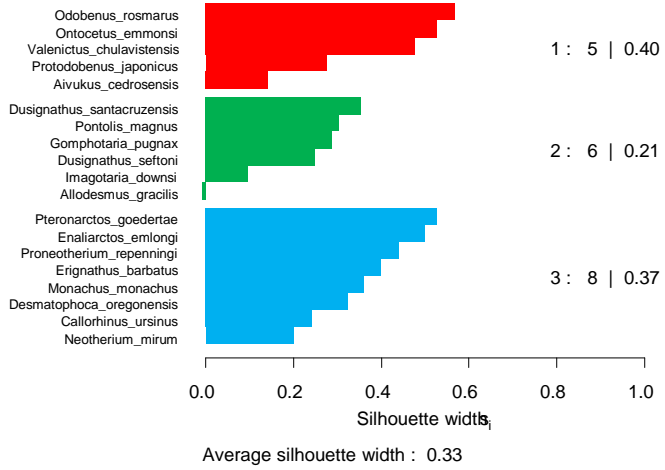


Silhouette plot, Fuzzy Analysis

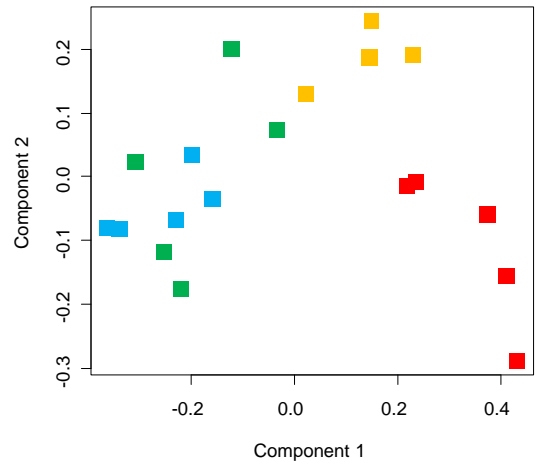
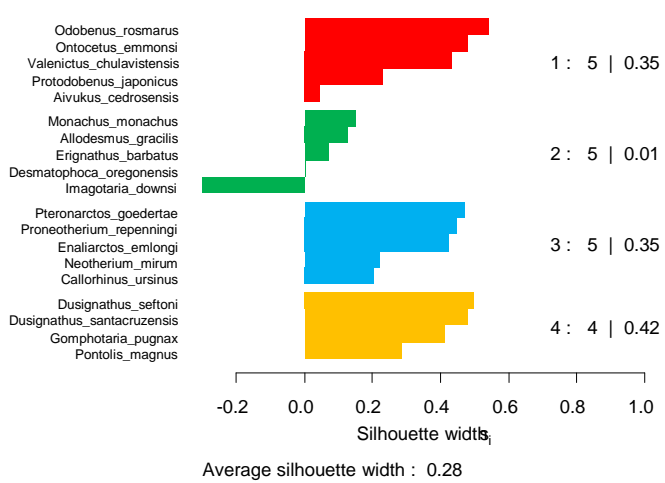
k=2



k=3



k=4



Family Mustelidae

Order Carnivora

Prevosti and Ferrero 2008

Pearson BDC

Negative: 16

Positive: 30

Clusters: 5

Clusterability

Hopkins Statistic: 0.749

Dip test: 0.056

Dip test p-value: 0.308

Spearman BDC

Negative: 16

Positive: 35

Clusters: 4

The Spearman BDC results exhibit an additional five instances of significant, positive correlation, all of which involve *Enhydra lutris* and members of the largest cluster evident in the Pearson BDC results. Thus, the number of clusters changes from five in the Pearson BDC to four in the Spearman BDC, with a cluster membership difference of 7%. The average silhouette width for the Pearson BDC clusters is 0.49 and for the Spearman BDC clusters is 0.51.

The medoid partition at k=5 is substantially worse than the Pearson BDC clusters. The five-cluster medoid partition has an average silhouette width of 0.32 and two taxa with negative silhouette widths. The cluster membership difference between the five-cluster medoid partition and the Pearson BDC clusters is 21%. The four-cluster medoid partition agrees exactly with the Spearman BDC clusters.

The five-cluster fuzzy analysis is substantially worse than the Pearson BDC clusters. The five-cluster fuzzy partition has an average silhouette width of 0.31 and has a cluster membership difference of 43% when compared to the Pearson BDC. At k=4, fuzzy analysis is not consistent with either the Spearman BDC clusters or the medoid partition. Instead, the four-cluster fuzzy partition has an average silhouette width of 0.3 and three taxa with negative silhouette values.

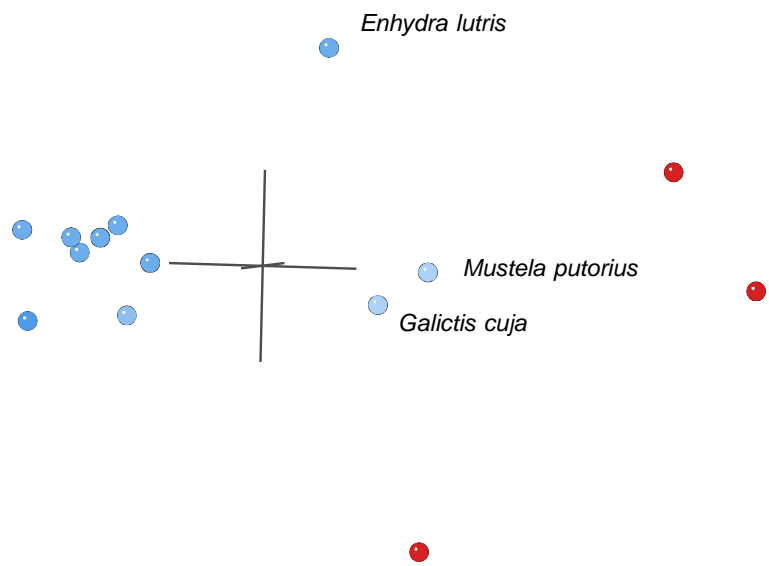
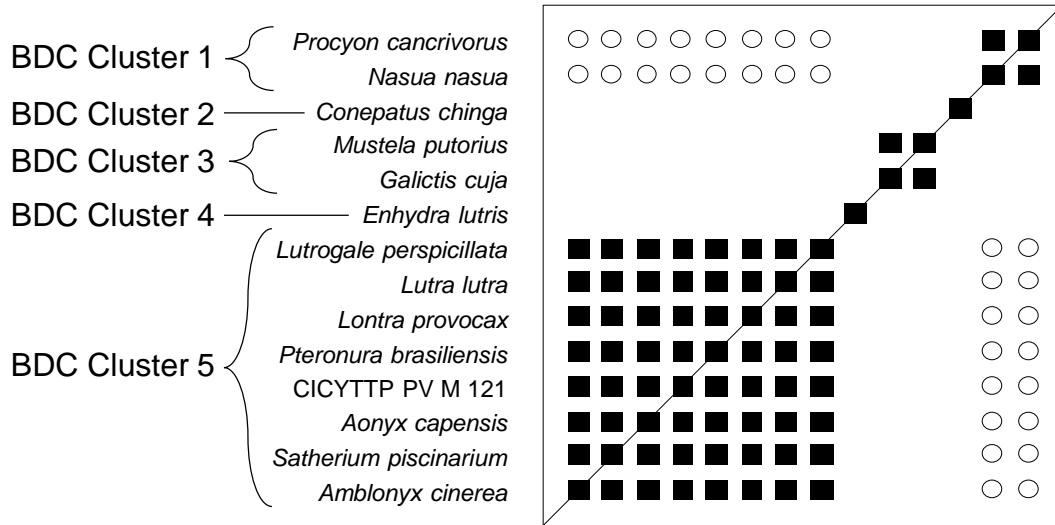
The original analysis concluded that a cluster of mustelid taxa could be a holobaramin, but that cluster excluded *Mustela*, *Talictis*, and *Enhydra*. Here the Spearman BDC and four-cluster medoid partition largely support this conclusion except they include *Enhydra* in the provisional holobaramin. As with the Pearson BDC, though, evidence of significant, negative correlation separating *Galictis* and *Mustela* from the other mustelids is lacking. Hence the membership of the holobaramin remains uncertain.

Original conclusion: HB?

Updated conclusion: HB?

Prevosti, F.J. and B.S. Ferrero. 2008. A Pleistocene giant river otter from Argentina: remarks on the fossil record and phylogenetic analysis. *Journal of Vertebrate Paleontology* 28:1171-1181.

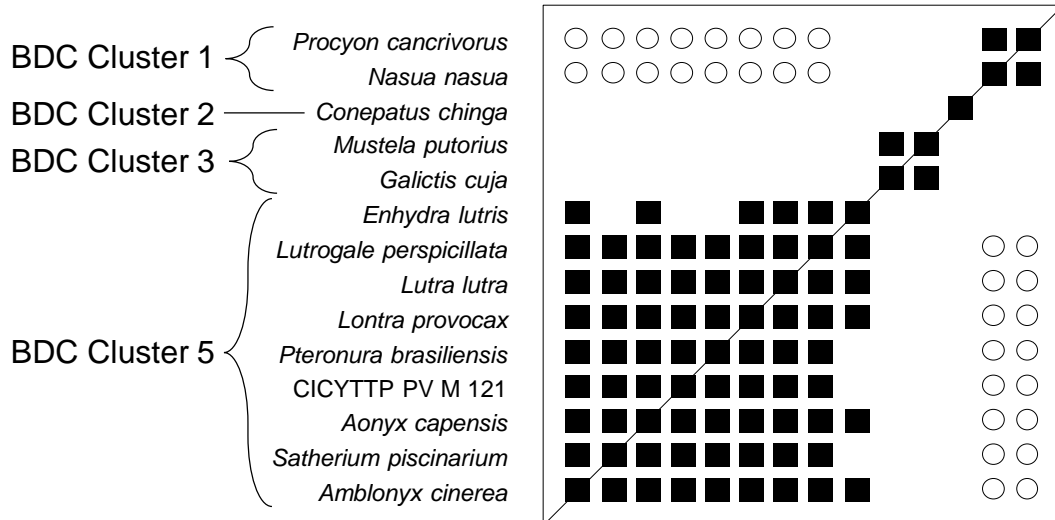
Characters: Craniodental



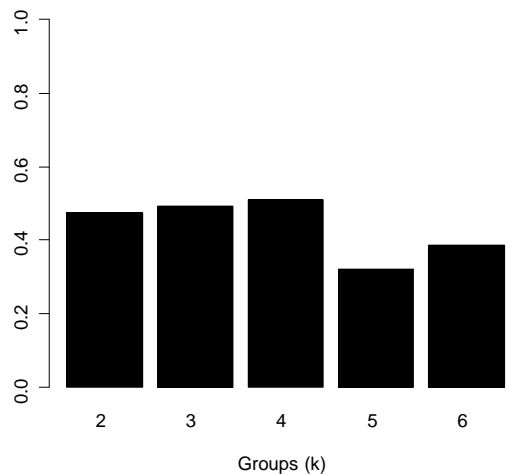
Order Carnivora
Family Mustelidae

Published taxa	41
Published characters	69
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	14
Characters used for calculations	64
Median bootstrap value	99
F ₉₀	0.78
Stress of 3D MDS	0.11
k _{min}	6
Conclusion	HB?

Notes: A cluster of mustelid taxa appear to be a holobaramin, but *Mustela*, *Galictis* and *Enhydra* are not connected to the main cluster of mustelid taxa in either the MDS or BDC results. This result should be examined further.



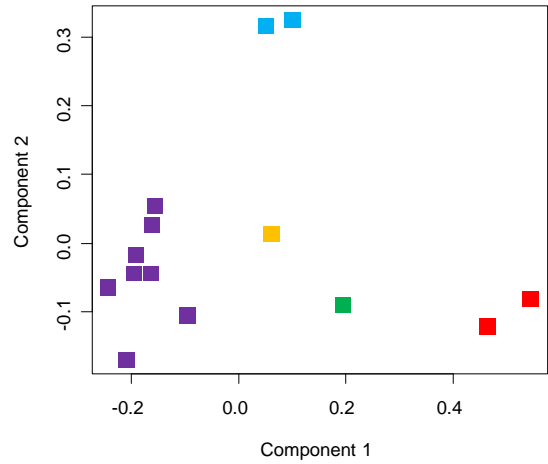
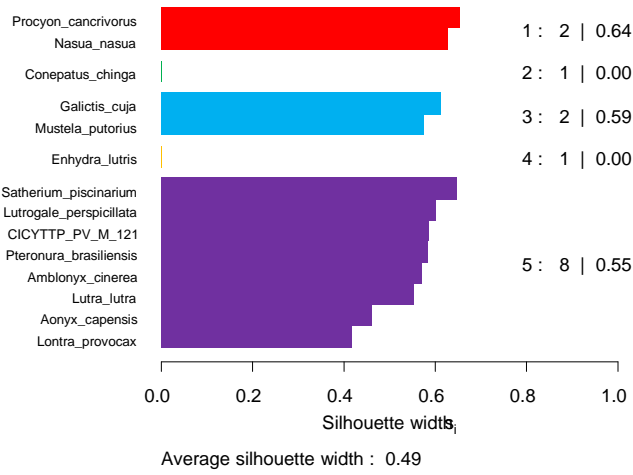
Average Silhouette Widths, Partion Around Medoids



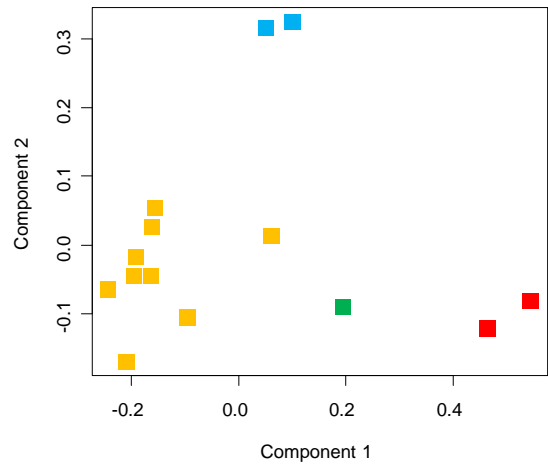
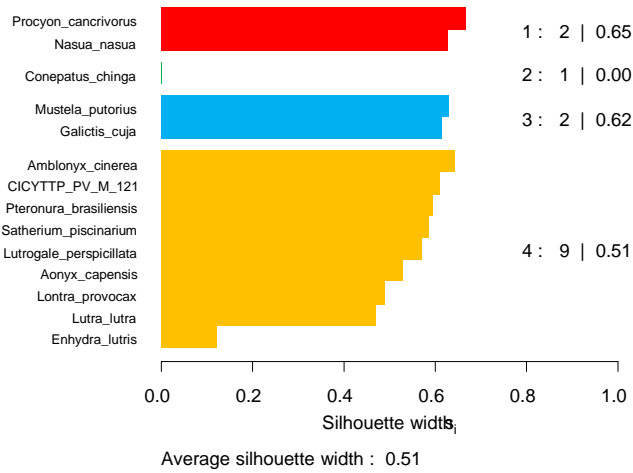
Clade Correspondence: Three of the five BDC clusters have two or more taxa each. All three are clades in the published phylogeny of Figure 5A in Prevosti and Ferrero (2008).

Silhouette plot, BDC partitions

Pearson Correlation

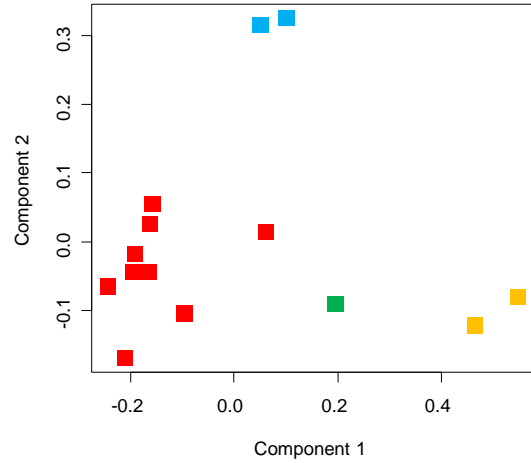
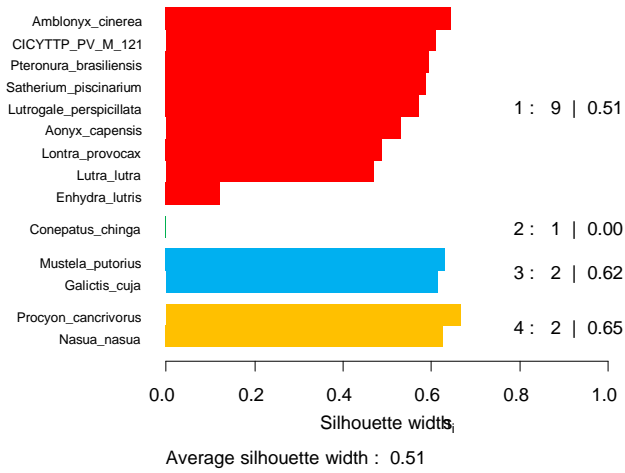


Spearman Correlation

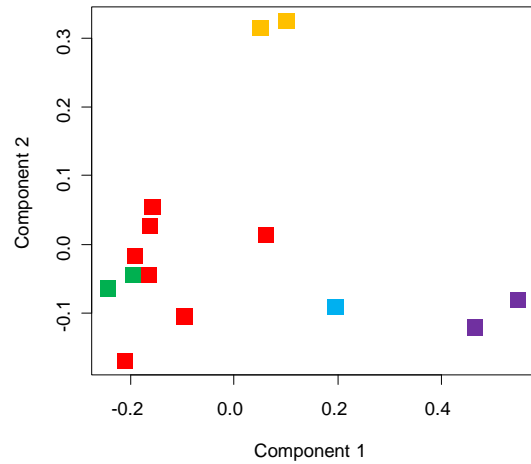
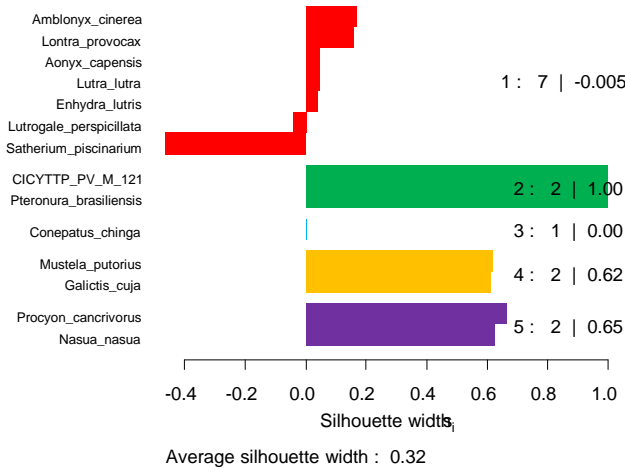


Silhouette plot, Partition Around Medoids

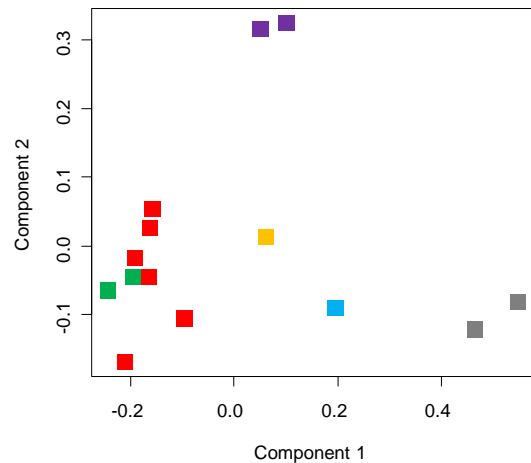
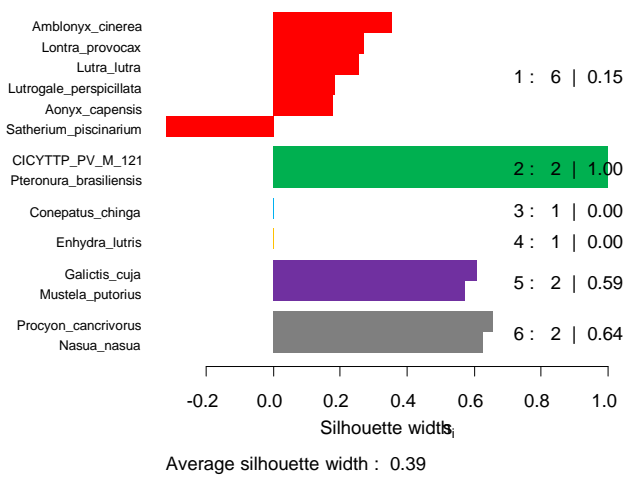
k=4



k=5

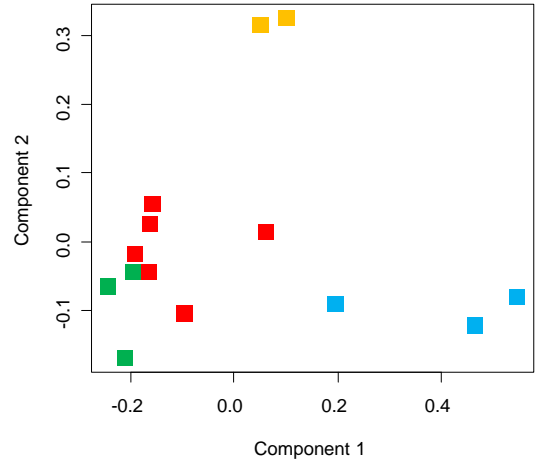
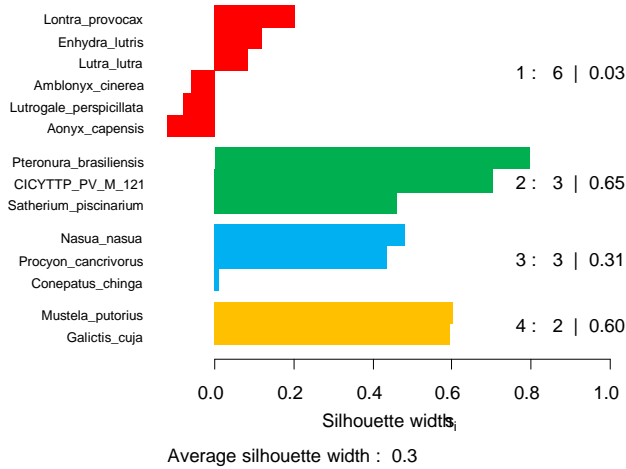


k=6

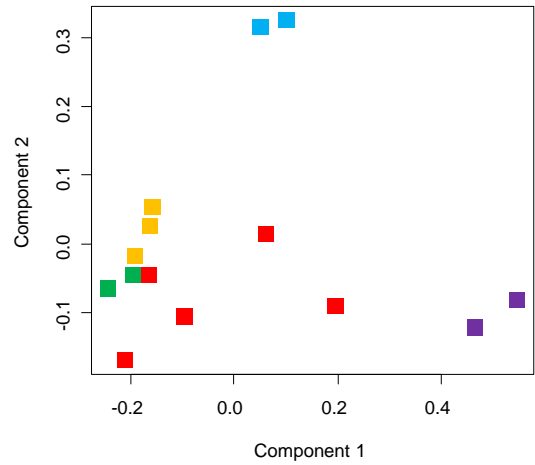
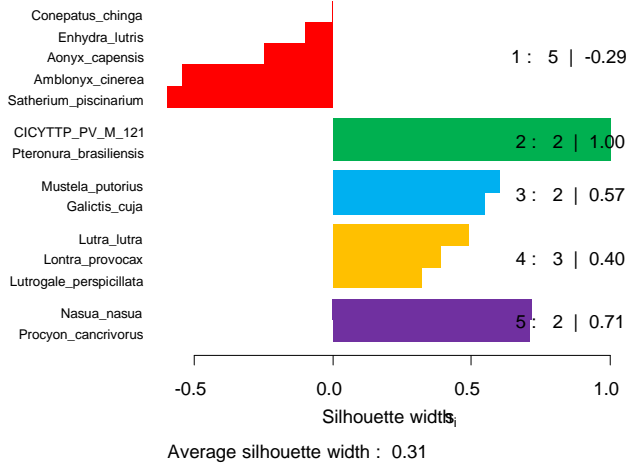


Silhouette plot, Fuzzy Analysis

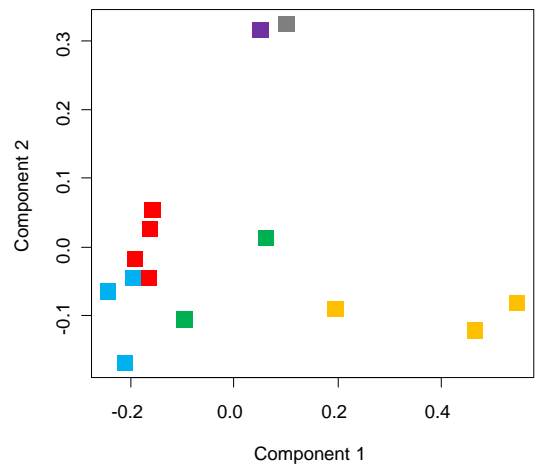
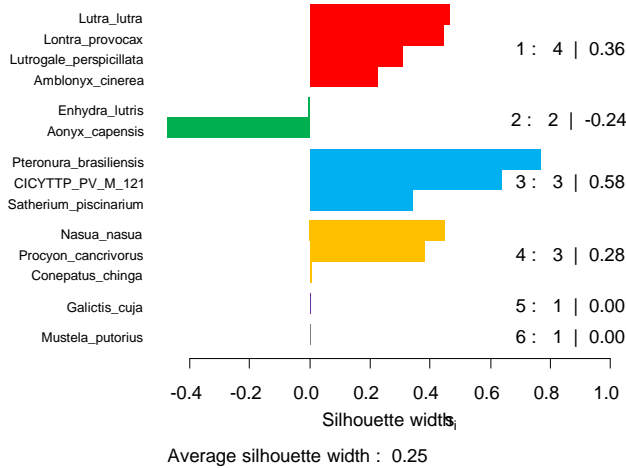
k=4



k=5



k=6



Family Mephitidae

Order Carnivora
Wang et al. 2014

Pearson BDC
Negative: 23
Positive: 55
Clusters: 3

Spearman BDC
Negative: 29
Positive: 50
Clusters: 3

Clusterability
Hopkins Statistic: 0.813
Dip test: 0.023
Dip test p-value: 0.886

The Spearman BDC rearranges the significant, positive correlation observed in the Pearson BDC results. Though both analyses recognize three clusters, the membership differs, and the cluster membership difference is 44%. The Spearman BDC clusters have the advantage in average silhouette width, with 0.4 compared to the 0.34 for the three Pearson BDC clusters.

The three-cluster medoid partition does not support the Pearson or the Spearman BDC results. Compared to the Pearson BDC clusters, the medoid partition at $k=3$ has a cluster membership difference of 39%. The three-cluster medoid partition has an average silhouette width of 0.43, which is slightly better than either the Pearson or Spearman BDC clusters. The two-cluster medoid partition also does not divide the taxa into ingroup and outgroup clusters.

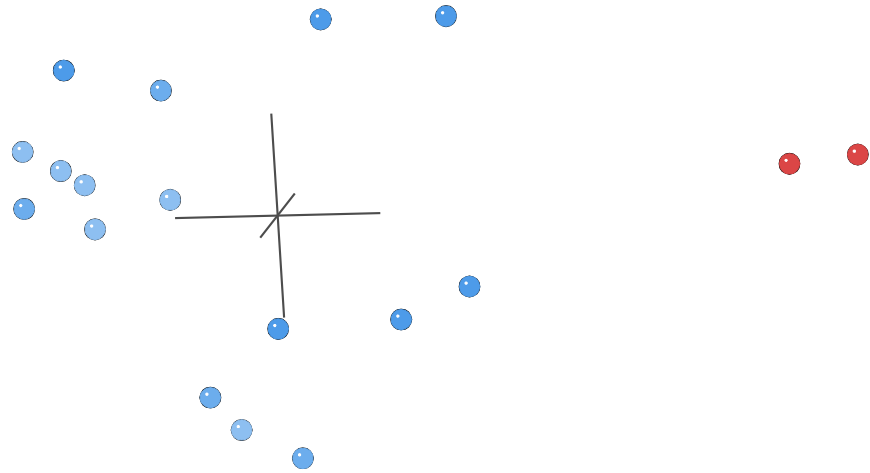
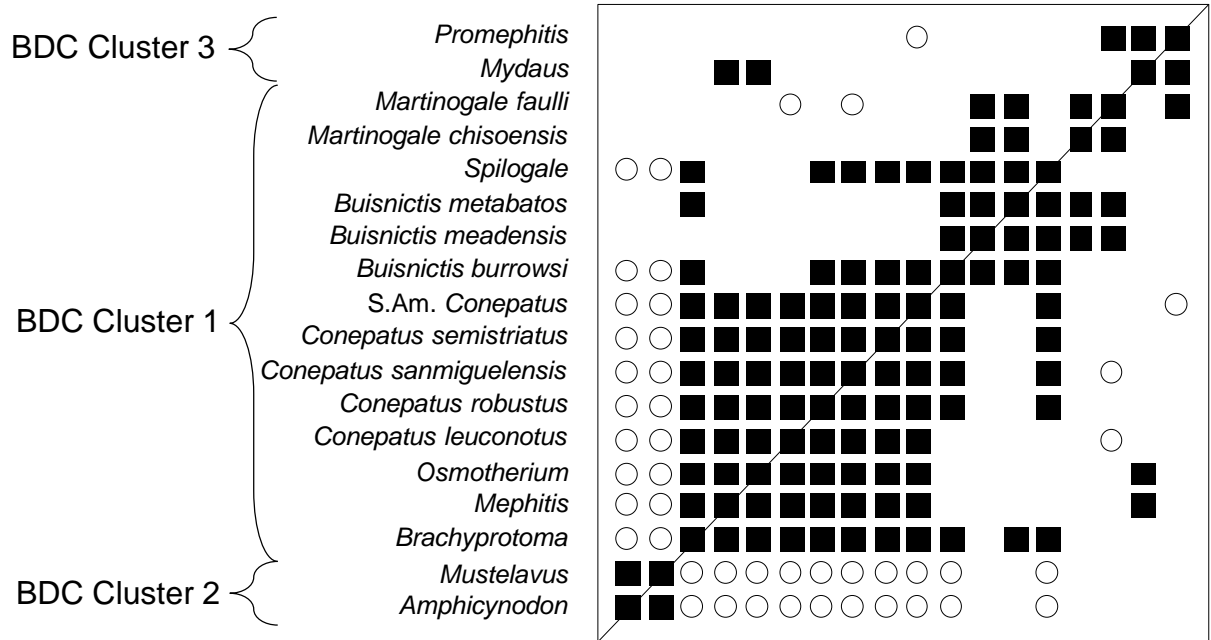
Fuzzy analysis at $k=3$ also does not support the Pearson or Spearman BDC results. The three-cluster fuzzy partition has an average silhouette value of 0.43. The two-cluster fuzzy partition also does not divide the taxa into ingroup and outgroup clusters.

These results cast substantial doubt on the original conclusion that Mephitidae is a holobaramin. Further investigation is warranted.

Original conclusion: HB
Updated conclusion: Inconclusive

Wang, X., Ó. Carranza-Castañeda, and J.J. Aranda-Gómez. 2014. A transitional skunk, *Buisnictis metabatos* sp. nov. (Mephitidae, Carnivora), from Baja California Sur and the role of southern refugia in skunk evolution. *Journal of Systematic Palaeontology* 12:291-302.

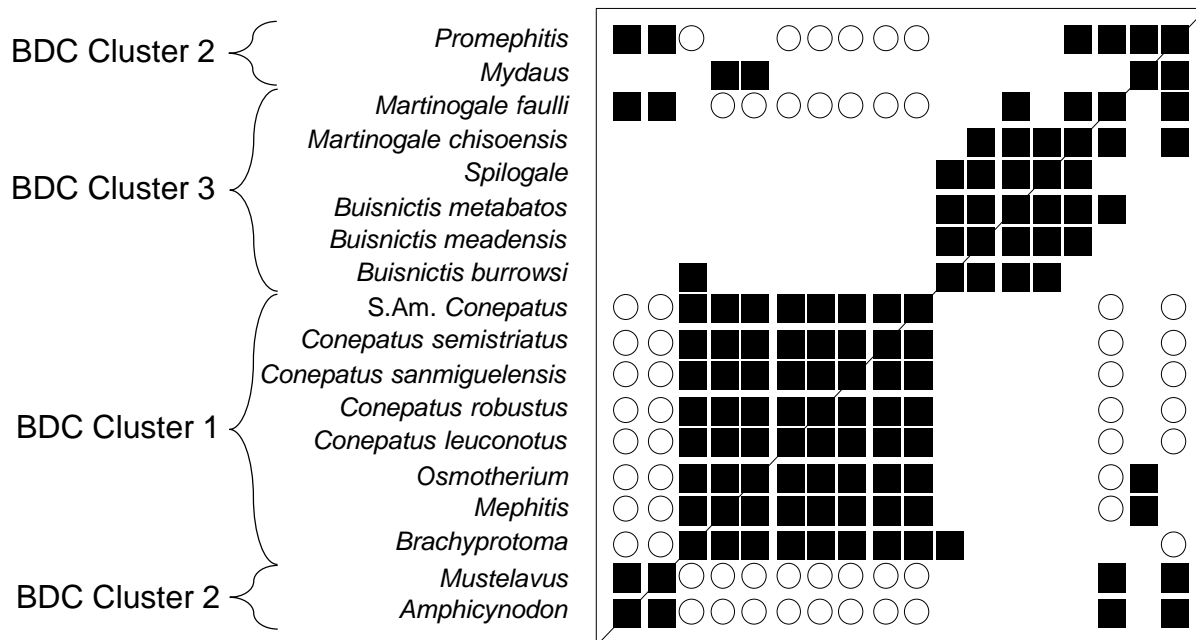
Characters: Craniodental



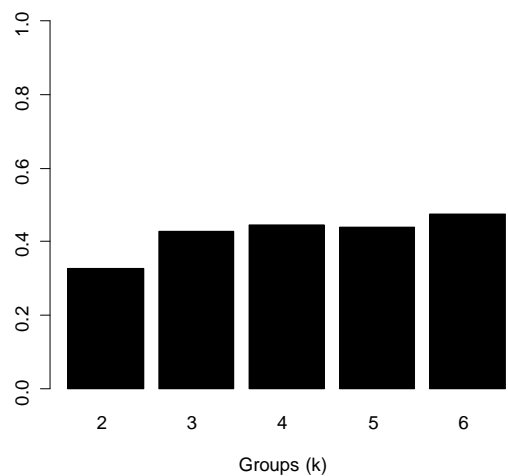
Order Carnivora
Family Mephitidae

Published taxa	21
Published characters	39
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	18
Characters used for calculations	31
Median bootstrap value	74
F ₉₀	0.26
Stress of 3D MDS	0.09
k _{min}	4
Conclusion	HB

Notes: Mephitidae is clearly separated from the outgroup taxa in both BDC and MDS results. Mephitidae is likely a holobaramin.



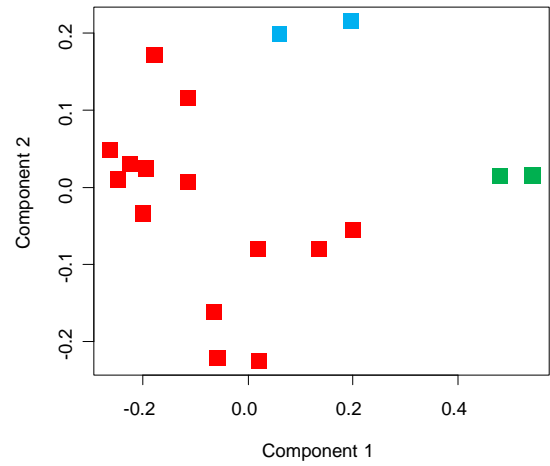
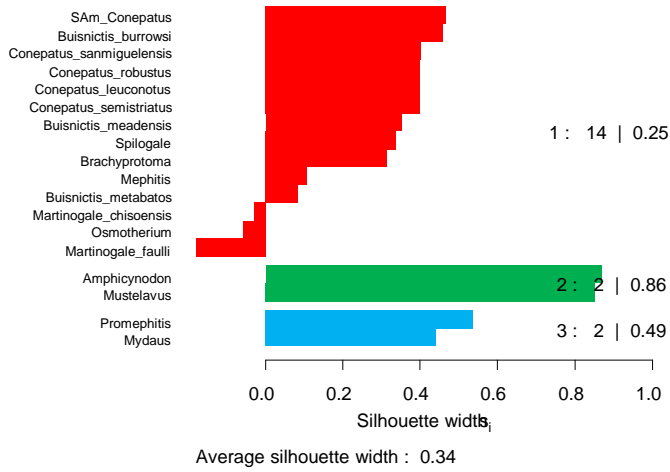
Average Silhouette Widths, Partion Around Medoids



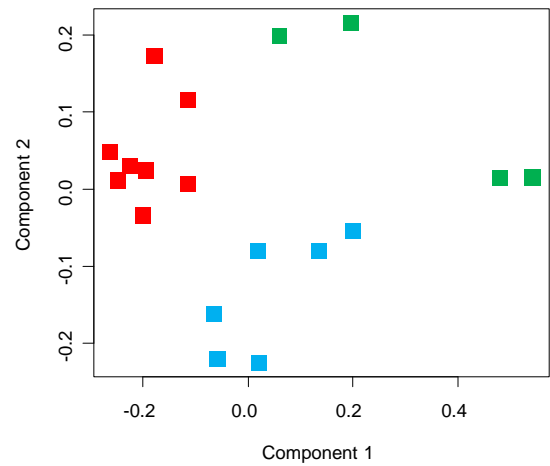
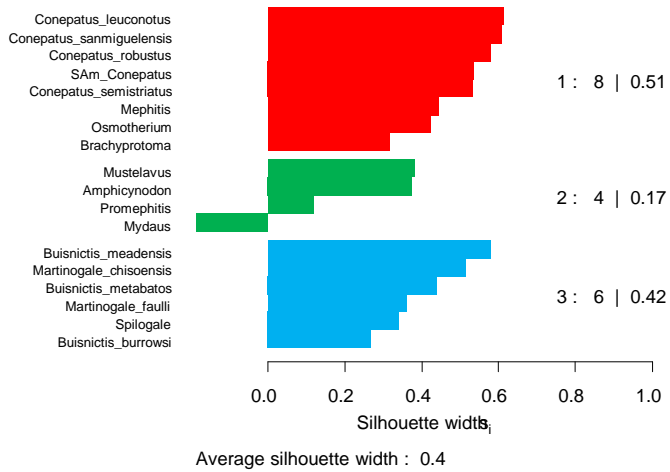
Clade Correspondence: All three taxa in the BDC results contain more than one taxon each. All three are monophyletic in the phylogeny of Figure 8A of Wang et al. (2014), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

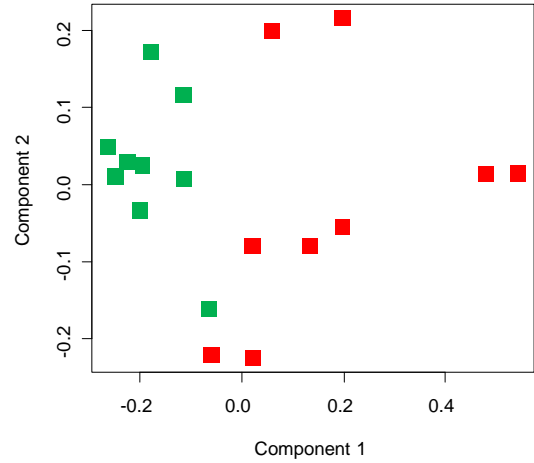
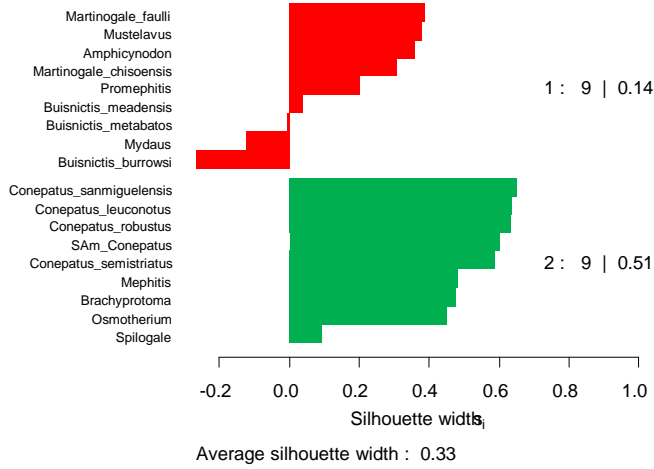


Spearman Correlation

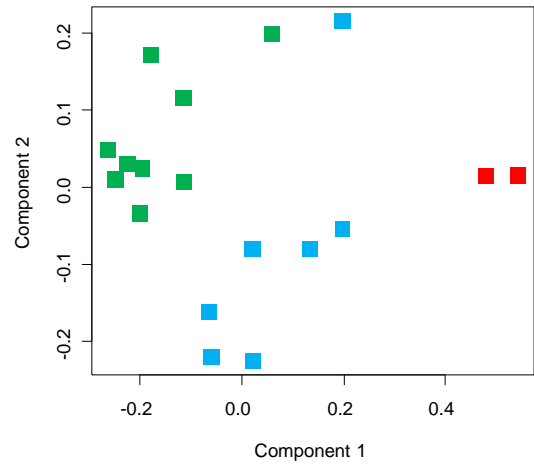
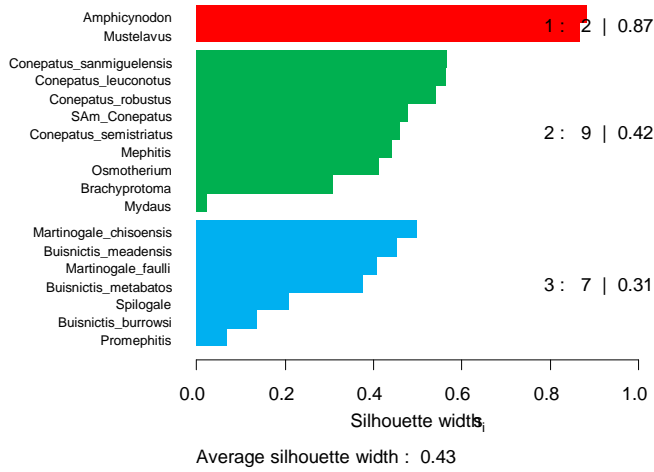


Silhouette plot, Partition Around Medoids

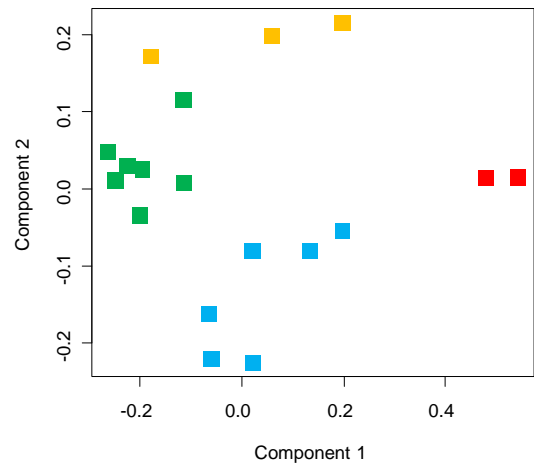
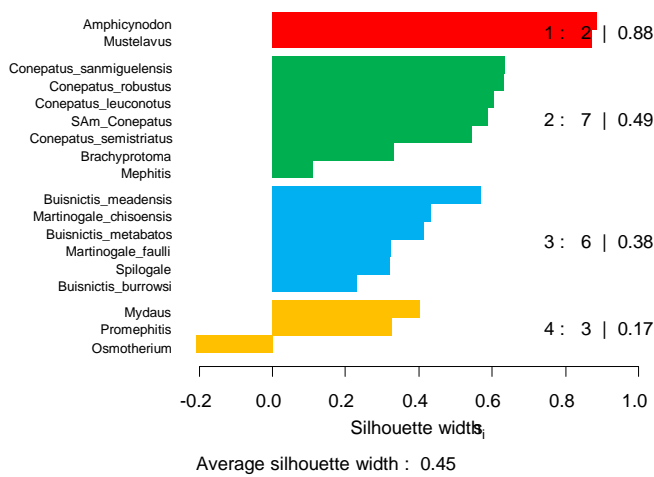
k=2



k=3

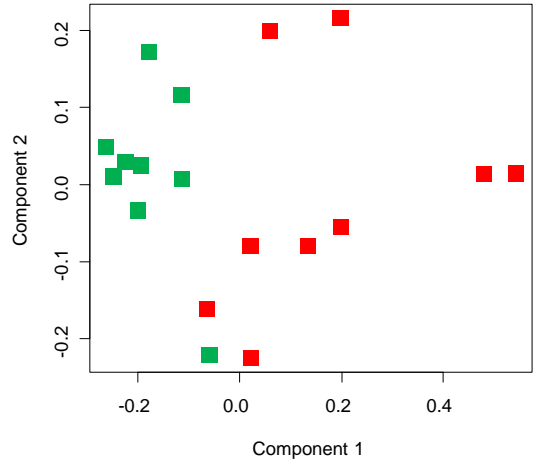
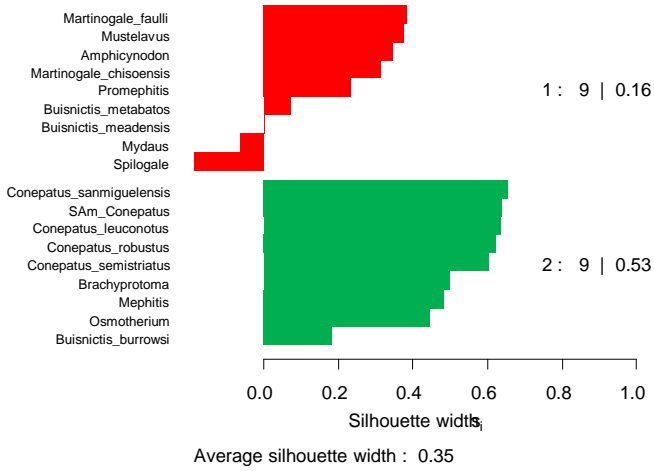


k=4

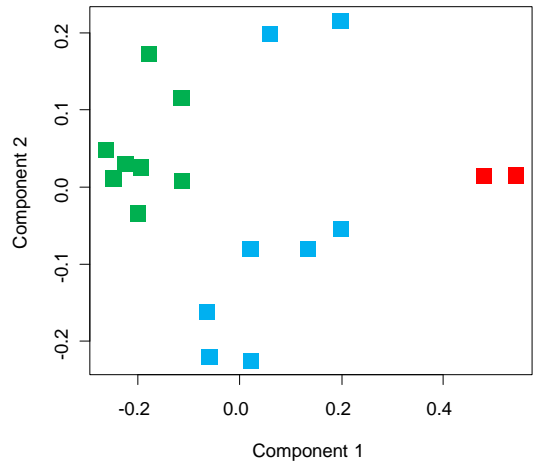
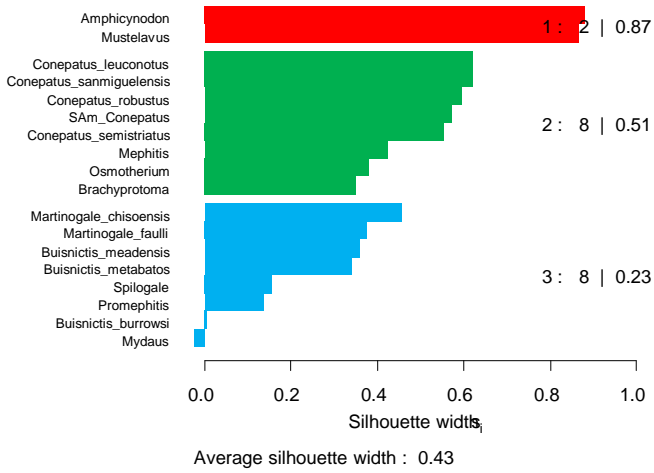


Silhouette plot, Fuzzy Analysis

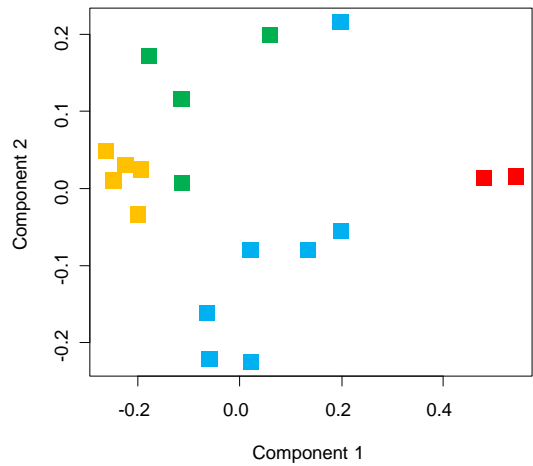
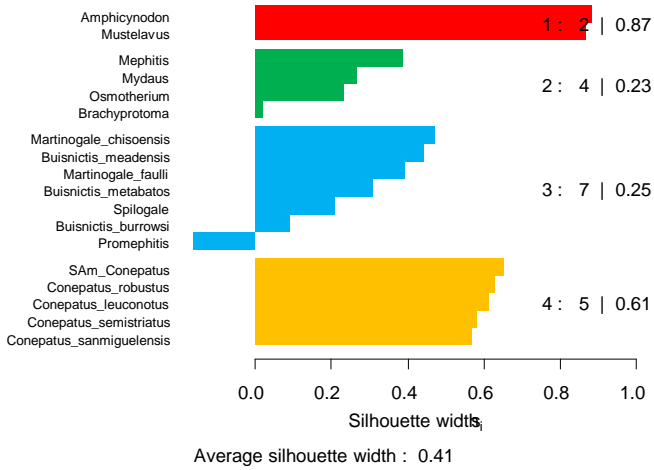
k=2



k=3



k=4



Family Procyonidae

Order Carnivora

Ahrens 2012

Pearson BDC

Negative: 16

Positive: 27

Clusters: 5

Clusterability

Hopkins Statistic: 0.676

Dip test: 0.022

Dip test p-value: 0.971

Spearman BDC

Negative: 20

Positive: 34

Clusters: 3

There are seven additional instances of significant, positive correlation in the Spearman BDC results when compared to the Pearson BDC results. This reduces the number of clusters from five to three. The principle changes involve three different singleton clusters from the Pearson BDC, two of which (*Potos* and *Bassaricyon*) join into a single cluster and the third (*Ailurus*) joins a larger cluster that contains the raccoon *Procyon lotor*. The cluster membership difference is 13%. The average silhouette value for the five-cluster Pearson BDC clusters is 0.19 and for the three-cluster Spearman BDC clusters is 0.31.

The average silhouette value for the five-cluster medoid partition is 0.2, but the cluster membership difference compared to the Pearson BDC clusters is 44%. At $k=3$, the medoid partition has an average silhouette value of 0.23 and does not match the Spearman BDC clusters.

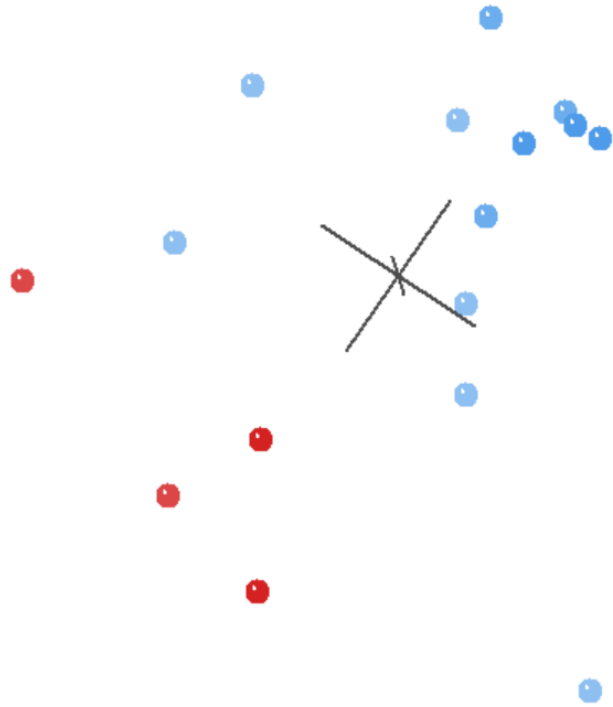
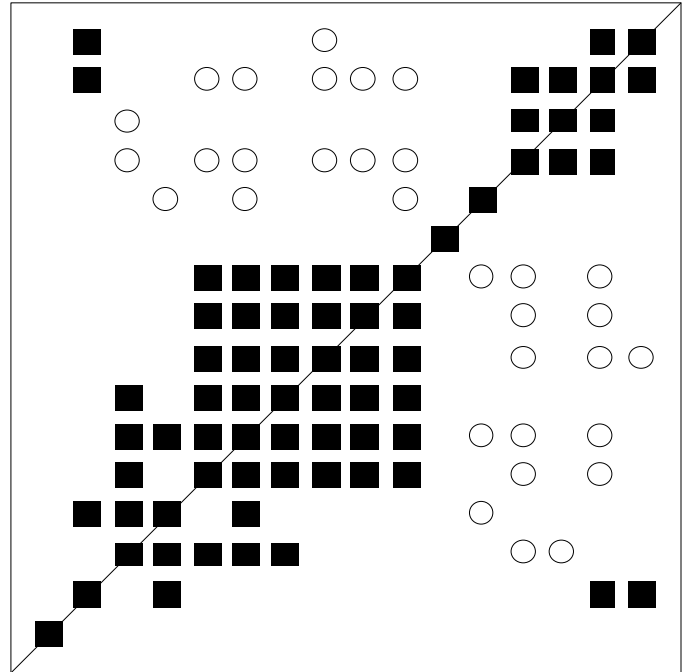
Fuzzy analysis at $k=5$ failed, but the three-cluster fuzzy partition had an average silhouette width of 0.24. The three-cluster fuzzy partition did not match the Spearman BDC clusters.

These results are inconclusive and reinforce the uncertainty of the original analysis.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

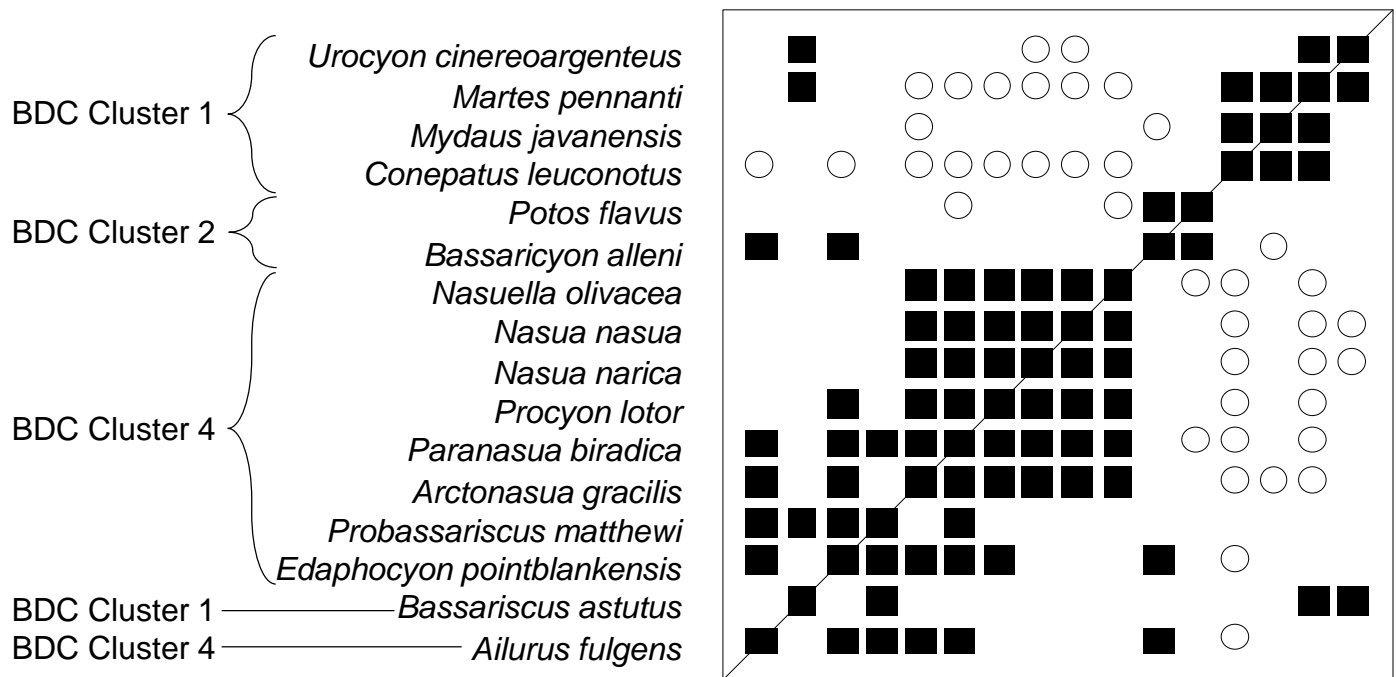
- BDC Cluster 1 { *Urocyon cinereoargenteus*
Martes pennanti
Mydaus javanensis
Conepatus leuconotus
- BDC Cluster 2 ————— *Potos flavus*
- BDC Cluster 3 ————— *Bassaricyon alleni*
- BDC Cluster 4 { *Nasuella olivacea*
Nasua nasua
Nasua narica
Procyon lotor
Paranasua biradica
Arctonasua gracilis
Probassariscus matthewi
Edaphocyon pointblankensis
- BDC Cluster 1 ————— *Bassariscus astutus*
- BDC Cluster 5 ————— *Ailurus fulgens*



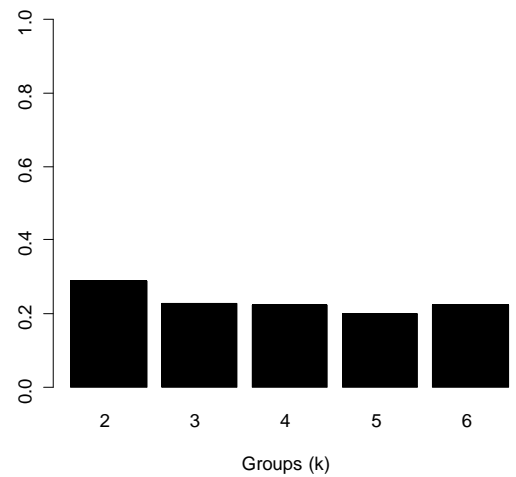
Order Carnivora
Family Procyonidae

Published taxa	20
Published characters	78
Character relevance	0.75
Taxic relevance	0.25
Taxa used for calculations	16
Characters used for calculations	69
Median bootstrap value	79
F ₉₀	0.32
Stress of 3D MDS	0.15
k _{min}	6
Conclusion	Inc

Notes: BDC results shows potential discontinuity around some procyonid taxa, but the MDS results show a diffuse cloud of all taxa. There is no clear evidence of discontinuity.



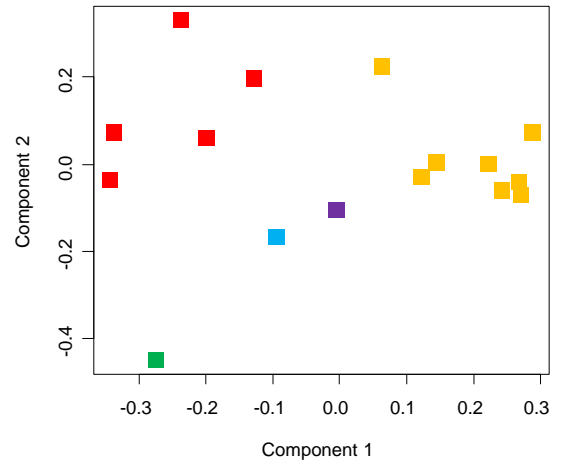
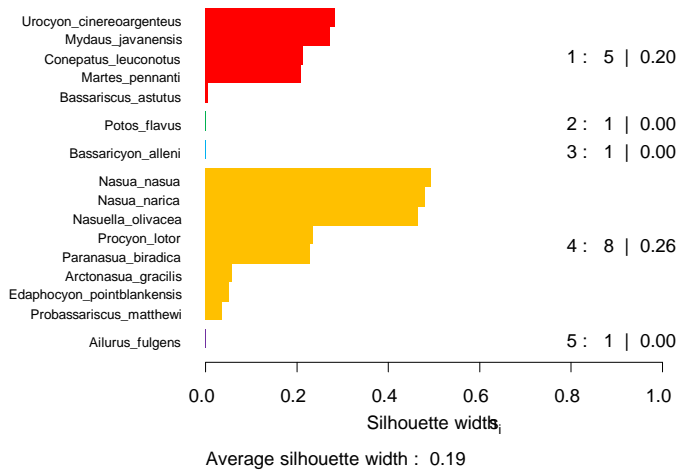
Average Silhouette Widths, Partion Around Medoids



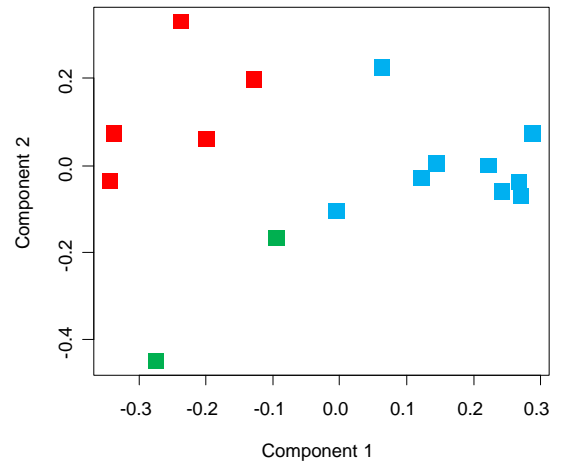
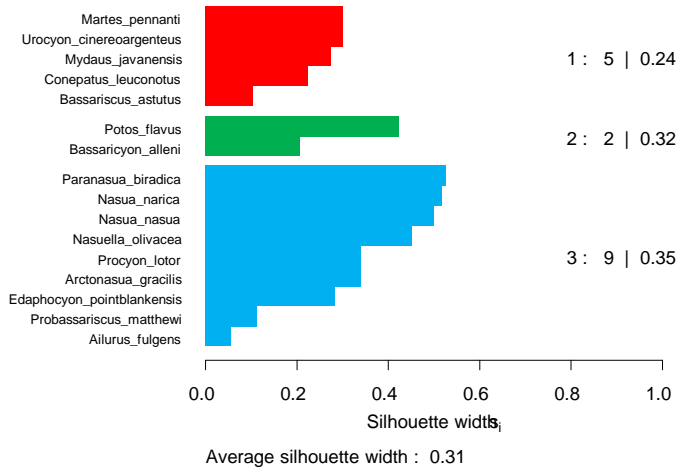
Clade Correspondence: Two of the five BDC clusters contain two or more taxa each. Only cluster 1, consisting of outgroups and associated taxa, forms a clade in phylogeny of Figure 35 of Ahrens (2012), if the phylogeny were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

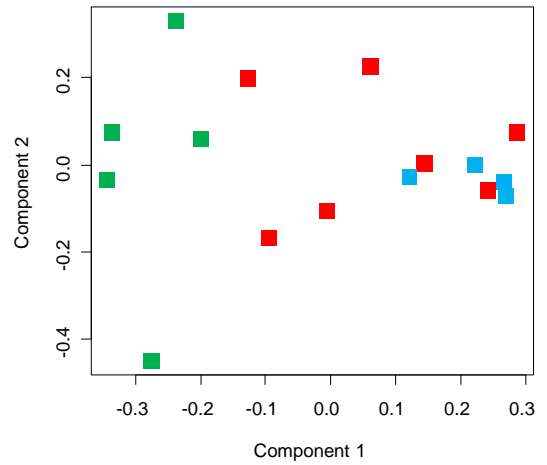
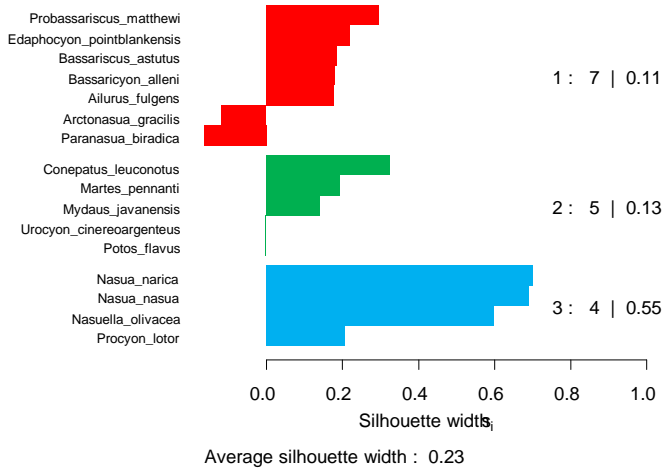


Spearman Correlation

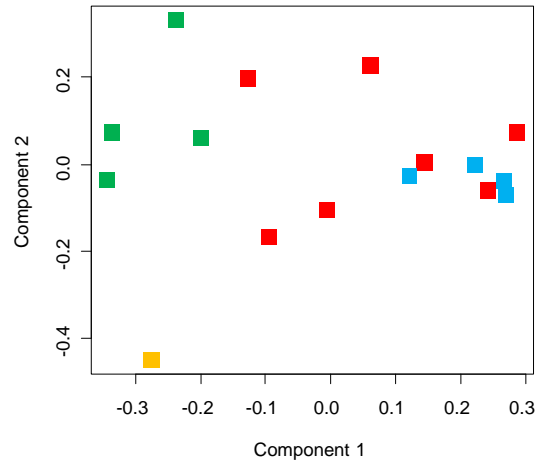
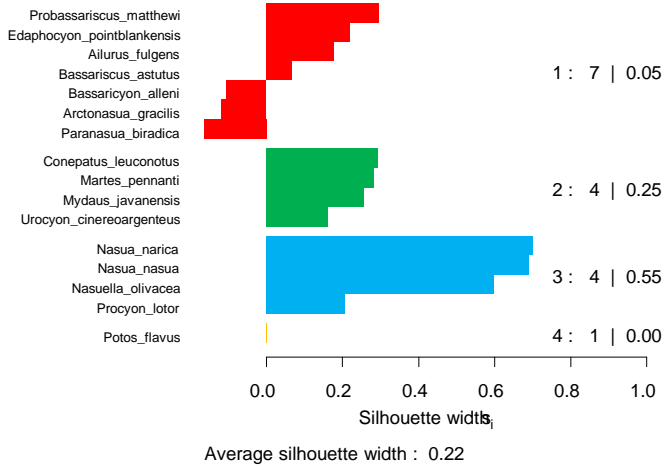


Silhouette plot, Partition Around Medoids

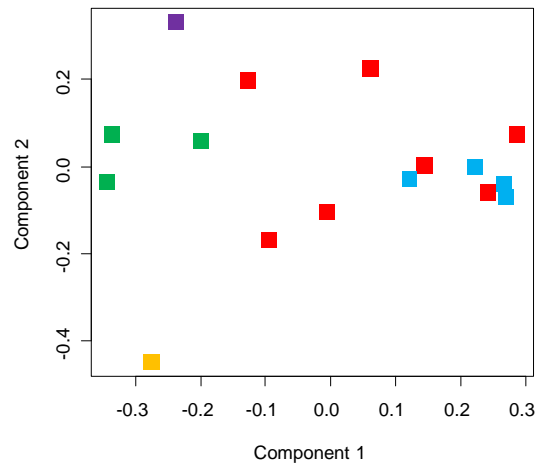
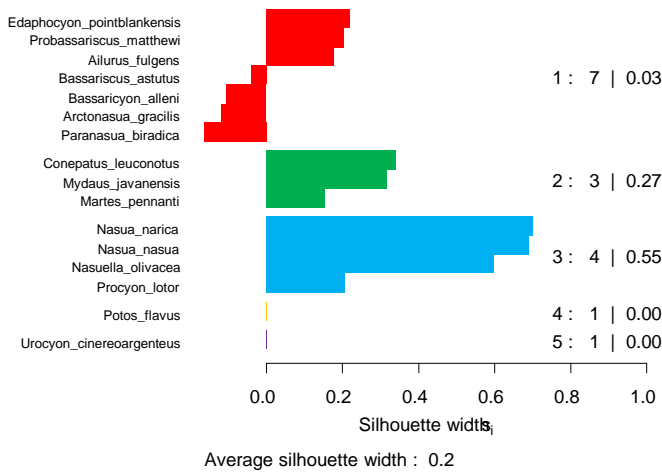
k=3



k=4

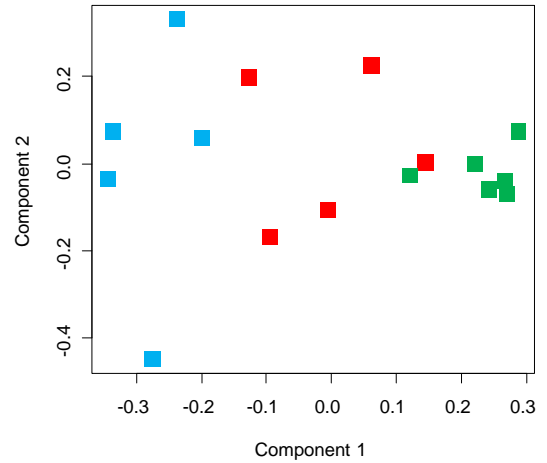
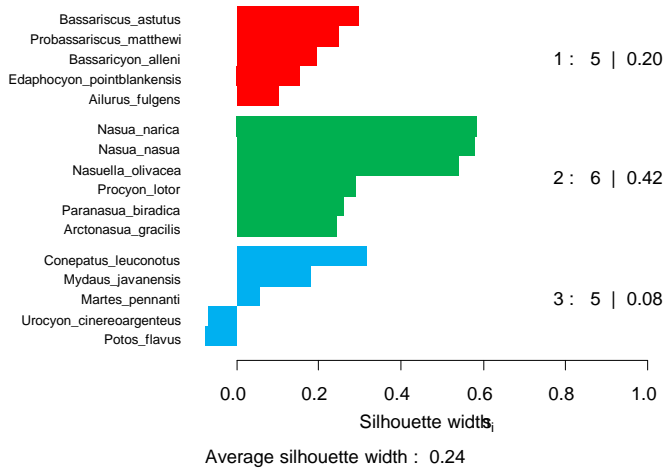


k=5

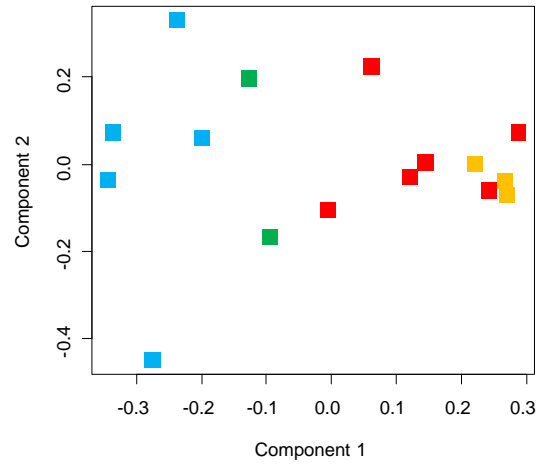
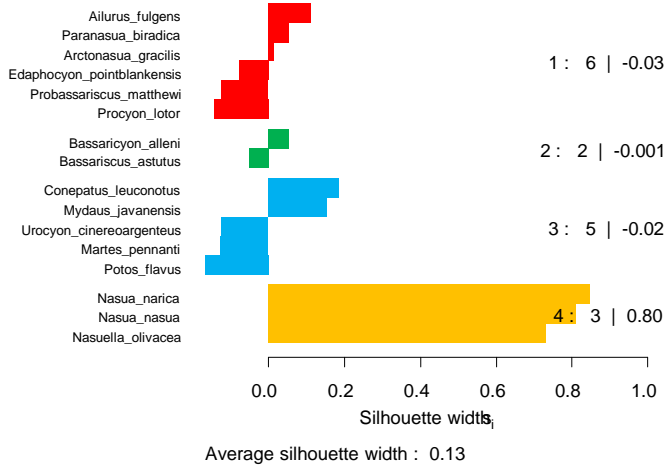


Silhouette plot, Fuzzy Analysis

k=3



k=4



Family Chrysochloridae

Order Chrysochloridea

Asher et al. 2010

Pearson BDC

Negative: 216

Positive: 205

Clusters: 2

Clusterability

Hopkins Statistic: 0.888

Dip test: 0.091

Dip test p-value: 2.20E-16

Spearman BDC

Negative: 216

Positive: 219

Clusters: 2

The Spearman BDC results show only 14 additional instances of significant, positive BDC when compared to the Pearson BDC results, but the difference only serves to complete the ideal pattern of a holobaramin in BDC: There are two groups of taxa evident in both BDC analysis, and in the Spearman BDC results, all taxon pairs within each cluster exhibit significant, positive correlation and all taxon pairs between the two clusters exhibit significant, negative BDC. The average silhouette width for this partition is 0.65.

The two-cluster medoid partition and the two-cluster fuzzy analysis both return exactly the same clusters as the BDC results.

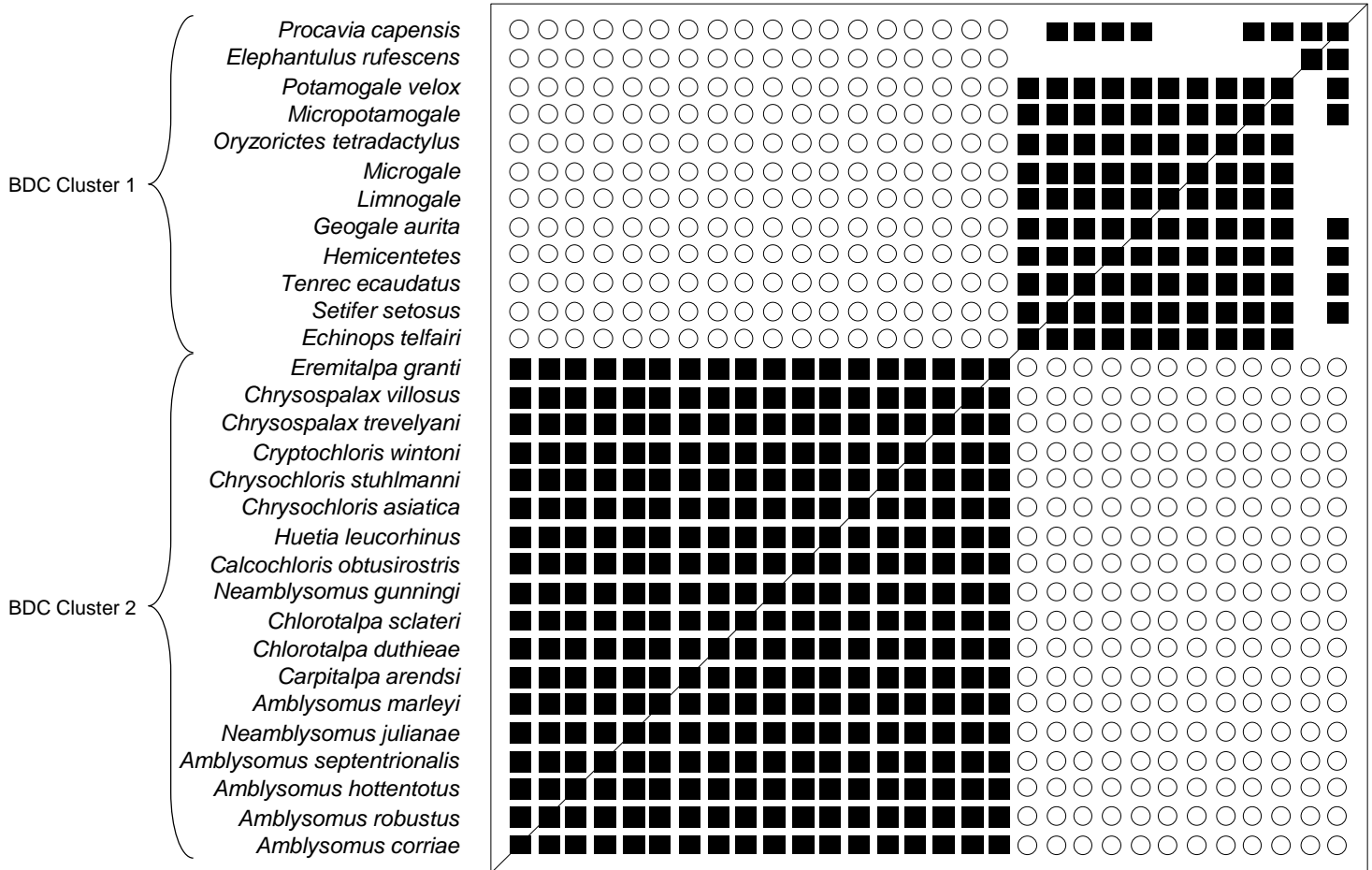
These results reinforce the original conclusion that the Chrysochloridae are a holobaramin.

Original conclusion: HB

Updated conclusion: HB

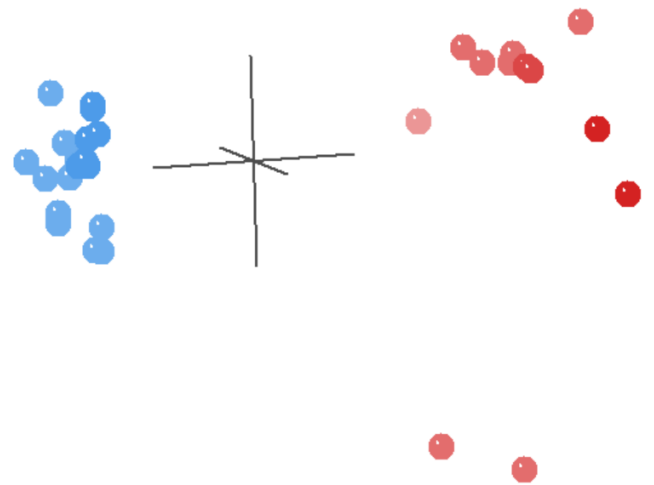
Asher, R.J., S. Maree, G. Bronner, N.C. Bennett, P. Bloomer, P. Czechowski, M. Meyer, and M. Hofreiter. 2010. A phylogenetic estimate for golden moles (Mammalia, Afrotheria, Chrysochloridae). *BMC Evolutionary Biology* 10:69.

Characters: Craniodental and postcranial



Order Chrysochloridea
Family Chrysochloridae

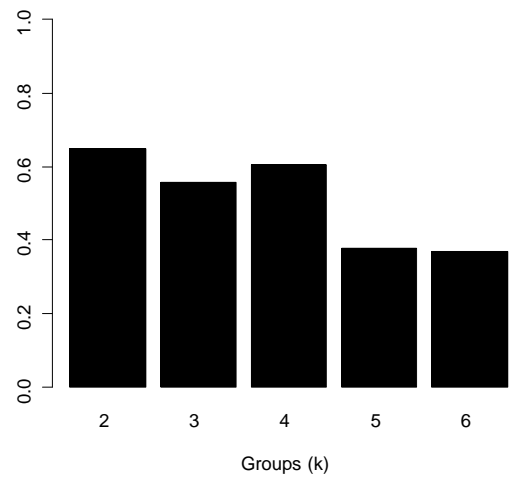
Published taxa	30
Published characters	144
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	30
Characters used for calculations	134
Median bootstrap value	100
F ₉₀	0.93
Stress of 3D MDS	0.11
k _{min}	6
Conclusion	HB



Notes: Chrysochloridae is well-separated from the outgroup taxa in MDS and BDC results. Chrysochloridae is a holobaramin.



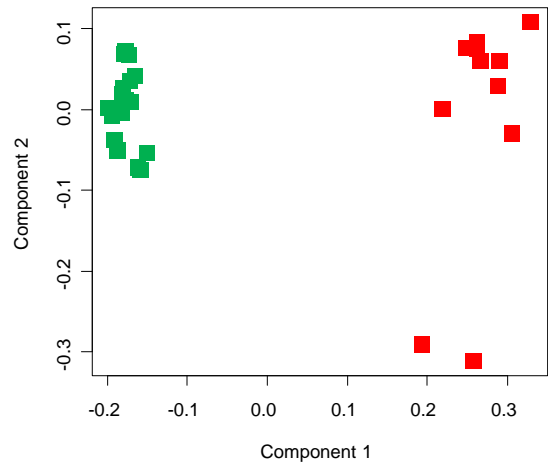
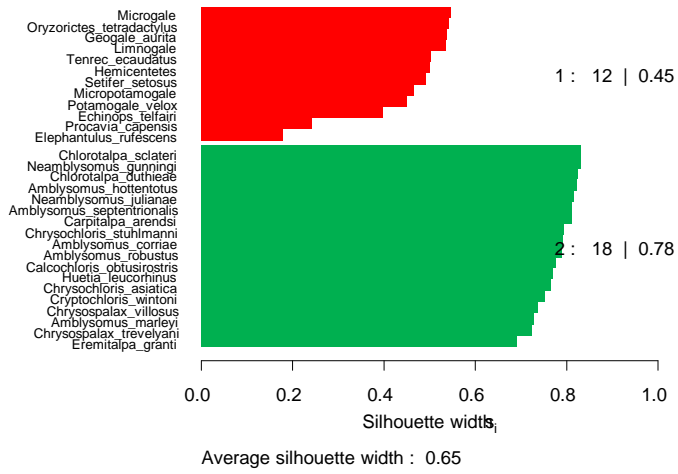
Average Silhouette Widths, Partion Around Medoids



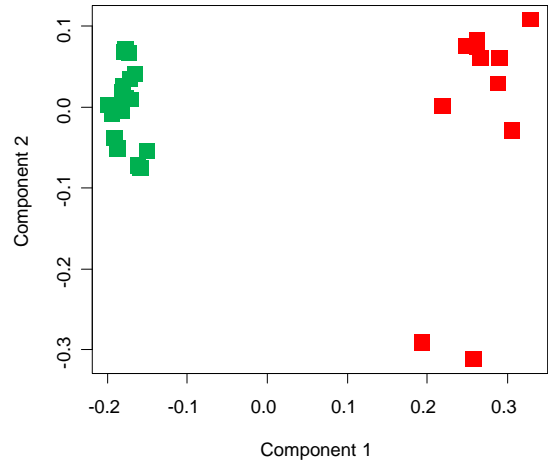
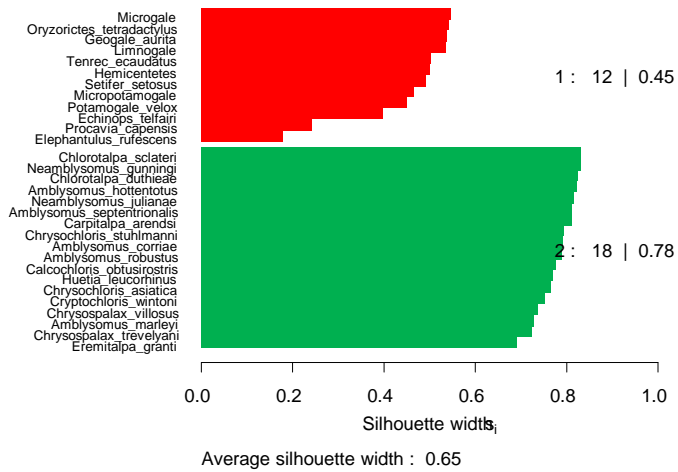
Clade Correspondence: The two clear BDC clusters both have more than two taxa each. Both are monophyletic in the phylogeny of Figure 4C of Asher et al. (2010).

Silhouette plot, BDC partitions

Pearson Correlation

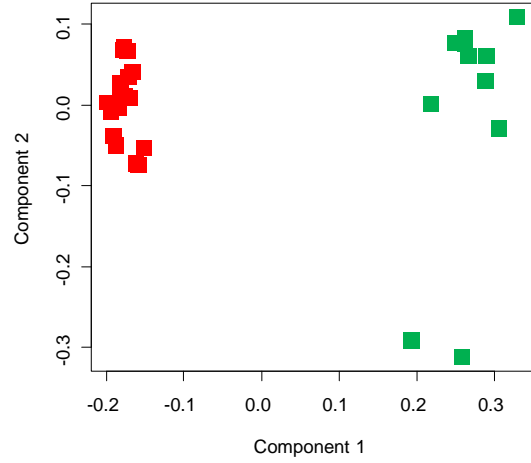
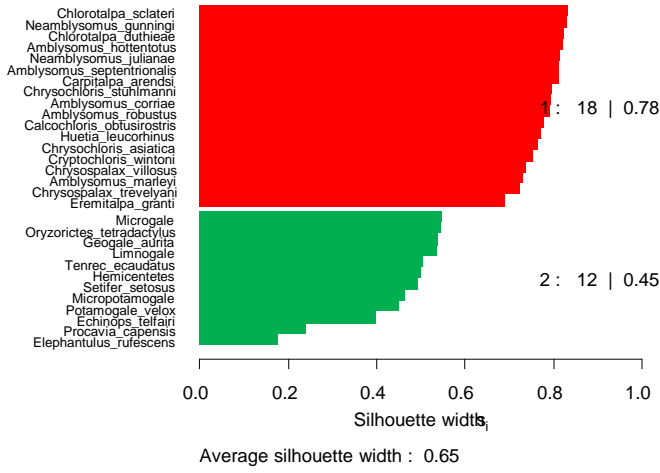


Spearman Correlation

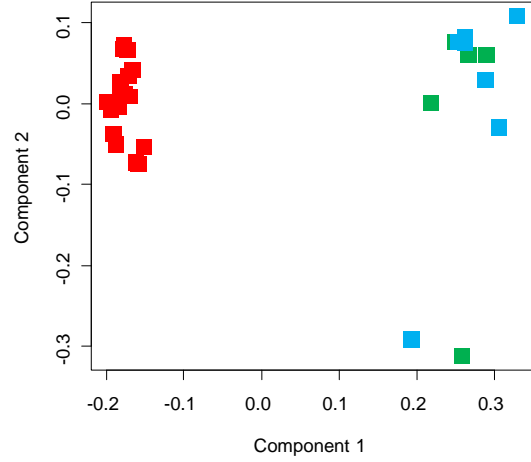
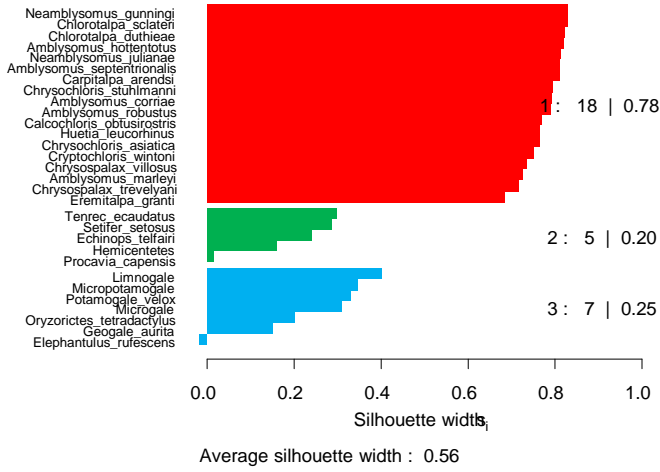


Silhouette plot, Partition Around Medoids

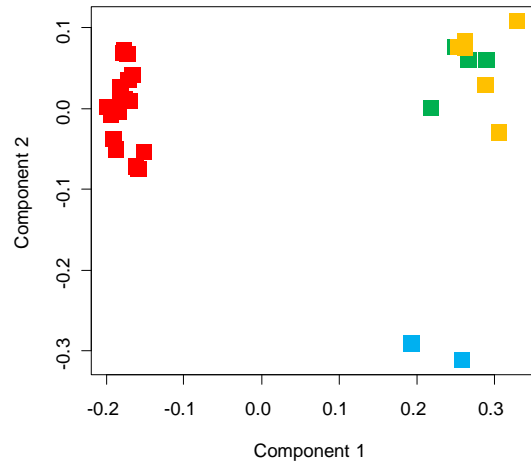
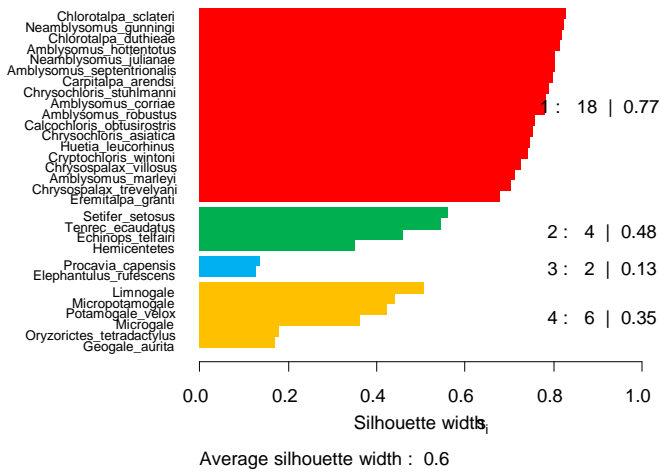
k=2



k=3

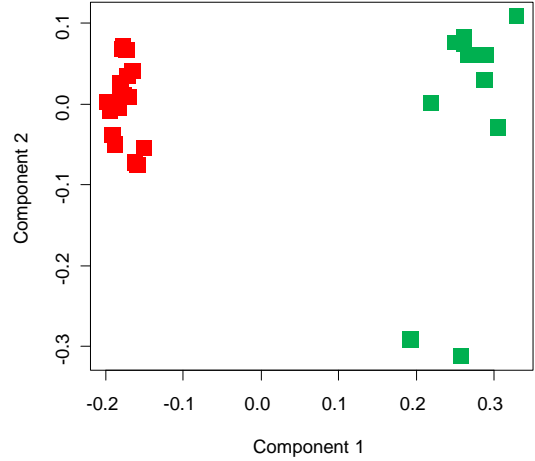
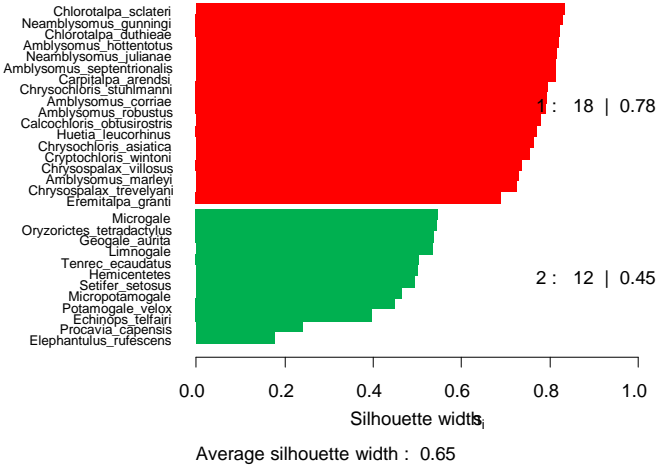


k=4

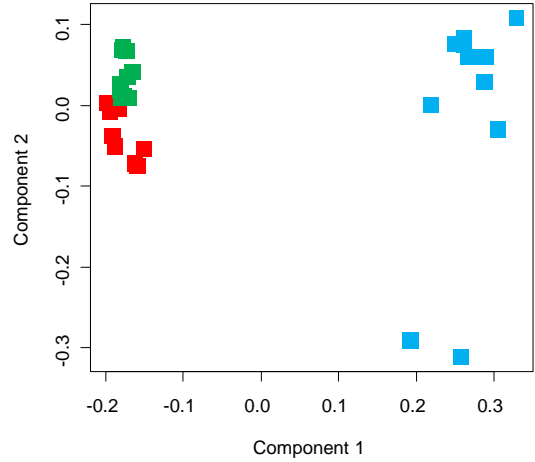
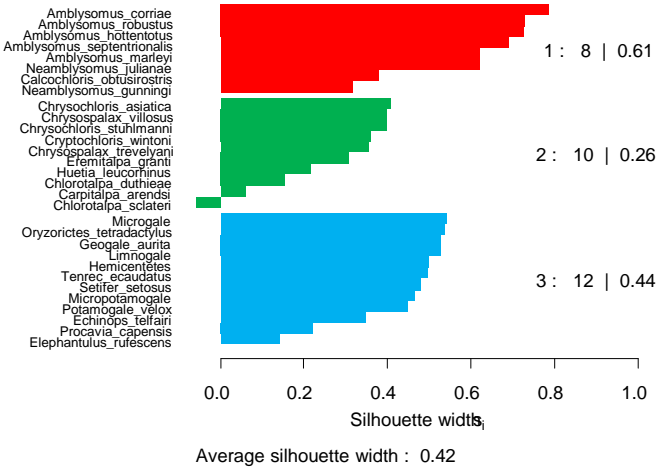


Silhouette plot, Fuzzy Analysis

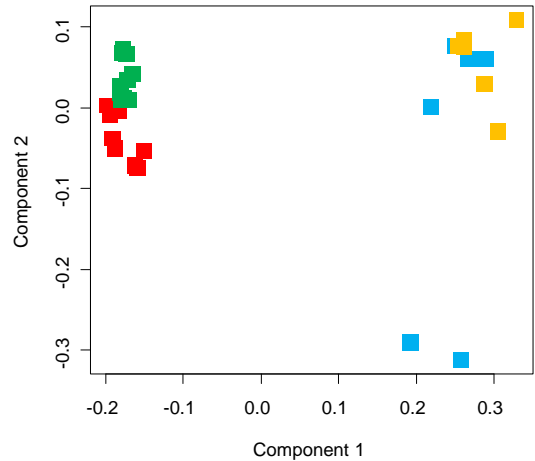
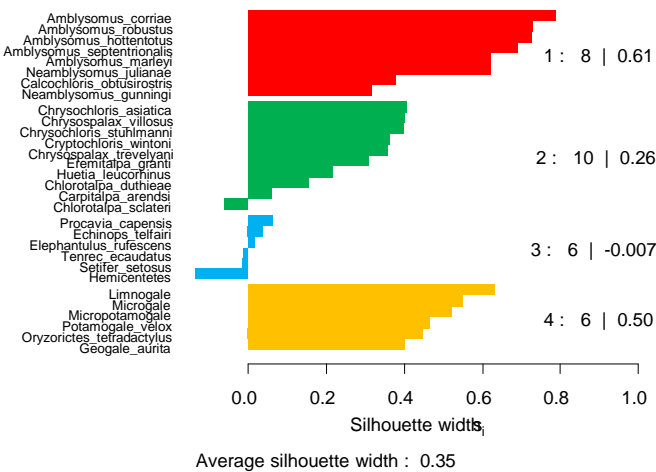
k=2



k=3



k=4



Family Erinaceidae

Order Erinaceomorpha

He et al. 2012

Pearson BDC

Negative: 112

Positive: 119

Clusters: 2

Spearman BDC

Negative: 112

Positive: 119

Clusters: 2

Clusterability

Hopkins Statistic: 0.934

Dip test: 0.124

Dip test p-value: 2.20E-16

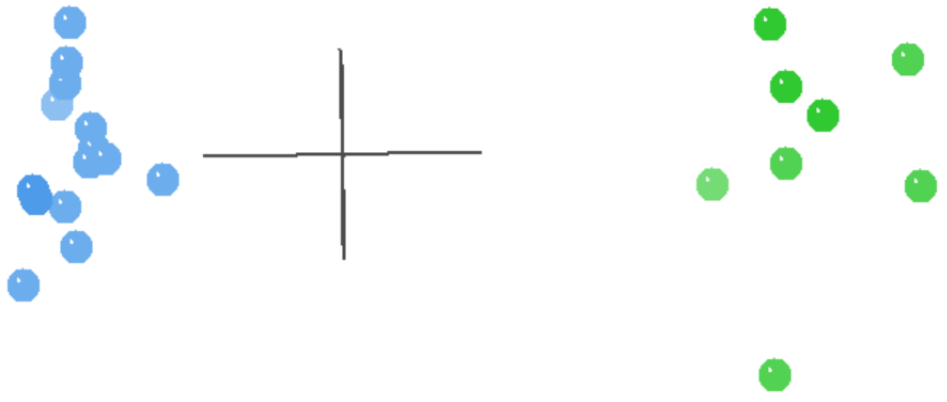
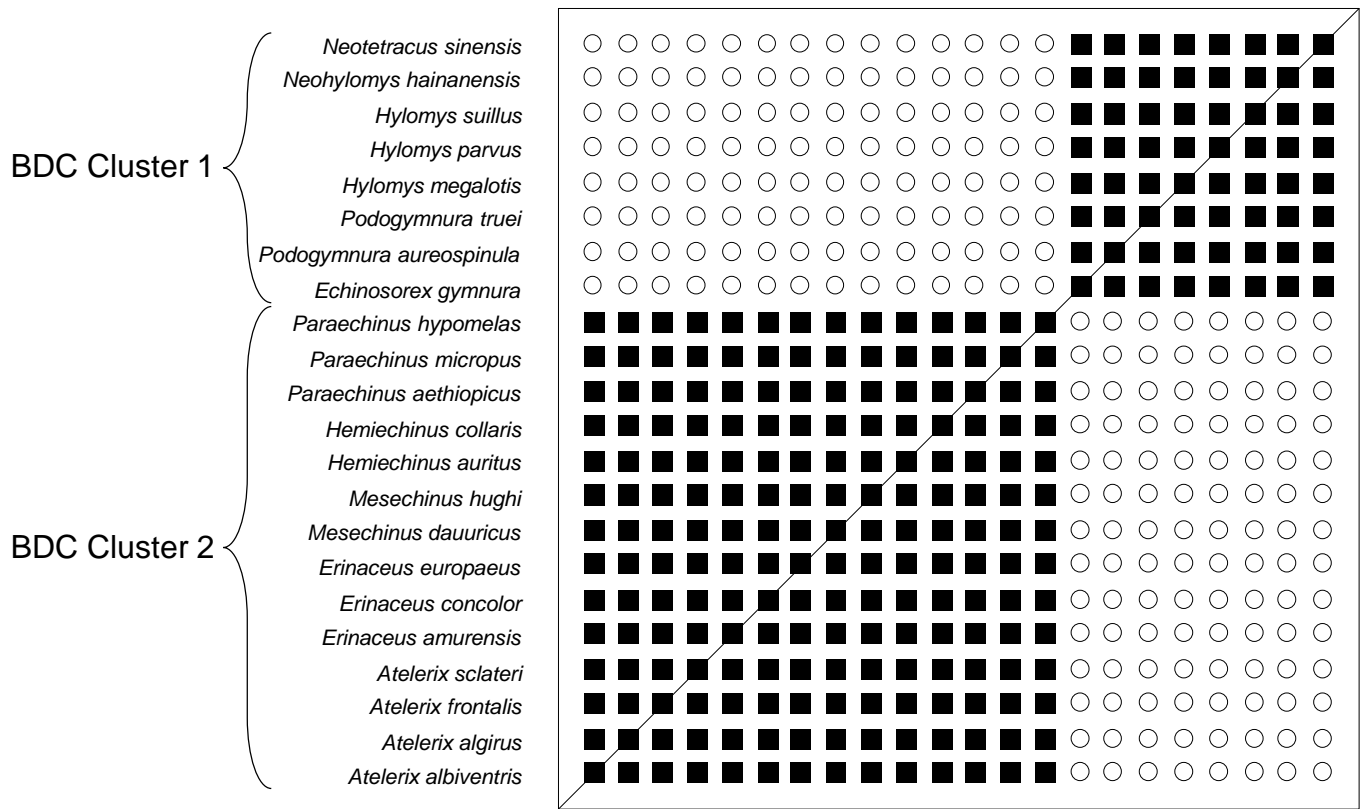
The Spearman and Pearson BDC results are identical. The two-cluster medoid partition and fuzzy analysis also agree exactly with the BDC results. These results reinforce the original conclusion that Erinaceinae and Galericinae are holobaramins.

Original conclusion: HB

Updated conclusion: HB

He, K., J.-H. Chen, G.C. Gould, N. Yamaguchi, H.-S. Ai, Y.-X. Wang, Y.-P. Zhang, and X.-L. Jiang. 2012. An estimation of Erinaceidae phylogeny: a combined analysis approach. *PLoS ONE* 7(6):e39304.

Characters: Craniodental, postcranial, external morphology



Order Erinaceomorpha
Family Erinaceidae

Published taxa	23
Published characters	135
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	22
Characters used for calculations	97
Median bootstrap value	100
F ₉₀	1
Stress of 3D MDS	0.07
k _{min}	4
Conclusion	HB

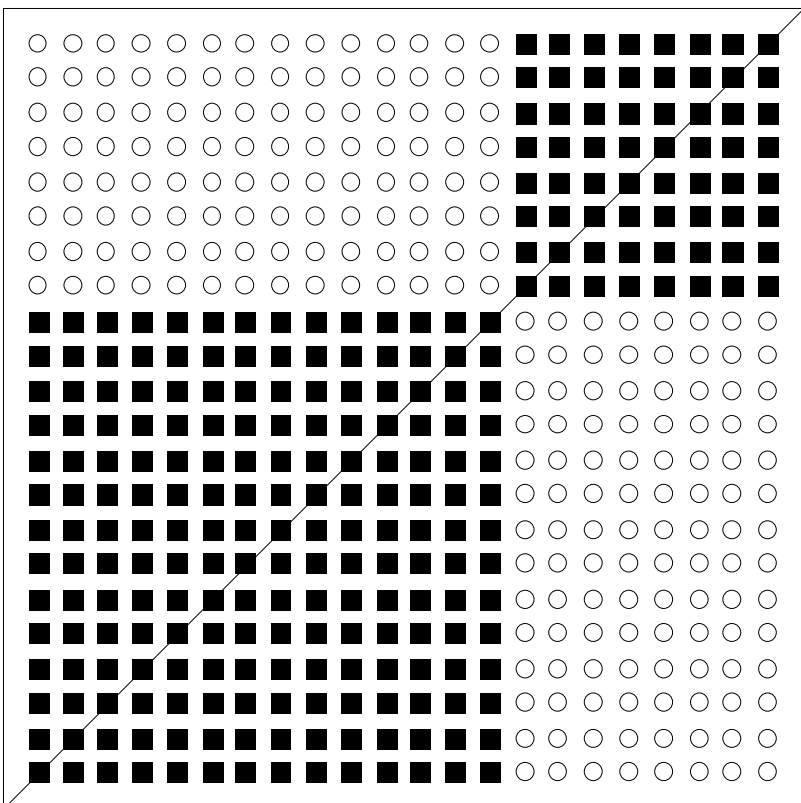
Notes: Subfamilies Erinaceinae and Galericinae are both well-separated in the BDC and MDS results. Both are likely holobaramins.

BDC Cluster 1

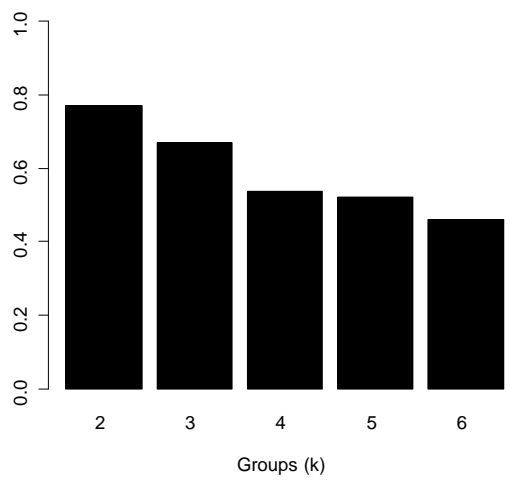
- Neotetracus sinensis*
- Neohylomys hainanensis*
- Hylomys suillus*
- Hylomys parvus*
- Hylomys megalotis*
- Podogymnura truei*
- Podogymnura aureospinula*
- Echinosorex gymnura*

BDC Cluster 2

- Paraechinus hypomelas*
- Paraechinus micropus*
- Paraechinus aethiopicus*
- Hemiechinus collaris*
- Hemiechinus auritus*
- Mesechinus hughi*
- Mesechinus dauuricus*
- Erinaceus europaeus*
- Erinaceus concolor*
- Erinaceus amurensis*
- Atelerix sclateri*
- Atelerix frontalis*
- Atelerix algirus*
- Atelerix albiventris*



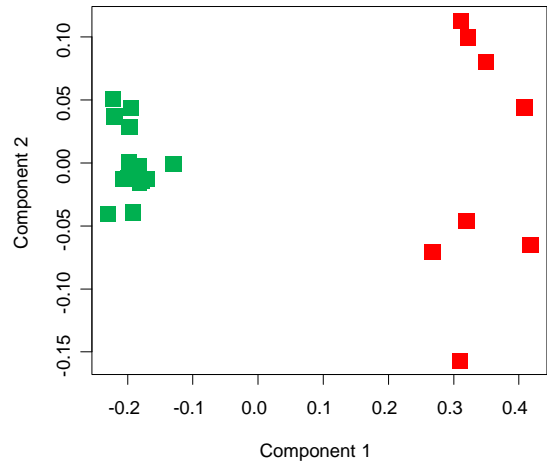
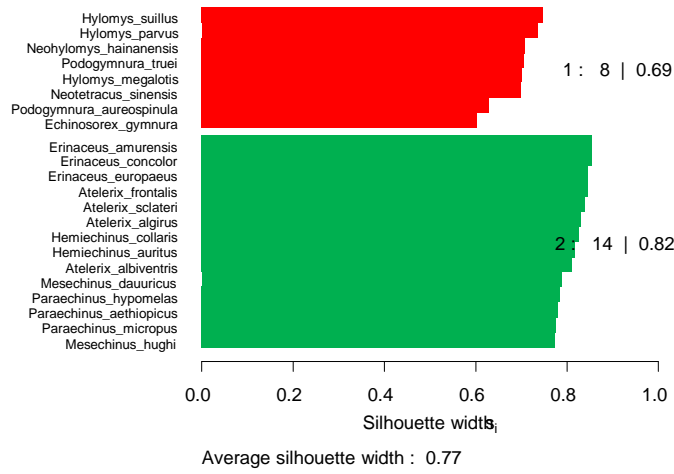
Average Silhouette Widths, Partition Around Medoids



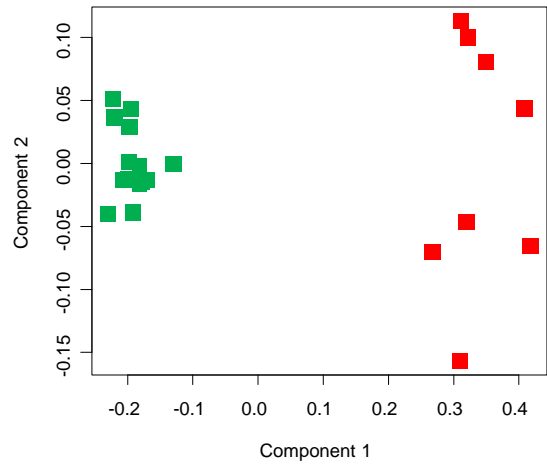
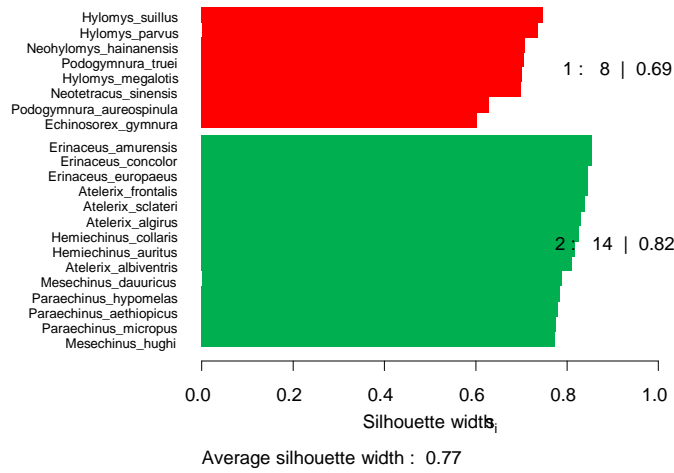
Clade Correspondence: The two clear BDC clusters both have more than two taxa each. Both are clades in the phylogeny of Figure 5D of He et al. (2012), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

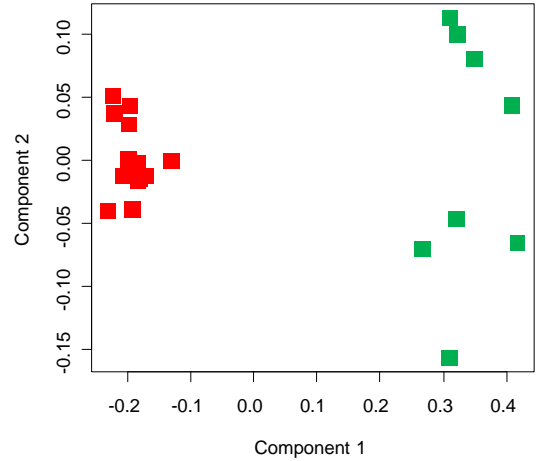
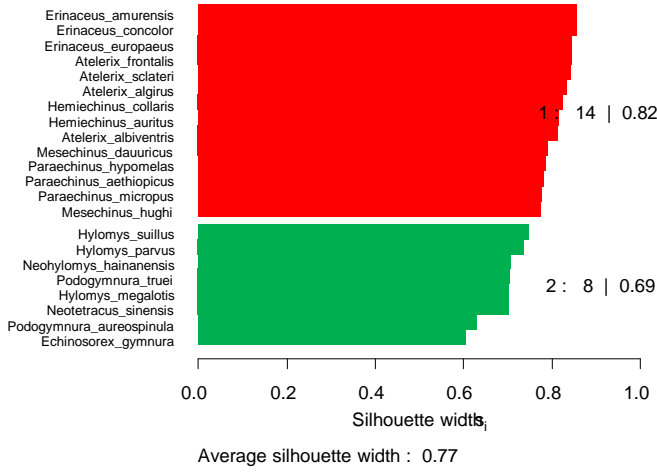


Spearman Correlation

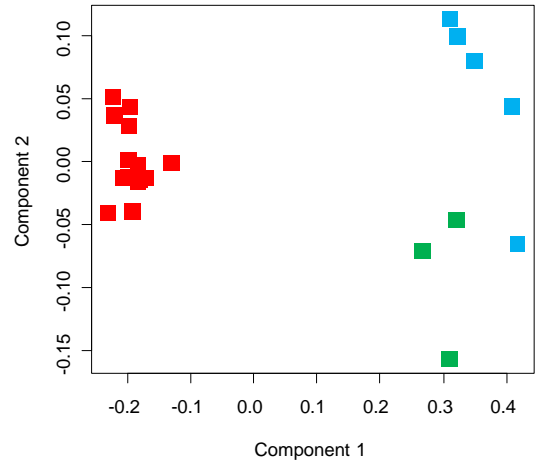
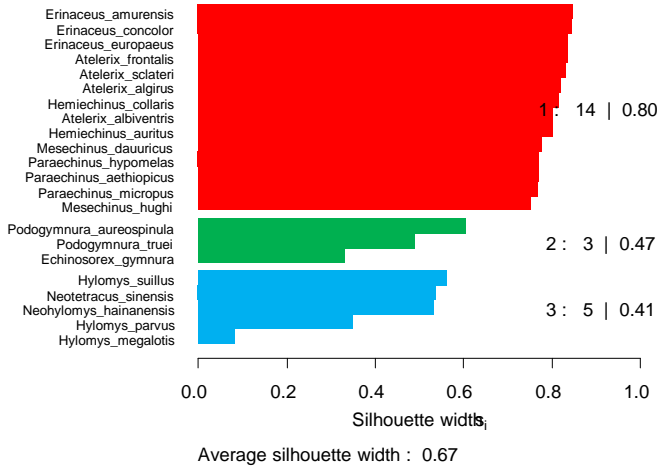


Silhouette plot, Partition Around Medoids

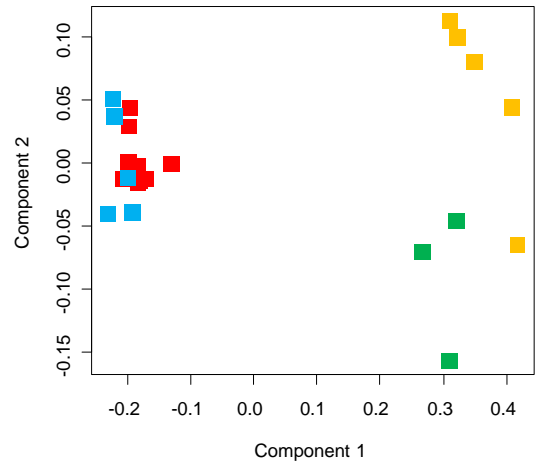
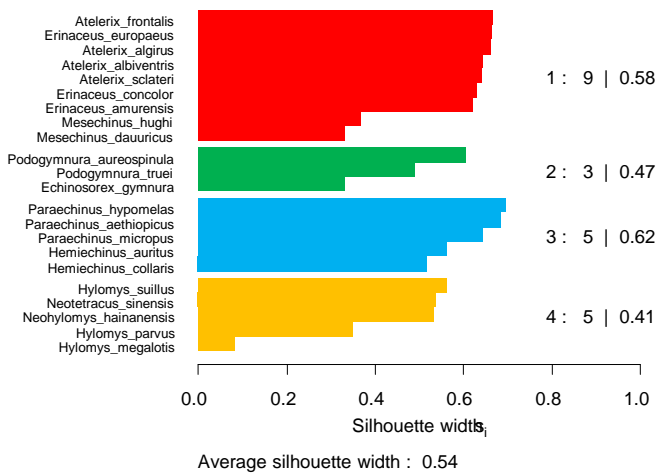
k=2



k=3

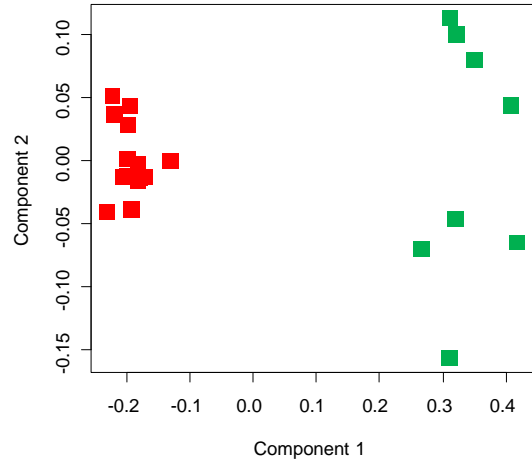
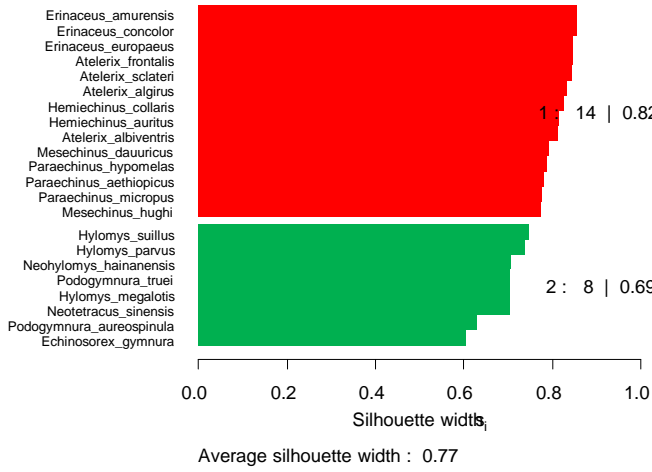


k=4

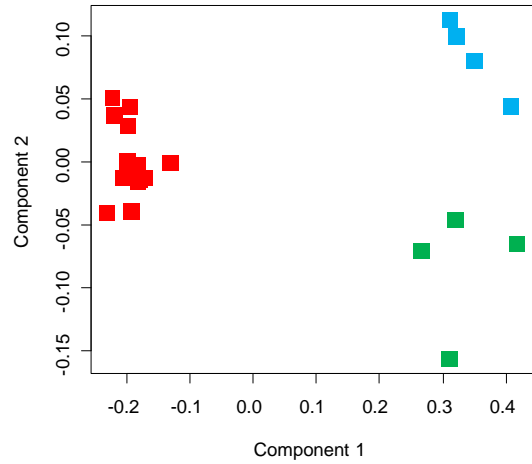
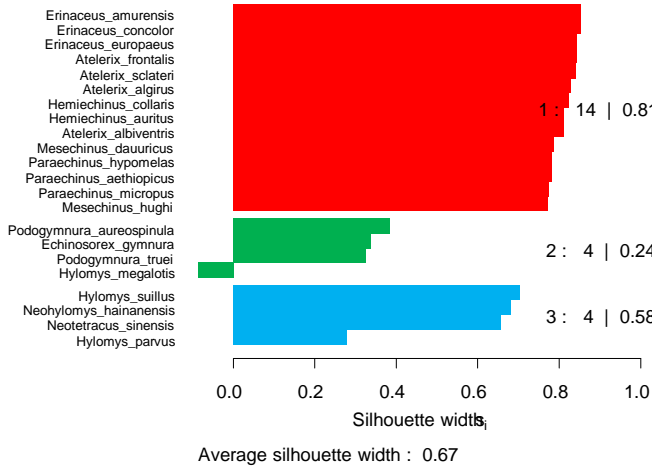


Silhouette plot, Fuzzy Analysis

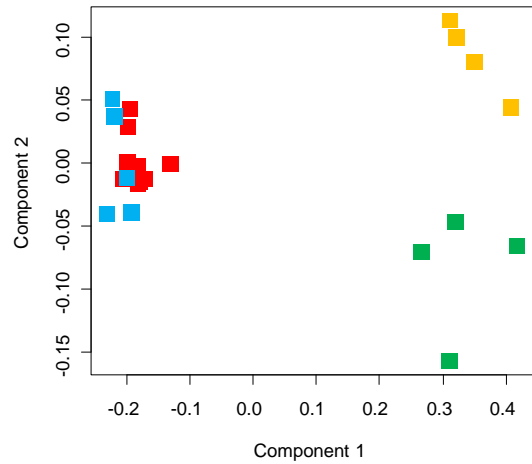
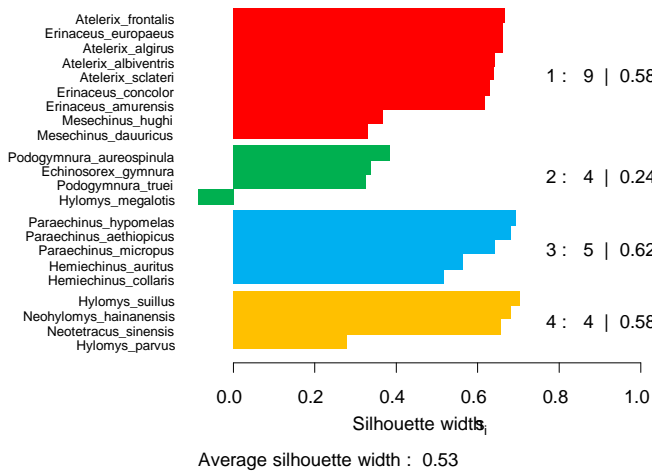
k=2



k=3



k=4



Family Talpidae

Order Erinaceomorpha

Sánchez-Villagra et al. 2006

Pearson BDC

Negative: 71

Positive: 84

Clusters: 3

Clusterability

Hopkins Statistic: 0.744

Dip test: 0.032

Dip test p-value: 0.142

Spearman BDC

Negative: 61

Positive: 92

Clusters: 2

In the Pearson BDC, three clusters are evident, with significant, negative correlation widespread between them. In the Spearman BDC, *Uropsilus*, which is a singleton cluster in the Pearson BDC results, shares significant, positive correlation with every member of the outgroup cluster. Thus, the number of clusters is reduced from three to two. The average silhouette width for the three Pearson BDC clusters is 0.3 and for the two Spearman BDC clusters is 0.42.

Medoid partitioning at $k=3$ has an average silhouette width of 0.29 and does not agree with the Pearson BDC clusters. The cluster membership difference is 24%. Two-cluster medoid partitioning agrees exactly with the Spearman BDC clusters.

Fuzzy analysis at $k=3$ yields a partition with an average silhouette width of 0.28 and also does not agree with the Pearson BDC clusters. The cluster membership difference is 33%. At $k=2$, the fuzzy partition does not agree with the Spearman BDC nor the two-cluster medoid partition; however, the average silhouette value of 0.29 is substantially lower than the Spearman BDC clusters.

These results are very consistent with the original analysis. Here we find that the Chinese shrew mole *Uropsilus* may not be a member of the Talpidae holobaramin. Nevertheless, the remainder of the membership of the talpid holobaramin is supported by the Spearman BDC and two-cluster medoid partition. Though the two-cluster fuzzy analysis does not support this partition, it is a lesser quality partition as revealed by its average silhouette width. The original conclusion is therefore largely confirmed.

Original conclusion: HB

Updated conclusion: HB

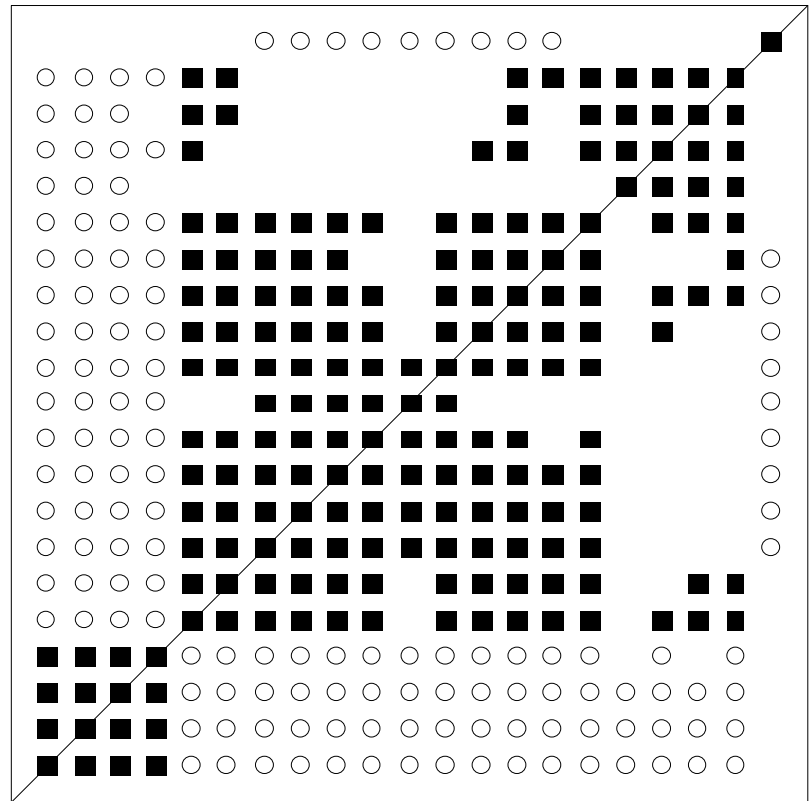
Characters: Craniodental and postcranial

BDC Cluster 1

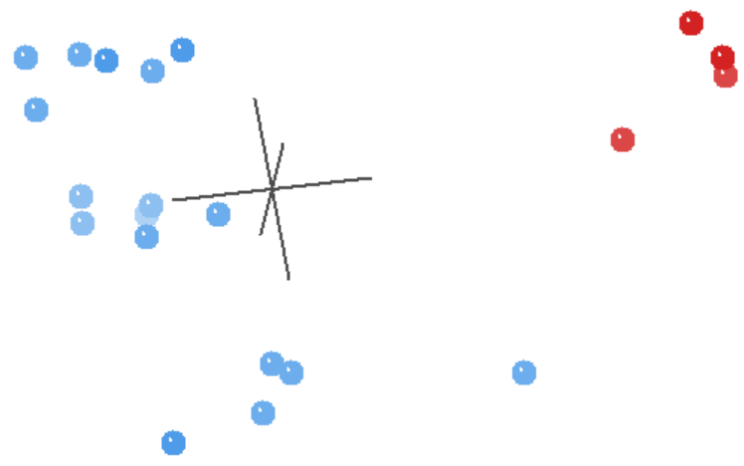
BDC Cluster 2

BDC Cluster 3

- Uropsilus* spp.
- Urotrichus talpoides*
- Dymecodon pilirostris*
- Galemys pyrenaicus*
- Desmana moschata*
- Scapanus* spp.
- Scalopus aquaticus*
- Scapanulus oweni*
- Parascalops breweri*
- Scaptonyx fuscicaudus*
- Scaptochirus moschatus*
- Parascaptor leucura*
- Talpa europaea*
- Mogera wogura*
- Euroscaptor* spp.
- Neurotrichus gibbsii*
- Condylura cristata*
- Erinaceus europaeus*
- Crocidura russula*
- Sorex araneus californicus*
- Blarina brevicauda*



Order Erinaceomorpha
Family Talpidae



Published taxa	21
Published characters	157
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	21
Characters used for calculations	135
Median bootstrap value	90
F ₉₀	0.49
Stress of 3D MDS	0.21
k _{min}	9
Conclusion	HB

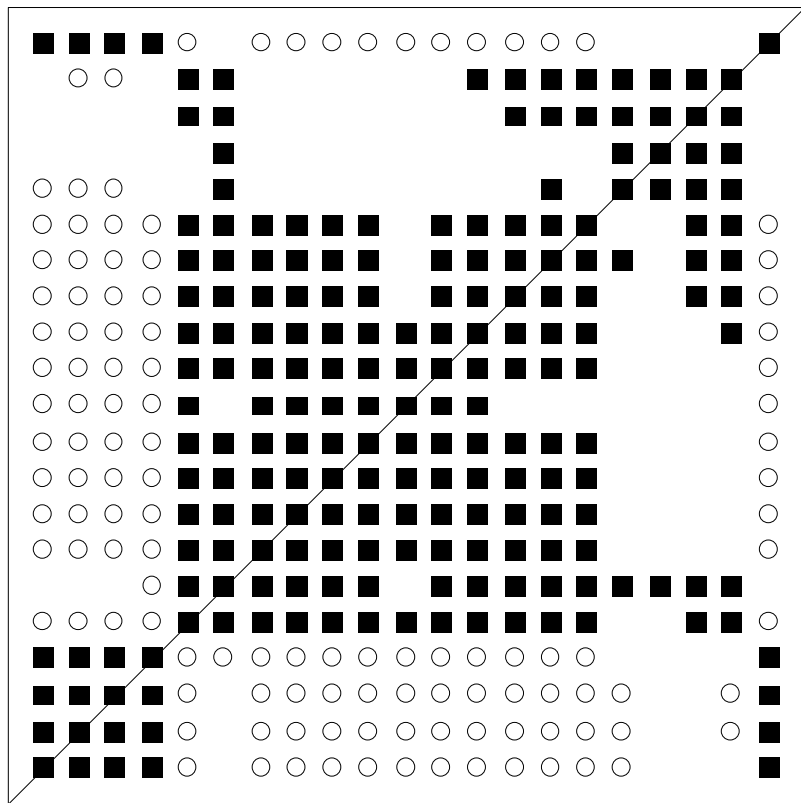
Notes: Talpidae is well-separated from the outgroup taxa in both the BDC and MDS results. Talpidae is likely a holobaramin.

BDC Cluster 3

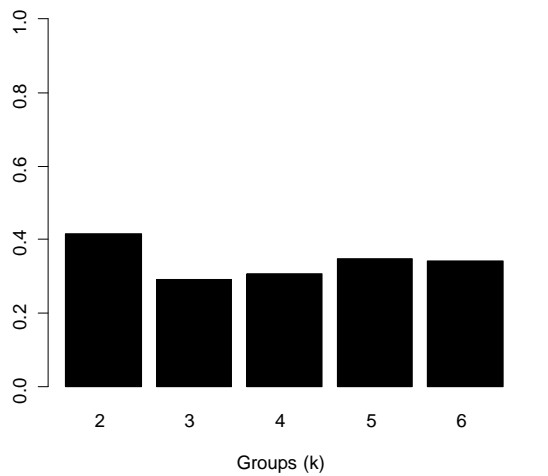
BDC Cluster 2

BDC Cluster 3

- Uropsilus* spp.
- Urotrichus talpoides*
- Dymecodon pilirostris*
- Galemys pyrenaicus*
- Desmana moschata*
- Scapanus* spp.
- Scalopus aquaticus*
- Scapanulus oweni*
- Parascalops breweri*
- Scaptonyx fuscicaudus*
- Scaptochirus moschatus*
- Parascaptor leucura*
- Talpa europaea*
- Mogera wogura*
- Euroscaptor* spp.
- Neurotrichus gibbsii*
- Condylura cristata*
- Erinaceus europaeus*
- Crocidura russula*
- Sorex araneus californicus*
- Blarina brevicauda*



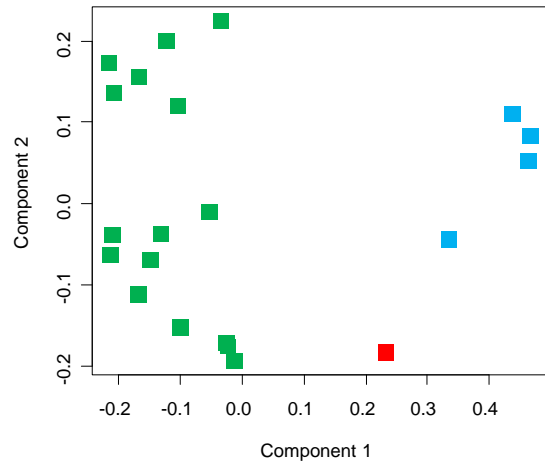
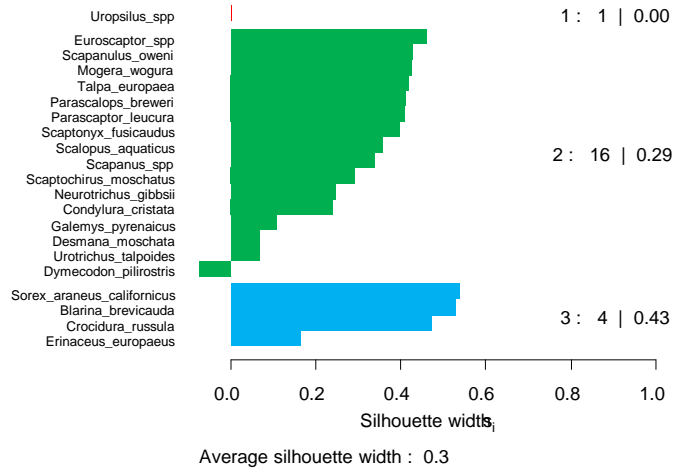
Average Silhouette Widths, Partion Around Medoids



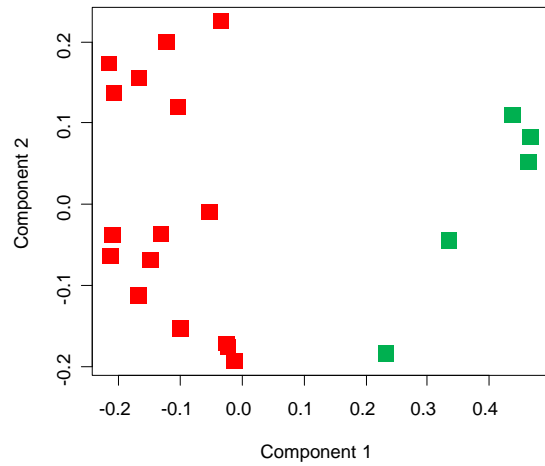
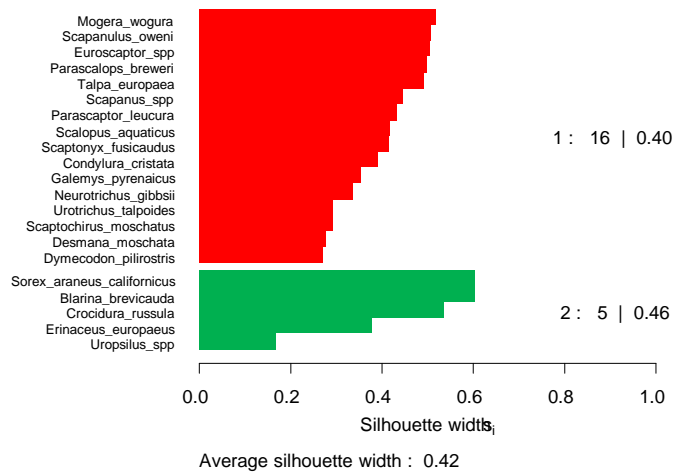
Clade Correspondence: Two of the BDC clusters contain two or more taxa each. Both are monophyletic in the phylogeny of Figure 1 in Sánchez-Villagra et al. (2006).

Silhouette plot, BDC partitions

Pearson Correlation

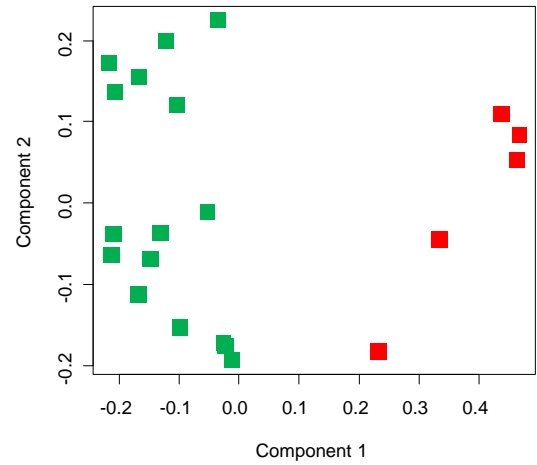
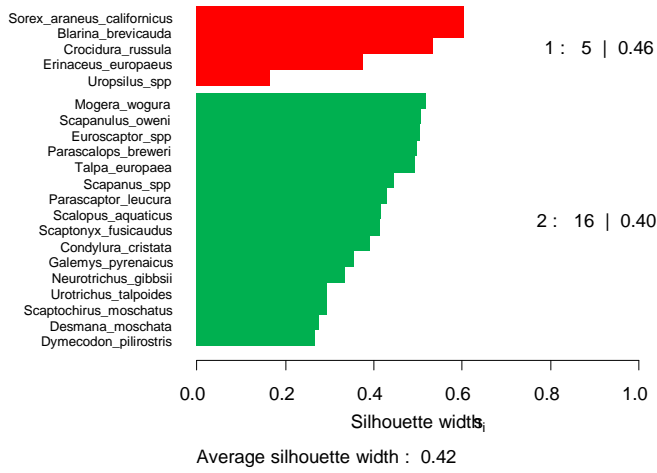


Spearman Correlation

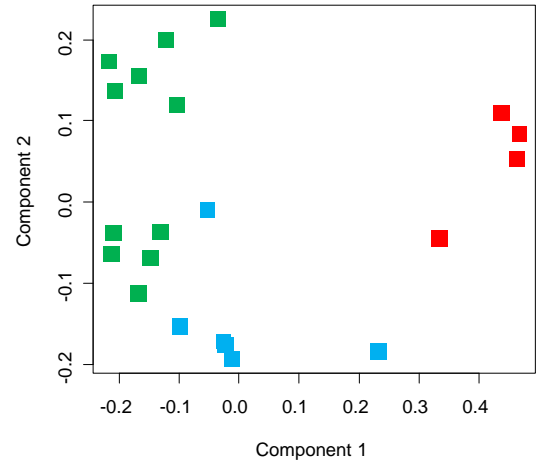
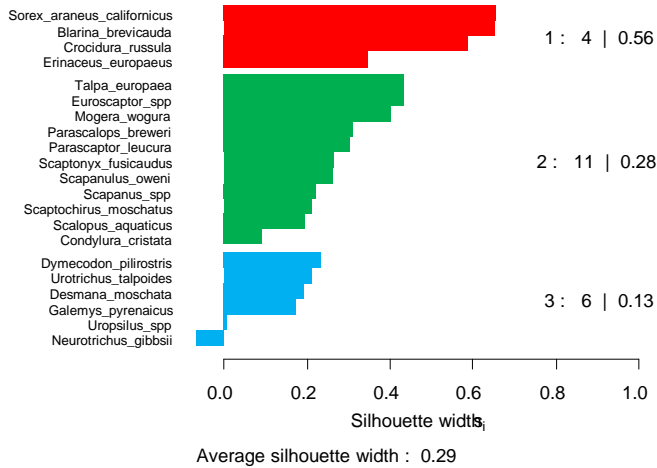


Silhouette plot, Partition Around Medoids

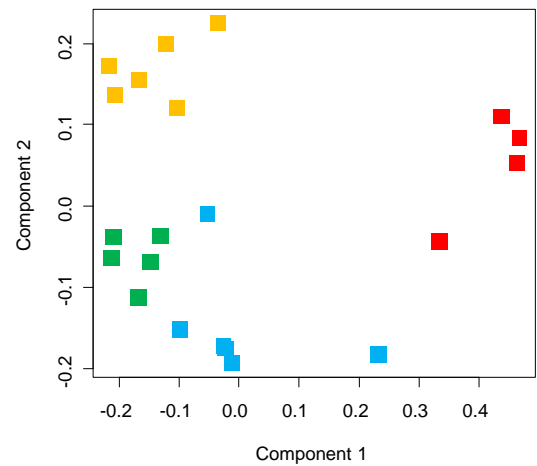
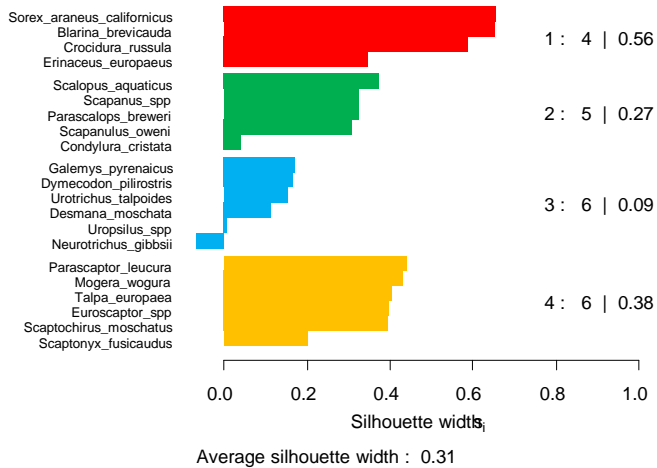
k=2



k=3

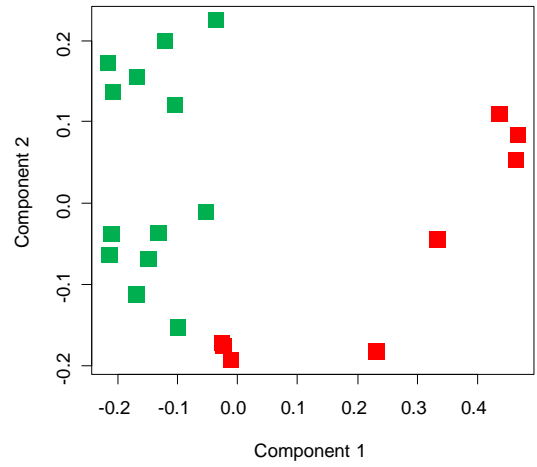
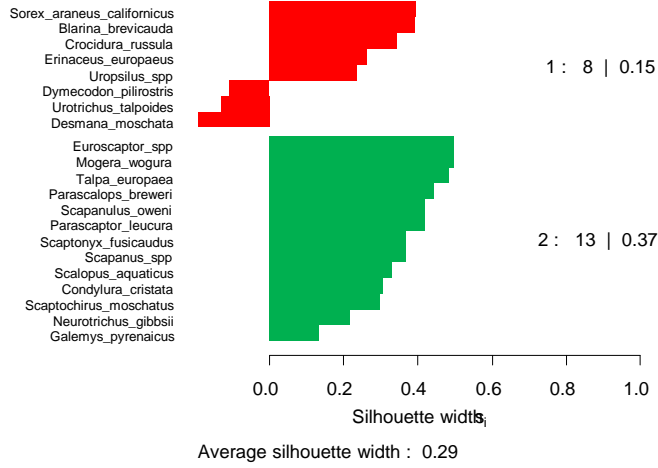


k=4

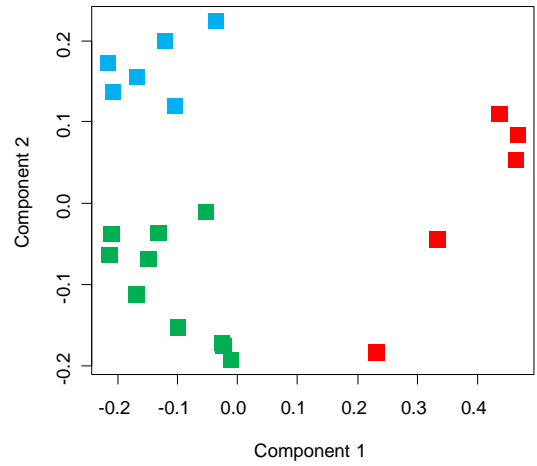
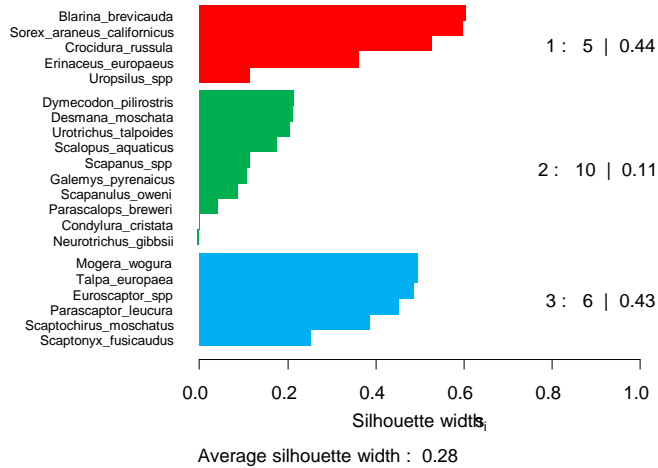


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Nyctitheriidae

Order Soricomorpha

Manz and Bloch 2015

Pearson BDC

Negative: 69

Positive: 353

Clusters: 4

Clusterability

Hopkins Statistic: 0.756

Dip test: 0.025

Dip test p-value: 0.00038

Spearman BDC

Negative: 36

Positive: 398

Clusters: 3

The original Pearson BDC results included two outgroup taxa *Maelestes* and *Macrocranion* that formed a single cluster that shared mostly significant, negative correlation with three ingroup clusters. In the Spearman BDC results, the outgroup taxa are split up and attached to different ingroup clusters. Hence, the cluster count goes from four in the Pearson BDC results to three in the Spearman BDC results. The cluster membership difference is 5%. The Pearson BDC clusters have an average silhouette width of 0.25, and the Spearman BDC clusters have an average silhouette width of 0.23, with two taxa exhibiting negative silhouette widths.

The four-cluster medoid partition has an average silhouette width of 0.19 and does not agree with the Pearson BDC clusters. The cluster membership difference is 39%. Likewise, the three-cluster medoid partition has an average silhouette width of 0.23 and does not agree with the Spearman BDC clusters.

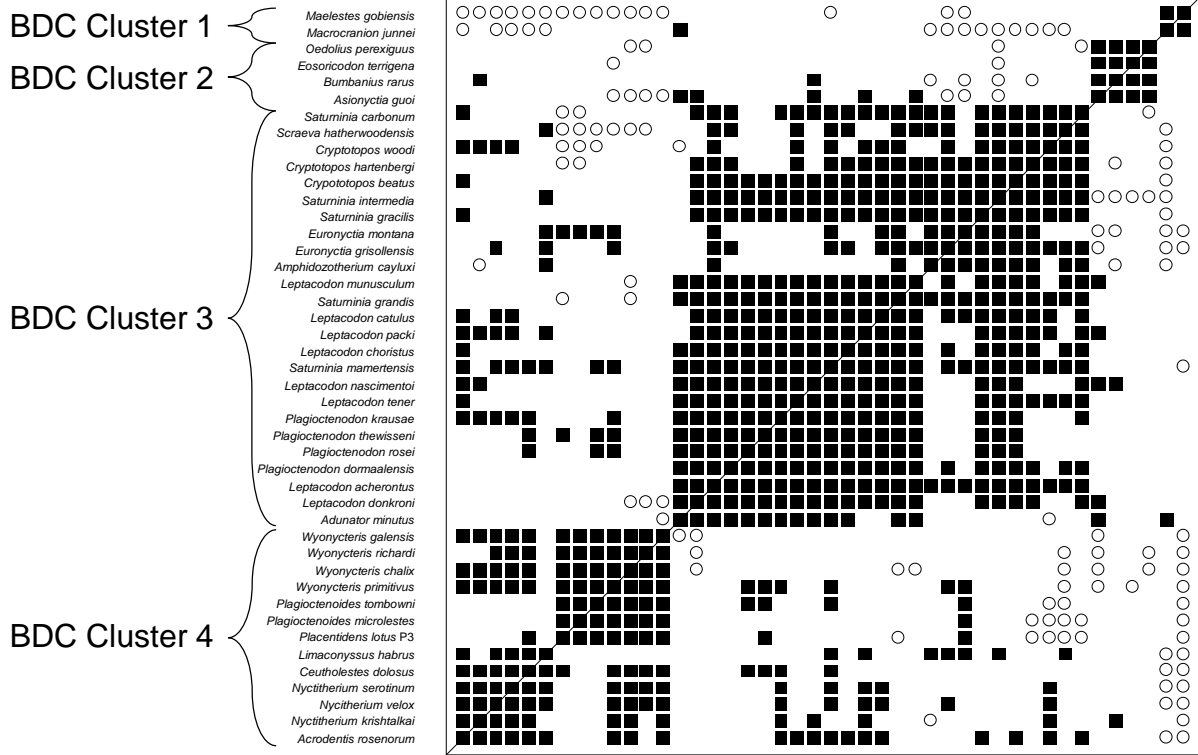
The original conclusion was based on a single cluster of outgroup taxa that exhibited mostly significant, negative BDC with the ingroup taxa. Because the MDS results did not reveal an obvious discontinuity, the conclusion of holobaramin was qualified as uncertain. Here the uncertainty has multiplied. The Pearson BDC results are not confirmed by the Spearman BDC results or by the medoid partition. We ought therefore to change the original conclusion to inconclusive.

Original conclusion: HB?

Updated conclusion: Inconclusive

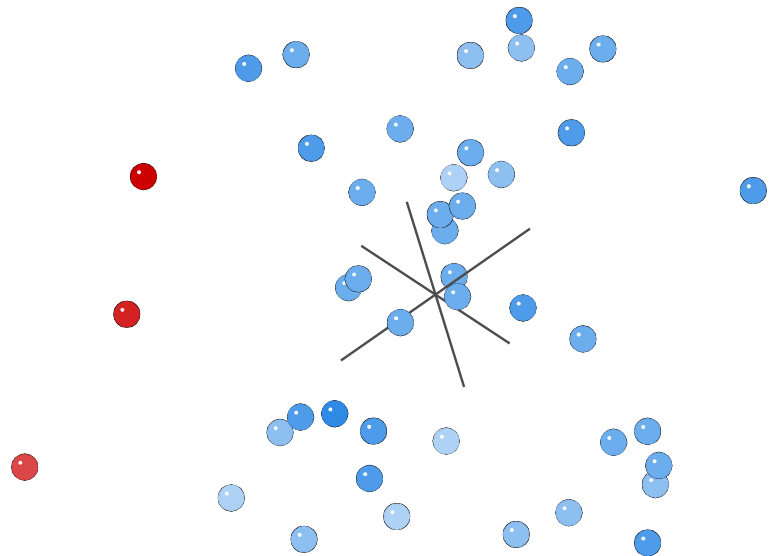
Manz, C.L. and J.I. Bloch. 2015. Systematics and phylogeny of Paleocene-Eocene Nyctitheriidae (Mammalia, Eulipotyphla?) with description of a new species from the Late Paleocene of the Clarks Fork Basin, Wyoming, USA. *Journal of Mammalian Evolution* 22:307-342.

Characters: Dental

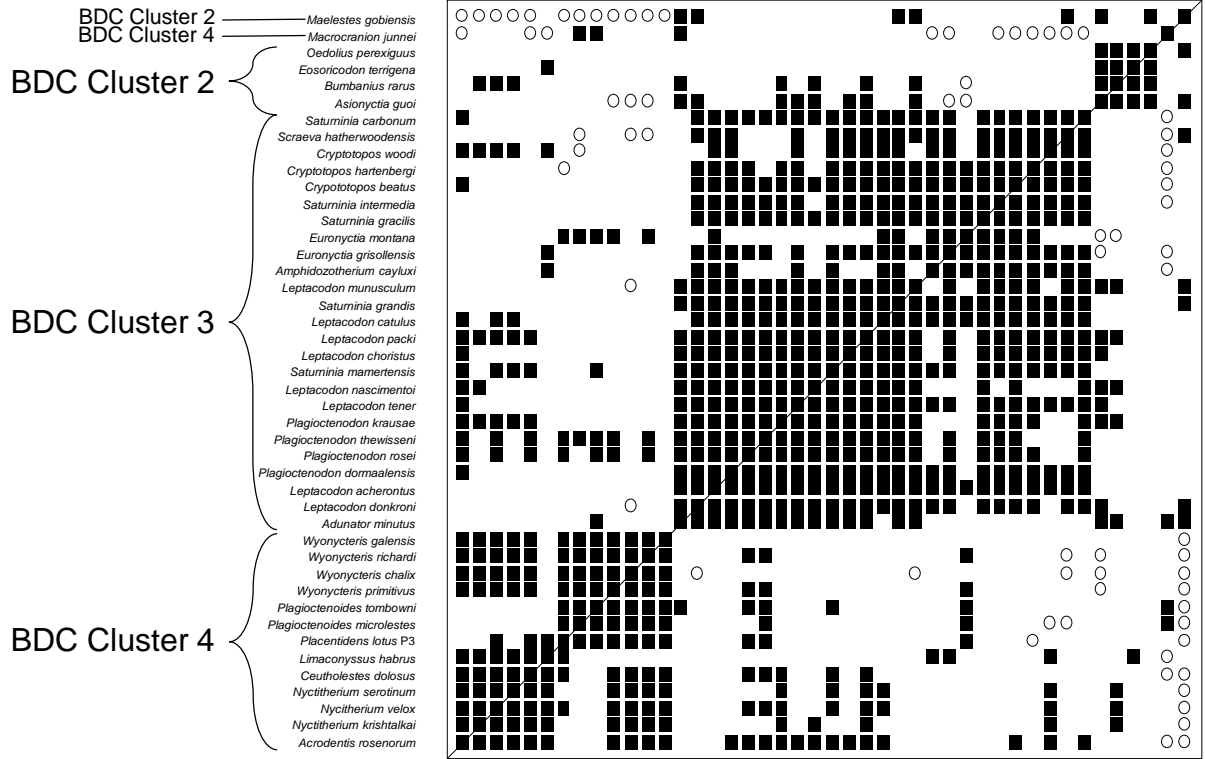


Order Soricomorpha
Family Nyctitheriidae

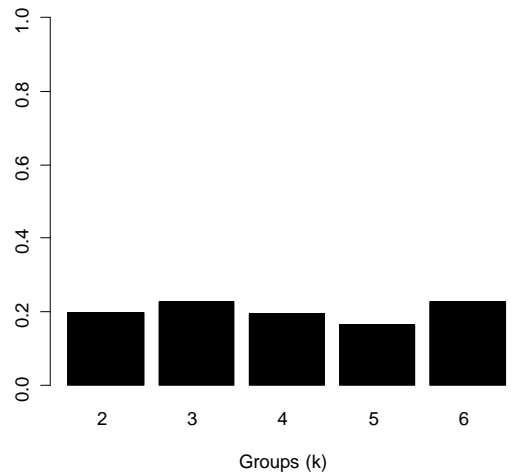
Published taxa	54
Published characters	66
Character relevance	0.75
Taxic relevance	0.5
Taxa used for calculations	44
Characters used for calculations	34
Median bootstrap value	65
F ₉₀	0.1
Stress of 3D MDS	0.3
k _{min}	7
Conclusion	HB?



Notes: BDC seems to support separation between the outgroup taxa and ingroup taxa, but the MDS results are far less clear. Given that the 3D stress is high (0.3), we may very tentatively accept Nyctitheriidae as a holobaramin.



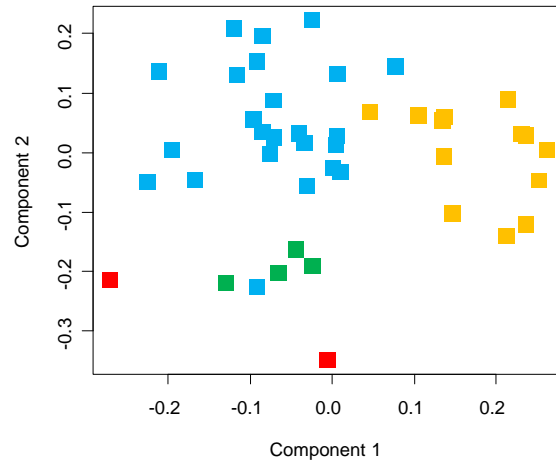
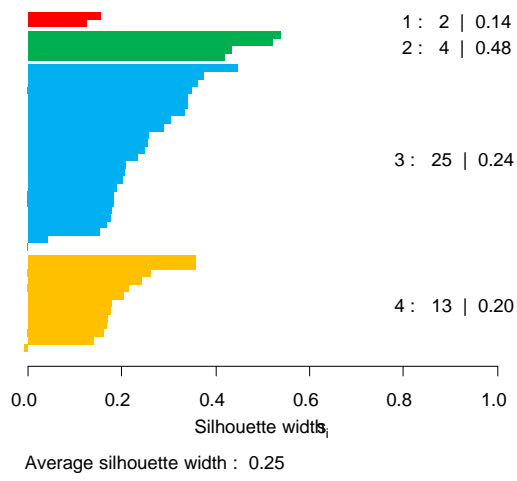
Average Silhouette Widths, Partion Around Medoids



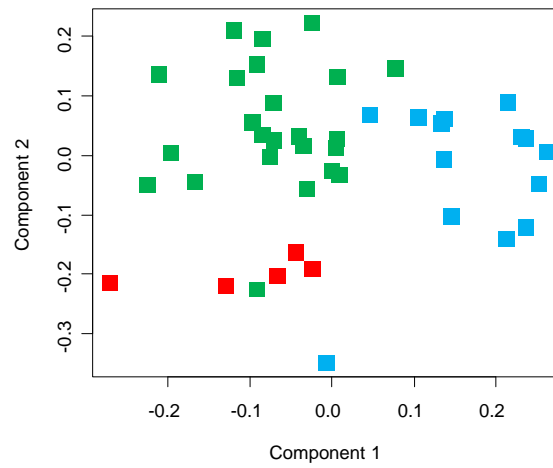
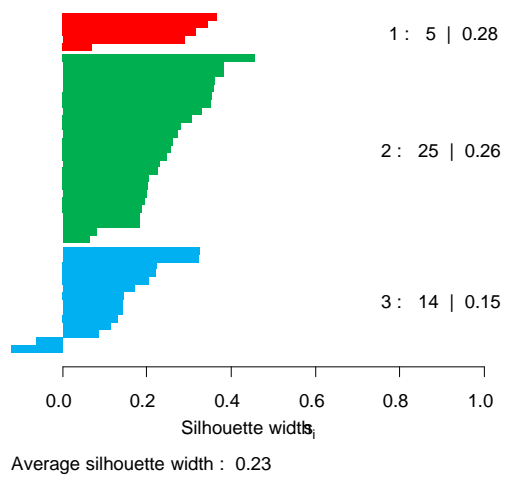
Clade Correspondence: All four BDC clusters contain two or more taxa each. Only cluster 1, consisting of two outgroup taxa, appears as a clade, if the phylogeny of Figure 6 in Manz and Bloch (2015) were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

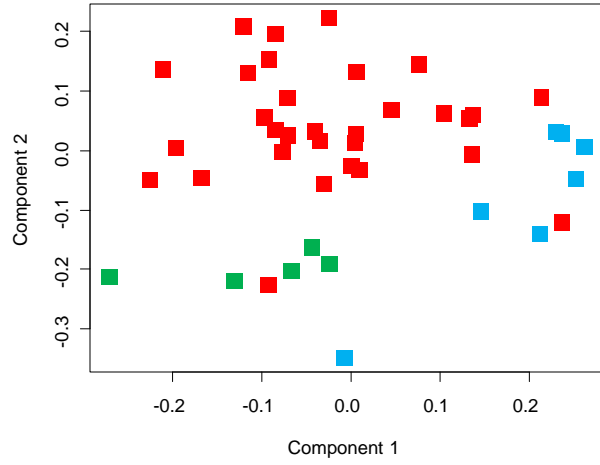
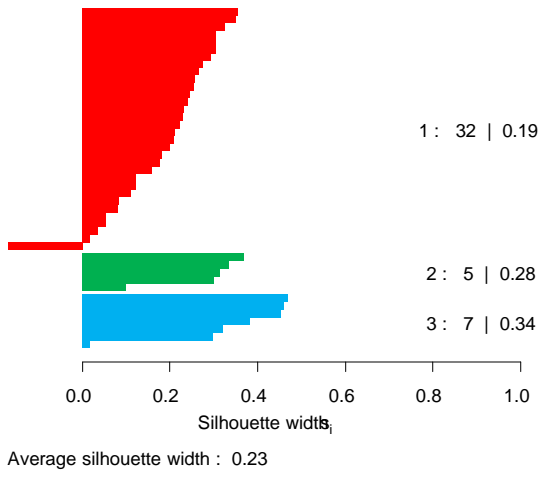


Spearman Correlation

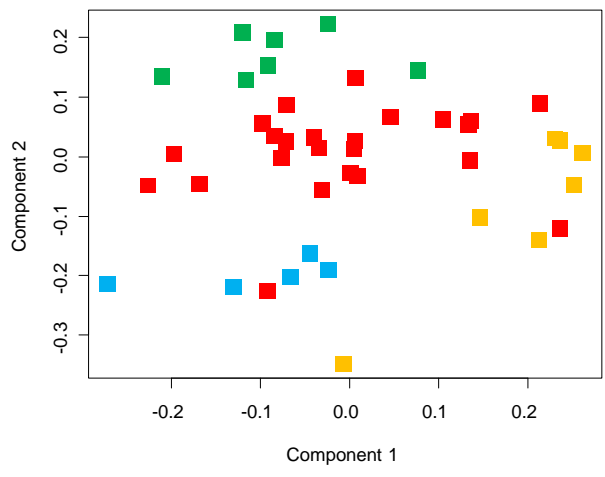
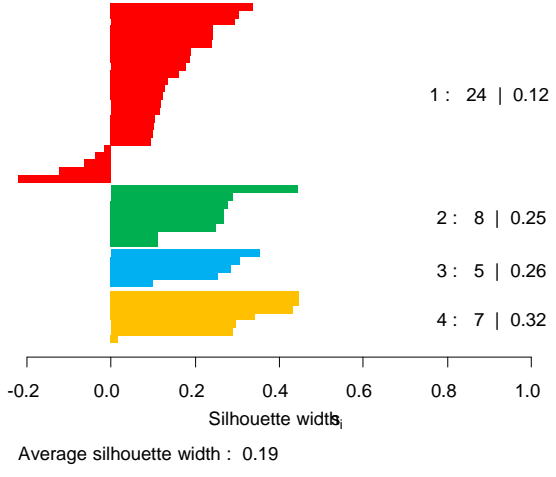


Silhouette plot, Partition Around Medoids

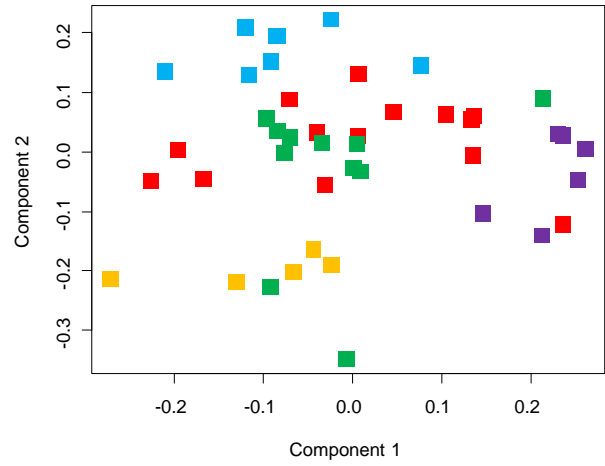
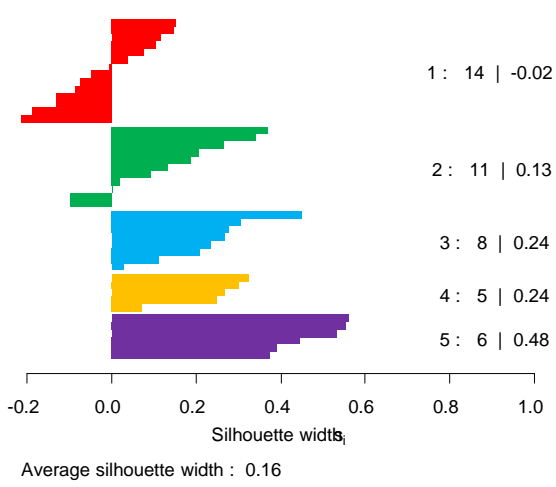
k=3



k=4



k=5



Family Soricidae

Order Soricomorpha

Hugueney and Maridet 2011

Pearson BDC

Negative: 12

Positive: 63

Clusters: 3

Clusterability

Hopkins Statistic: 0.681

Dip test: 0.048

Dip test p-value: 0.074

Spearman BDC

Negative: 8

Positive: 41

Clusters: 2

The original Pearson BDC results gave three clusters, including a singleton cluster of the outgroup *Saturninia gracilis*, which was negatively correlated with all members of the ingroup except one (*Srinitium marteli*). The Spearman BDC results place *Srinitium marteli* in the same cluster as the other ingroup taxa, but reduce the frequency of significant, negative correlation from twelve taxon pairs to eight. The Pearson BDC clusters have an average silhouette width of 0.33, with two taxa exhibiting negative silhouette widths. The Spearman BDC clusters have a much higher average silhouette width of 0.58, and no taxa have negative silhouette widths.

At $k=3$, the medoid partition agrees exactly with the Pearson BDC clusters, and at $k=2$, medoid partitioning agrees exactly with the Spearman BDC.

Fuzzy analysis agrees with none of the other clusterings, but the fuzzy analyses produced partitions with substantially lower average silhouette widths of 0.19 ($k=3$) and 0.29 ($k=2$). Hence we have good reason to doubt the fuzzy partition.

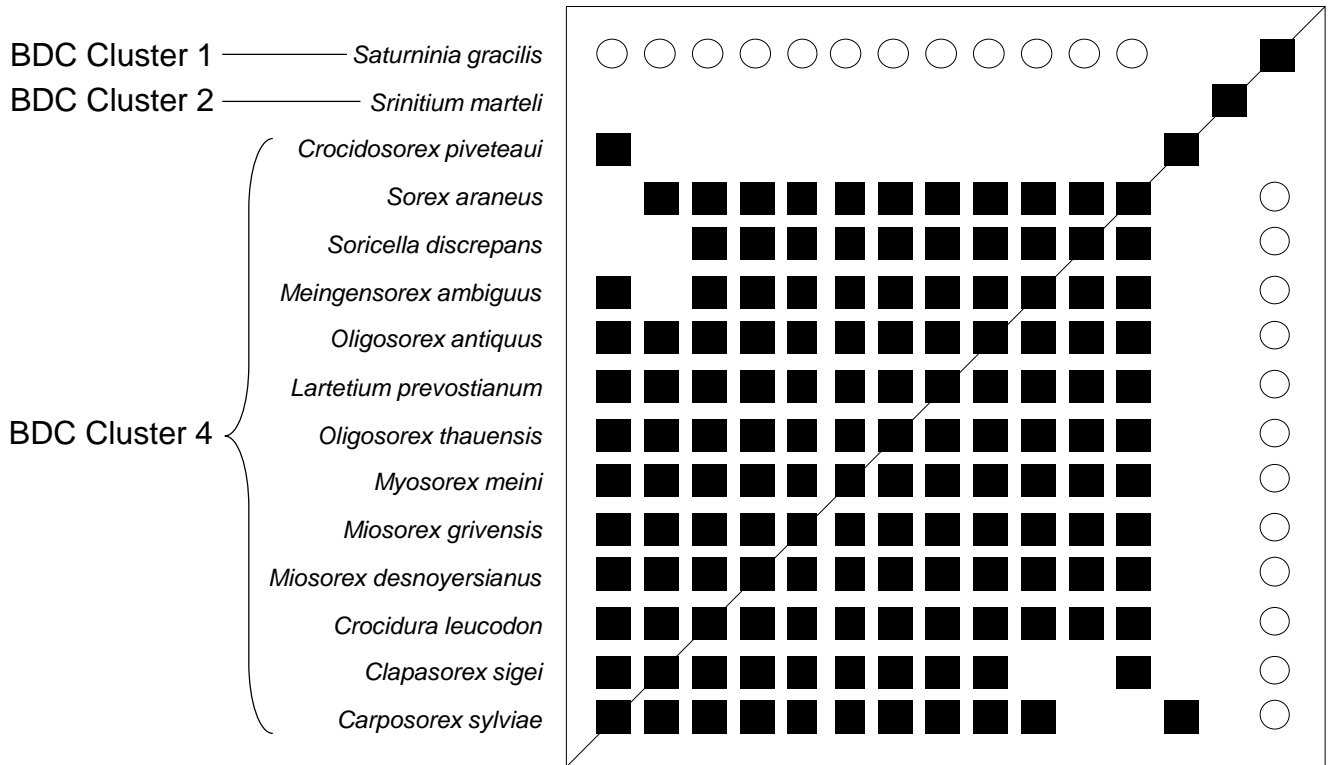
Given these results, the original conclusion that Soricidae is a holobaramin is strongly confirmed.

Original conclusion: HB?

Updated conclusion: HB

Hugueney, M. and O. Maridet. 2011. Early Miocene soricids (Insectivora, Mammalia) from Limagne (Central France): new systematic comparisons, updated biostratigraphic data and evolutionary implications. *Geobios* 44:225-236.

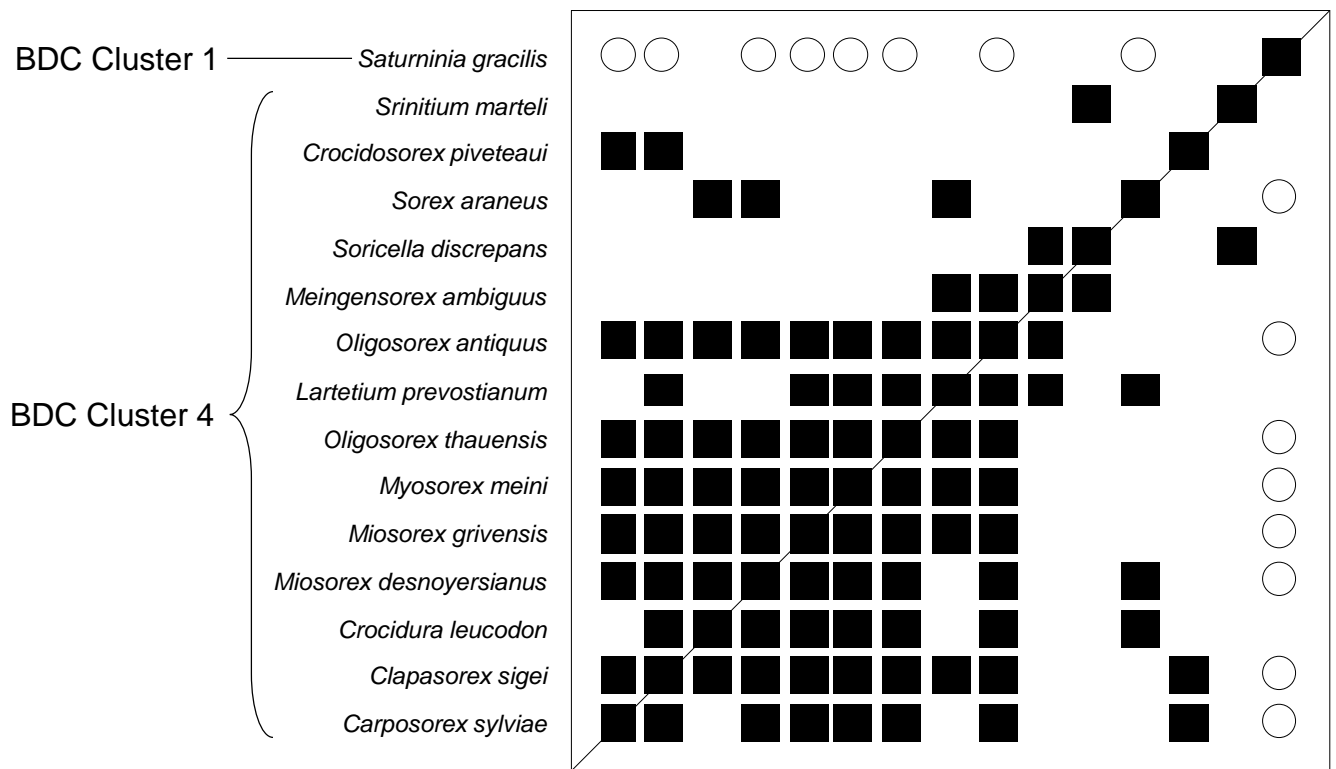
Characters: Craniodental



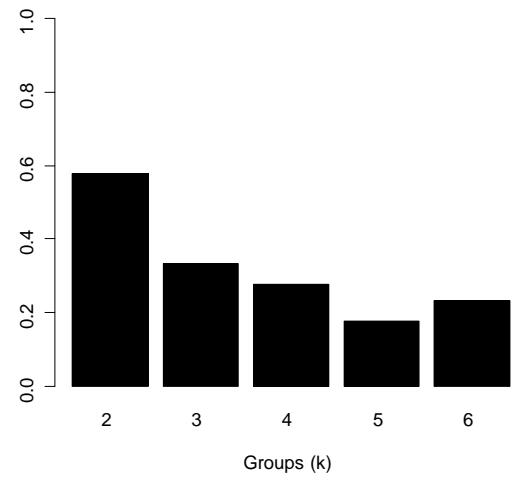
Order Soricomorpha
Family Soricidae

Published taxa	15
Published characters	27
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	15
Characters used for calculations	21
Median bootstrap value	79
F ₉₀	0.34
Stress of 3D MDS	0.22
k _{min}	5
Conclusion	HB?

Notes: Soricidae is well separated from the outgroup in BDC and MDS results. Soricidae is likely a holobaramin based on these characters.



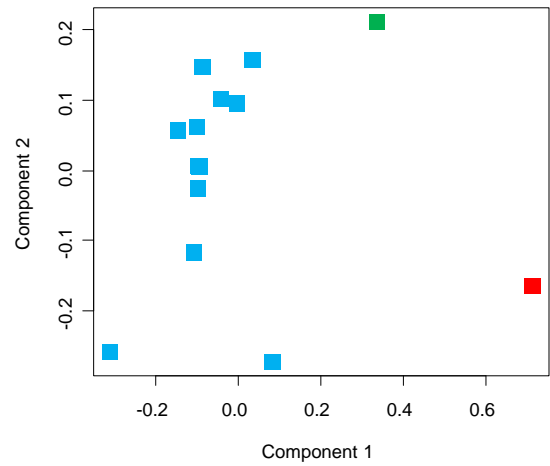
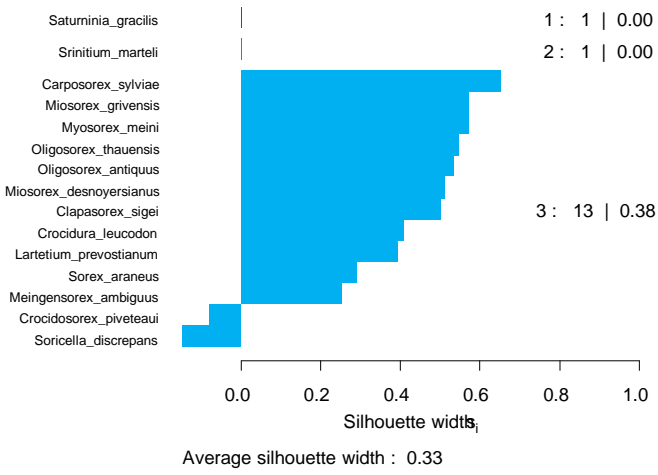
Average Silhouette Widths, Partion Around Medoids



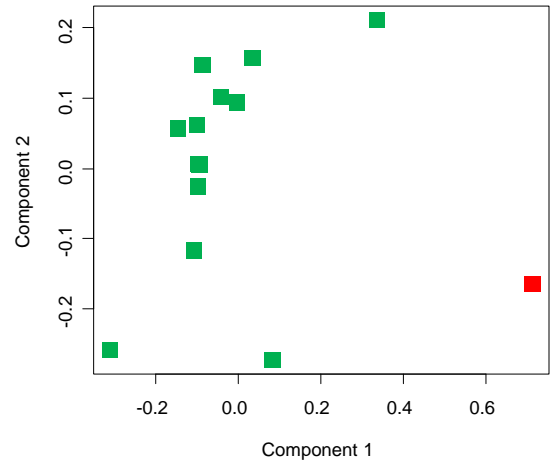
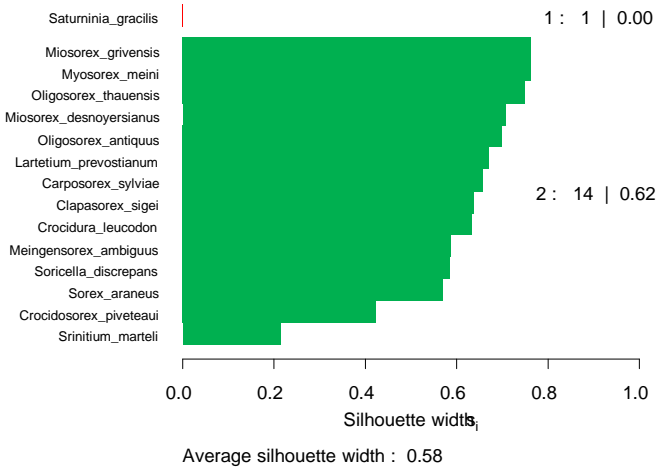
Clade Correspondence: The BDC results show one large cluster of 13 taxa and two singletons. That cluster is monophyletic in the published phylogeny (Hugueney and Maridet 2011, Figure 6).

Silhouette plot, BDC partitions

Pearson Correlation

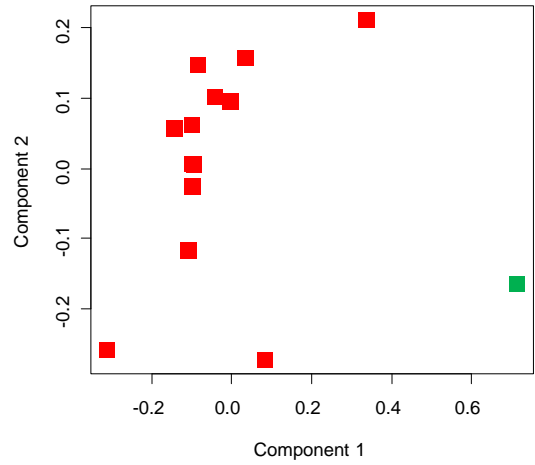
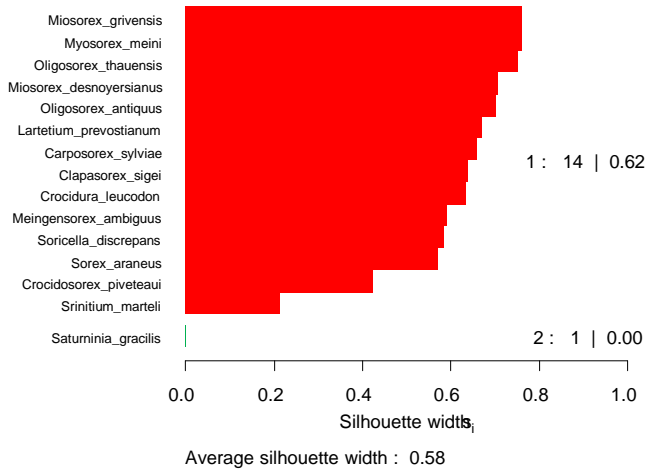


Spearman Correlation

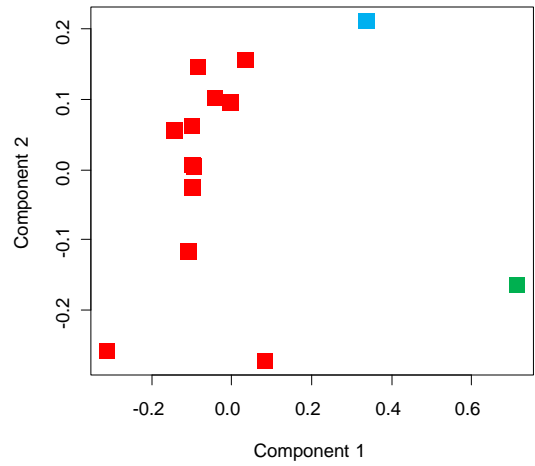
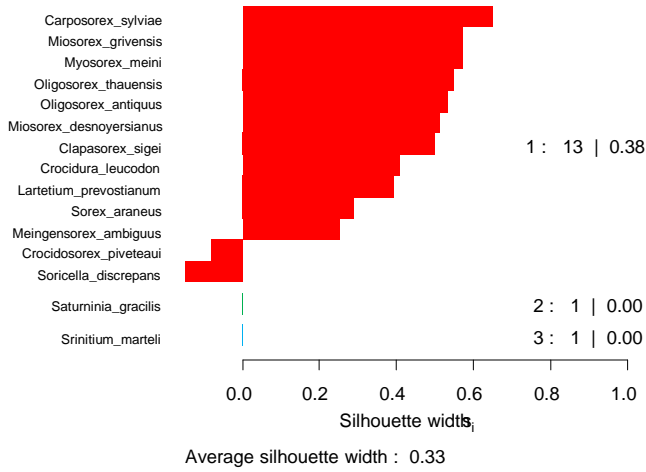


Silhouette plot, Partition Around Medoids

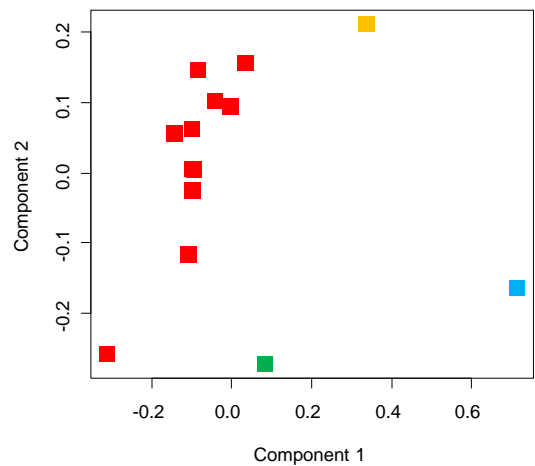
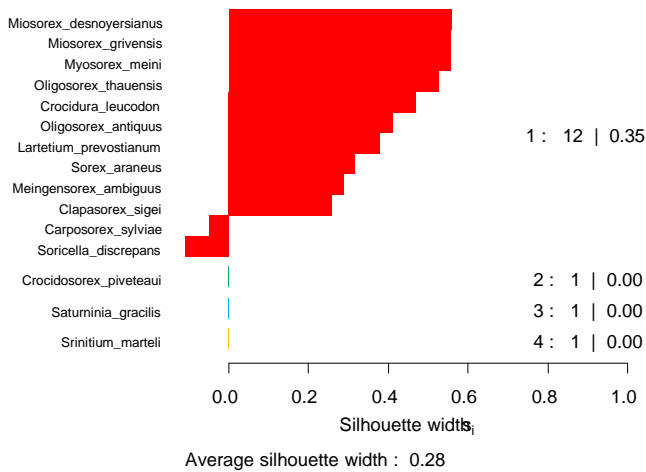
k=2



k=3

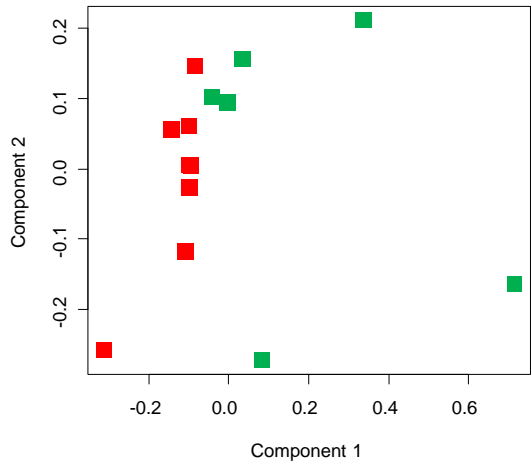
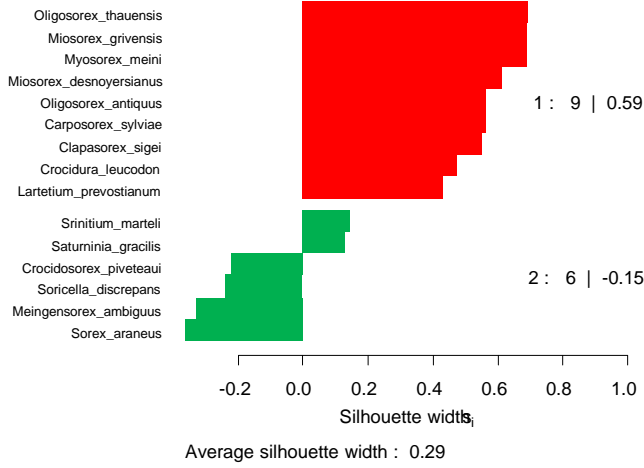


k=4

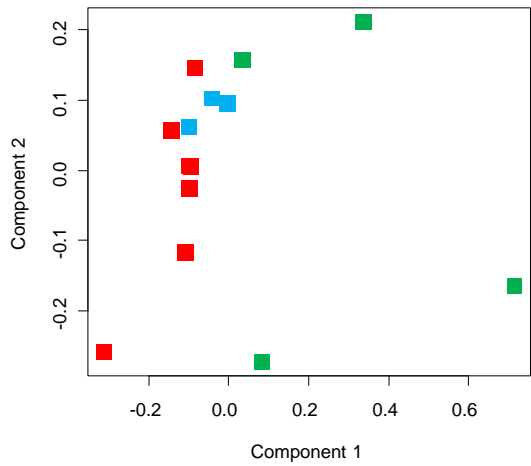
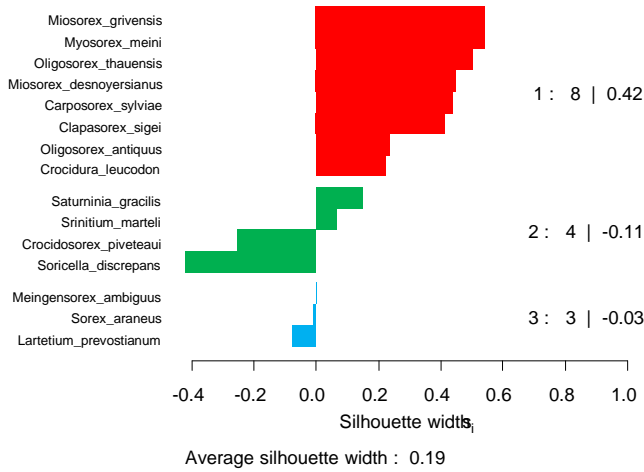


Silhouette plot, Fuzzy Analysis

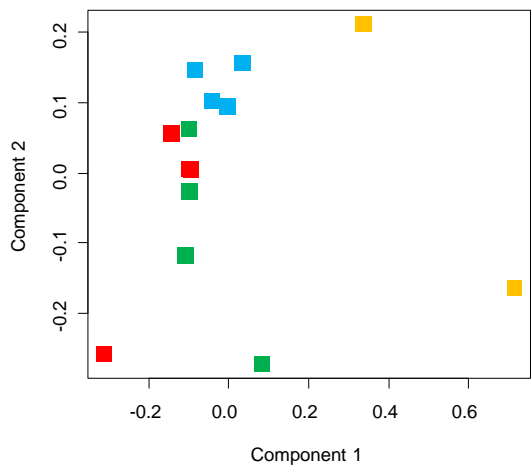
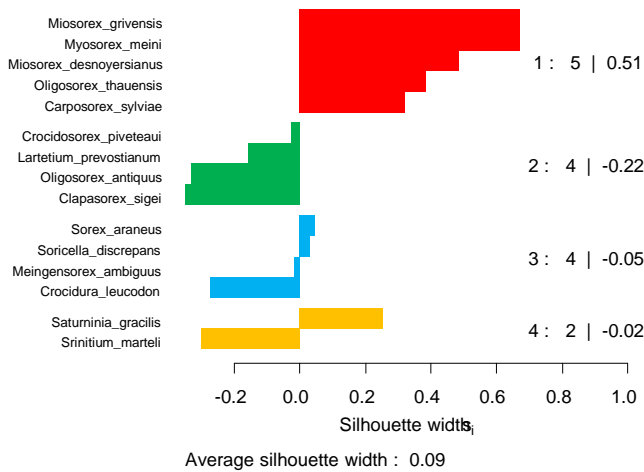
k=2



k=3



k=4



Family Rhinolophidae

Order Chiroptera

Hand and Kirsch 2003

Pearson BDC

Negative: 130

Positive: 394

Clusters: 3

Spearman BDC

Negative: 101

Positive: 429

Clusters: 2

Clusterability

Hopkins Statistic: 0.721

Dip test: 0.011

Dip test p-value: 0.632

The Spearman BDC results reveal an additional 35 instances of significant, positive correlation, thereby reducing the number of clusters from three to two. The average silhouette width for the three Pearson BDC clusters is 0.24 and for the two Spearman BDC clusters is 0.3. The cluster membership difference is 26%.

The three-cluster medoid partition has an average silhouette width of 0.23 and does not agree with the Pearson BDC clusters. The cluster membership difference is 12%. The two-cluster medoid partition has an average silhouette width of 0.2 and also does not agree with the Spearman BDC clusters.

Fuzzy analysis for $k=3$ failed. For $k=2$, the fuzzy partition had an average silhouette width of 0.22 and did not agree with the Spearman BDC clusters or the two-cluster medoid partition.

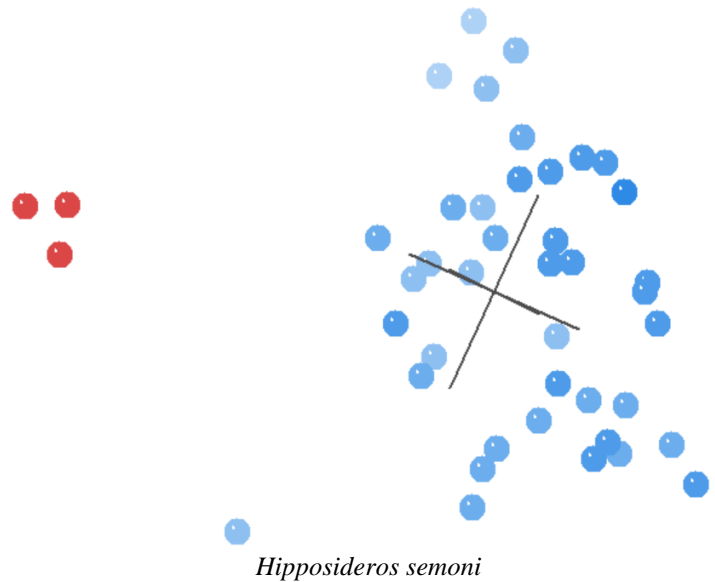
Given the lack of consistency from these analyses, these results should be judged inconclusive.

Original conclusion: HB?

Updated conclusion: Inconclusive

Hand, S.J. and J.A.W. Kirsch. 2003. *Archerops*, a new annectant hipposiderid genus (Mammalia: Microchiroptera) from the Australian Miocene. *Journal of Paleontology* 77:1139-1151.

Characters: Craniodental and postcranial



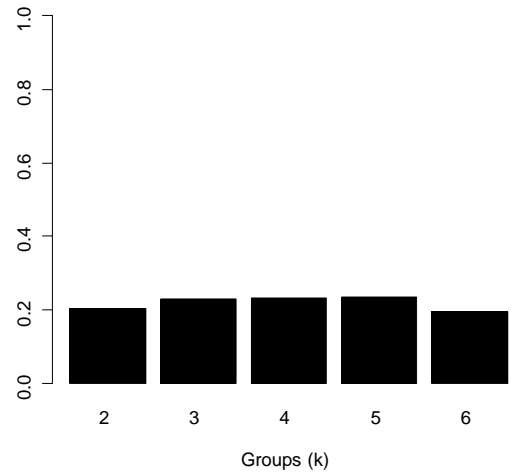
Order Chiroptera
Family Rhinolophidae

Published taxa	44
Published characters	64
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	43
Characters used for calculations	64
Median bootstrap value	73
F ₉₀	0.2
Stress of 3D MDS	0.32
k _{min}	11
Conclusion	HB?

Notes: BDC and MDS support a separation between Rhinolophidae and outgroup taxa. *Hipposideros semoni* shares positive BDC with all outgroup taxa and two other rhinolophids, but the MDS supports including *H. semoni* in the rhinolophid cluster. Rhinolophidae is likely a holobaramin.



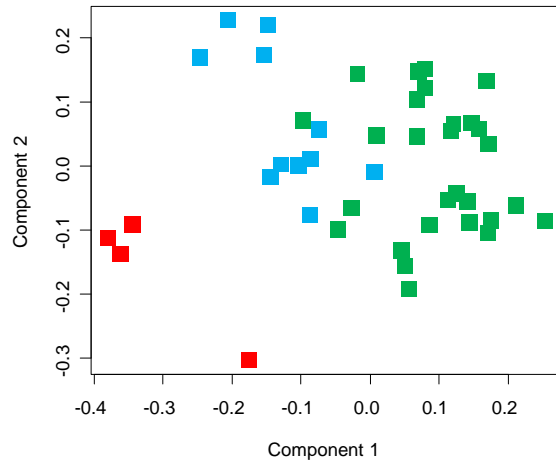
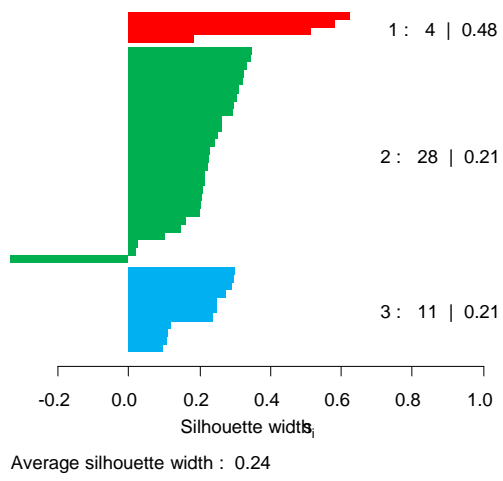
Average Silhouette Widths, Partion Around Medoids



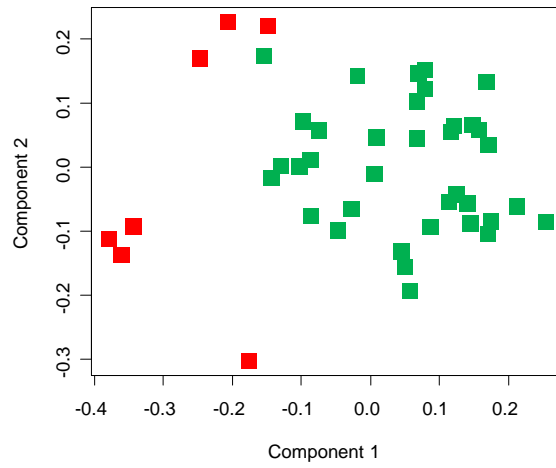
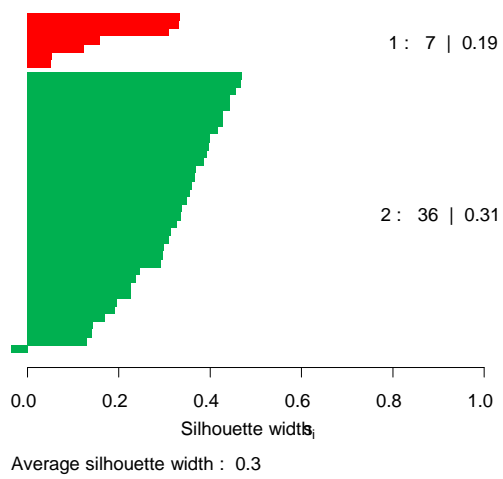
Clade Correspondence: All three clusters evident in the BDC results contain two or more taxa each. None of them are monophyletic in either of the published phylogenies in Figure 3 of Hand and Kirsch (2003).

Silhouette plot, BDC partitions

Pearson Correlation

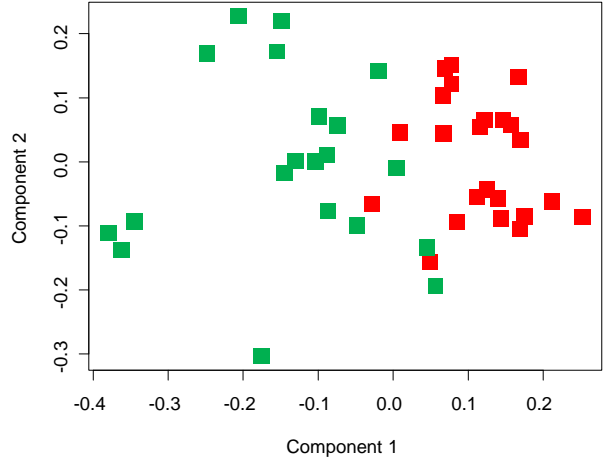
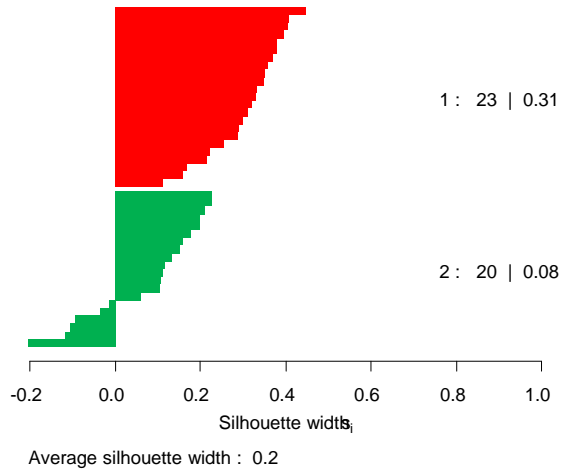


Spearman Correlation

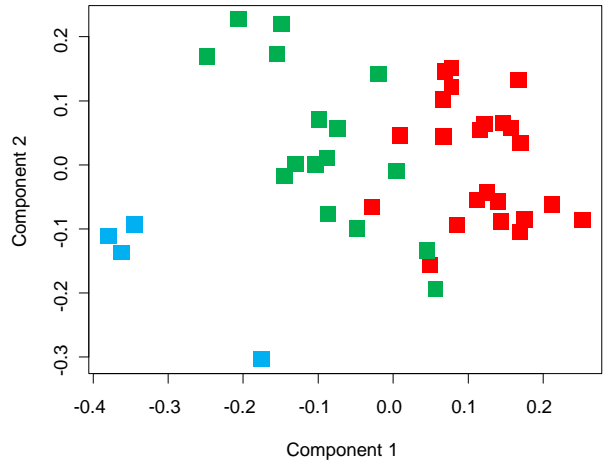
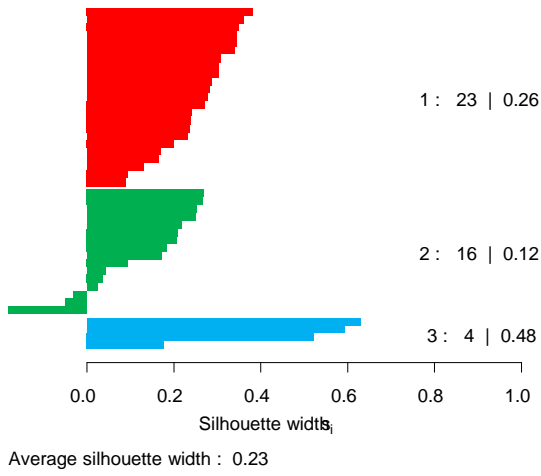


Silhouette plot, Partition Around Medoids

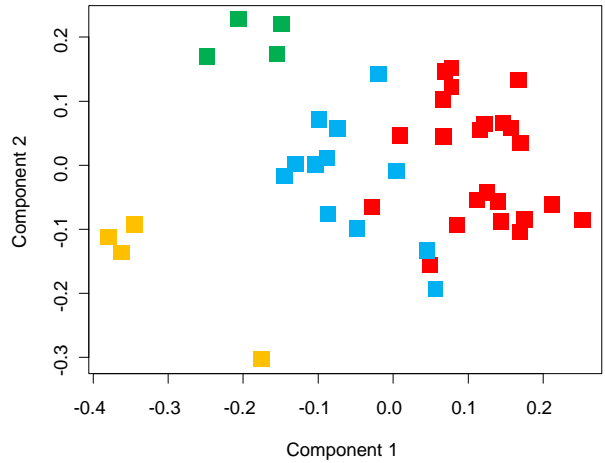
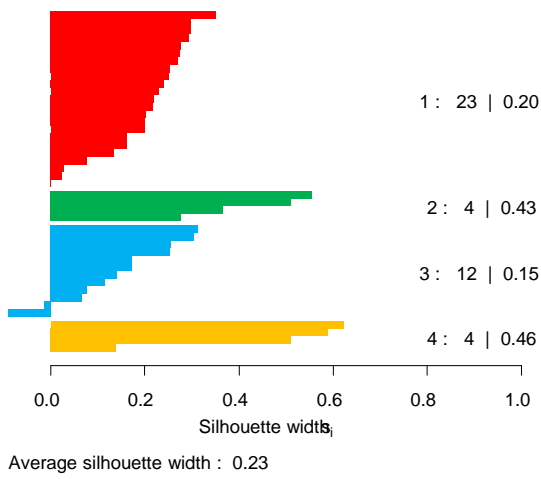
k=2



k=3

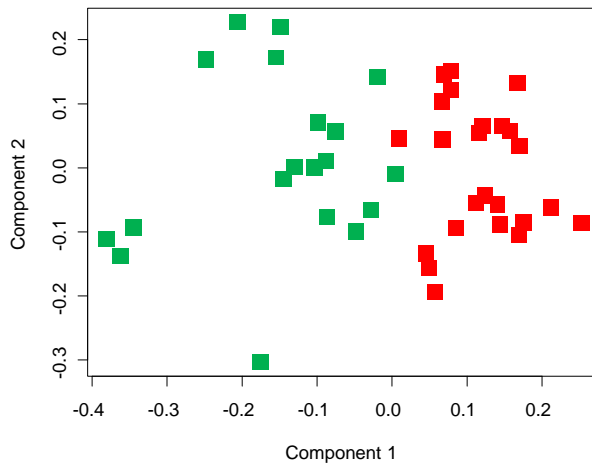
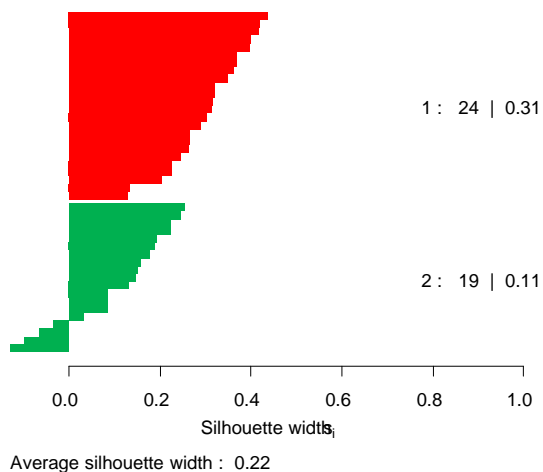


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Mormoopidae

Order Chiroptera

Simmons and Conway 2001

Pearson BDC

Negative: 7

Positive: 27

Clusters: 6

Clusterability

Hopkins Statistic: 0.878

Dip test: 0.041

Dip test p-value: 0.092

Spearman BDC

Negative: 30

Positive: 47

Clusters: 4

The original Pearson BDC results reveal six different clusters of taxa, but the Spearman BDC adds twenty more instances of significant, positive correlation, which reduce the number of clusters to four. The Pearson BDC clusters have an average silhouette width of 0.7, and the Spearman BDC clusters have an average silhouette of 0.51. The cluster membership difference is 24%.

At $k=6$, the medoid partition agrees exactly with the Pearson BDC clusters. At $k=4$, the medoid partition has an average silhouette width of 0.45, and it does not agree with the Spearman BDC clusters.

Fuzzy analysis disagrees with both the Pearson and Spearman clusters. The fuzzy partition has an average silhouette width of 0.45 at $k=6$ and 0.55 at $k=4$. The six-cluster fuzzy partition and the Pearson BDC have a cluster membership difference of 24%.

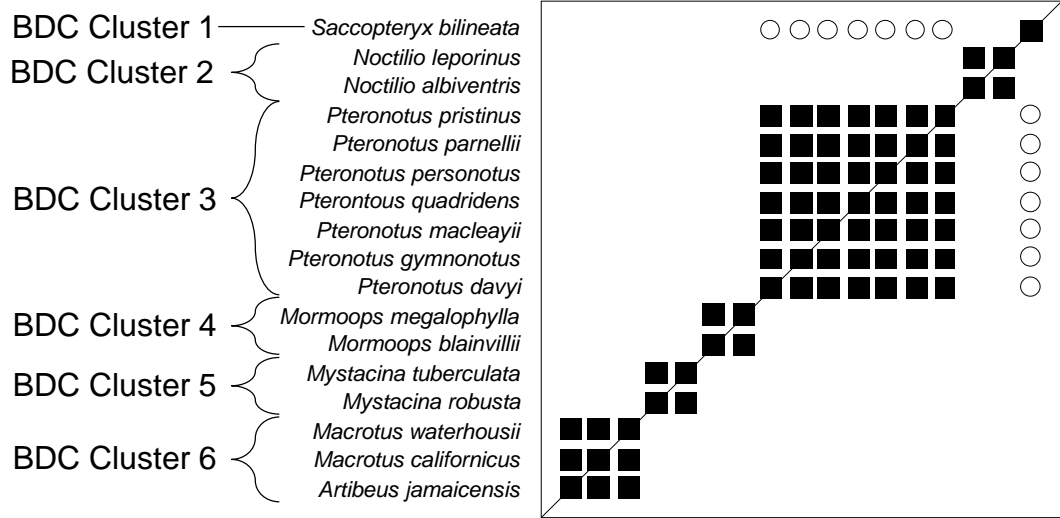
In the original analysis, we concluded that genus *Pteronotus* by itself was a monobaramin, based on significant, positive correlation between all six of its species. The Spearman BDC results support including genus *Mormoops* in the same monobaramin, and significant, negative BDC surrounding that monobaramin suggests it might be a holobaramin. However, a cluster consisting of the species of *Mormoops* and *Pteronotus* is not recovered in either the medoid partition or the fuzzy analysis. Therefore, the lack of consistency in these results ought to be judged as inconclusive.

Original conclusion: MB

Updated conclusion: Inconclusive

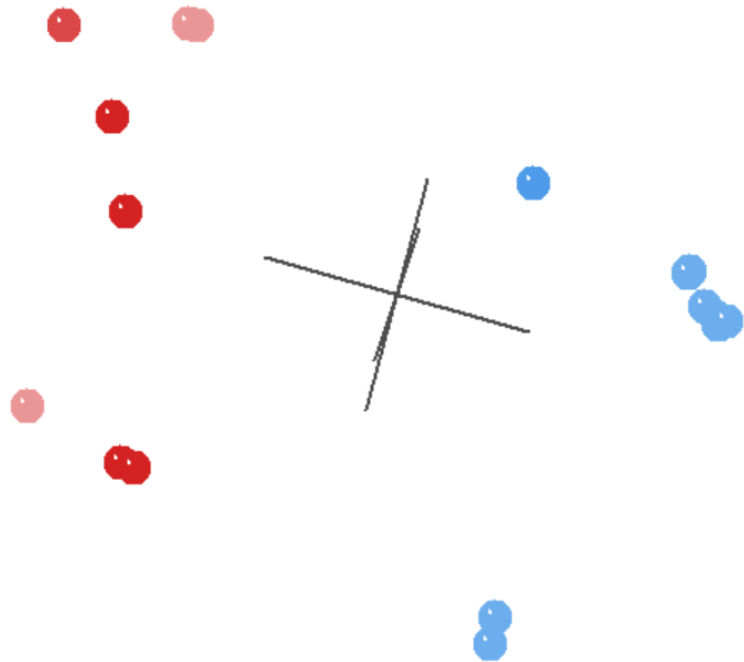
Simmons, N.B. and T.M. Conway. 2001. Phylogenetic relationships of mormoopid bats (Chiroptera: Mormoopidae) based on morphological data. *Bulletin of the American Museum of Natural History* 258:1-97.

Characters: Craniodental, postcranial, soft tissue

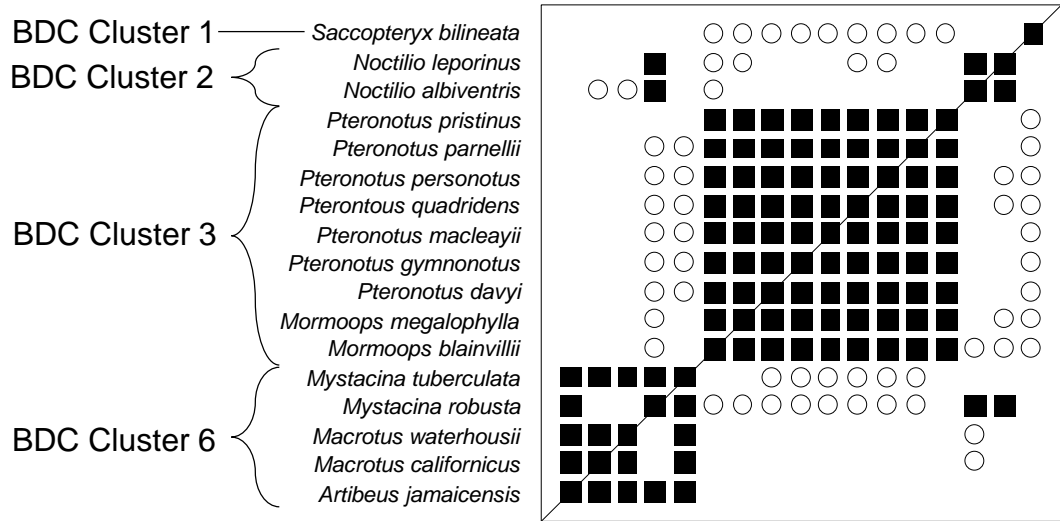


Order Chiroptera
Family Mormoopidae

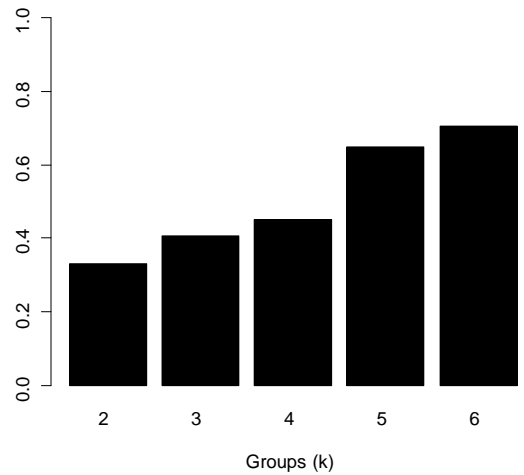
Published taxa	17
Published characters	209
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	17
Characters used for calculations	162
Median bootstrap value	92
F ₉₀	0.54
Stress of 3D MDS	0.19
k _{min}	7
Conclusion	MB



Notes: BDC reveals very little correlation between genera. *Pteronotus* appears to be a well-defined monobaramin in the BDC results. MDS reveals a distinction between ingroup and outgroup taxa, but both are diffuse and poorly clustered. We may provisionally accept *Pteronotus* as a monobaramin. Clear discontinuity is not evident.



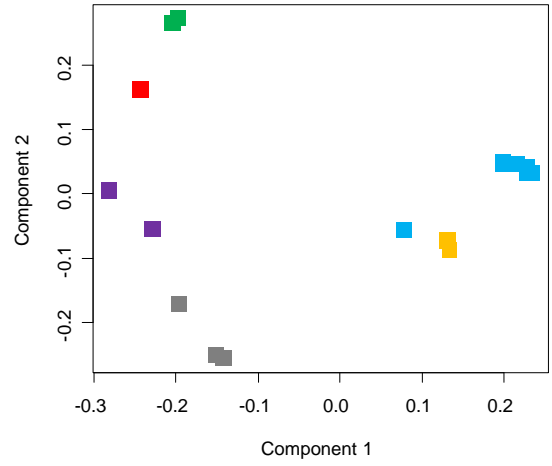
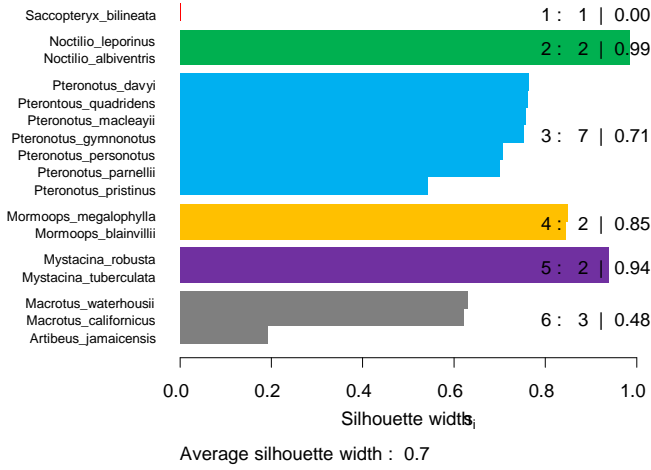
Average Silhouette Widths, Partion Around Medoids



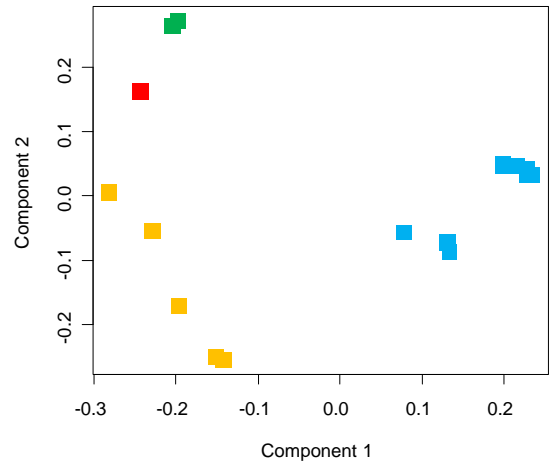
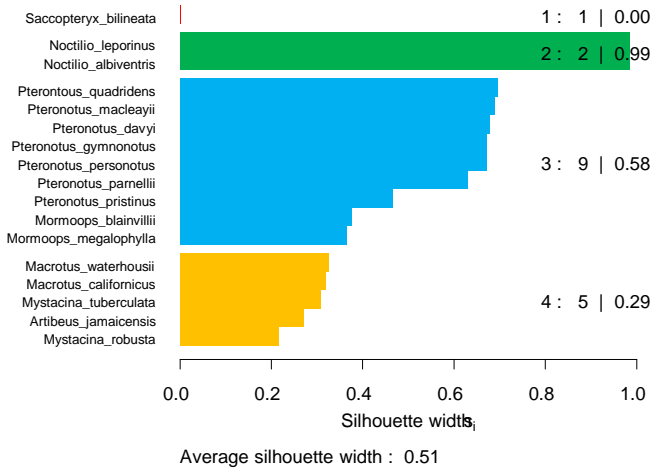
Clade Correspondence: Five of the six clusters in the BDC results have more than one taxon each. All of them are monophyletic in the phylogeny of Figure 12 of Simmons and Conway (2001).

Silhouette plot, BDC partitions

Pearson Correlation

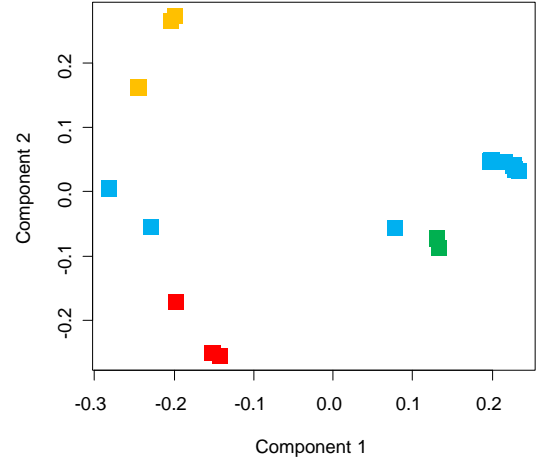
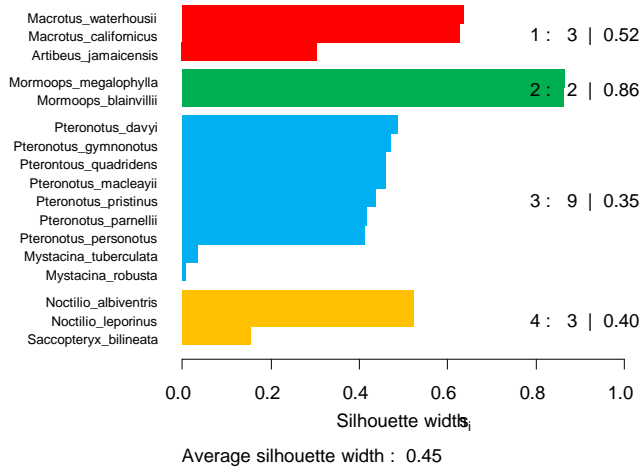


Spearman Correlation

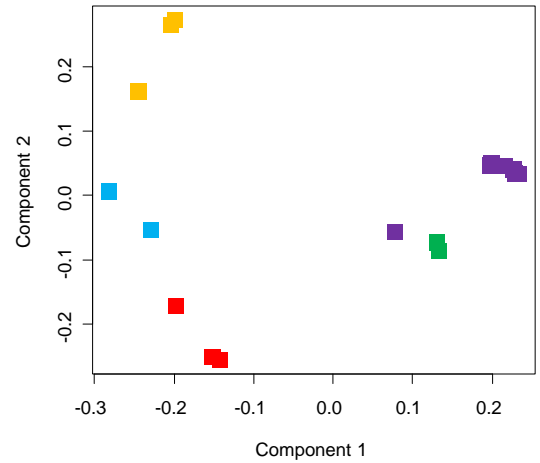
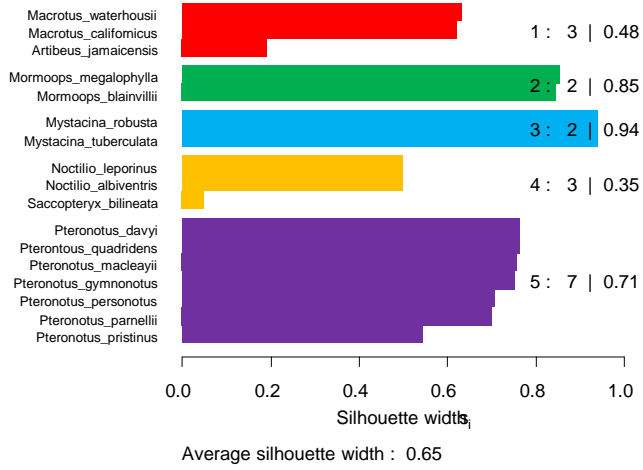


Silhouette plot, Partition Around Medoids

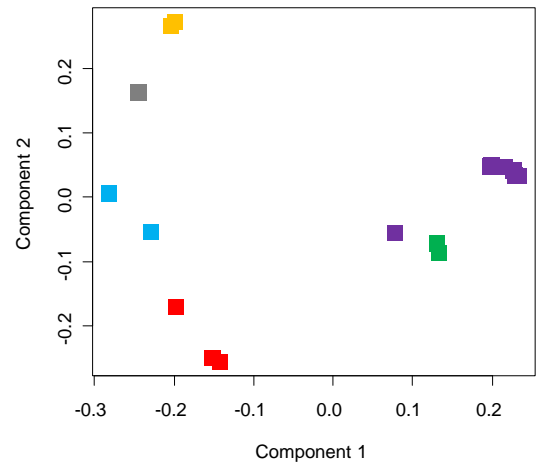
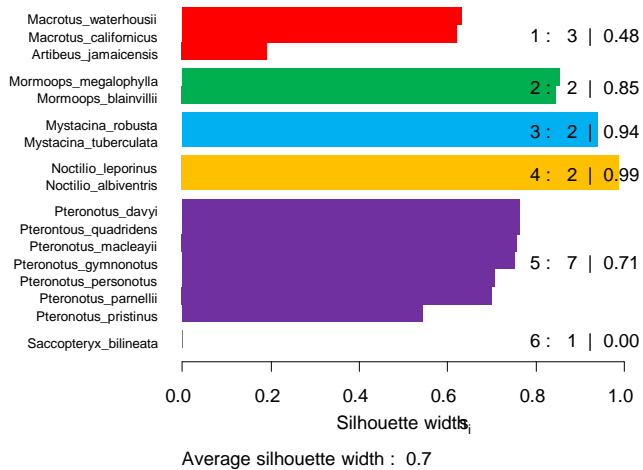
k=4



k=5

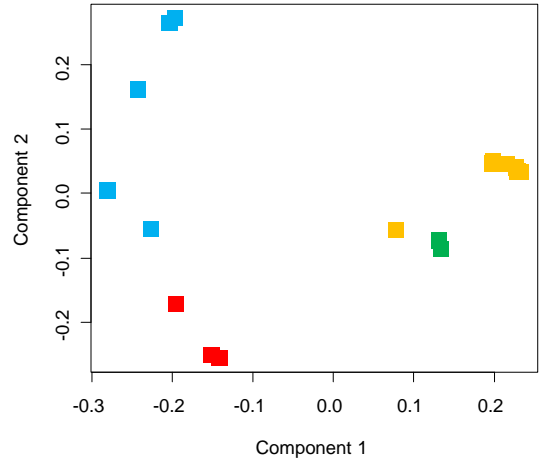
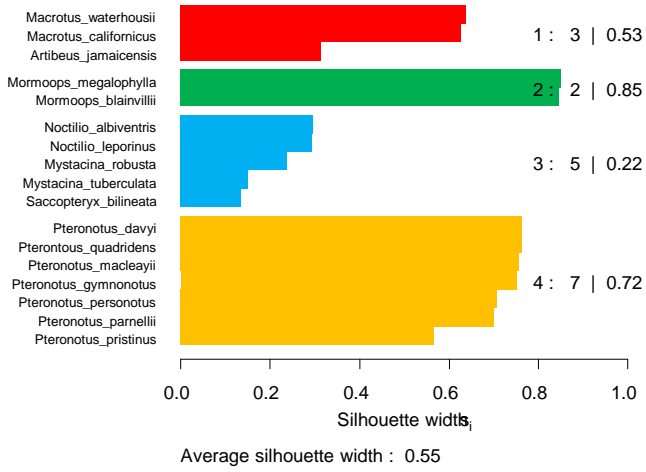


k=6

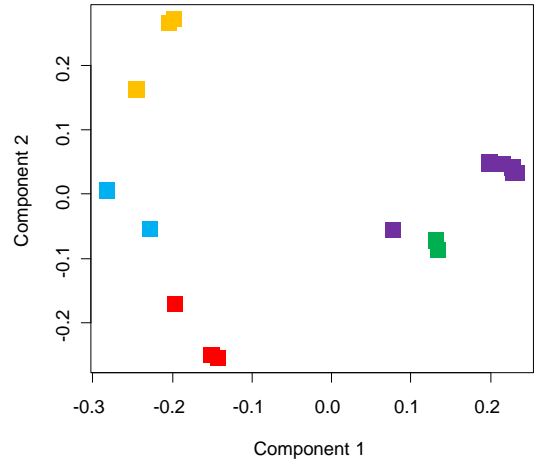
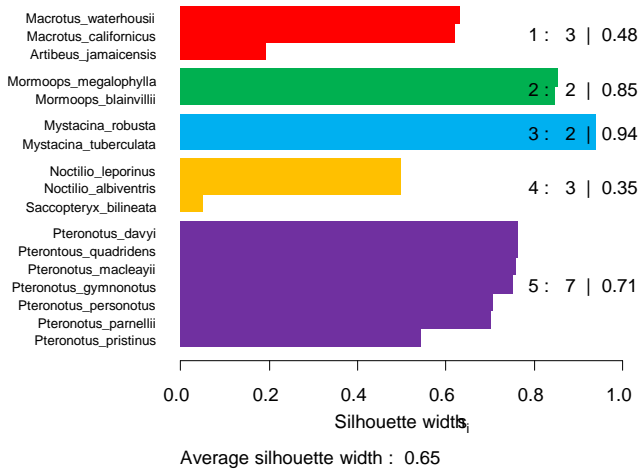


Silhouette plot, Fuzzy Analysis

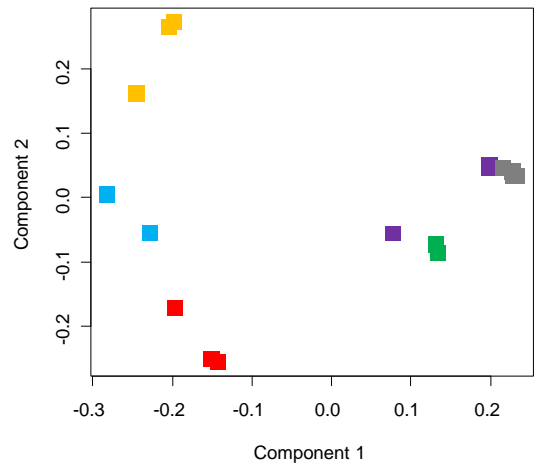
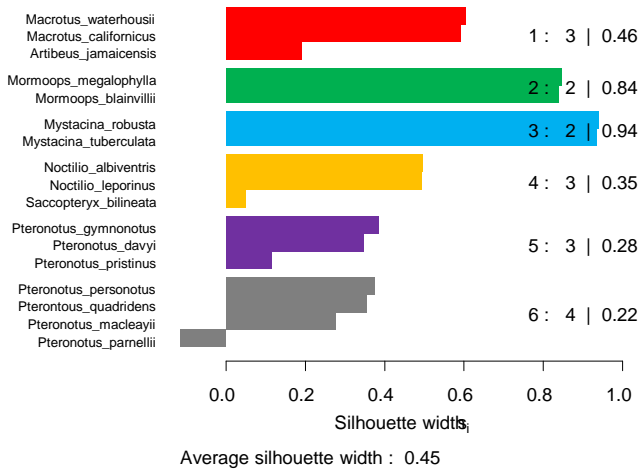
k=4



k=5



k=6



Family Phyllostomidae

Order Chiroptera
Wetterer et al. 2000

Pearson BDC
Negative: 402
Positive: 804
Clusters: 3

Spearman BDC
Negative: 298
Positive: 1114
Clusters: 2

Clusterability
Hopkins Statistic: 0.876
Dip test: 0.008
Dip test p-value: 0.61

The Spearman BDC results reveal an additional 310 instances of significant, positive correlation when compared to the Pearson BDC results. These additional correlations reduce the number of clusters from three to two. The average silhouette width was 0.37 for the Pearson BDC clusters and 0.32 for the Spearman BDC clusters. The cluster membership difference was 5%.

The three-cluster medoid partition has an average silhouette width of 0.36 and does not agree with the Pearson BDC clusters. The cluster membership difference is 30%. At $k=2$, the medoid partition has an average silhouette width of 0.26 and also does not agree with the Spearman BDC clusters.

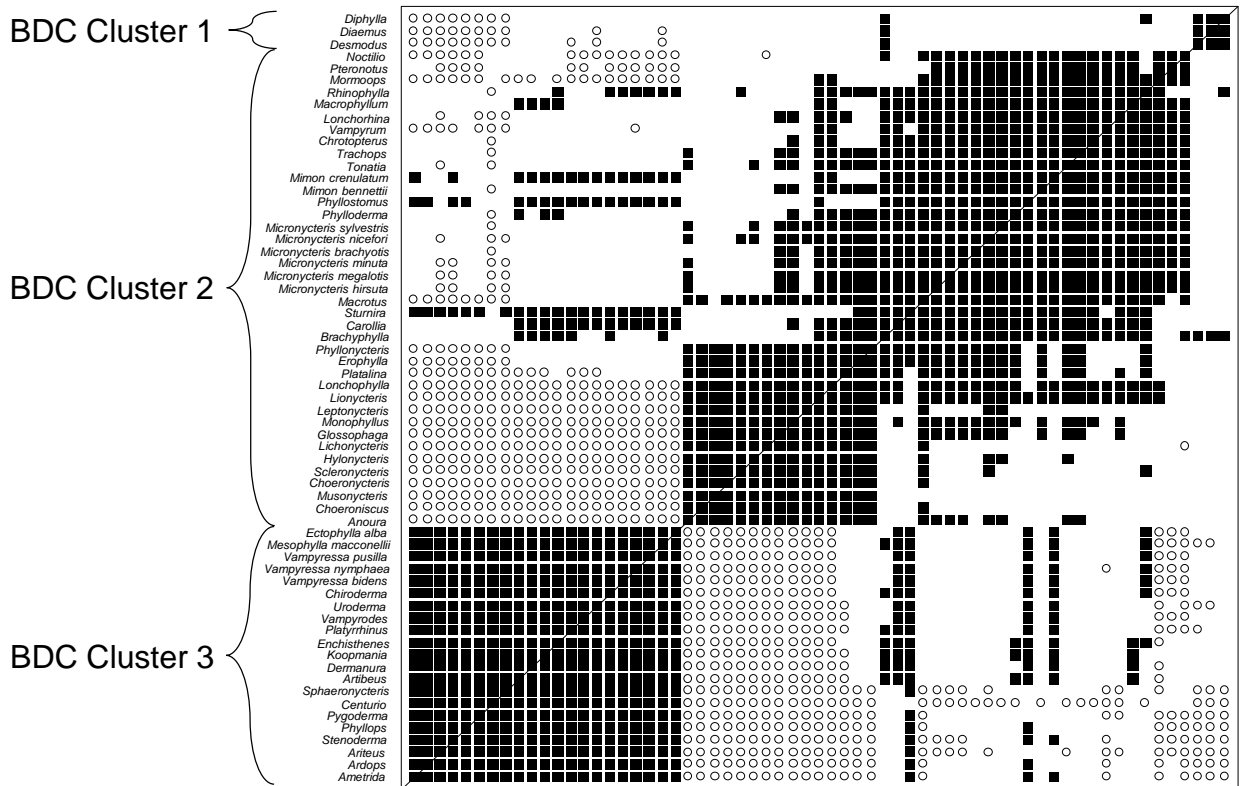
Fuzzy analysis failed at $k=3$, but at $k=2$, the fuzzy partition has an average silhouette width of 0.3.

The lack of consistency in these analyses suggests that these results are inconclusive.

Original conclusion: Inconclusive
Updated conclusion: Inconclusive

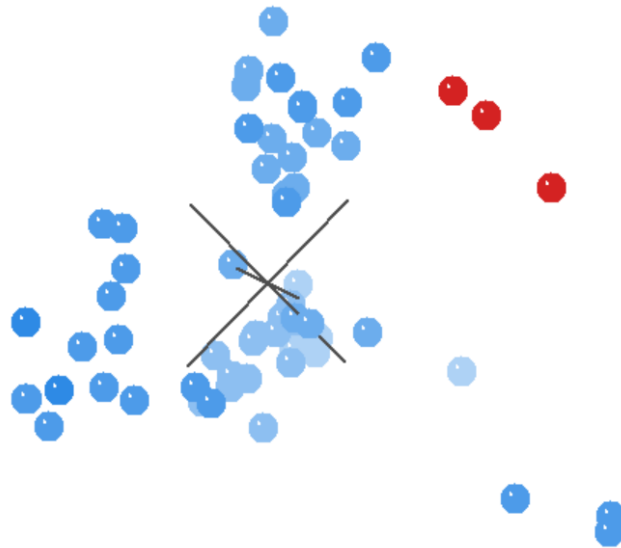
Wetterer, A.L., M.V. Rockman, and N.B. Simmons. 2000. Phylogeny of phyllostomid bats (Mammalia: Chiroptera): data from diverse morphological systems, sex chromosomes, and restriction sites. *Bulletin of the American Museum of Natural History* 248:1-200.

Characters: Craniodental, postcranial, soft issue, karyotype, restriction sites

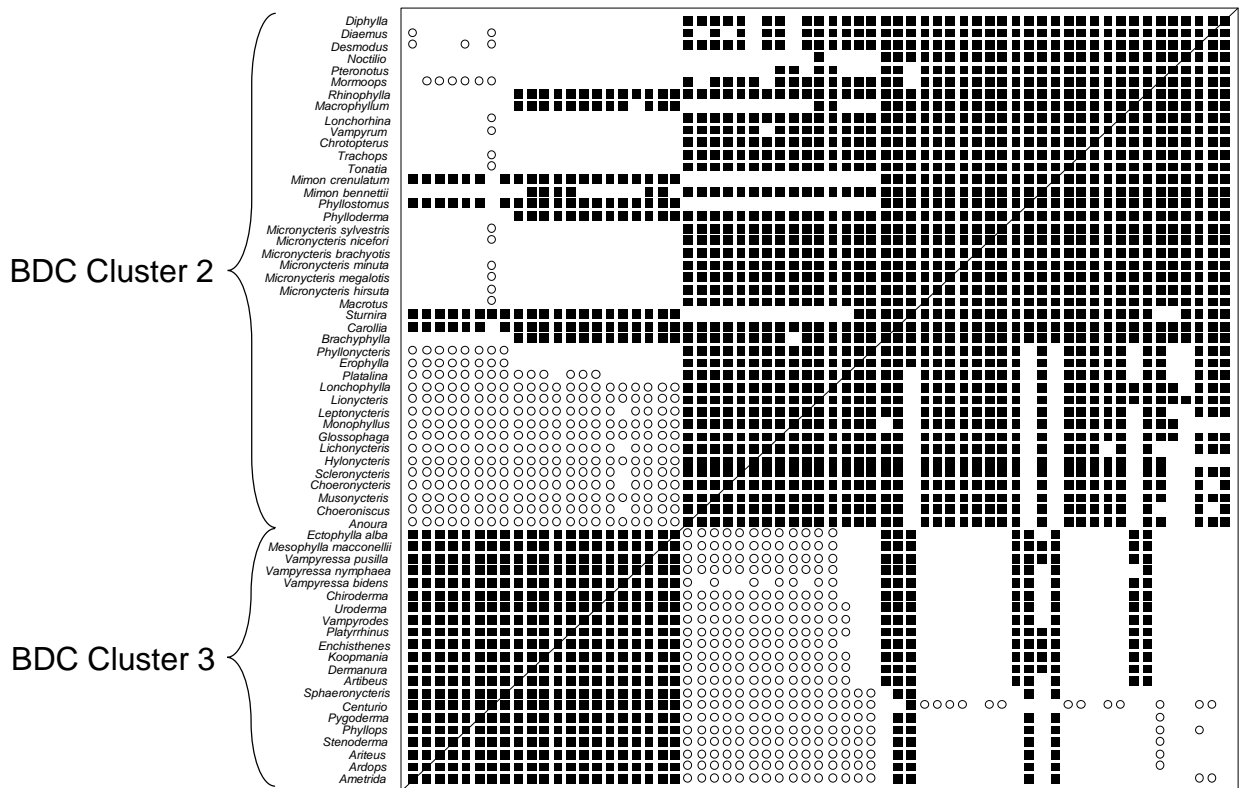


Order Chiroptera
Family Phyllostomidae

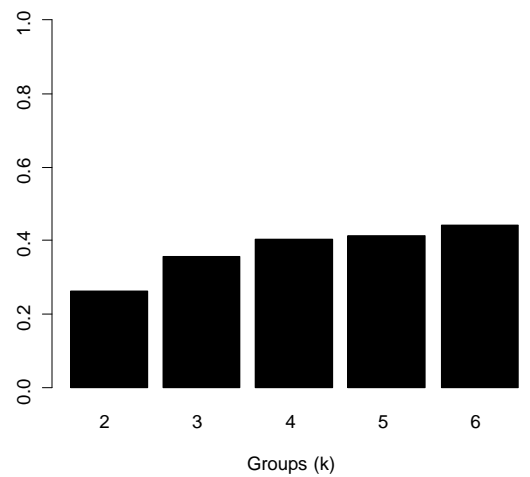
Published taxa	63
Published characters	150
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	63
Characters used for calculations	98
Median bootstrap value	77
F ₉₀	0.33
Stress of 3D MDS	0.24
k _{min}	10
Conclusion	Inc



Notes: No clear evidence of discontinuity in BDC or MDS results.



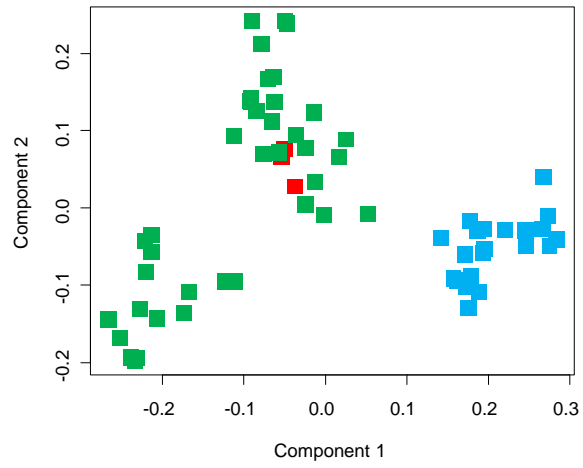
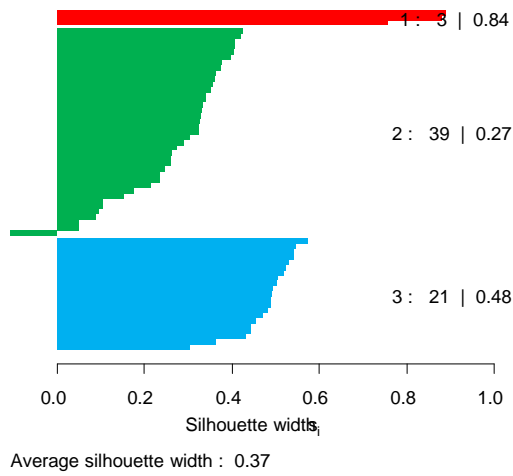
Average Silhouette Widths, Partion Around Medoids



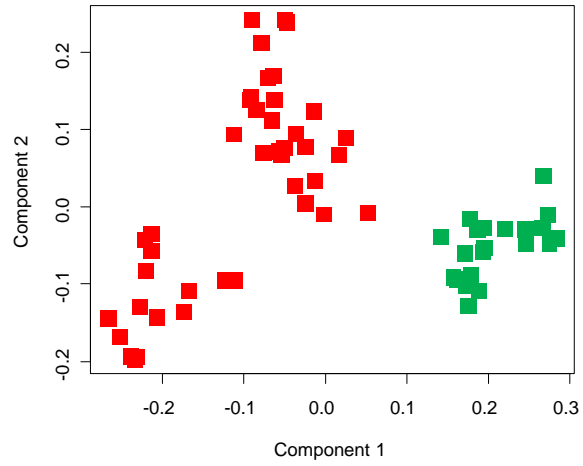
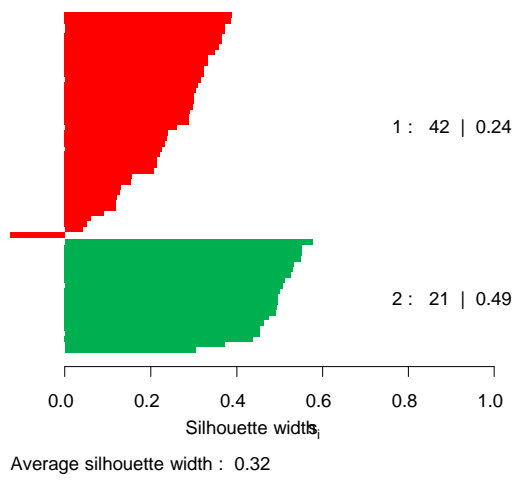
Clade Correspondence: There are three BDC clusters, and all three have more than one taxon. Clusters 1 and 3 are monophyletic in the phylogeny of Figure 49 in Wetterer et al. (2000). Cluster 2 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

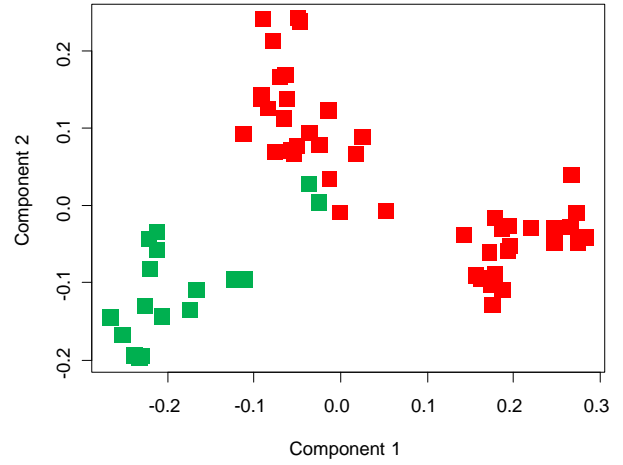
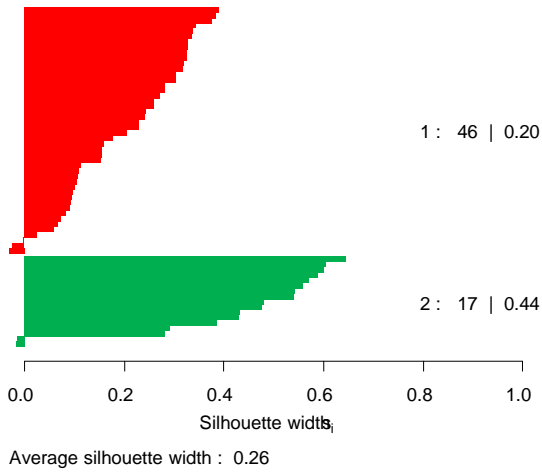


Spearman Correlation

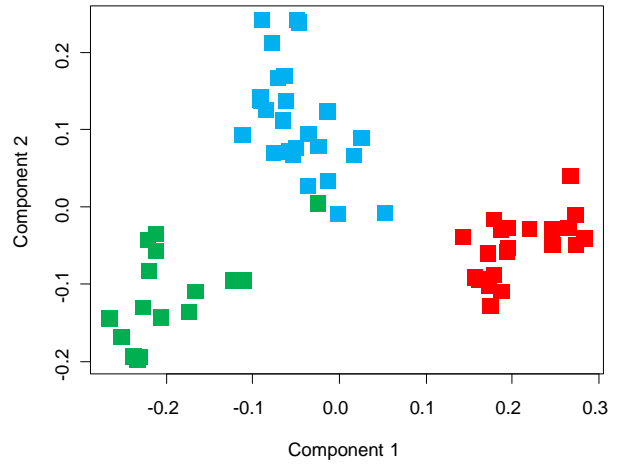
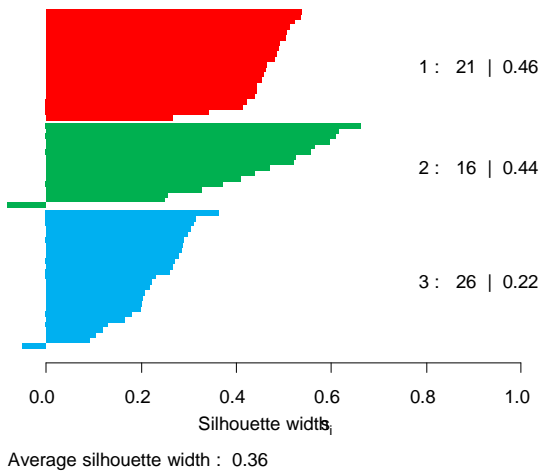


Silhouette plot, Partition Around Medoids

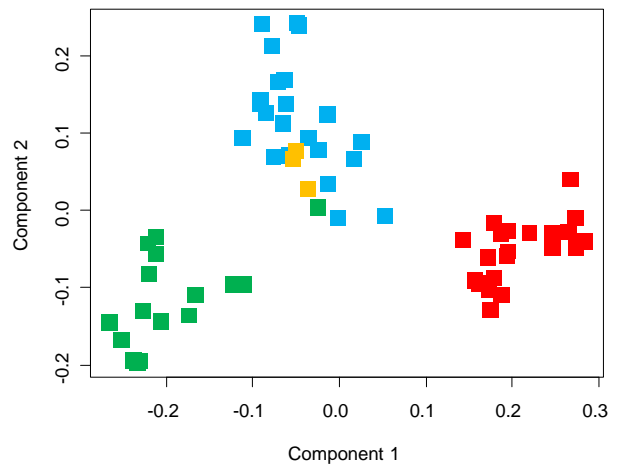
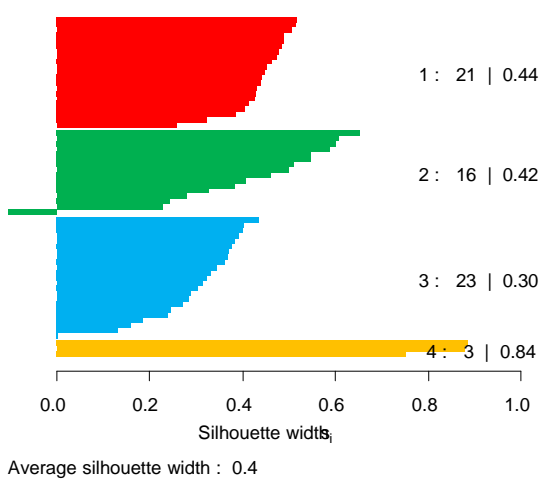
k=2



k=3

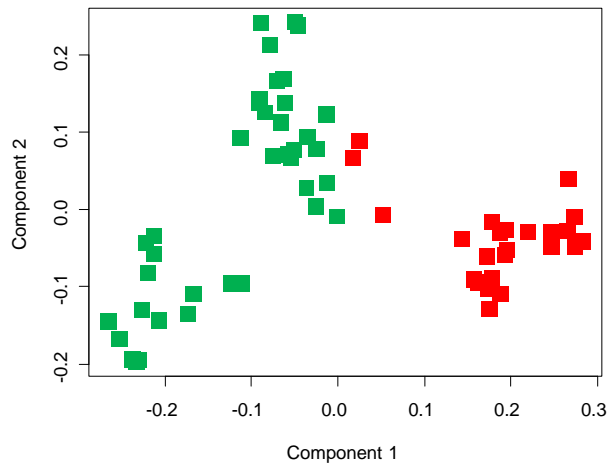
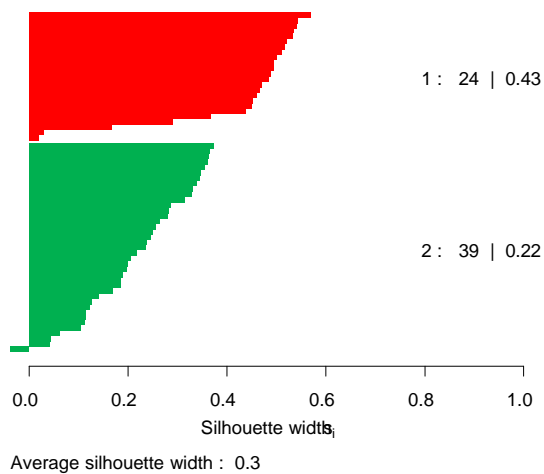


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Picodontidae

Order Primates

Burger 2013

Pearson BDC

Negative: 315

Positive: 718

Clusters: 2

Clusterability

Hopkins Statistic: 0.875

Dip test: 0.013

Dip test p-value: 0.052

Spearman BDC

Negative: 143

Positive: 952

Clusters: 2

Spearman BDC results reveal 234 additional instances of significant, positive correlation, including instances of positive correlation between picodontids and outgroup taxa. Despite that, the cluster partition is the same as in the Pearson BDC. Two clusters are recognized with an average silhouette width of 0.4.

The two-cluster medoid partition is identical to the Pearson BDC. At $k=3$ and $k=4$, the cluster of picodontids also appears (the outgroup are separated into smaller clusters). The three- and four-cluster medoid partitions have average silhouette values of 0.35 and 0.4 respectively.

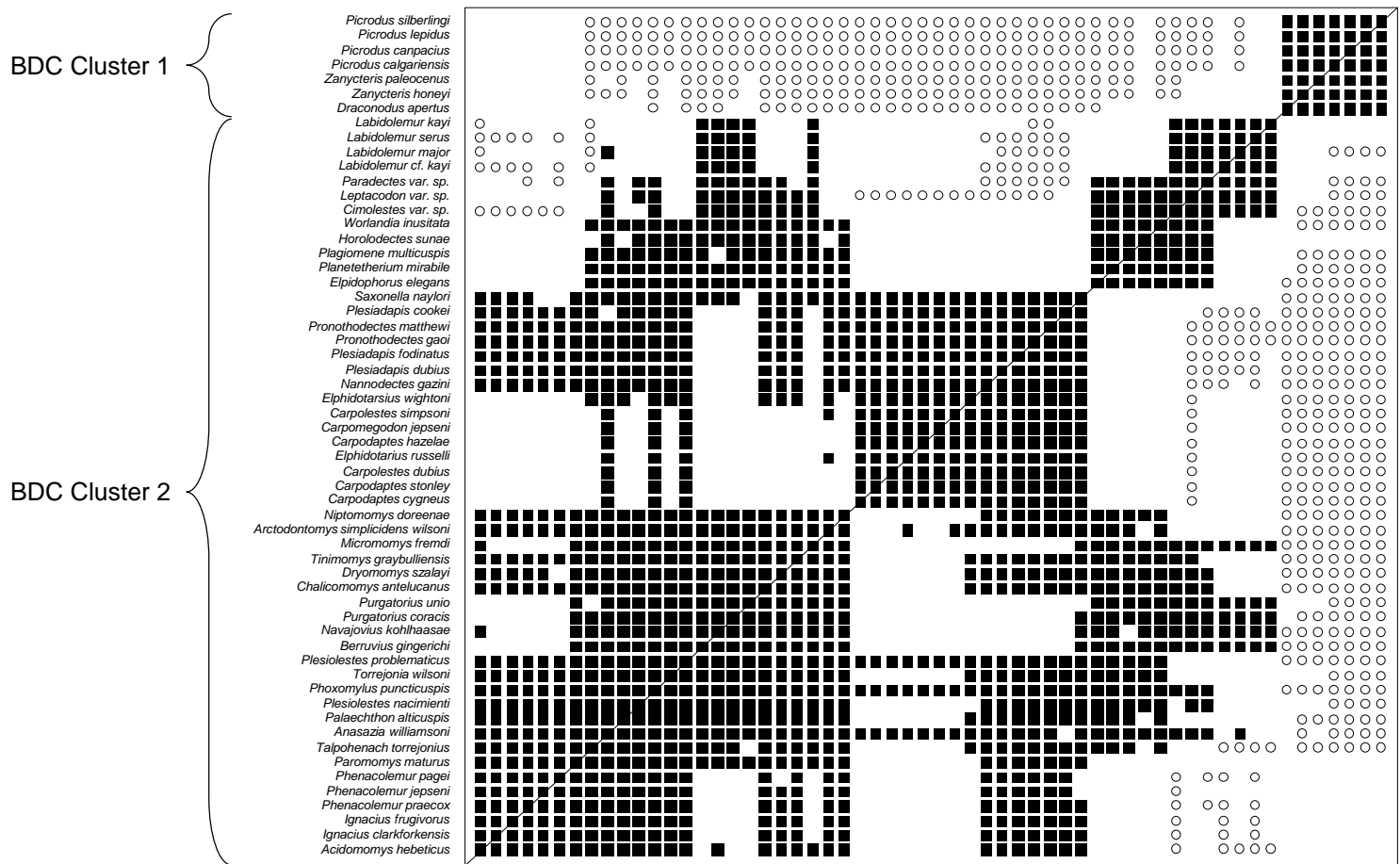
Fuzzy analysis at $k=3$ does not agree with the medoid partition or the BDC clusters, but the average silhouette value of 0.19 is much lower than the average silhouette value of the BDC clusters.

The presence of significant, positive correlation between the picodontids and outgroup taxa revealed in the Spearman BDC results warrants caution in affirming the original holobaramin diagnosis for the Picodontidae, but the strong support for the picodontid cluster in the the medoid partition suggests that the picodontids really are a holobaramin. In the Spearman BDC, the picodontids share significant, positive correlation with species of the genera *Phenacolemur* and *Ignacius*. The addendum figure shows the two-dimensional MDS results with the picodontids, *Phenacolemur*, and *Ignacius* highlighted. The outgroup form a long, quasi-linear structure with the picodontids, *Phenacolemur*, and *Ignacius* at the highest positions in the second component. Hence, the entire line of outgroup taxa is roughly equidistant from picodontids and *Phenacolemur* and *Ignacius*, thus generating positive correlation. Thus, these correlations do not warrant putting *Phenacolemur* and *Ignacius* in the same holobaramin, since the separation between them is visible in the MDS and by the constant recognition of the picodontid cluster in the medoid partitioning.

Original conclusion: HB

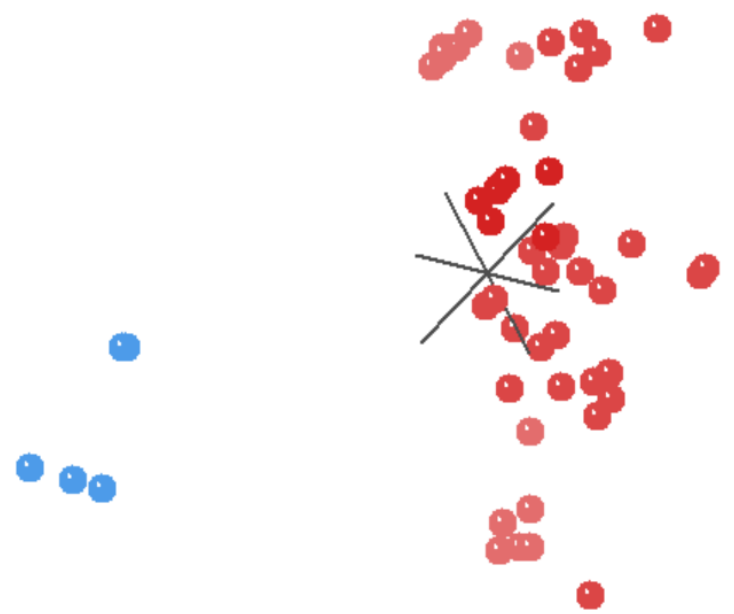
Updated conclusion: HB

Characters: Dental



Order Primates
Family Picrodontidae

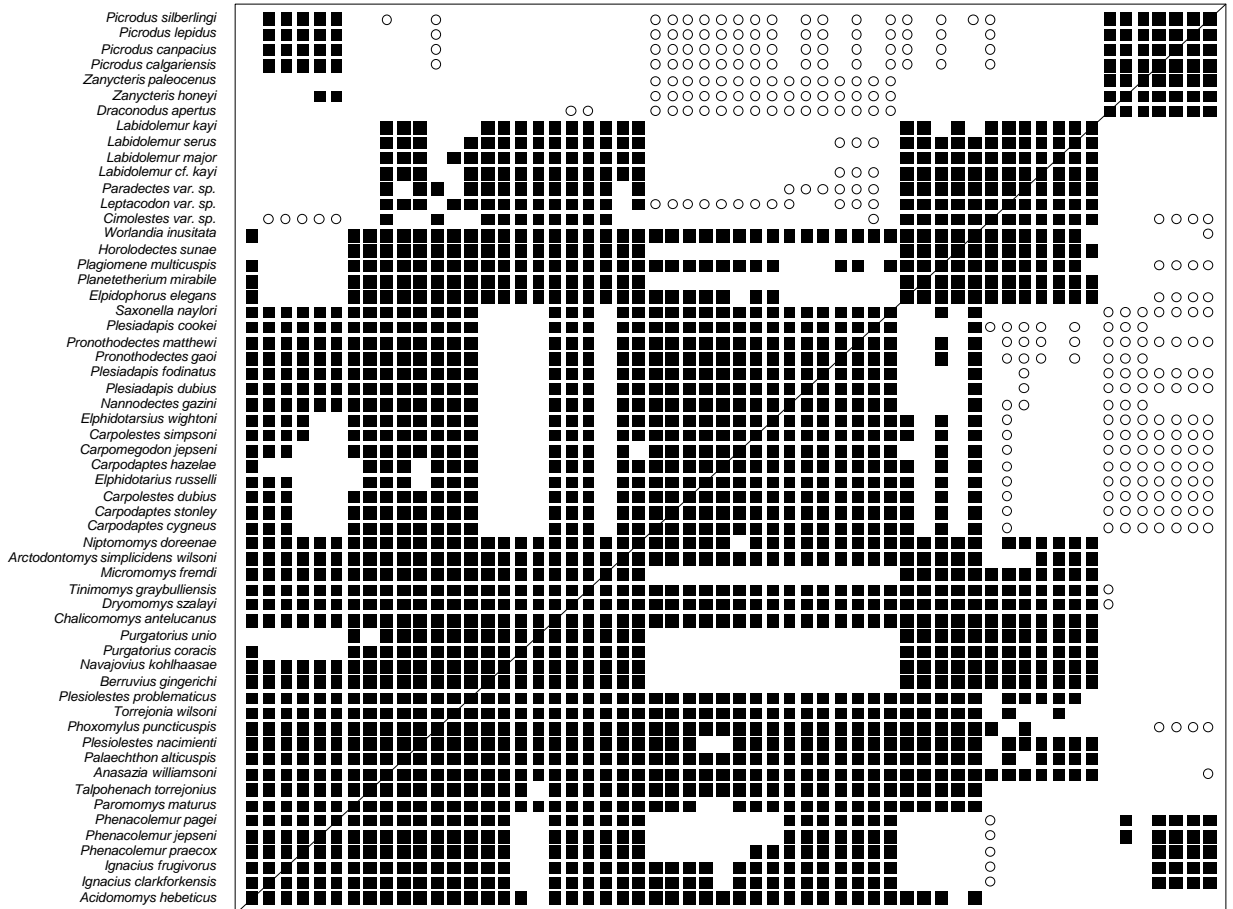
Published taxa	58
Published characters	113
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	58
Characters used for calculations	98
Median bootstrap value	79
F ₉₀	0.34
Stress of 3D MDS	0.24
k _{min}	7
Conclusion	HB



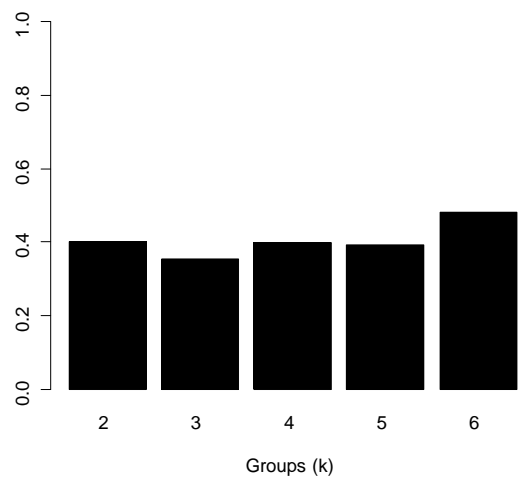
Notes: The taxa are trimmed to include Picrodontidae, with Plesiadapidae, and Carpolestidae as the outgroup. Picrodontidae is well-separated from the outgroup taxa in both BDC and MDS results. Picrodontidae is probably a holobaramin.

BDC Cluster 1

BDC Cluster 2



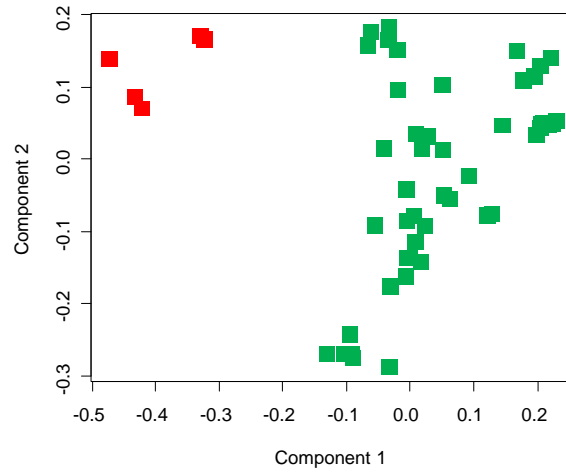
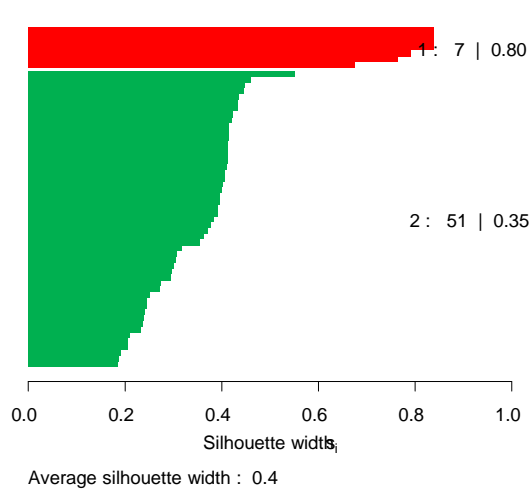
Average Silhouette Widths, Partion Around Medoids



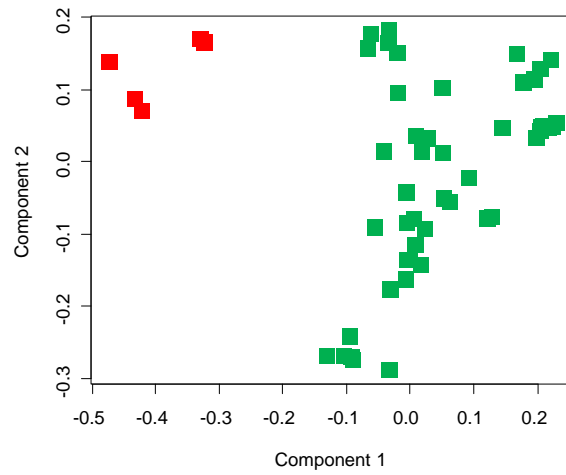
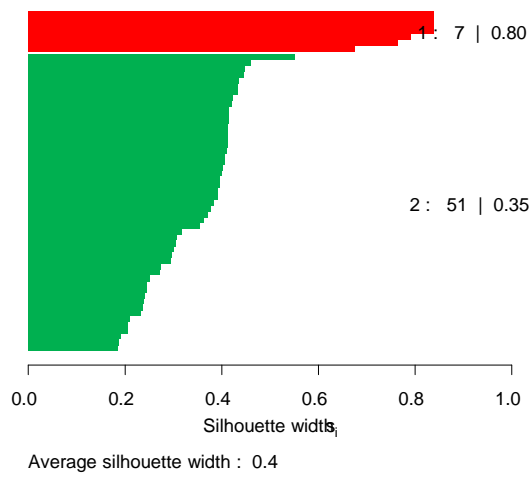
Clade Correspondence: Two large clusters of taxa are evident in the BDC results. Both are monophyletic in the phylogeny in Figure 2 of Burger (2013).

Silhouette plot, BDC partitions

Pearson Correlation

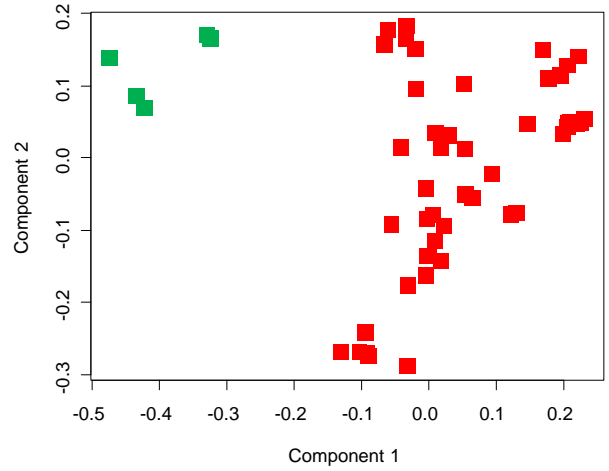
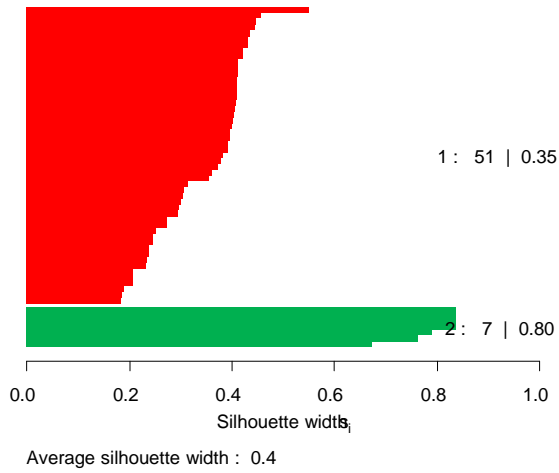


Spearman Correlation

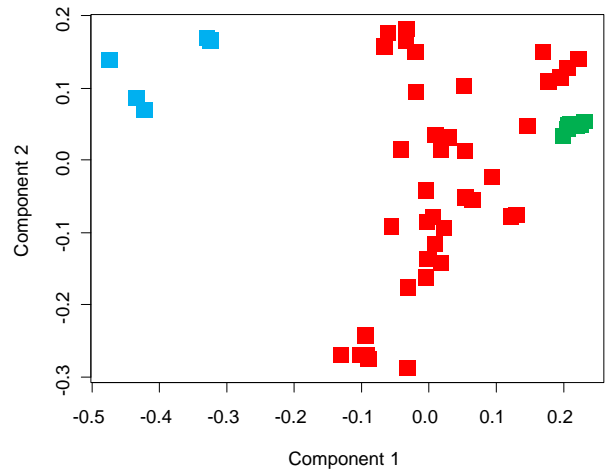
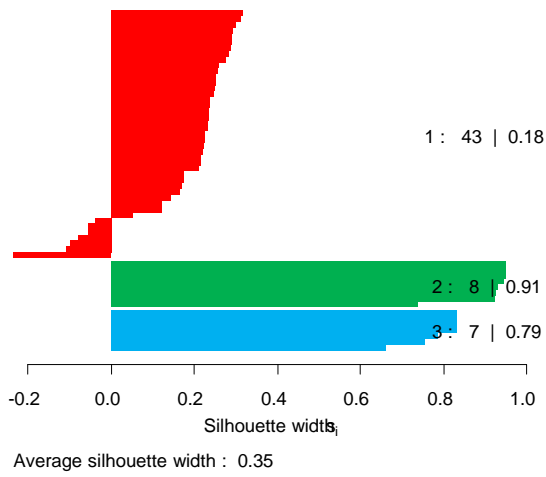


Silhouette plot, Partition Around Medoids

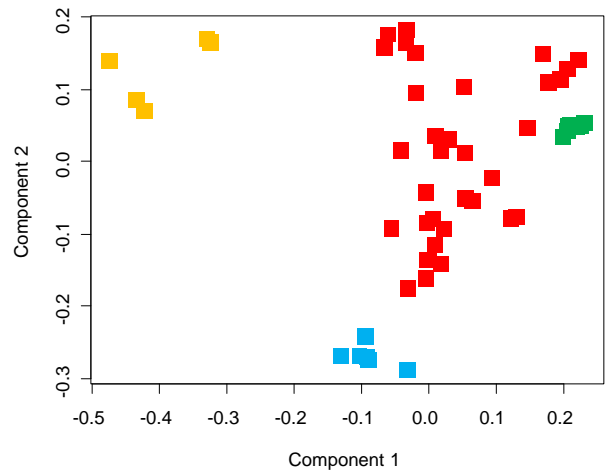
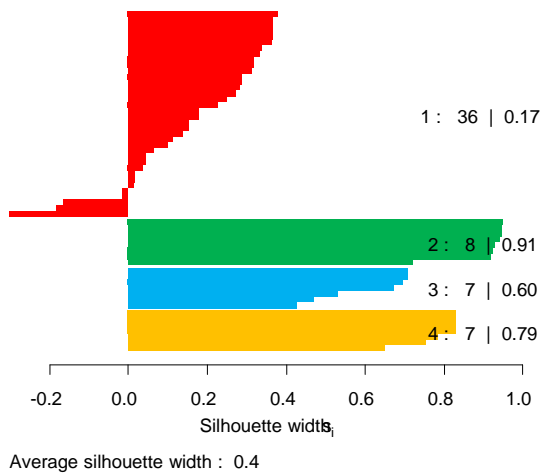
k=2



k=3

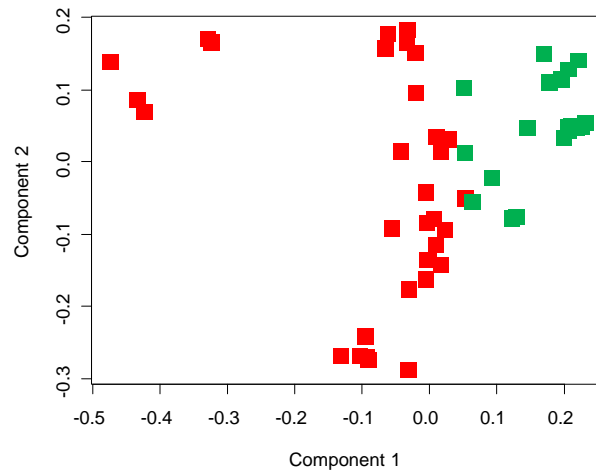
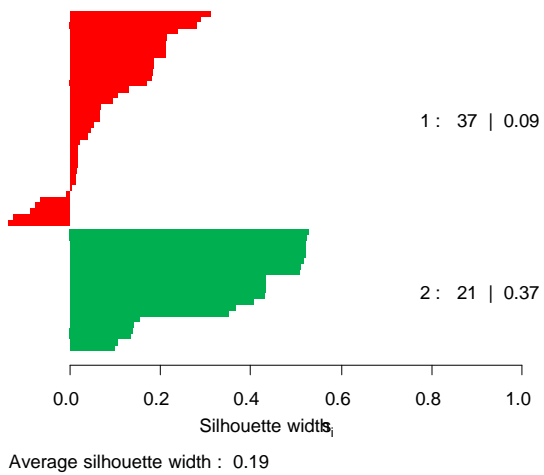


k=4

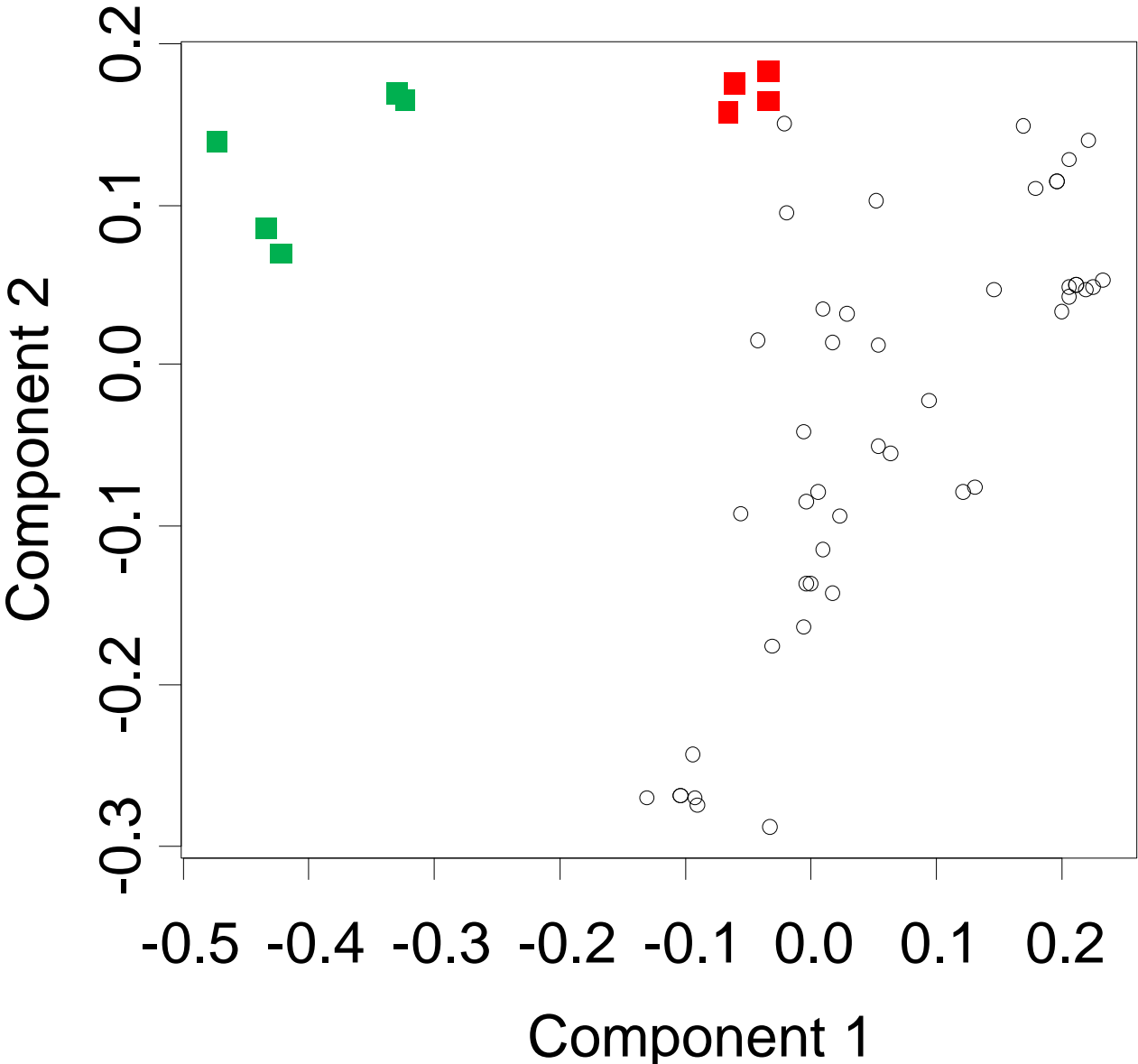


Silhouette plot, Fuzzy Analysis

k=2



Addendum: Two dimensional MDS showing the picrodontids in green and the species of *Phenacolemur* and *Ignacius* in red.



Family Plesiadapidae

Order Primates

Burger 2013

Pearson BDC

Negative: 48

Positive: 43

Clusters: 3

Clusterability

Hopkins Statistic: 0.919

Dip test: 0.096

Dip test p-value: 2.20E-16

Spearman BDC

Negative: 54

Positive: 49

Clusters: 2

The Spearman BDC reveals six additional instances of significant, positive correlation that unite the singleton cluster *Saxonella* with the ingroup plesiadapid cluster. The Pearson BDC results reveal three clusters that correspond exactly to the outgroup taxon *Saxonella* and the two families Plesiadapidae and Carpolestidae. The average silhouette width for this partition is 0.71. The Spearman BDC partition, which combines *Saxonella* and Plesiadapidae, has an average silhouette width of 0.72.

At k=3, medoid partitioning supports the exact clustering of the Pearson BDC results, and at k=2, medoid partitioning supports the exact clustering of the Spearman BDC results.

Fuzzy analysis at k=2 yields a partition that is identical to the Spearman BDC clusters, but at k=3, the fuzzy partition differs from the Pearson BDC clusters. *Saxonella* is combined with *Pronothodectes matthewi*, *Plesiadapis cookei*, and *Pronothodectes gaoi* to form a single cluster separate from the rest of the plesiadapids. The result is a cluster containing *Saxonella* in which all members have a negative silhouette width, and the overall partition has an average silhouette width of 0.54.

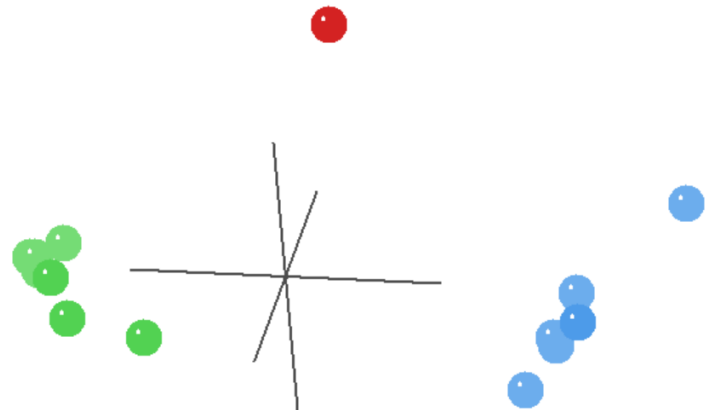
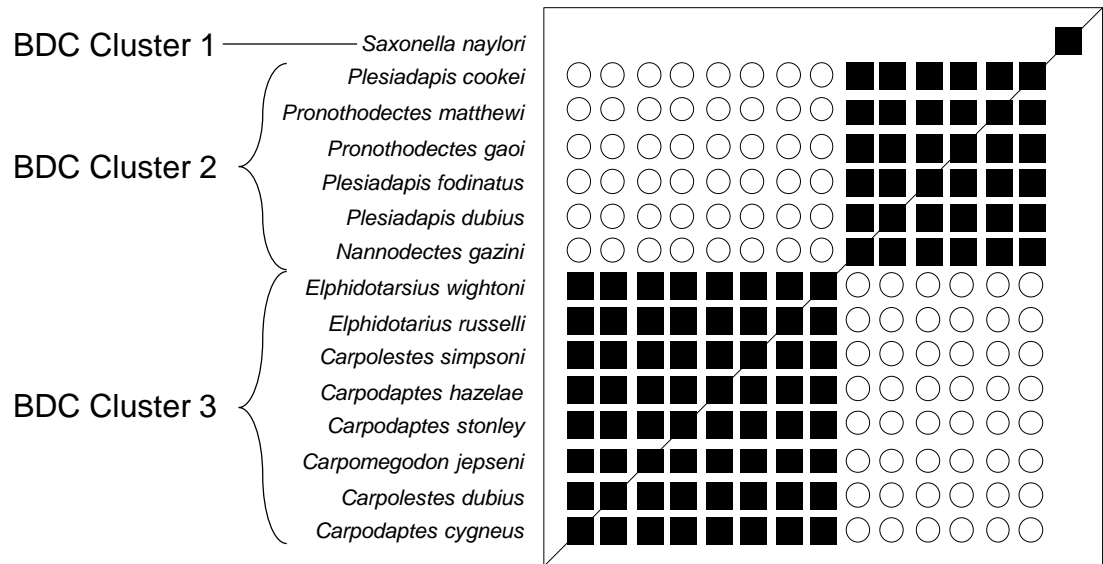
The original conclusion was that both Plesiadapidae and Carpolestidae were holobaramins separate from the outgroup *Saxonella*. These new results create a question regarding the status of *Saxonella*. The Spearman BDC unequivocally places it with the Plesiadapidae, but the MDS still shows a good separation between the plesiadapids and *Saxonella*. Three-cluster medoid partition supports the division of Carpolestidae, Plesiadapidae, and *Saxonella*, but the two-cluster medoid partition combines *Saxonella* with the plesiadapids. Two-cluster fuzzy analysis agrees with the medoid partition and the Spearman BDC clustering; however, the membership coefficient for *Saxonella* is only 64% compared to >86% for all other plesiadapids. Nevertheless, whether or not *Saxonella* belongs with the plesiadapids, there is clear evidence of two holobaramins in these results, thus confirming the original conclusion.

Original conclusion: HB

Updated conclusion: HB

Burger, B.J. 2013. A new species of the archaic primate *Zanycteris* from the late Paleocene of western Colorado and the phylogenetic position of the family Picrodontidae. *PeerJ* 1:e191.

Characters: Dental

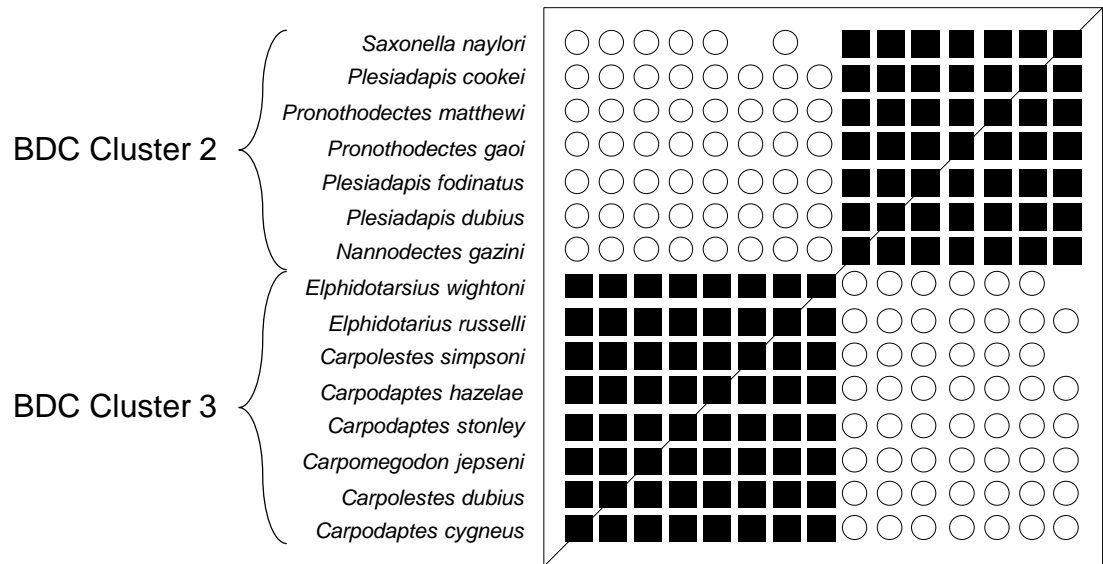


Order Primates
 Family Plesiadapidae

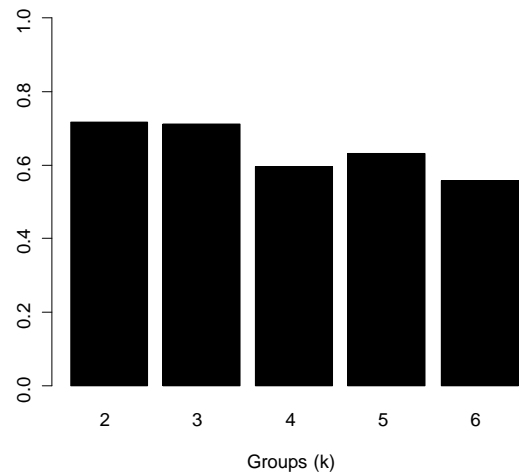
Published taxa	58
Published characters	113
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	15
Characters used for calculations	110
Median bootstrap value	100
F ₉₀	0.86
Stress of 3D MDS	0.09
k _{min}	4
Conclusion	HB

Green: Carpolestidae
 Blue: Plesiadapidae
 Red: *Saxonella*

Notes: Taxa from the previous analysis are further subdivided to remove the picrodontids. Plesiadapidae and Carpolestidae are well separated from each other and from the outgroup *Saxonella* in BDC and MDS results. Both are likely holobaramins.



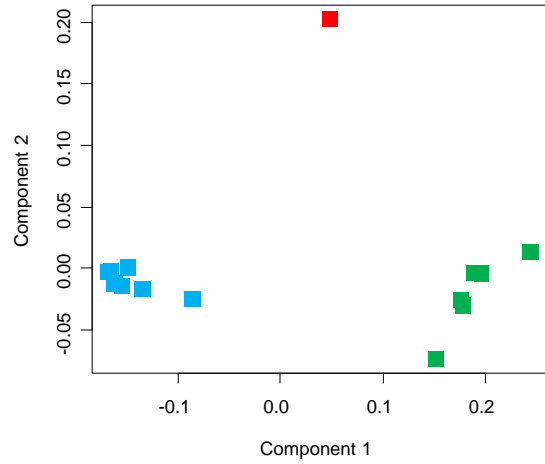
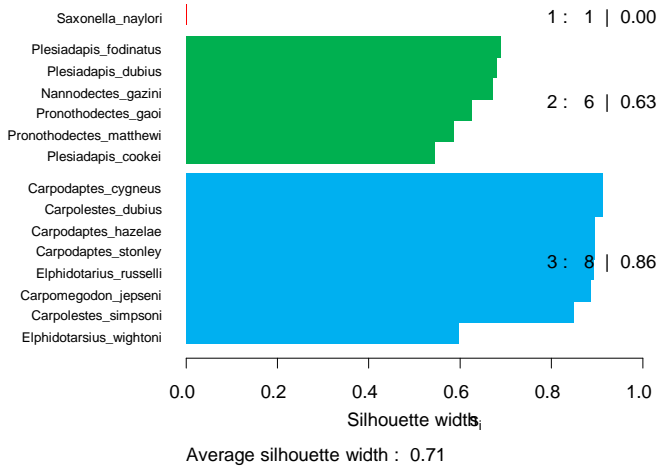
Average Silhouette Widths, Partion Around Medoids



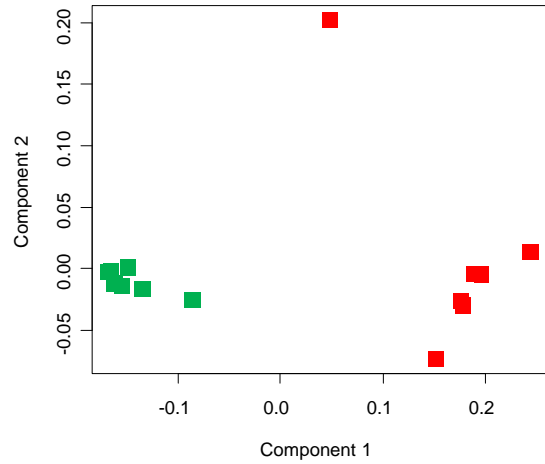
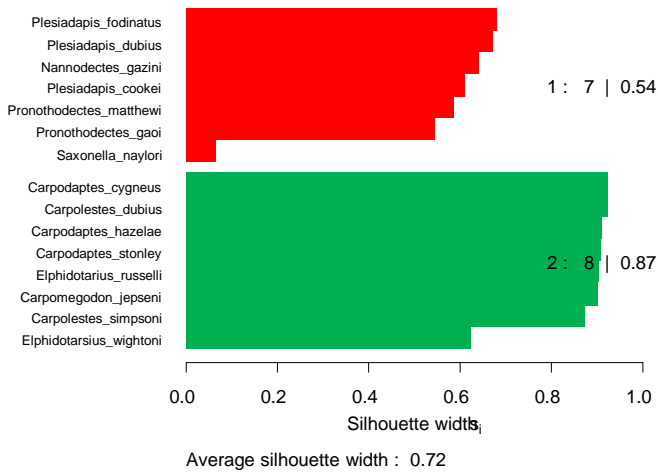
Clade Correspondence: Of the three BDC clusters, only one is a singleton. Both of the larger clusters correspond to clades in the phylogeny in Figure 2 of Burger (2013).

Silhouette plot, BDC partitions

Pearson Correlation

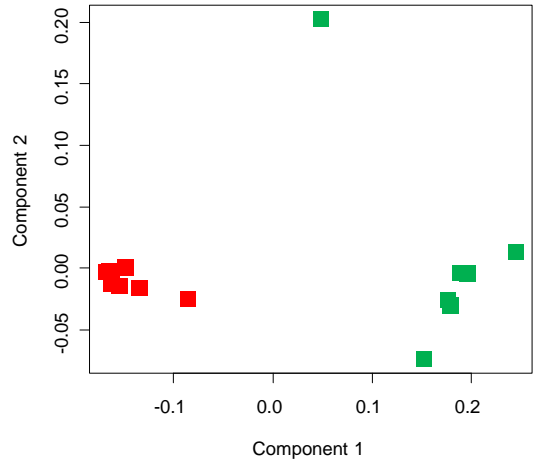
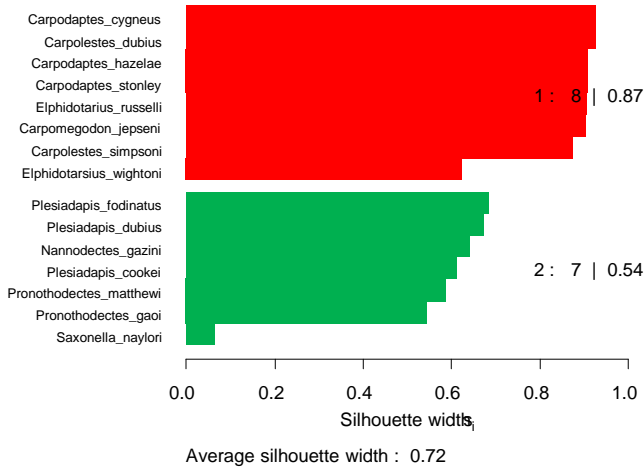


Spearman Correlation

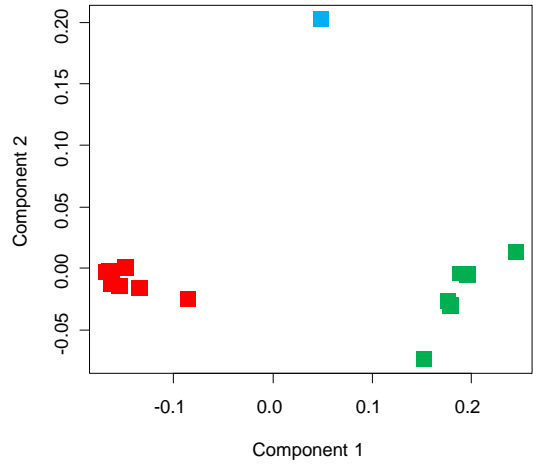
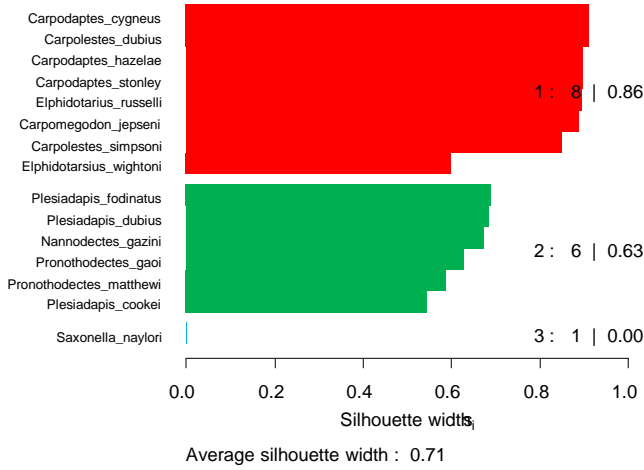


Silhouette plot, Partition Around Medoids

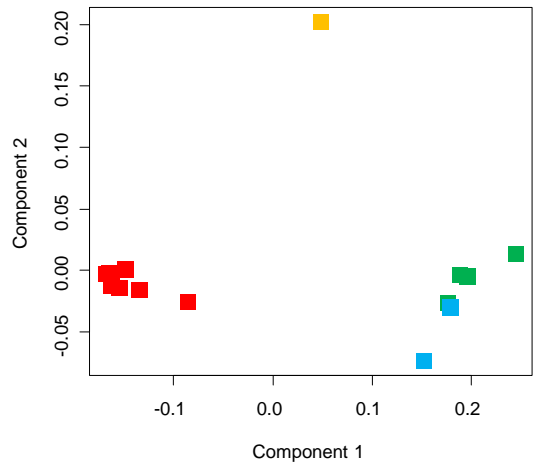
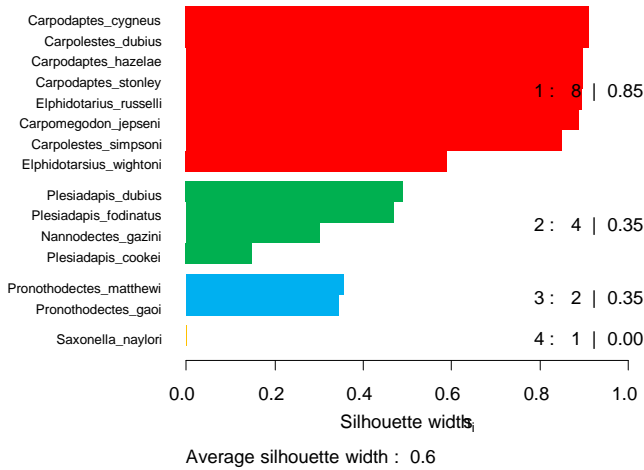
k=2



k=3

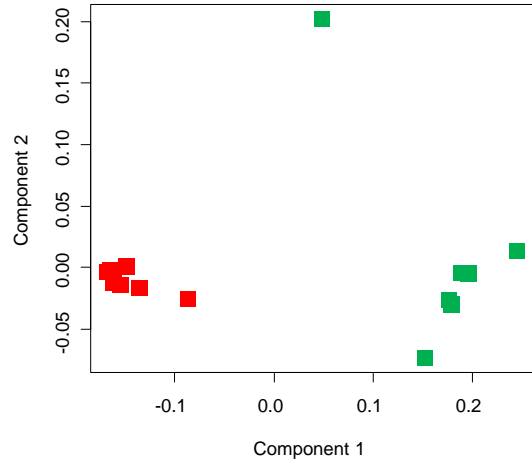
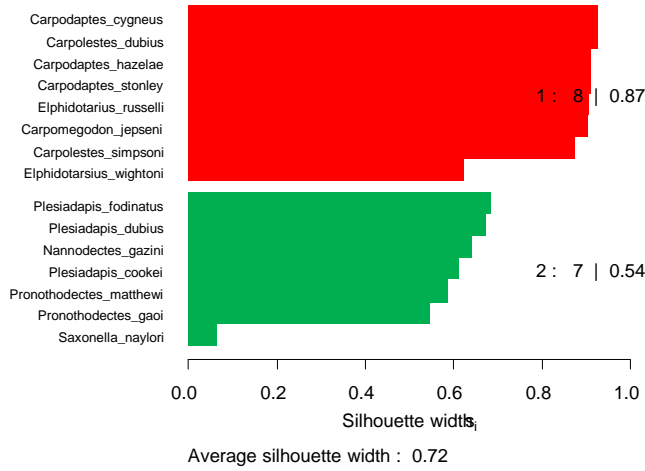


k=4

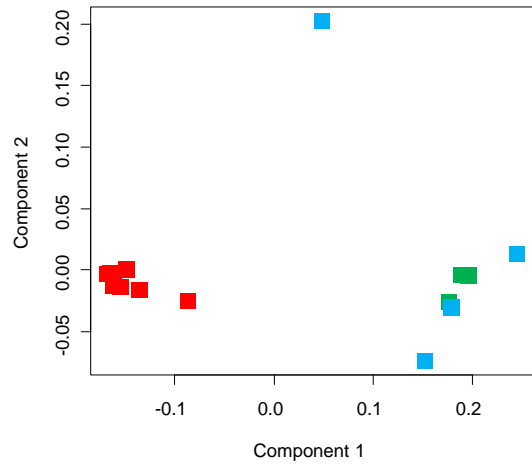
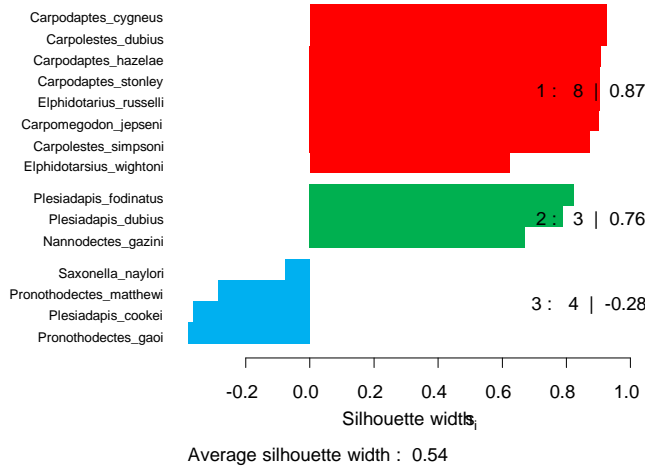


Silhouette plot, Fuzzy Analysis

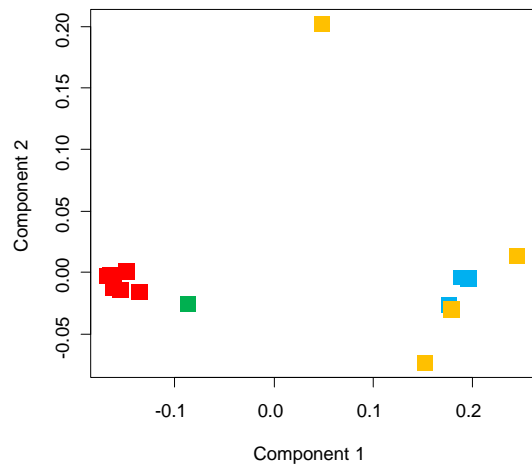
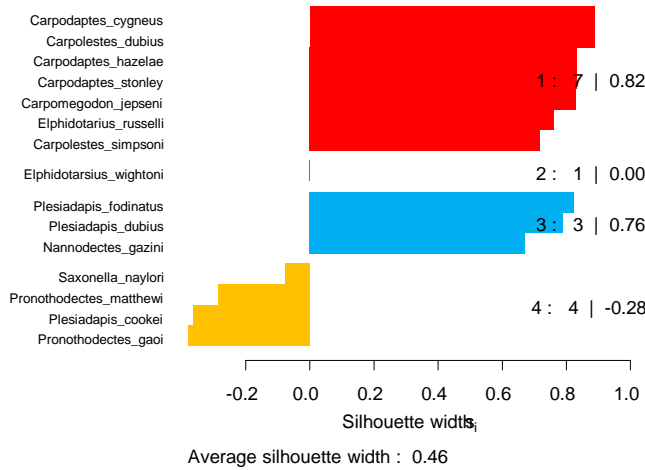
k=2



k=3



k=4



Family Lemuridae

Order Primates

Herrera and Dávalos 2016

Pearson BDC

Negative: 157

Positive: 190

Clusters: 3

Clusterability

Hopkins Statistic: 0.861

Dip test: 0.046

Dip test p-value: 6.14E-06

Spearman BDC

Negative: 99

Positive: 201

Clusters: 2

Spearman BDC adds only eleven instances of significant, positive correlation to the Pearson BDC results, but these correlations rearrange the membership of one of the Pearson BDC clusters. The smallest Pearson BDC cluster is split and reassigned to the other two larger clusters, thus reducing the cluster number from three in the Pearson BDC results to two in the Spearman BDC results. The cluster membership difference is 10%. The average silhouette widths are 0.47 for the three-cluster Pearson BDC partition and 0.44 for the two-cluster Spearman BDC partition. In addition, the Spearman BDC partition leaves one taxon (*Archaeolemur edwardsi*) with a negative silhouette width.

Two-cluster medoid partitioning exactly matched the clusters of the Spearman BDC results. Three-cluster medoid partitioning was very similar to the Pearson BDC clusters (cluster membership difference: 3%), with a single taxon (*Avahi occidentalis*) assigned to a different cluster, resulting in a negative silhouette width.

Fuzzy analysis at k=2 produced a partition very similar to the Spearman BDC clusters (cluster membership difference: 3%), with one taxon (*Archaeolemur majori*) assigned to a different cluster. The average silhouette width for the two-cluster fuzzy partition is 0.42. At k=3, the fuzzy partition differs substantially from the Pearson BDC results, with a cluster membership difference of 41%. The average silhouette width of the three-cluster fuzzy partition was only 0.26.

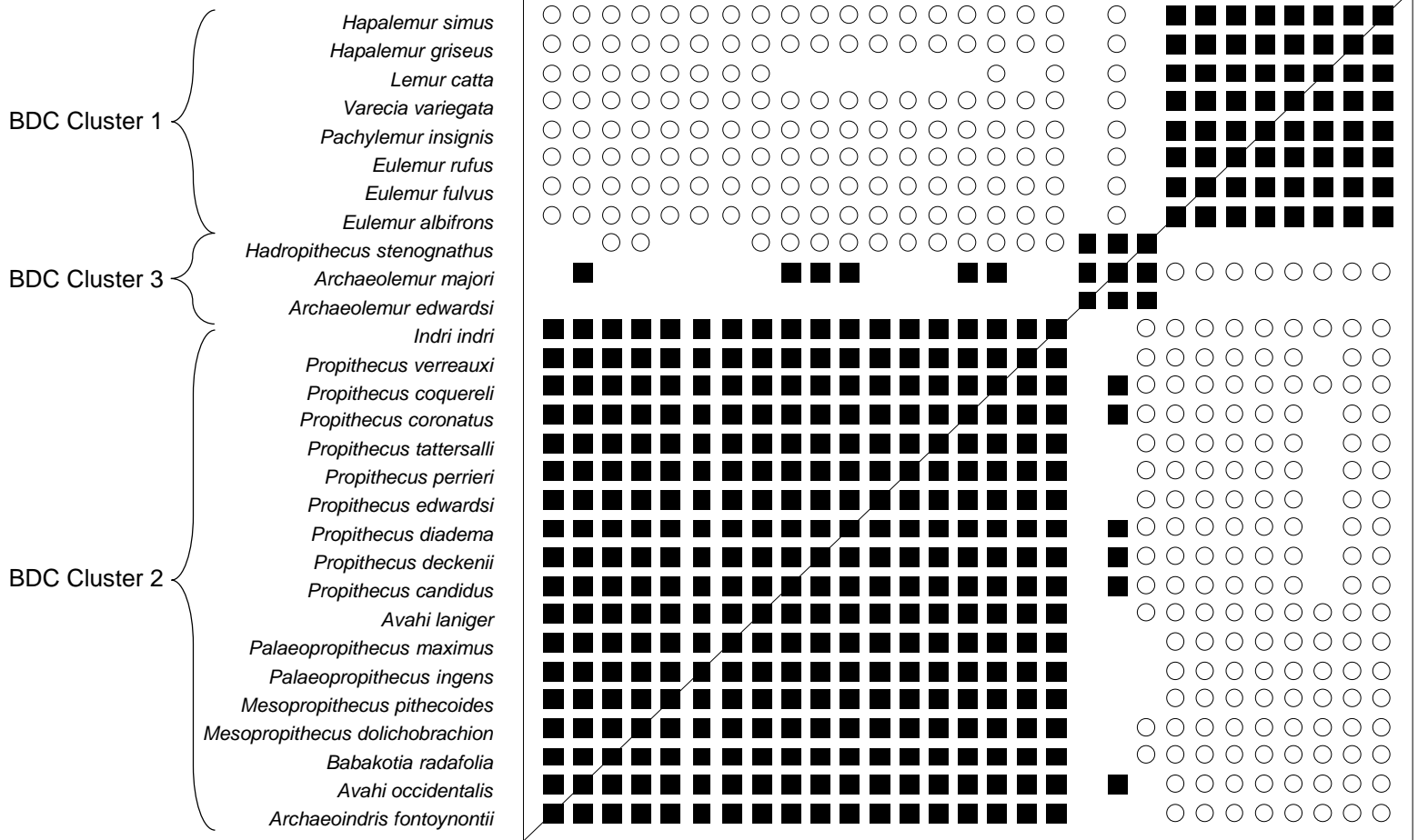
The small cluster recognized by the Pearson BDC but divided by the Spearman BDC is a diffuse set of three taxa in the MDS and consists of the three species of Archaeolemuridae (*Archaeolemur majori*, *Archaeolemur edwardsi*, and *Hadropithecus stenognathus*). Whatever the exact status of the archaeolemurids, every new analysis recognized the Lemuridae as a separate group from the Paleopropithecidae, thus supporting the original conclusion that these groups are holobaramins.

Original conclusion: HB

Updated conclusion: HB

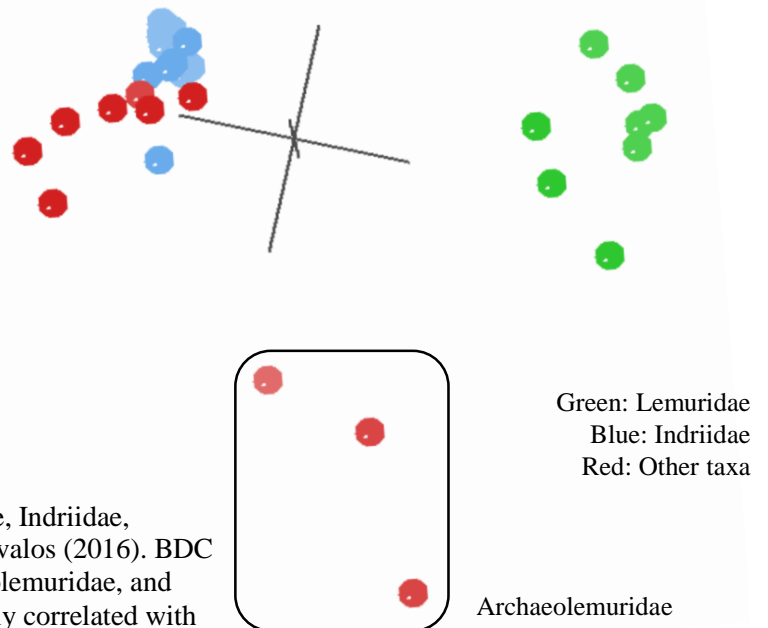
Herrera, J.P. and L.M. Dávalos. 2016. Phylogeny and divergence times of lemurs inferred with recent and ancient fossils in the tree. *Systematic Biology* 65:772-791.

Characters: Craniodental and postcranial

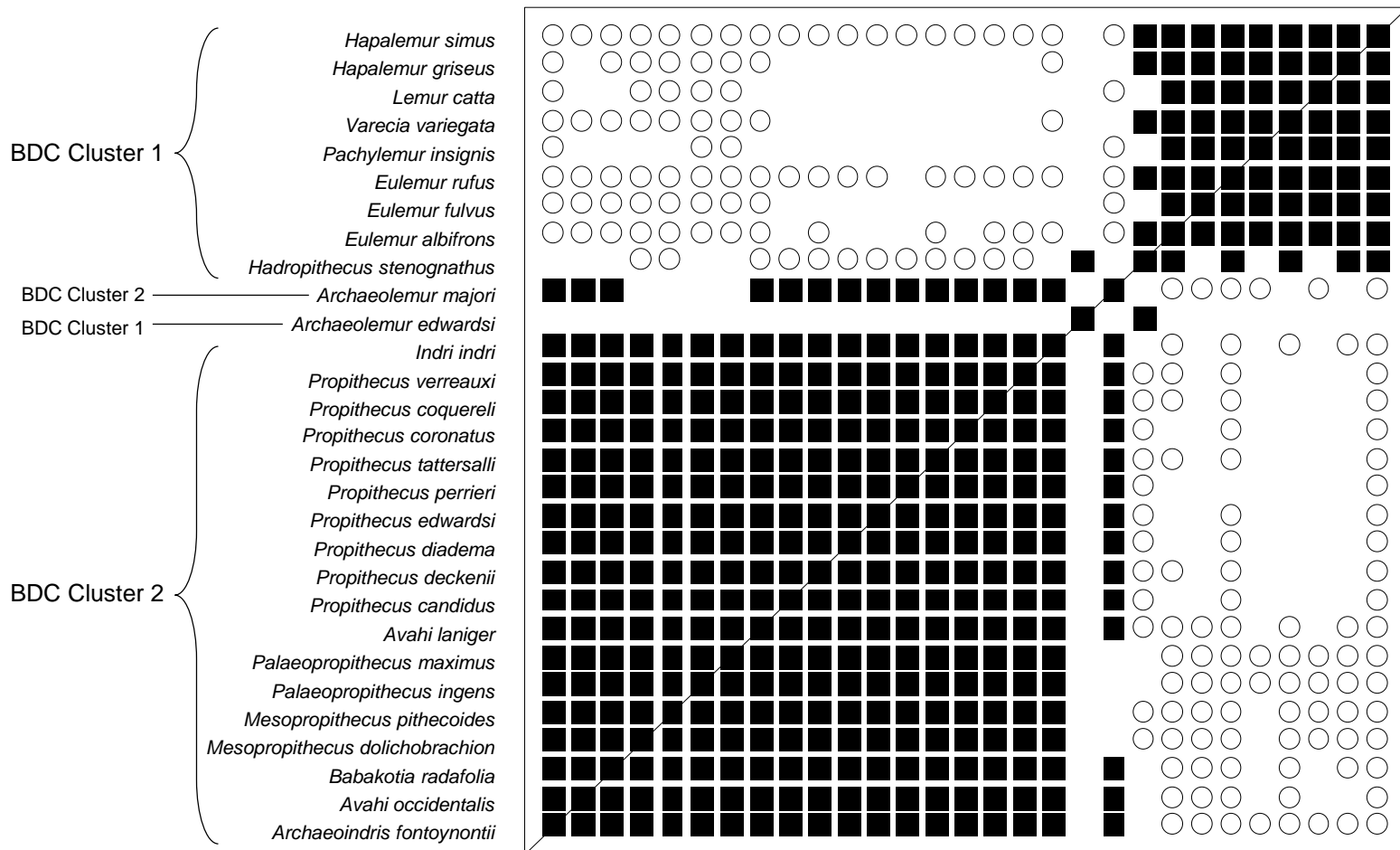


Order Primates
Family Lemuridae

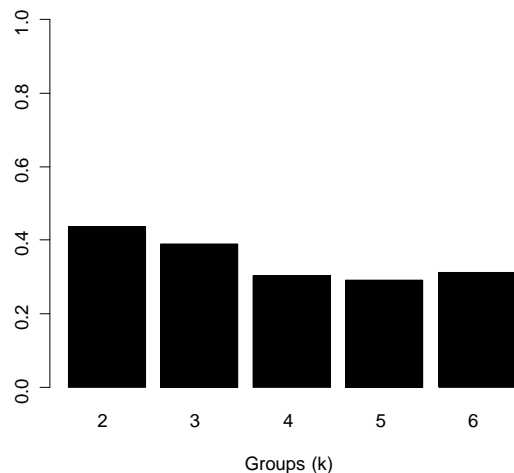
Published taxa	29
Published characters	421
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	29
Characters used for calculations	157
Median bootstrap value	98
F ₉₀	0.67
Stress of 3D MDS	0.23
k _{min}	11
Conclusion	HB



Notes: Taxon sample has been trimmed here to include Lemuridae, Indriidae, Palaeopropithecidae, and Archaeolemuridae from Herrera and Dávalos (2016). BDC reveals three groups of taxa corresponding to Lemuridae, Archaeolemuridae, and Indriidae + Palaeopropithecidae. *Archaeolemur majori* is positively correlated with six members of the Indriidae + Palaeopropithecidae group, but all but one BDC with *Archaeolemur majori* have poor bootstrap values. All comparisons between the groups Lemuridae and Indriidae + Palaeopropithecidae share significant, negative BDC. The MDS results support the three groups observed in the BDC, but *Archaeolemur majori* is clearly separated from the Indriidae + Palaeopropithecidae. Hence we may conclude that Lemuridae and Indriidae + Palaeopropithecidae are both likely holobaramins.



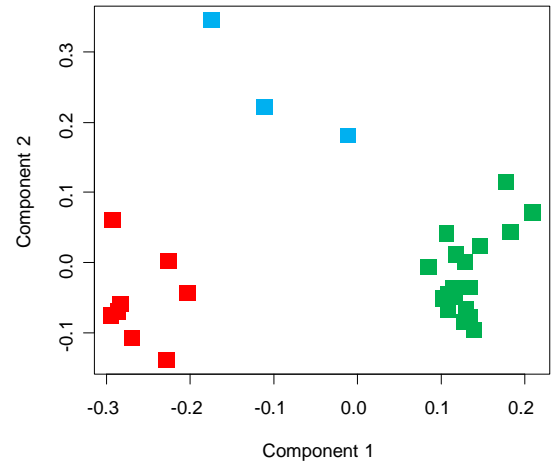
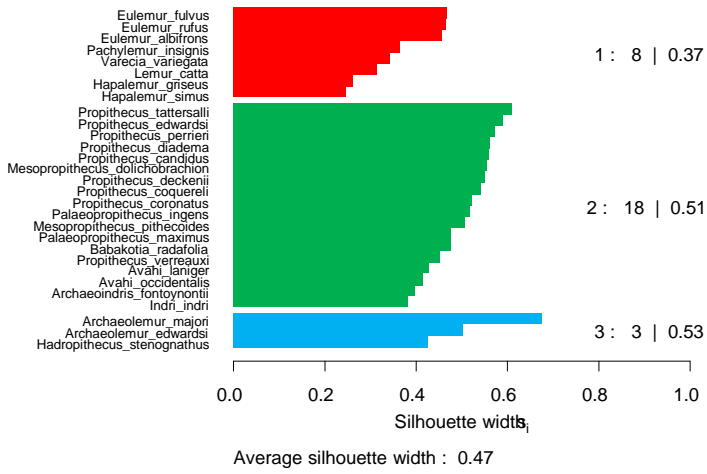
Average Silhouette Widths, Partion Around Medoids



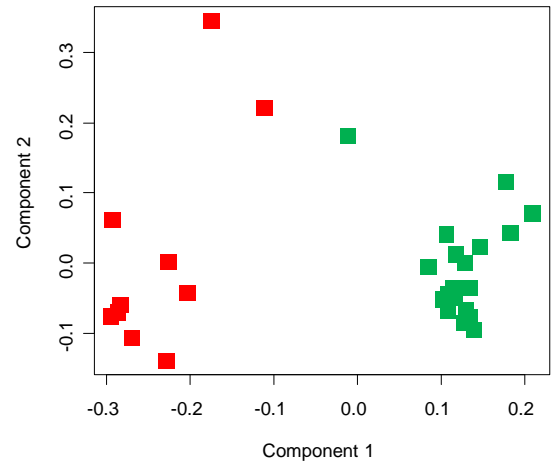
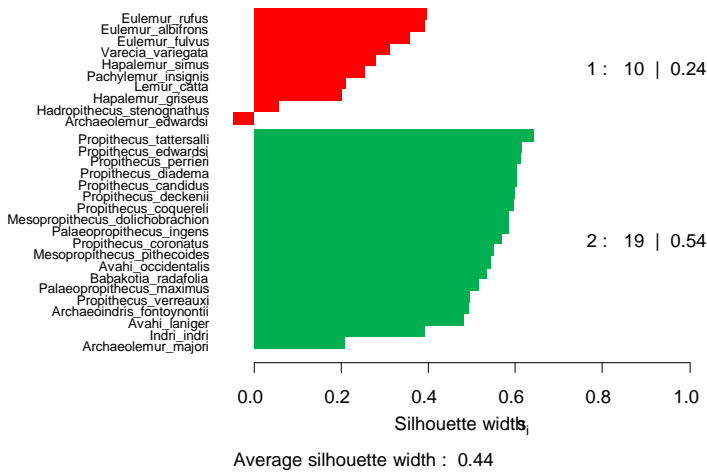
Clade Correspondence: The smallest of the three BDC clusters contains three taxa. All three are monophyletic in the phylogeny in Figure 2 of Burger (2013).

Silhouette plot, BDC partitions

Pearson Correlation

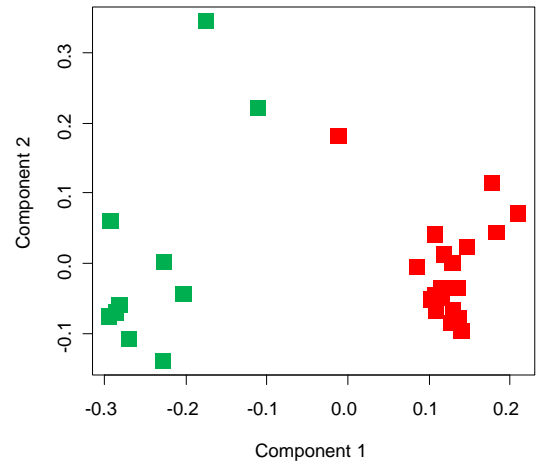
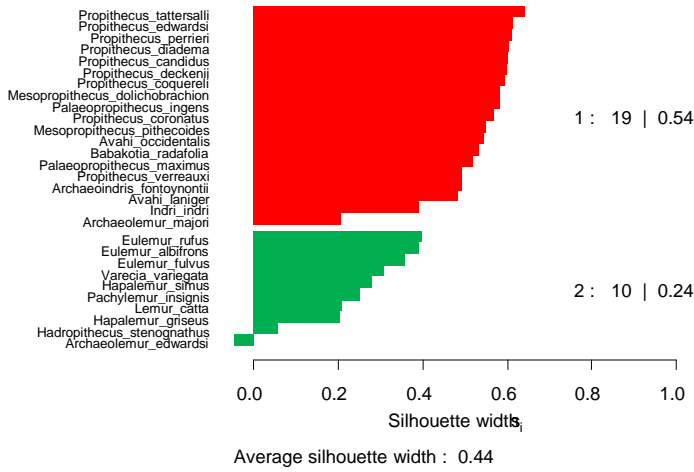


Spearman Correlation

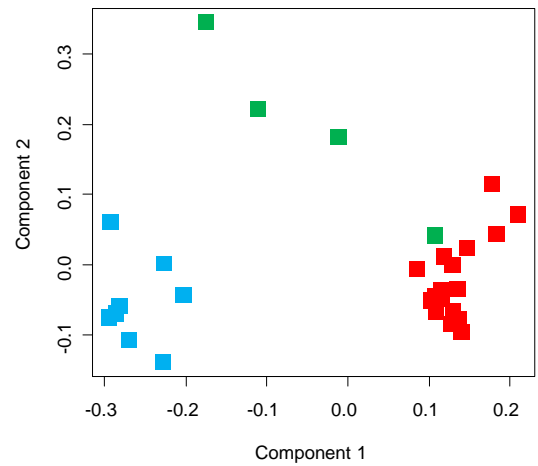
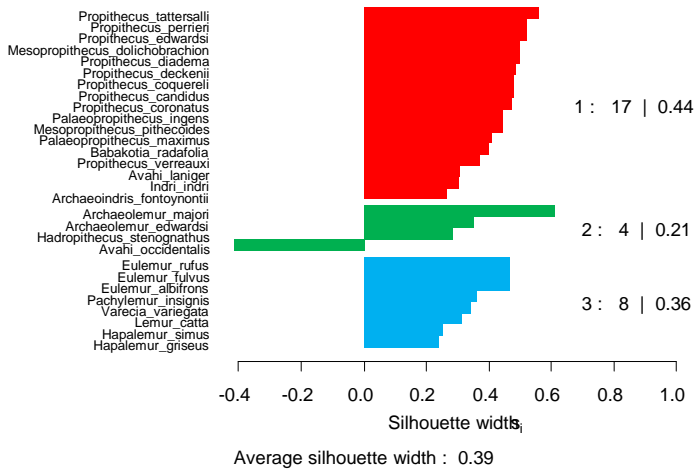


Silhouette plot, Partition Around Medoids

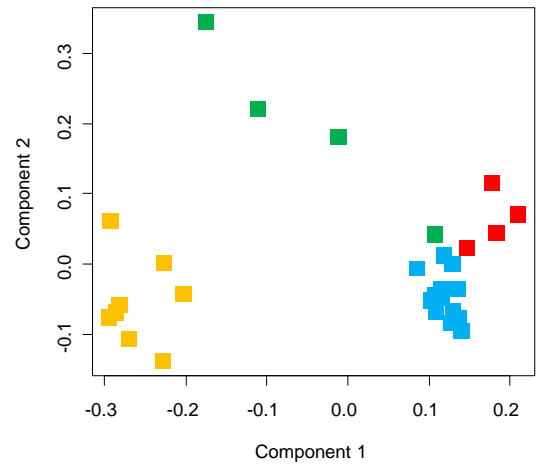
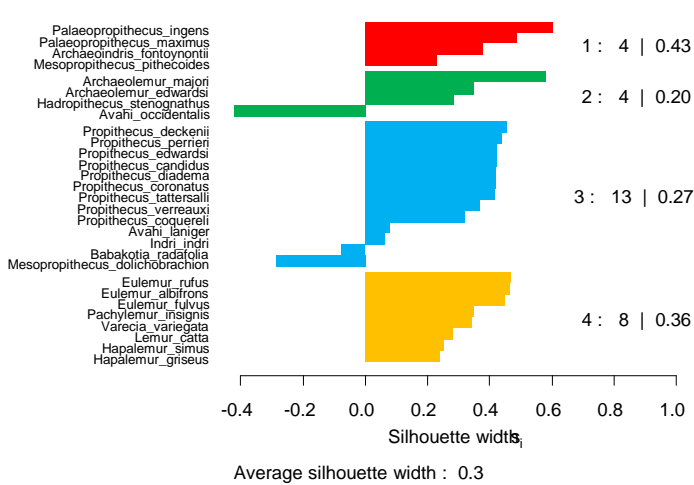
k=2



k=3

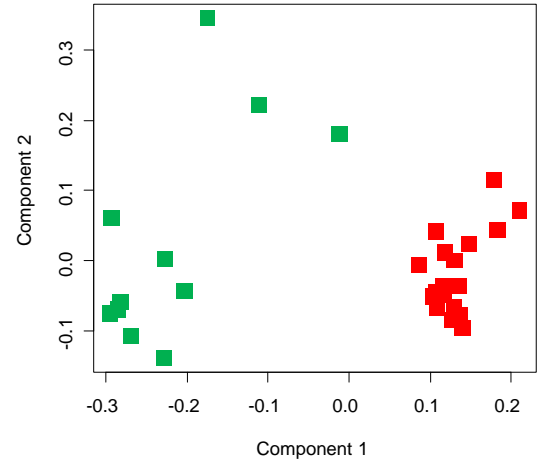
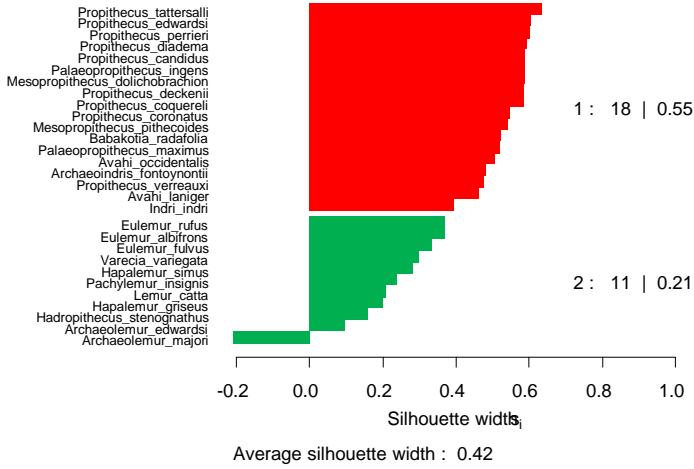


k=4

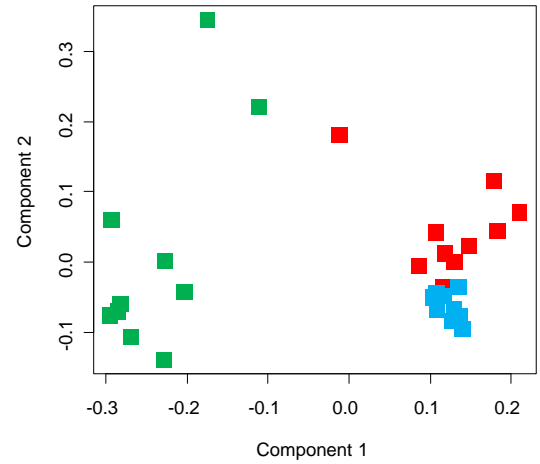
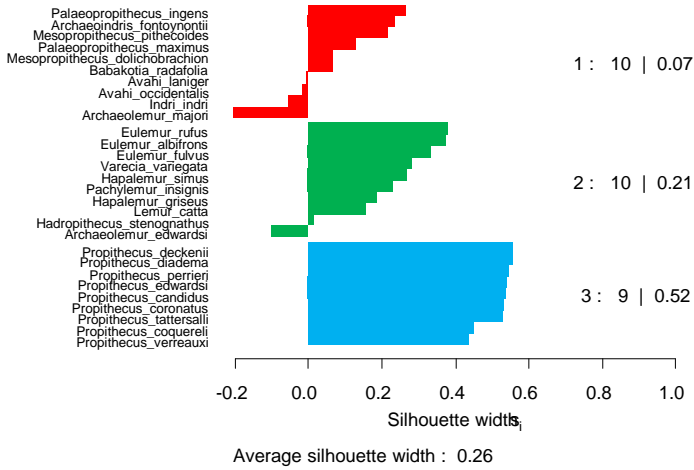


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Lepilemuridae

Order Primates

Herrera and Dávalos 2016

Pearson BDC

Negative: 18

Positive: 24

Clusters: 3

Clusterability

Hopkins Statistic: 0.85

Dip test: 0.027

Dip test p-value: 0.931

Spearman BDC

Negative: 18

Positive: 28

Clusters: 3

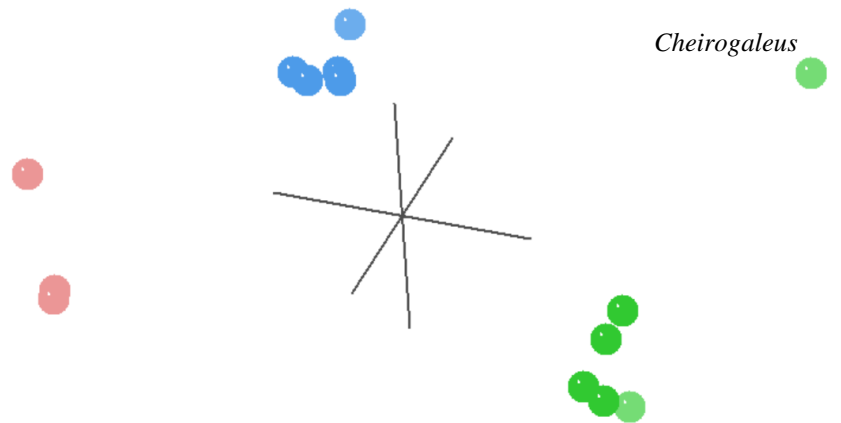
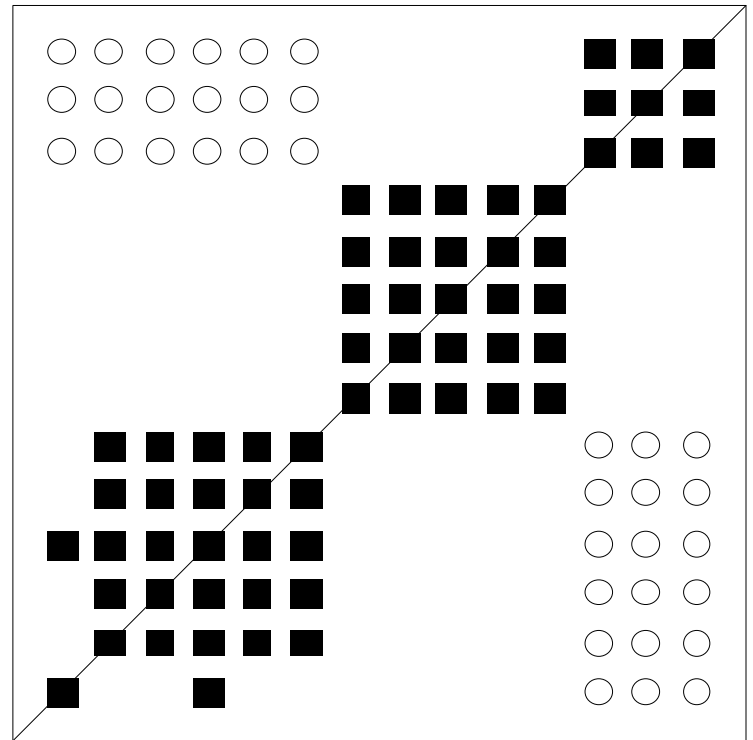
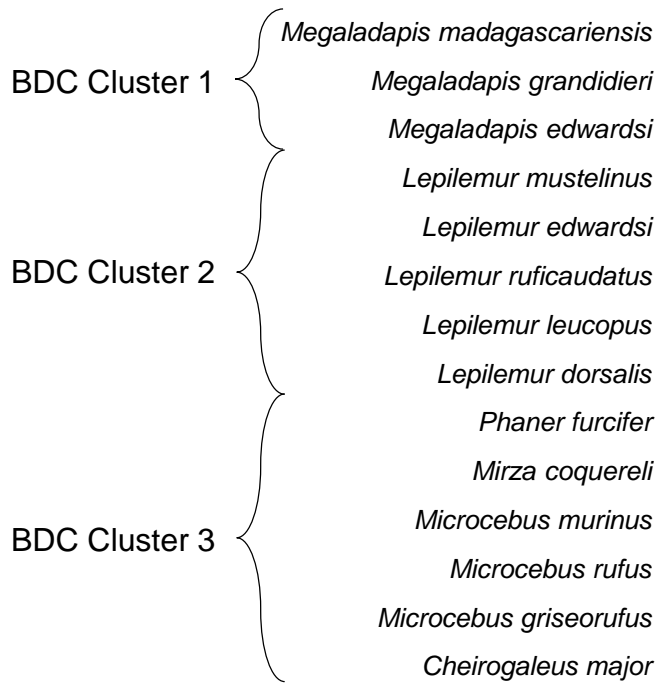
The Spearman BDC results reveal four additional instances of significant, positive correlation that firmly place *Cheirogaleus major* in a cluster with the rest of the cheirogaleids. The clustering is the same between the Spearman and Pearson BDC results, with an average silhouette width of 0.5. The three-cluster medoid partition agrees exactly with the BDC clusters, and the three-cluster fuzzy analysis produces the same partition as well.

These results confirm precisely the original conclusion that these clusters represent two holobarmins, Cheirogaleidae and Lepilemuridae.

Original conclusion: HB

Updated conclusion: HB

Craniodental and postcranial

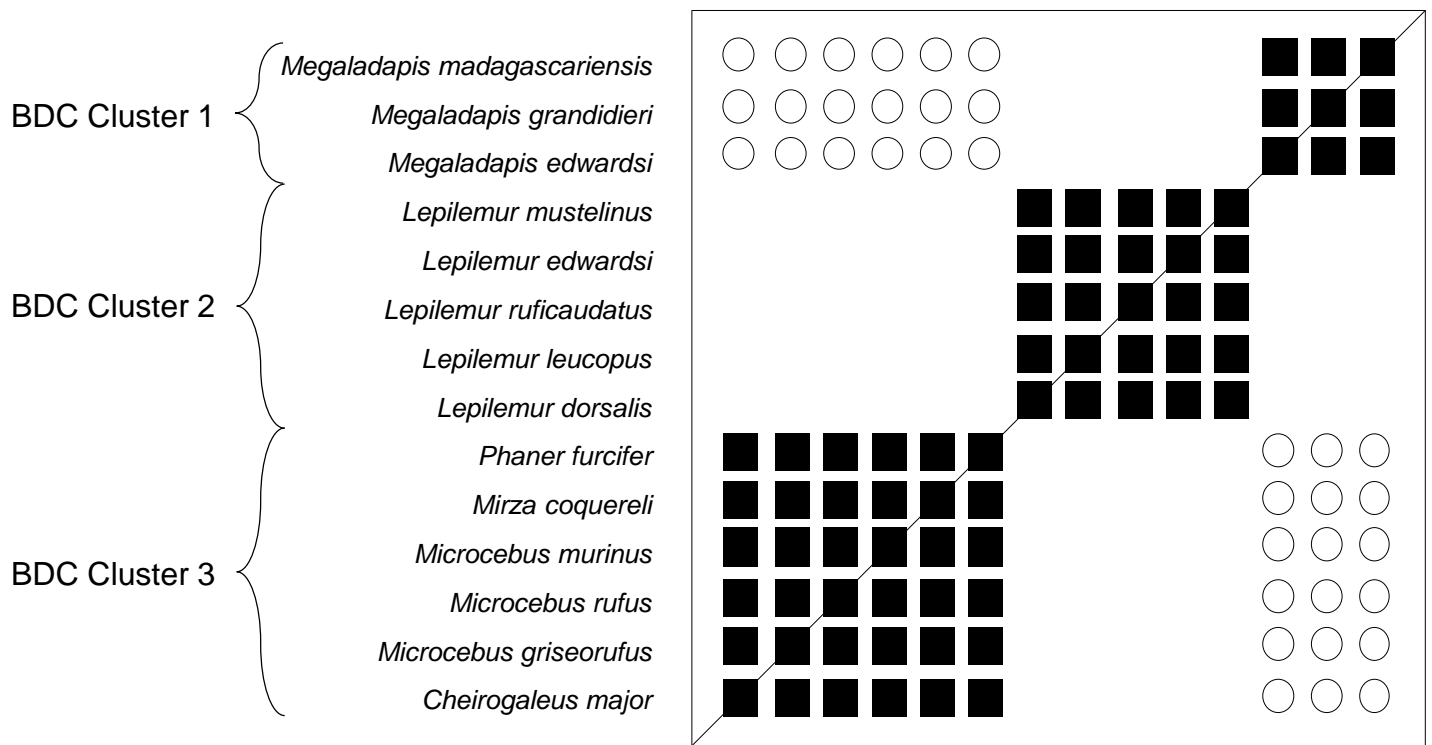


Order Primates
Family Lepilemuridae

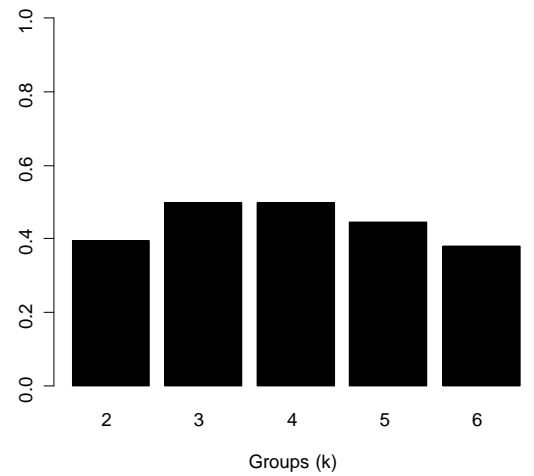
Published taxa	14
Published characters	421
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	14
Characters used for calculations	161
Median bootstrap value	93
F ₉₀	0.575
Stress of 3D MDS	0.16
k _{min}	7
Conclusion	HB

Red: Megaladapidae
Green: Cheirogaleidae
Blue: Lepilemuridae

Notes: Taxa have been trimmed to include Lepilemuridae, Cheirogaleidae, and Megaladapidae. BDC reveals three clear groups corresponding to the three families. MDS confirms these three groups. The position of *Cheirogaleus major* is uncertain in both BDC and MDS results. Lepilemuridae and Cheirogaleidae (excluding *Cheirogaleus major*) are likely holobaramins.



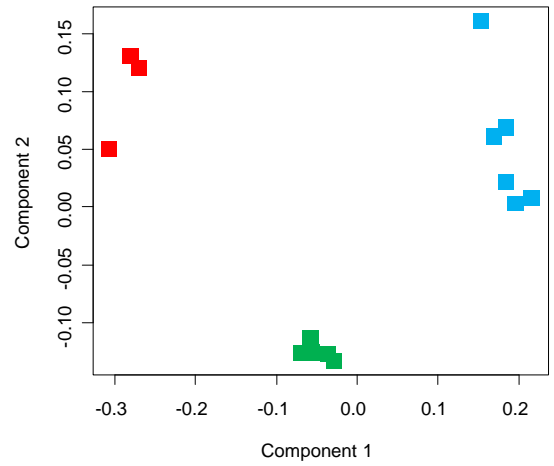
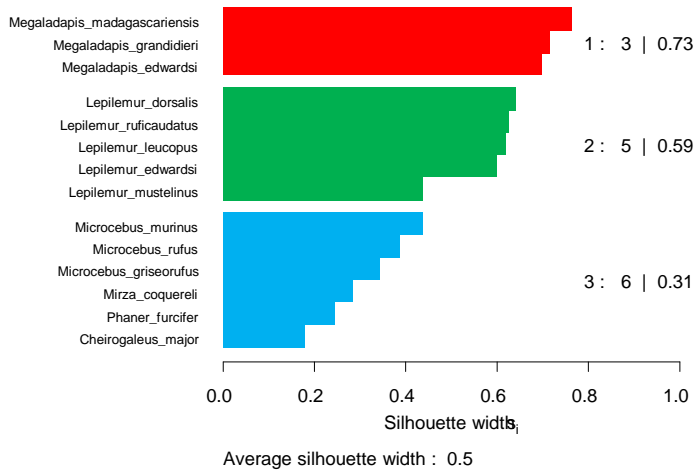
Average Silhouette Widths, Partion Around Medoids



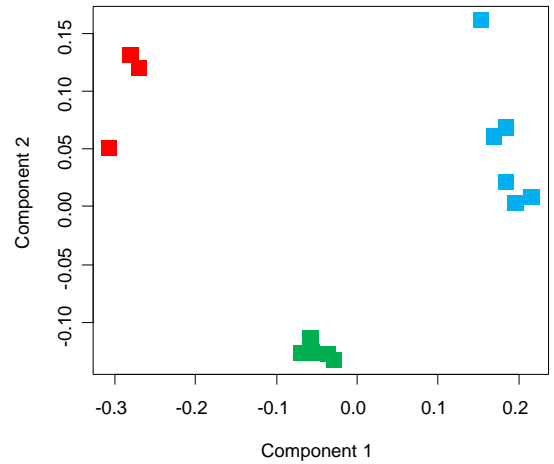
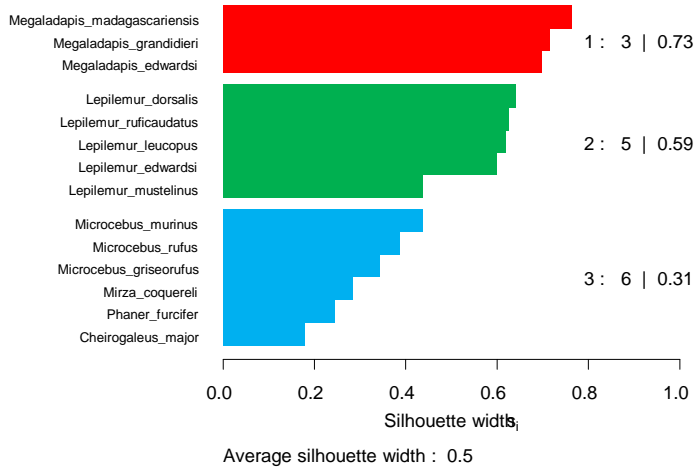
Clade Correspondence: All three BDC clusters contain more than one taxon each. All three are monophyletic in the phylogeny in Figure 2 of Burger (2013).

Silhouette plot, BDC partitions

Pearson Correlation

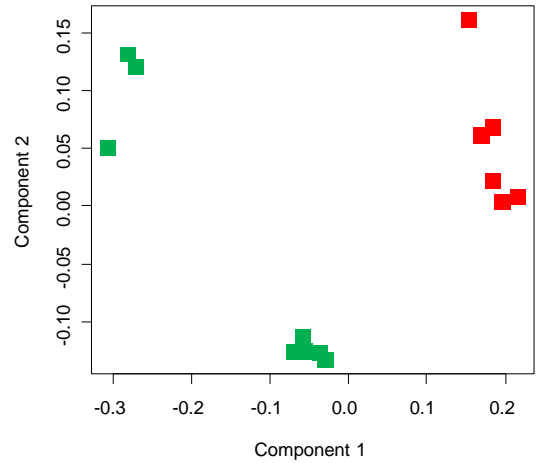
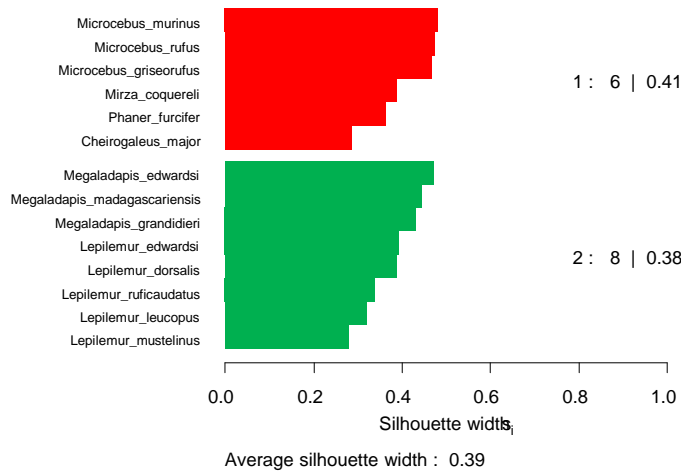


Spearman Correlation

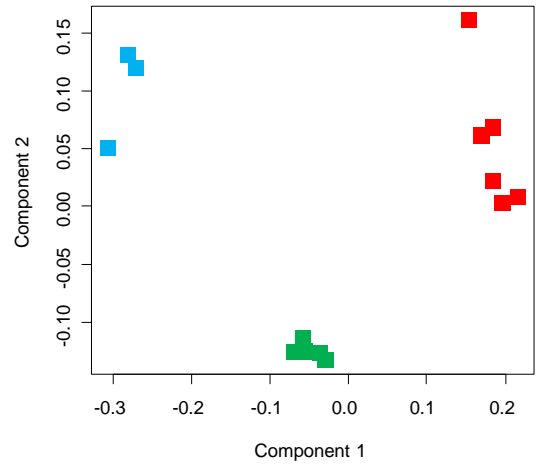
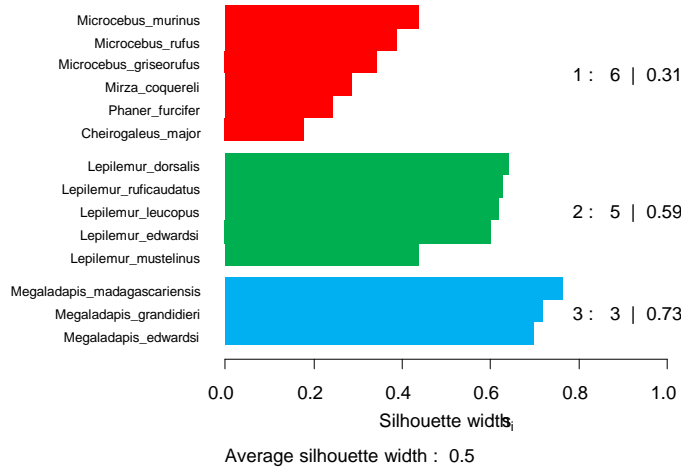


Silhouette plot, Partition Around Medoids

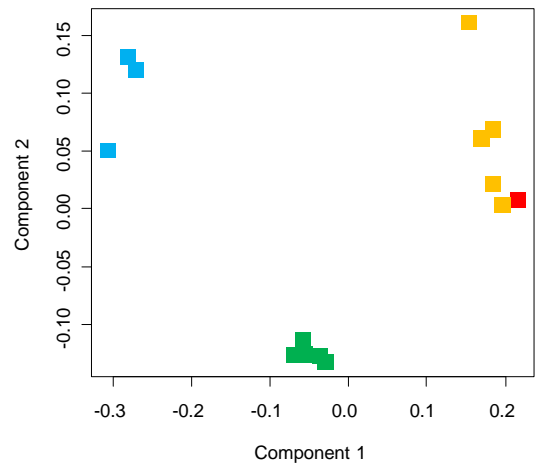
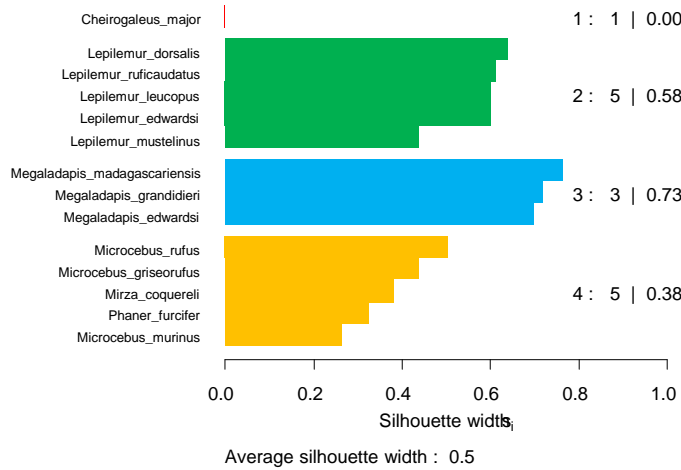
k=2



k=3

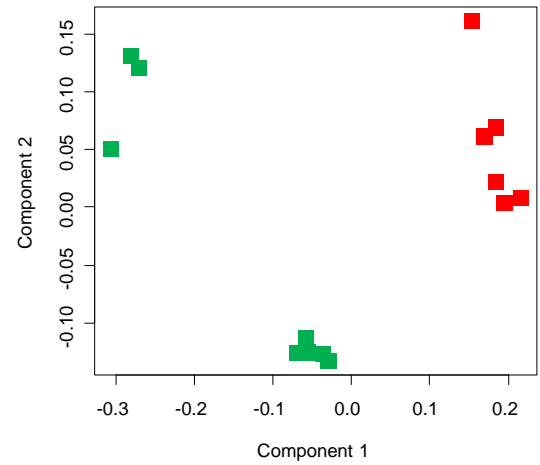
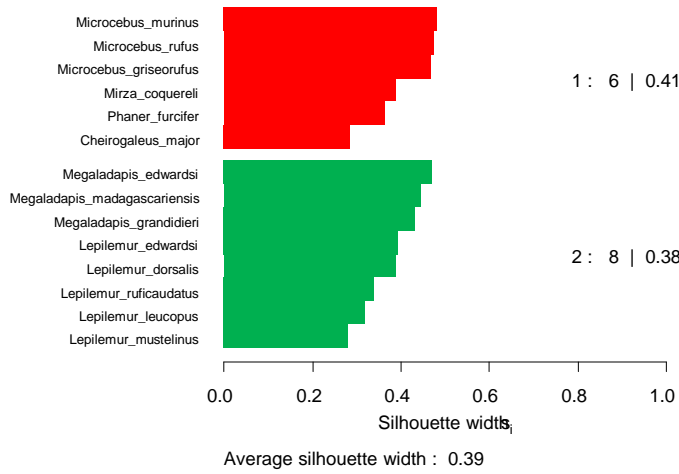


k=4

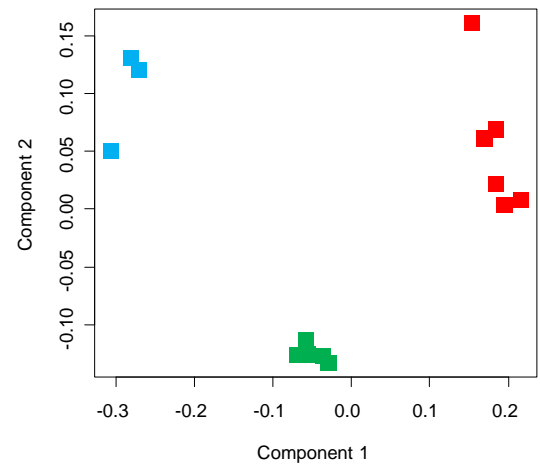
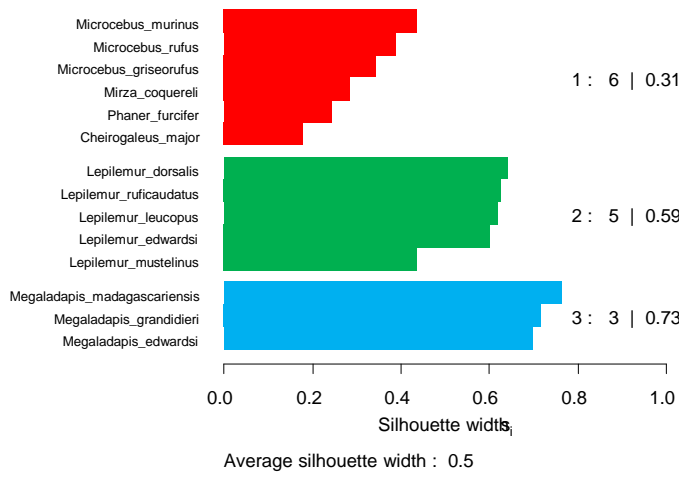


Silhouette plot, Fuzzy Analysis

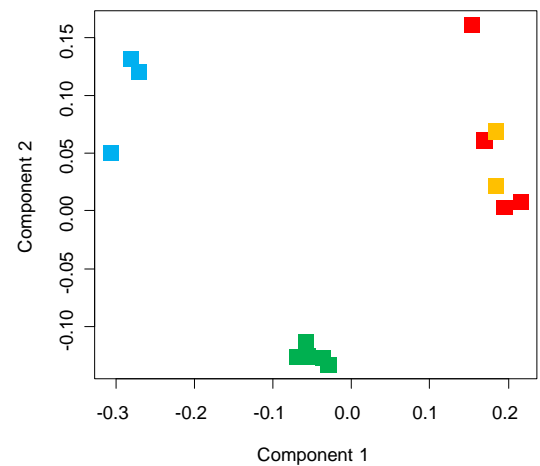
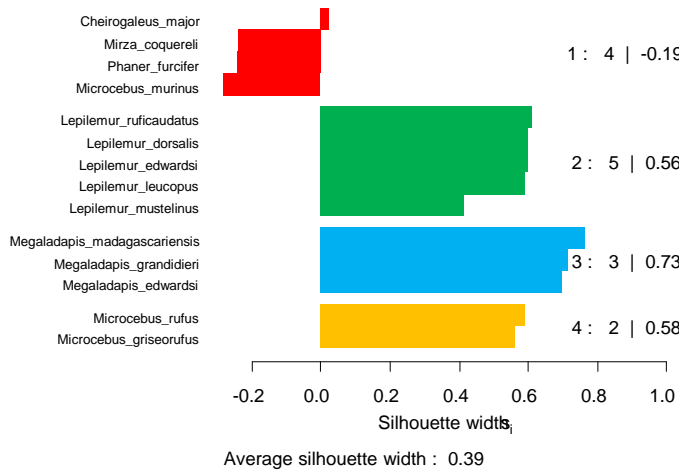
k=2



k=3



k=4



Family Loridae

Order Primates

Masters et al. 2005

Pearson BDC

Negative: 4

Positive: 4

Clusters: 6

Spearman BDC

Negative: 4

Positive: 6

Clusters: 5

Clusterability

Hopkins Statistic: 0.697

Dip test: 0.042

Dip test p-value: 0.936

The original Pearson BDC results revealed very few instances of significant correlation (eight out of 36 possible). As a result, there were six different clusters evident, with four of them being singletons. The Spearman BDC results add only two more instances of significant, positive correlation, resulting in the addition of *Loris tardigradus*, a singleton cluster from the Pearson BDC results, to the cluster consisting of the two *Arctocebus* species. The six-cluster Pearson BDC partition has an average silhouette width of 0.38, and the five-cluster Spearman BDC partition has an average silhouette width of 0.32.

The medoid partition at $k=6$ agrees exactly with the Pearson BDC results, and the five-cluster medoid partition agrees exactly with the Spearman BDC clustering. Fuzzy analysis was not possible for this large number of clusters.

These results confirm the original diagnosis that these taxa do not form clusters and cannot be interpreted as a holobaramin.

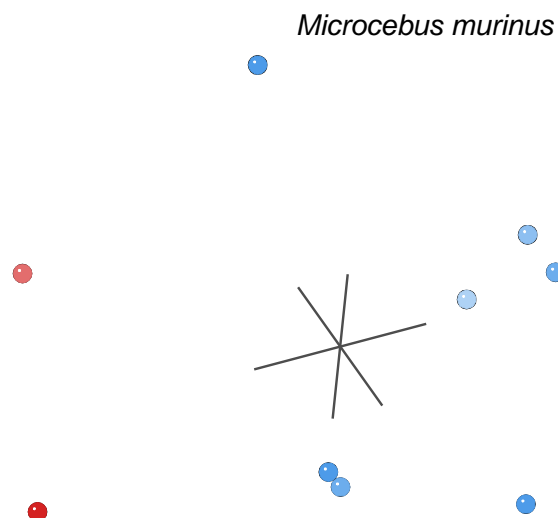
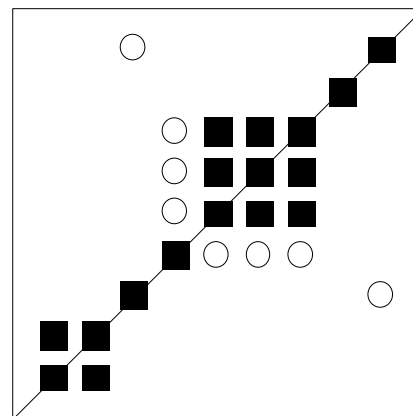
Original conclusion: Inconclusive

Updated conclusion: Inconclusive

Masters, J.C., N.M. Anthony, M.J. De Wit, and A. Mitchell. 2005. Reconstructing the evolutionary history of the Lorisidae using morphological, molecular, and geological data. *American Journal of Physical Anthropology* 127:465-480.

Characters: Craniodental

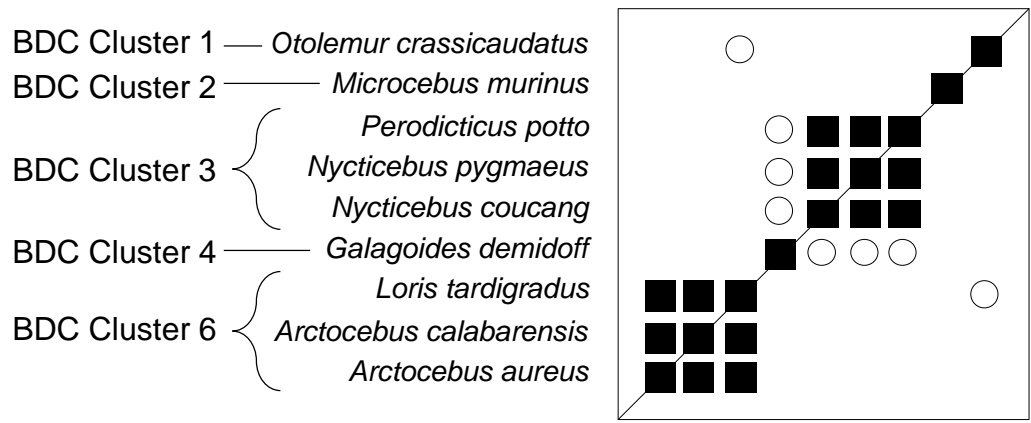
- BDC Cluster 1 — *Otolemur crassicaudatus*
- BDC Cluster 2 — *Microcebus murinus*
- BDC Cluster 3 { *Perodicticus potto*
Nycticebus pygmaeus
Nycticebus coucang
- BDC Cluster 4 — *Galagoides demidoff*
- BDC Cluster 5 — *Loris tardigradus*
- BDC Cluster 6 { *Arctocebus calabarensis*
Arctocebus aureus



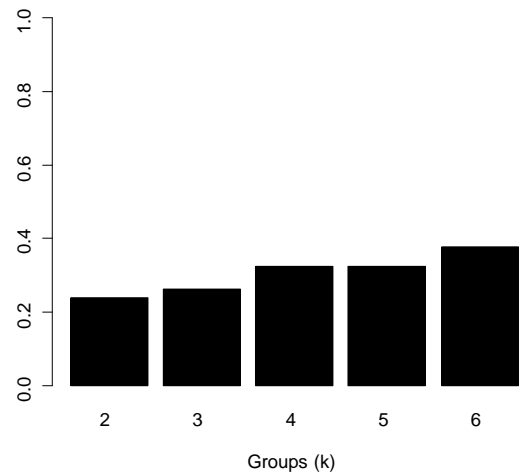
Order Primates
Family Loridae

Published taxa	9
Published characters	36
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	9
Characters used for calculations	36
Median bootstrap value	95.5
F ₉₀	0.64
Stress of 3D MDS	0.07
k _{min}	4
Conclusion	Inc

Notes: BDC has few correlations, and MDS results show a diffuse cluster of taxa. No clear evidence of discontinuity is present.



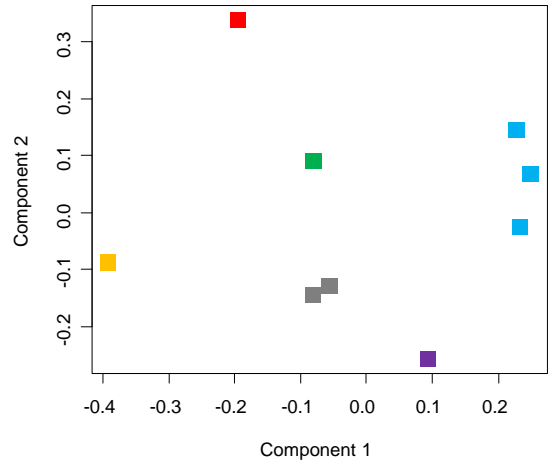
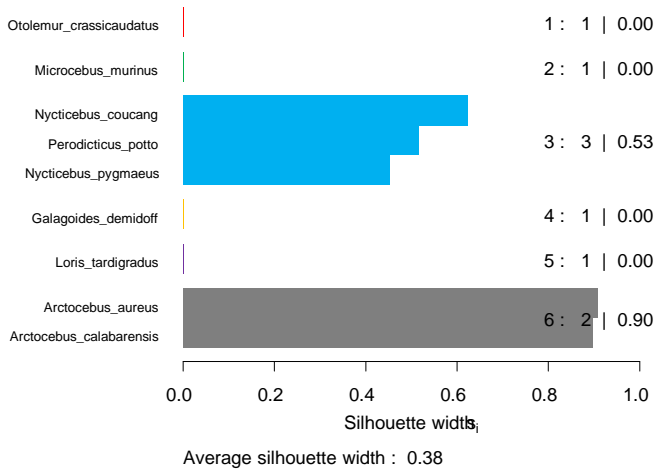
Average Silhouette Widths, Partion Around Medoids



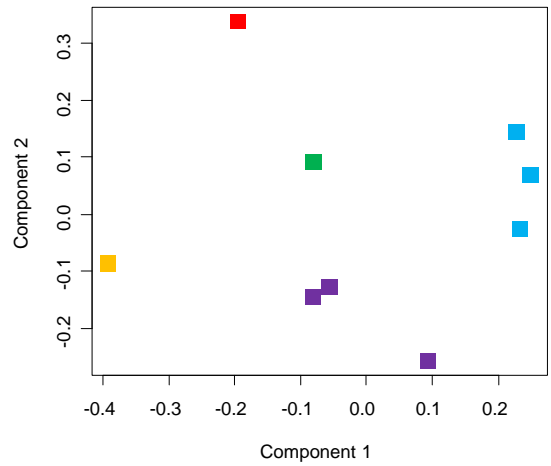
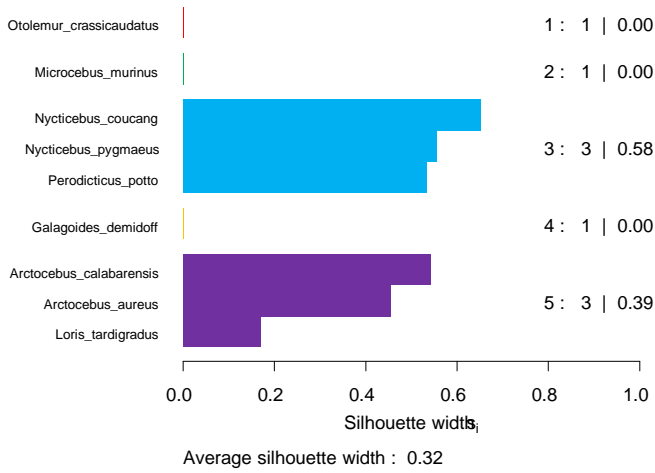
Clade Correspondence: Only clusters 3 and 6 of the six BDC clusters contain more than one taxon each. Both are monophyletic in both phylogenies depicted in Figure 1 of Masters et al. (2005).

Silhouette plot, BDC partitions

Pearson Correlation

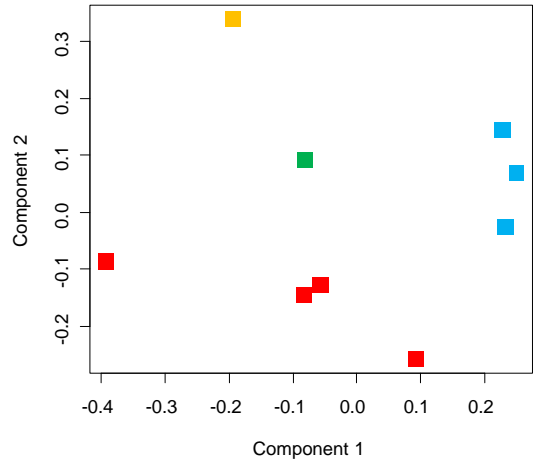
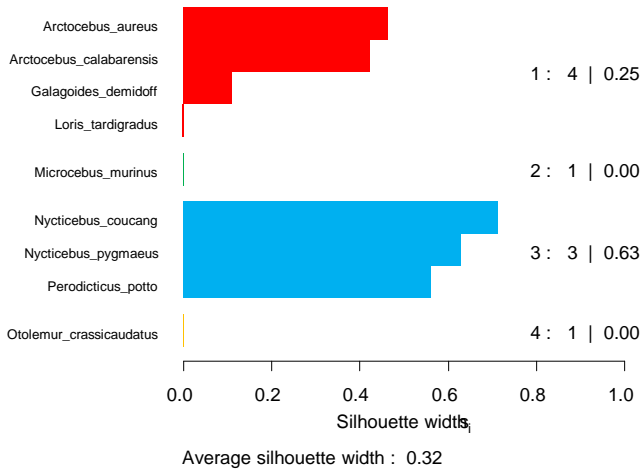


Spearman Correlation

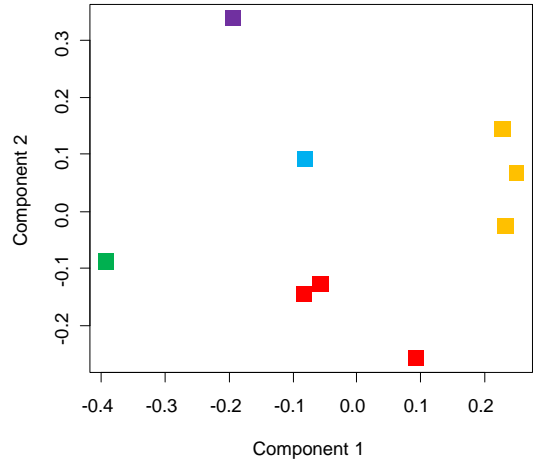
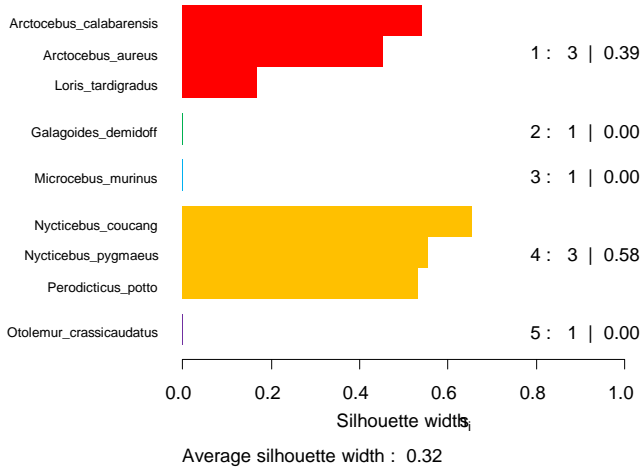


Silhouette plot, Partition Around Medoids

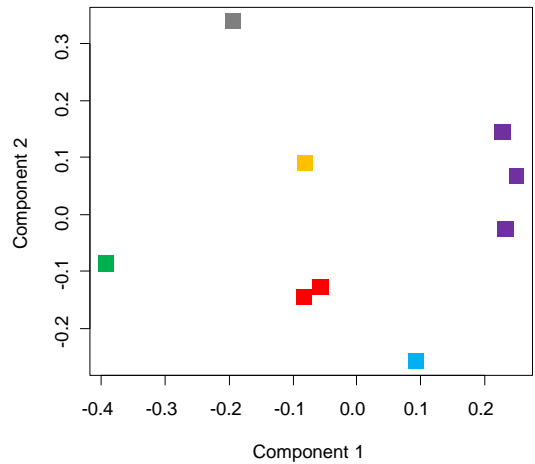
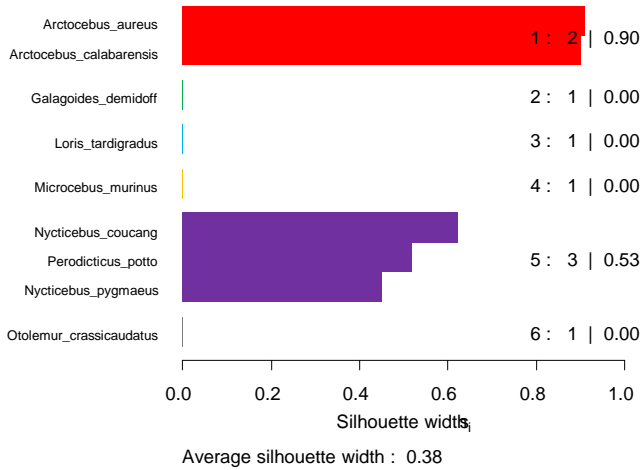
k=4



k=5



k=6



Family Carpolestidae

Order Primates
Bloch et al. 2001

Pearson BDC
Negative: 22
Positive: 31
Clusters: 3

Clusterability
Hopkins Statistic: 0.796
Dip test: 0.04
Dip test p-value: 0.375

Spearman BDC
Negative: 15
Positive: 31
Clusters: 2

The original Pearson BDC analysis revealed three clusters corresponding to the two outgroup taxa, the genus *Elphidotarsius*, and the remaining carpolestids. The Spearman BDC results combine the outgroup with the cluster of *Elphidotarsius* taxa, thus reducing the number of clusters from three to two. The three-cluster Pearson BDC partition has an average silhouette width of 0.48, and the two-cluster Spearman BDC partition has an average silhouette width of 0.45. The cluster membership difference is 14%.

Medoid partitioning at k=2 exactly matches the Spearman BDC clusters. At k=3, the medoid partition and the Pearson BDC clusters have a cluster membership difference of 36%. The average silhouette width for the three-cluster medoid partition is 0.4.

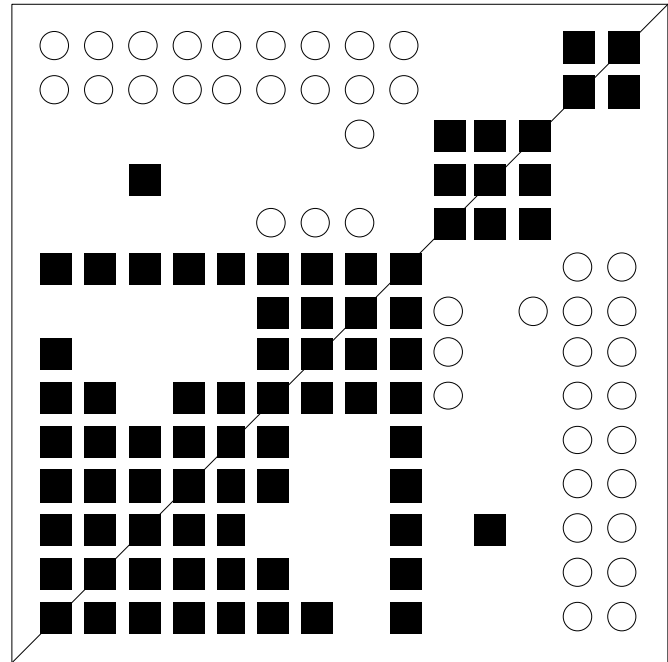
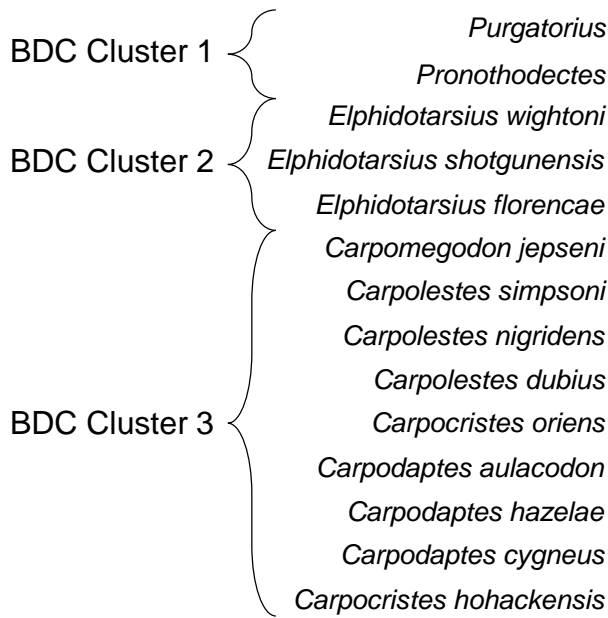
Two-cluster fuzzy partition also matches exactly the Spearman BDC clusters. At k=3, the fuzzy partition and the Pearson BDC clusters have a cluster membership difference of 43%. The average silhouette width for the three-cluster fuzzy partition is 0.39.

These results modify the original conclusion that Carpolestidae is possibly a holobaramin. The Spearman BDC results, two-cluster medoid partition, and two-cluster fuzzy analysis all support separating genus *Elphidotarsius* from the remaining carpolestids. These results therefore raise additional uncertainty about the position of *Elphidotarsius*, but still support recognizing the remaining carpolestids as a holobaramin.

Original conclusion: HB?
Updated conclusion: HB?

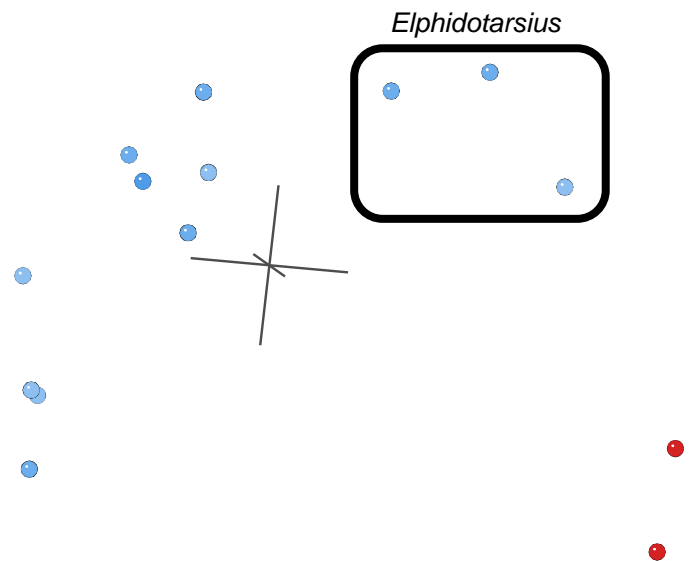
Bloch, J.I., D.C. Fisher, K.D. Rose, and P.D. Gingerich. 2001. Stratocladistic analysis of Paleocene Carpolestidae (Mammalia, Plesiadapiformes) with description of a new late Tiffanian genus. *Journal of Vertebrate Paleontology* 21:119-131.

Characters: Dental

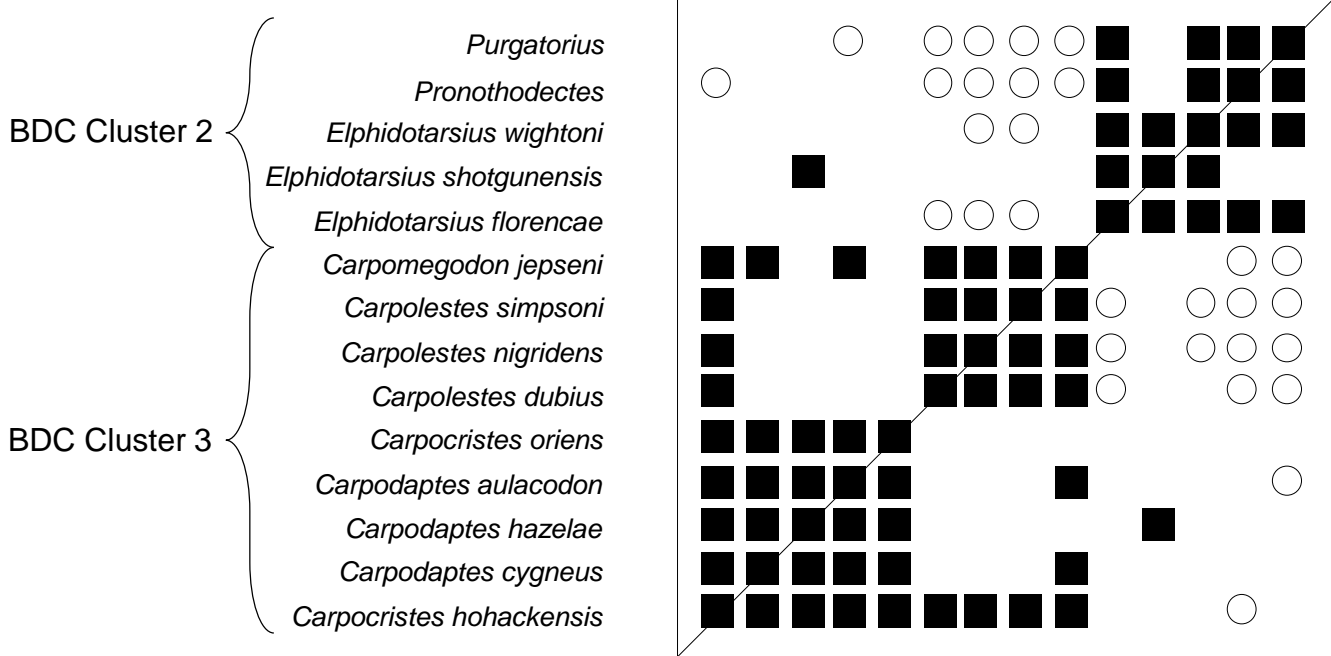


Order Primates
Family Carpolestidae

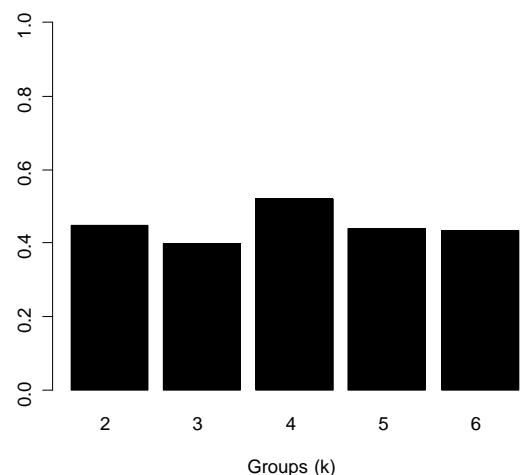
Published taxa	15
Published characters	33
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	14
Characters used for calculations	30
Median bootstrap value	88
F ₉₀	0.46
Stress of 3D MDS	0.09
k _{min}	4
Conclusion	HB?



BDC reveals three groups: outgroup taxa, genus *Elphidotarsius*, and the remaining carpolestids. Significant, negative BDC occurs between the outgroup and the remaining carpolestids but not between the outgroup and *Elphidotarsius*. There is very little significant BDC between *Elphidotarsius* and the remaining carpolestids, and none have bootstrap values >90%. MDS results reveal a good separation between the outgroup taxa and the Carpolestidae, including *Elphidotarsius*, which is part of an arc of carpolestid taxa. Taken together, MDS and BDC support recognizing Carpolestidae as a provisional holobaramin.



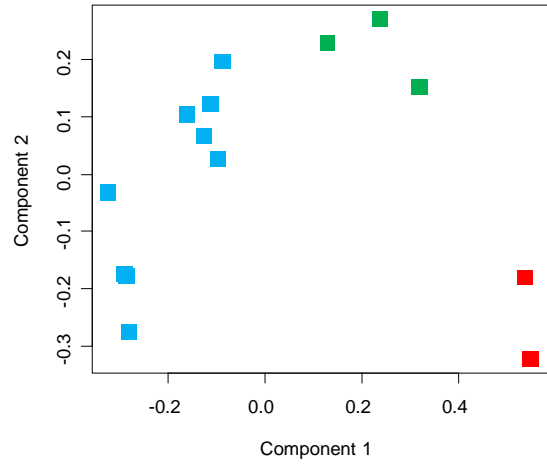
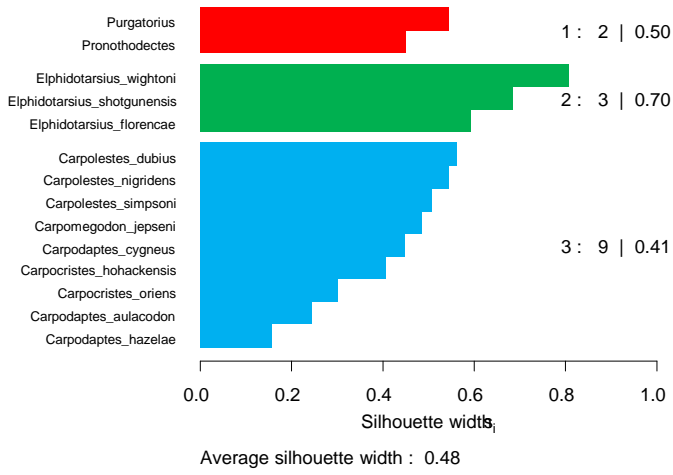
Average Silhouette Widths, Partion Around Medoids



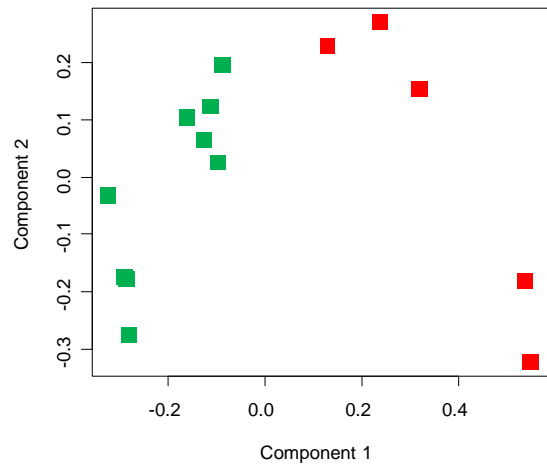
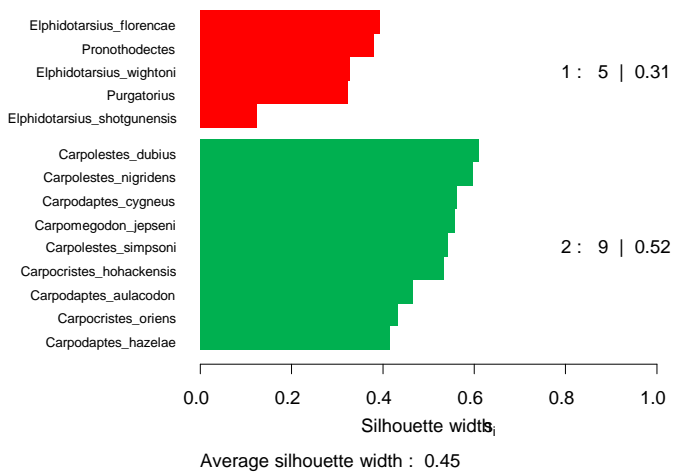
Clade Correspondence: All three BDC clusters contain more than one taxon each. Clusters 1 and 3 appear as clades in the phylogeny shown in Figure 10A in Bloch et al. (2001), if the phylogeny were drawn unrooted. Cluster 2 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

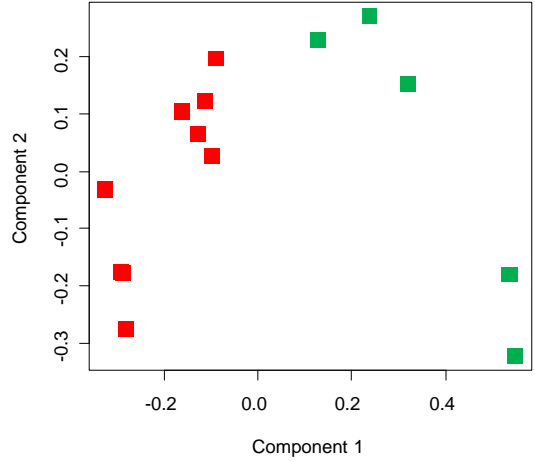
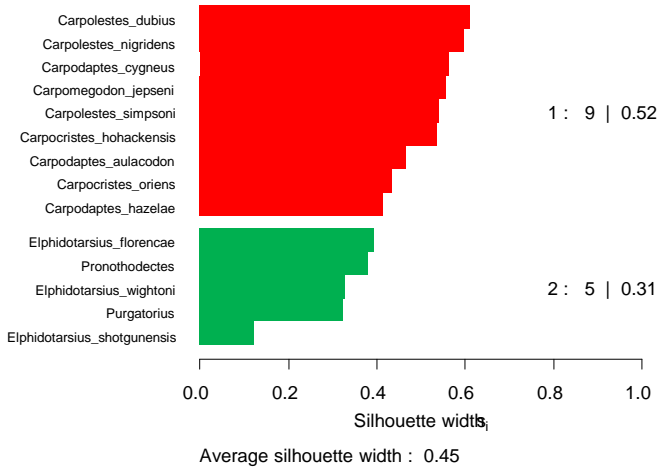


Spearman Correlation

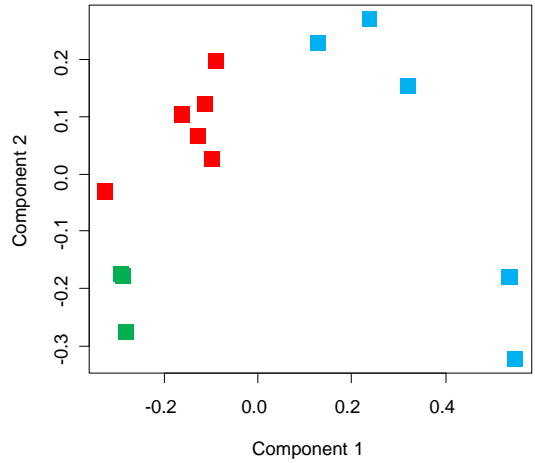
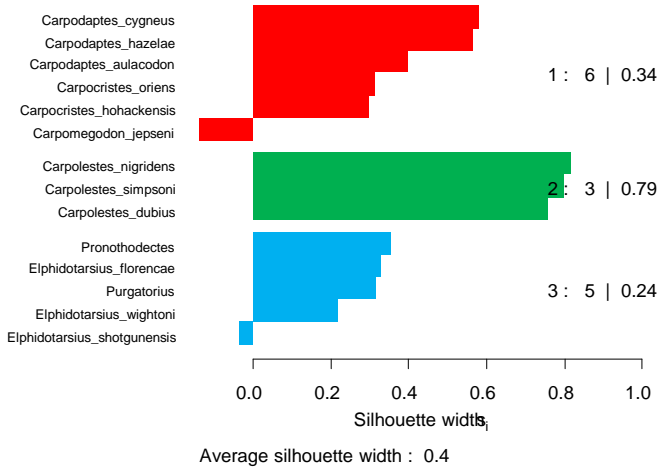


Silhouette plot, Partition Around Medoids

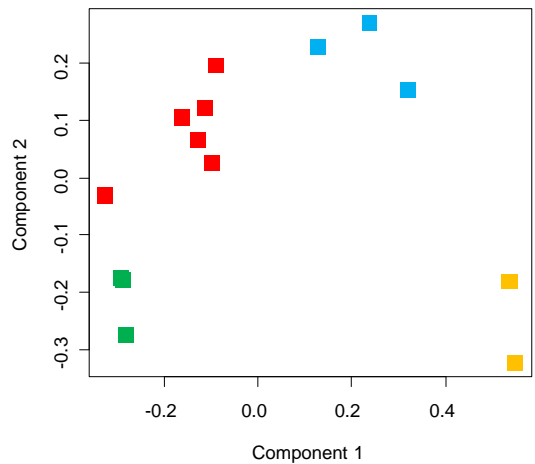
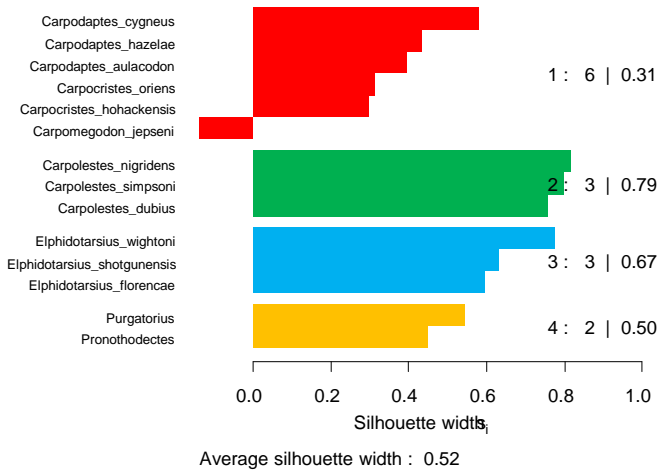
k=2



k=3

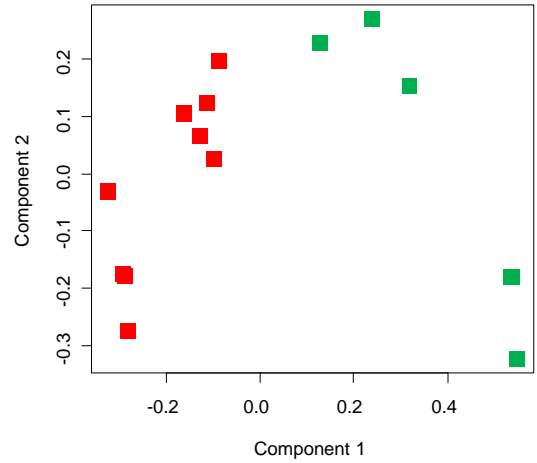
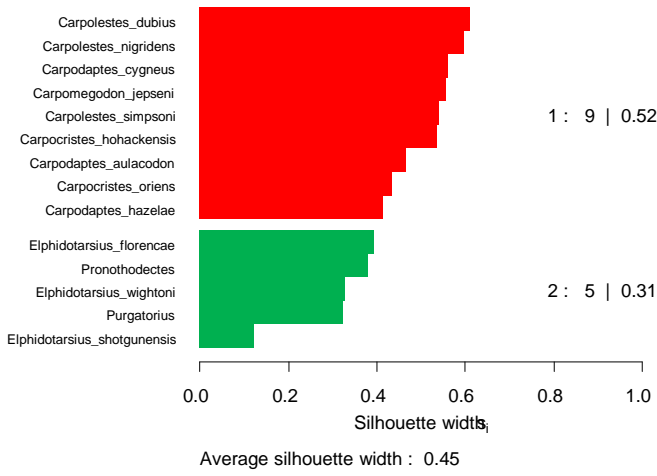


k=4

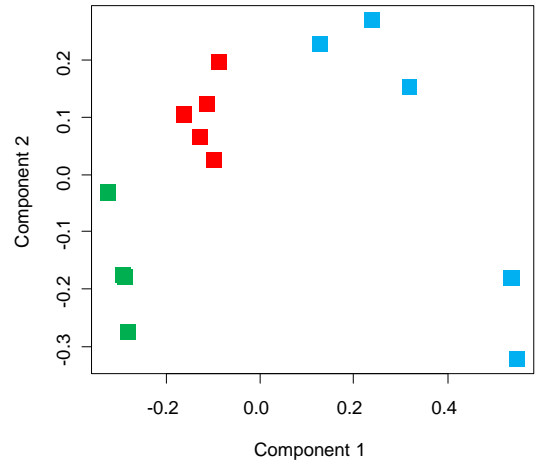
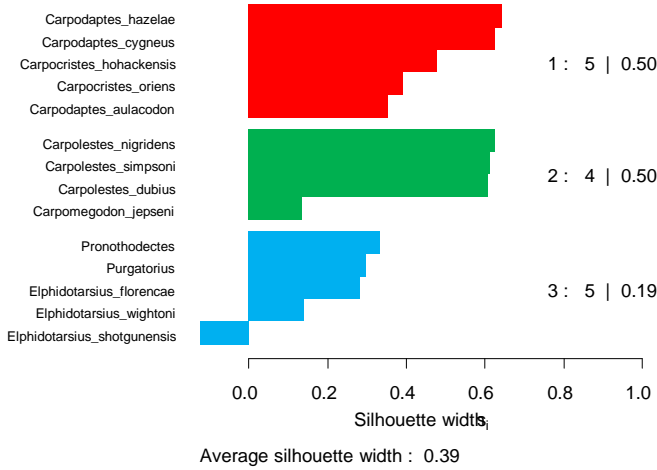


Silhouette plot, Fuzzy Analysis

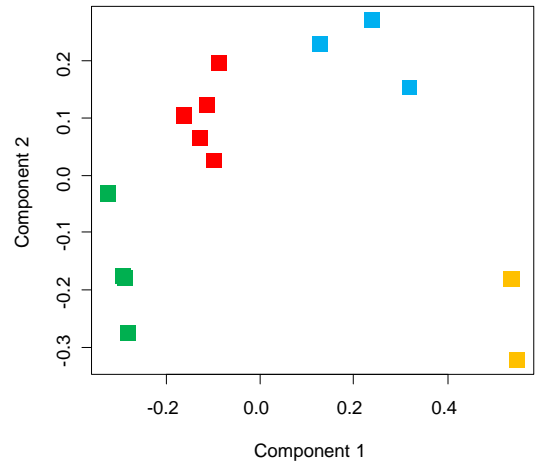
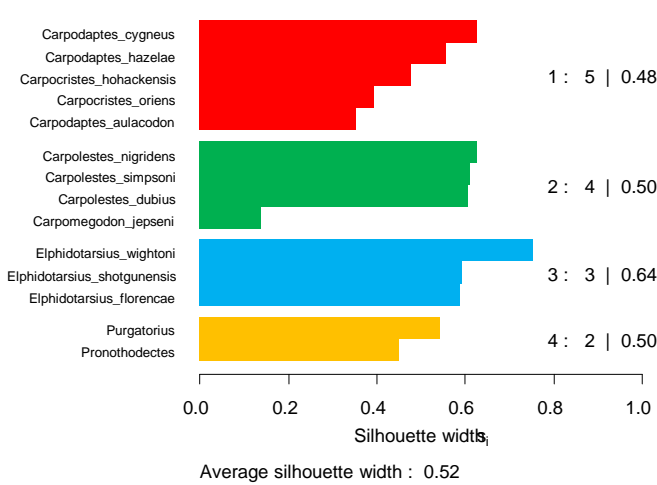
k=2



k=3



k=4



Family Omomyidae

Order Primates

Ni et al. 2004

Pearson BDC

Negative: 174

Positive: 278

Clusters: 3

Spearman BDC

Negative: 171

Positive: 304

Clusters: 2

Clusterability

Hopkins Statistic: 0.786

Dip test: 0.022

Dip test p-value: 0.07

The Pearson BDC results revealed three clusters that correspond to a large set of omomyid ingroup taxa and two smaller clusters of outgroup taxa. Spearman BDC adds 26 more instances of significant, positive correlation that combine the two outgroup clusters into one. Average silhouette widths for the three-cluster Pearson BDC partition is 0.29 and for the two-cluster Spearman BDC partition is 0.38. The cluster membership difference is 6%.

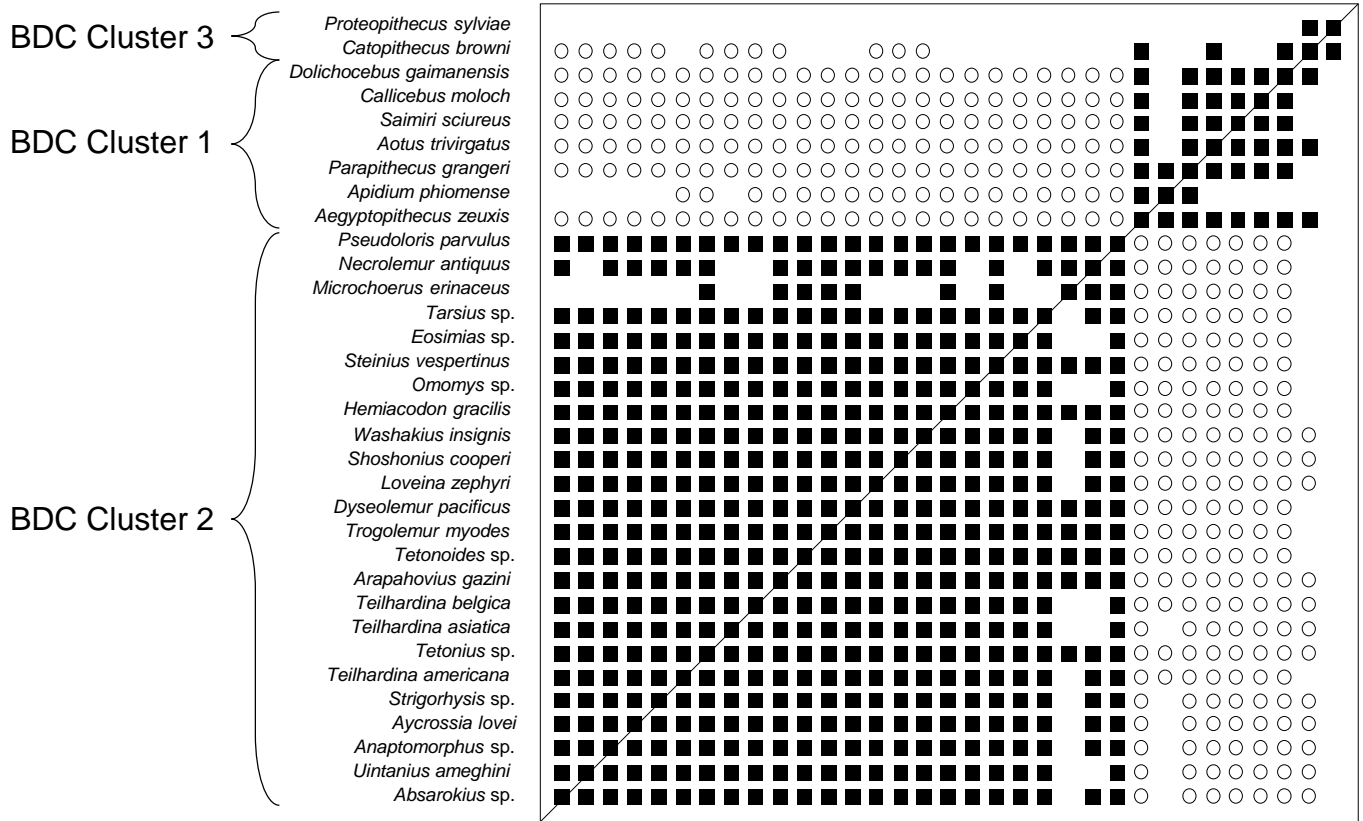
Three-cluster medoid partition has an average silhouette width of 0.18 and matches the Pearson BDC clusters very poorly (cluster membership difference: 30%). However, at $k=2$, the medoid partition matches the Spearman BDC clusters very closely, with one taxon (*Proteopithecus sylviae*) placed in a different cluster (cluster membership difference: 3%). The two-cluster medoid partition has an average silhouette width of 0.38.

Fuzzy analysis at $k=3$ failed, but at $k=2$, the fuzzy partition again resembles the Spearman BDC clusters. The two-cluster fuzzy partition has an average silhouette width of 0.33 and places *Necrolemur antiquus* and *Microchoerus erinaceus* in different cluster (cluster membership difference: 6%).

In all analyses the majority of the 24-taxon omomyid cluster is recognized, as in the original Pearson BDC analysis. The inclusion of three outlier taxa is, however, questionable based on the medoid partition and fuzzy analysis. These taxa are *Necrolemur antiquus*, *Microchoerus erinaceus*, and *Proteopithecus sylviae*. Spearman and Pearson BDC clustering places *N. antiquus* and *M. erinaceus* in the omomyid cluster and *P. sylviae* with the outgroup taxa. Thus, we find some uncertainty in these results that was not evident in the original analysis.

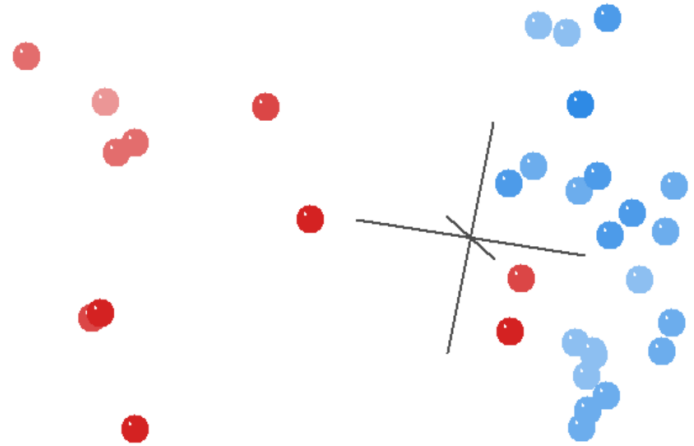
Original conclusion: HB

Updated conclusion: HB?

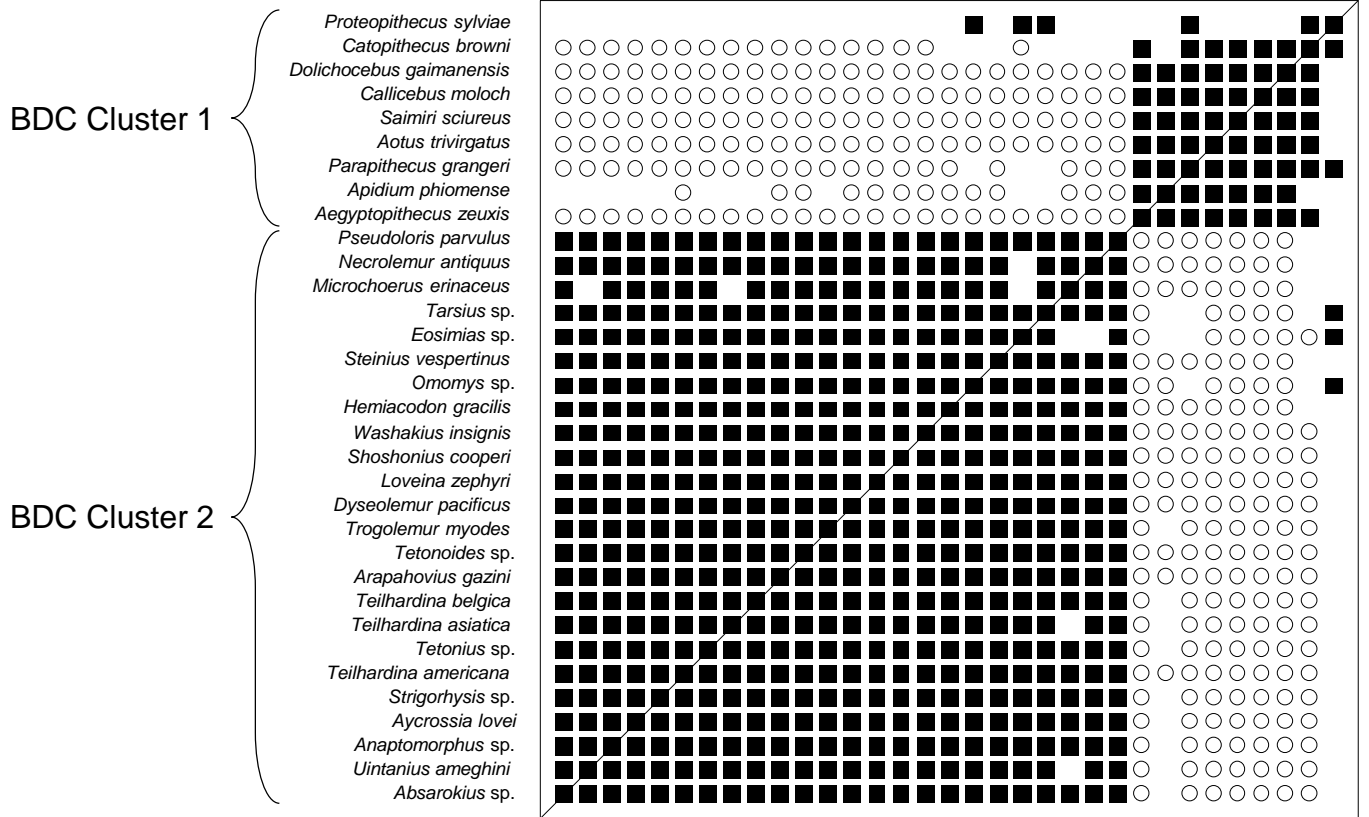


Order Primates
 Family Omomyidae

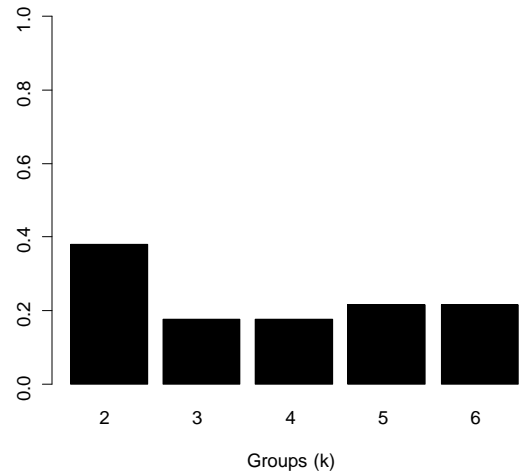
Published taxa	52
Published characters	303
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	33
Characters used for calculations	152
Median bootstrap value	97
F ₉₀	0.66
Stress of 3D MDS	0.27
k _{min}	12
Conclusion	HB



Notes: Taxa have been reduced to the Omomyidae and their sister clade, the anthropoids, from Ni et al.'s (2004) phylogeny. Both BDC and MDS reveal a clear distinction between anthropoids and Omomyidae. *Eosimias* and *Tarsius* cluster with Omomyidae in both BDC and MDS results. Omomyidae + *Eosimias* + *Tarsius* is likely a holobaramin.



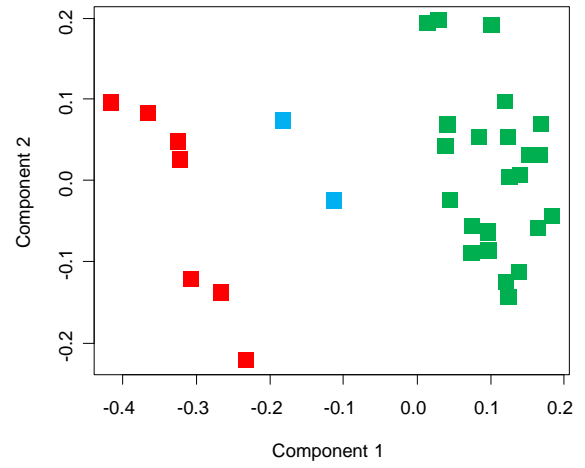
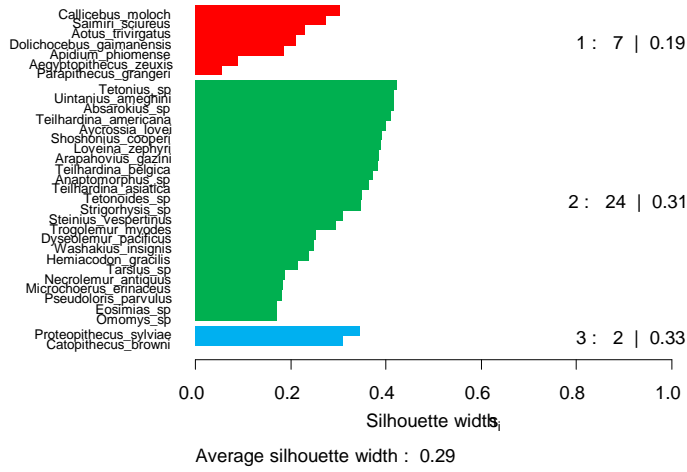
Average Silhouette Widths, Partion Around Medoids



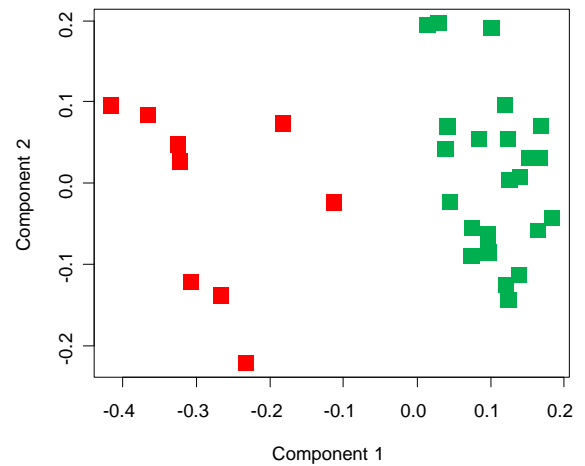
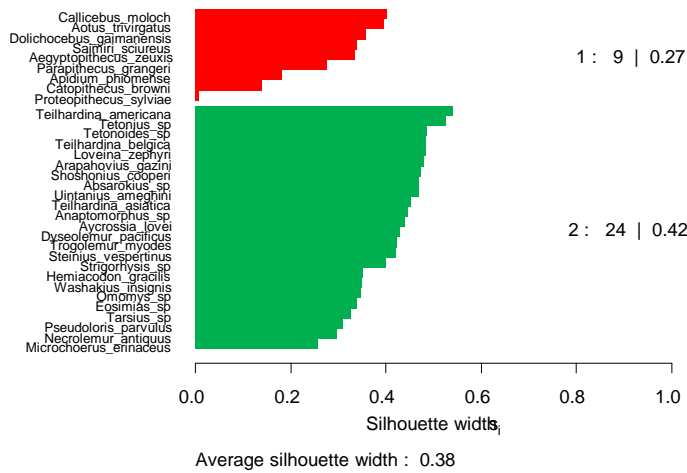
Clade Correspondence: Three clusters are evident in the BDC results, and all three contain at least two taxa each. Cluster 1 and 2 are monophyletic in the phylogeny in Figure 3 of Ni et al. (2004). Cluster 3, consisting of only two taxa, is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

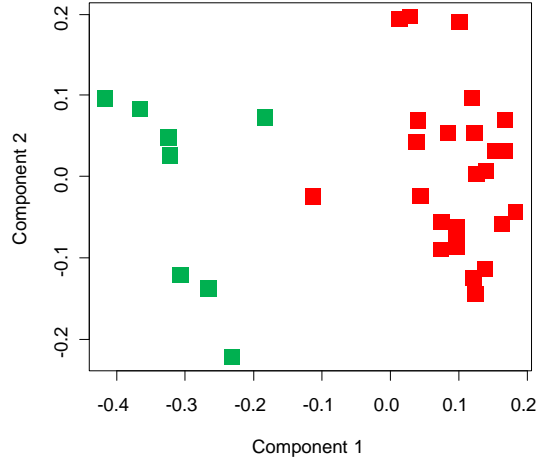
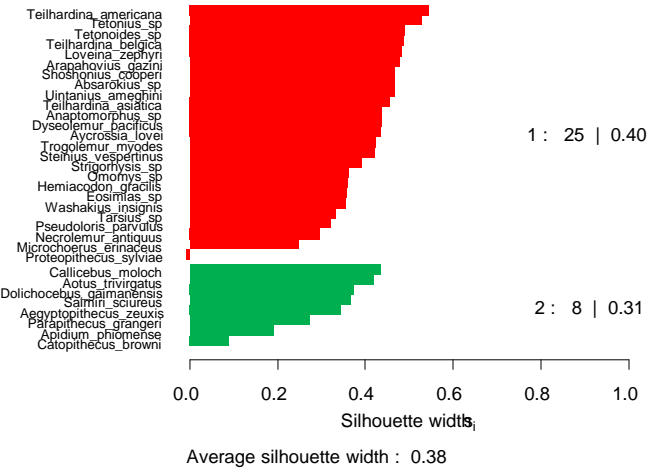


Spearman Correlation

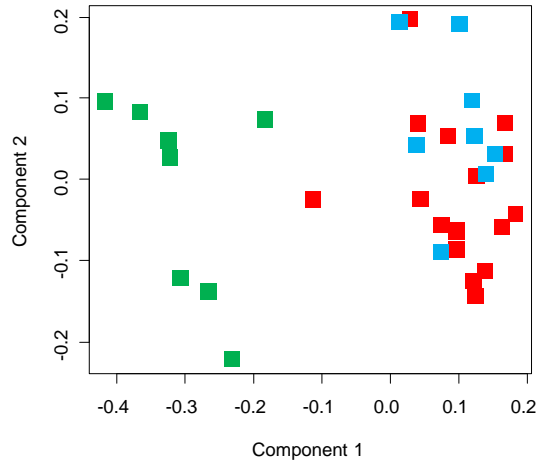
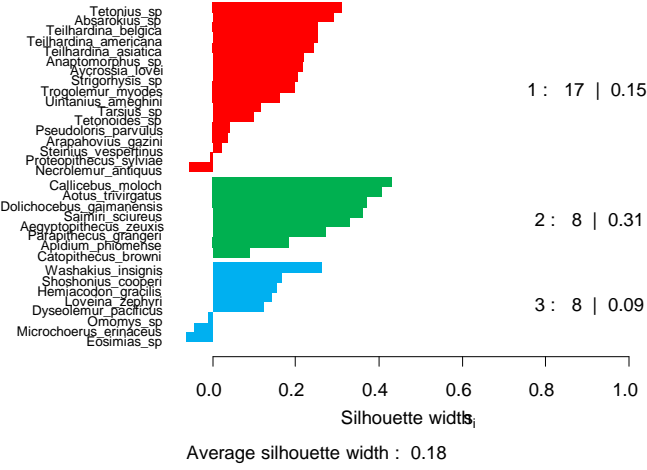


Silhouette plot, Partition Around Medoids

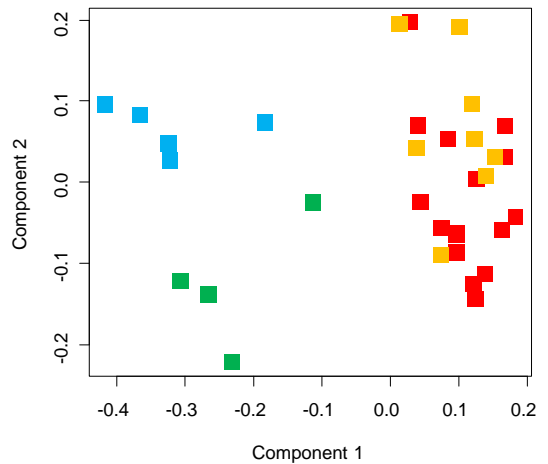
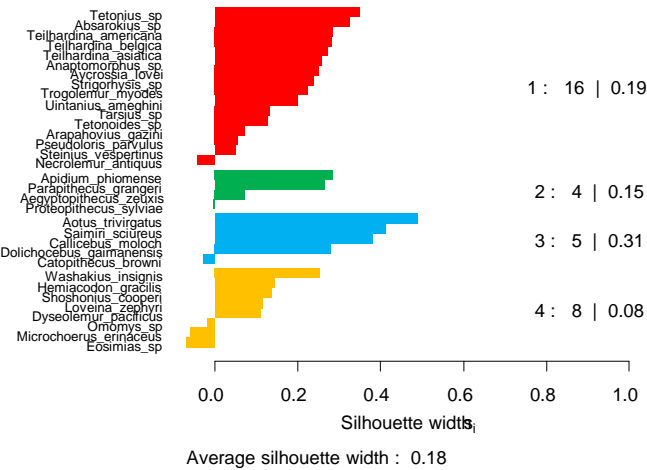
k=2



k=3

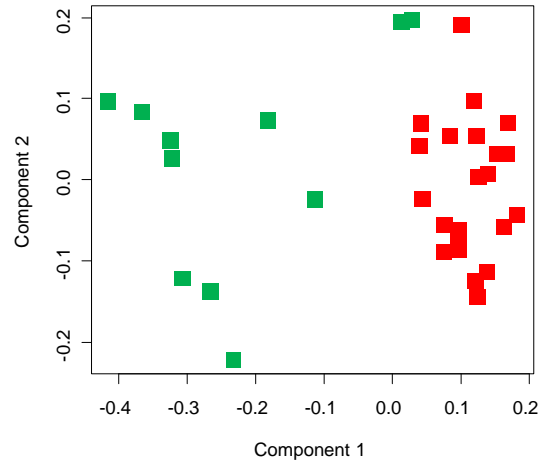
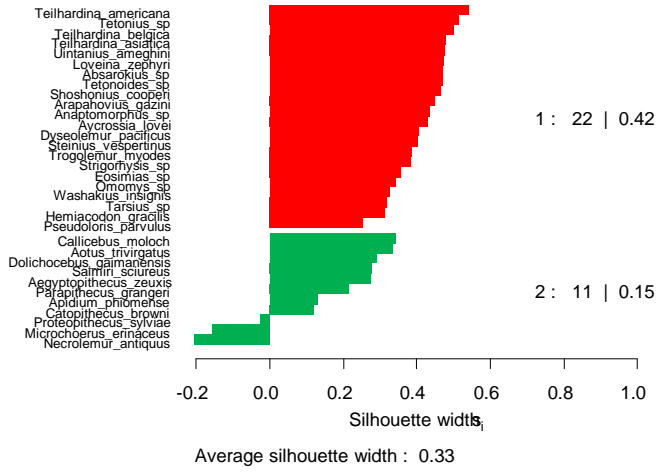


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Cebidae

Order Primates

Garbino 2015

Pearson BDC

Negative: 109

Positive: 183

Clusters: 2

Clusterability

Hopkins Statistic: 0.857

Dip test: 0.012

Dip test p-value: 0.99

Spearman BDC

Negative: 112

Positive: 148

Clusters: 3

Spearman BDC results in 35 fewer instances of significant, positive correlation, thus increasing the number of clusters from two in the Pearson BDC results to three. Average silhouette values for the two-cluster Pearson BDC partition is 0.49 and for the three-cluster Spearman BDC partition is 0.48. The cluster membership difference is 21%. The new cluster is formed by dividing the larger of the two Pearson BDC clusters.

Two-cluster medoid partition exactly matches the Pearson BDC clusters, and three-cluster medoid partition exactly matches the Spearman BDC clusters.

Three-cluster fuzzy analysis produced a partition exactly matching the Spearman BDC clusters, but at $k=2$, the fuzzy partition poorly matches the Pearson BDC results (cluster membership difference: 21%). Average silhouette width for the two-cluster fuzzy partition is 0.34.

The original analysis suggested that Callitrichinae, the larger cluster evident in the Pearson BDC results, was a holobaramin. These results support recognizing three clusters rather than two. These three clusters are evident in the Spearman BDC results, the medoid partition, and the fuzzy analysis. The two-cluster medoid partition matches the Pearson BDC clusters, but the two-cluster fuzzy partition differs by placing one of the callitrichine clusters together with the outgroup, which again suggests that these three clusters are distinct units and forcing a two-cluster partition differs only by which two of the clusters get combined into one.

Still, the significant, negative BDC evident in the Pearson and Spearman results does imply the presence of a discontinuity surrounding the Callitrichinae; however, it is less clear based on these results that the Callitrichinae are a single unit. Hence we may affirm that at least one holobaramin could be present here and possibly two. The results are not entirely confirmed, but the inferred discontinuity seems robust.

Original conclusion: HB?

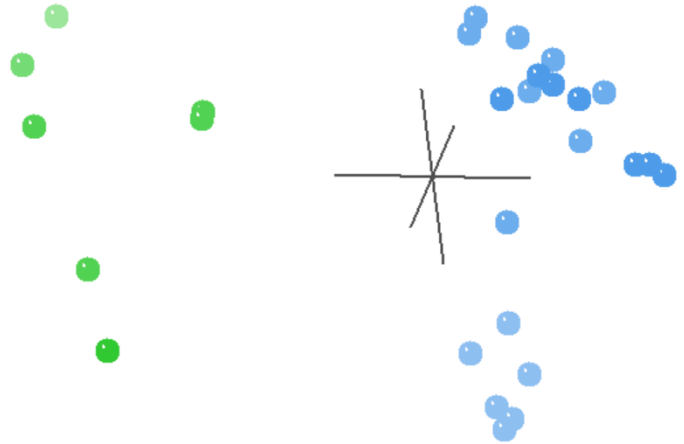
Updated conclusion: HB?

Garbino, G.S. 2015. How many marmoset (Primates: Cebidae: Callitrichinae) genera are there? A phylogenetic analysis based on multiple morphological systems. *Cladistics* 31:652-678.

Characters: Craniodental, postcranial, soft tissue, vocal



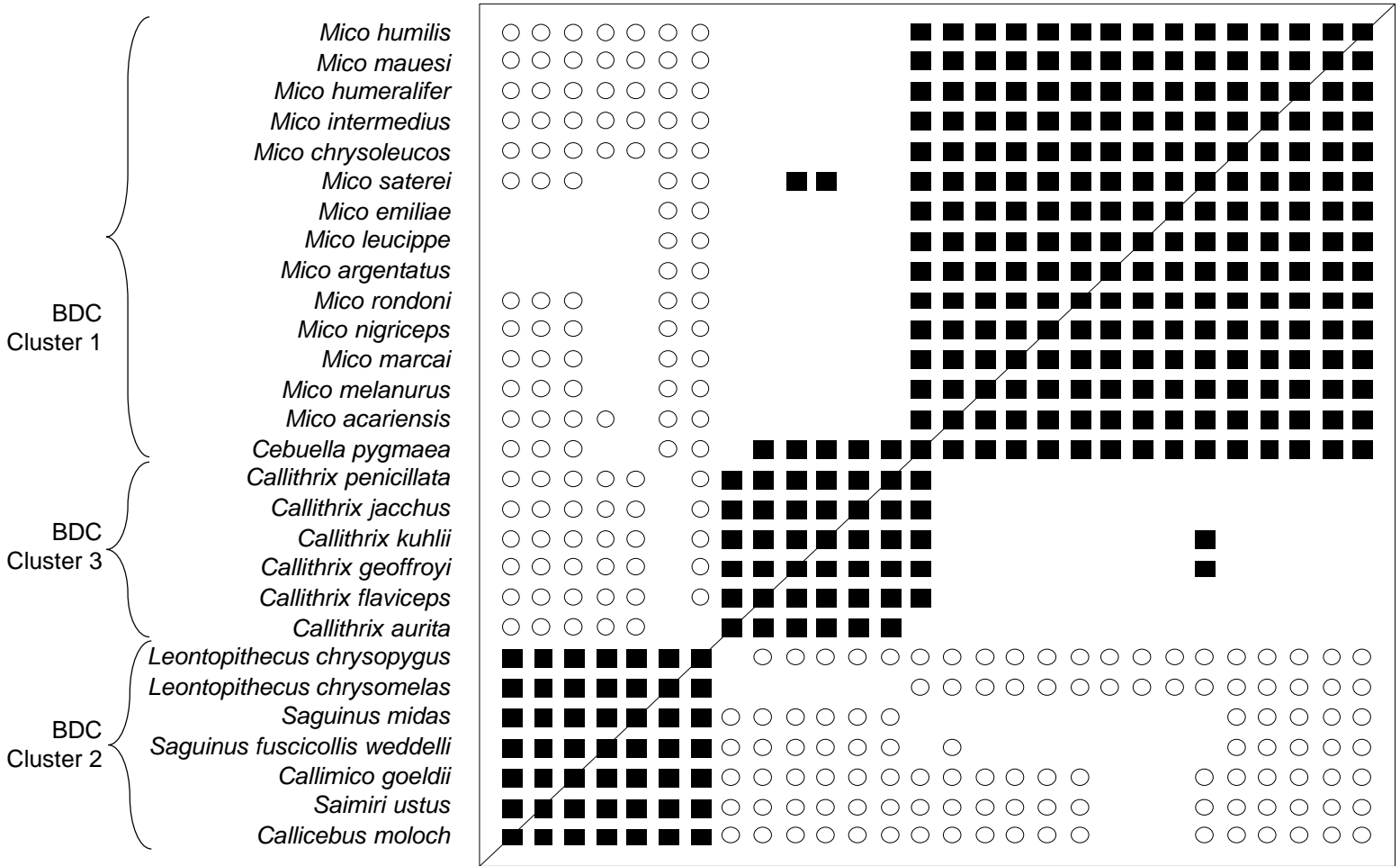
Blue: Callitrichinae
Green: other Cebidae



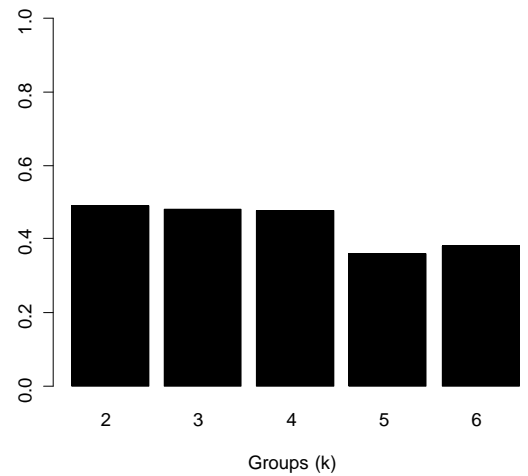
Order Primates
Family Cebidae

Published taxa	28
Published characters	83
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	28
Characters used for calculations	76
Median bootstrap value	83.5
F ₉₀	0.46
Stress of 3D MDS	0.14
k _{min}	7
Conclusion	HB?

Notes: BDC and MDS reveal two clear groups: Callitrichinae and the rest of the cebids. This suggests that Callitrichinae is a holobaramin.



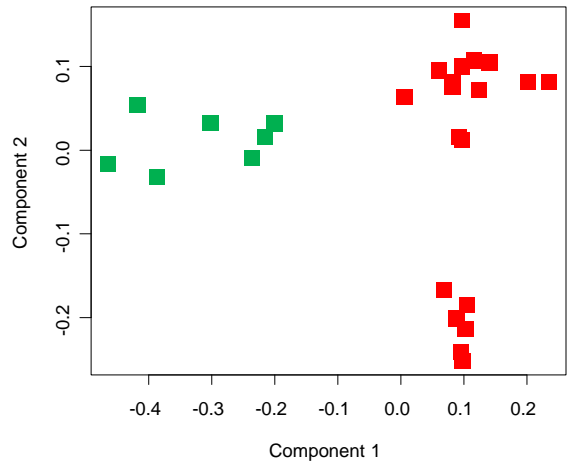
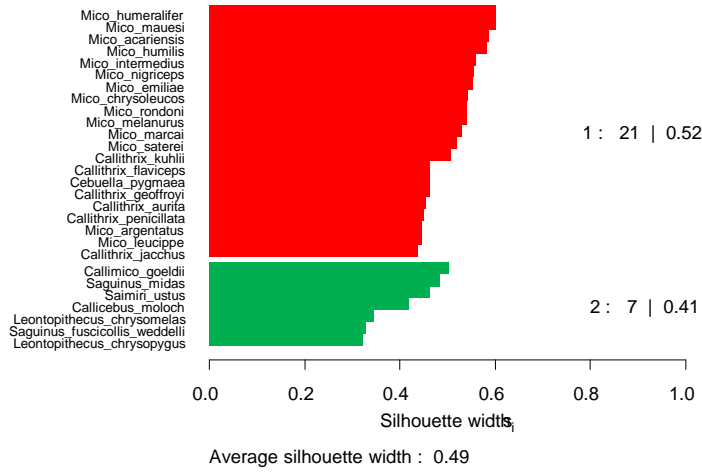
Average Silhouette Widths, Partion Around Medoids



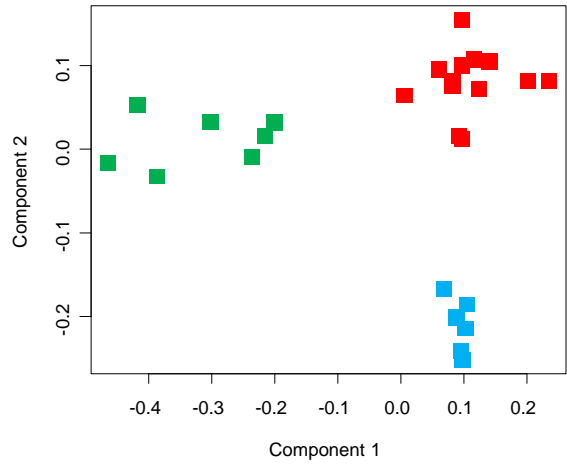
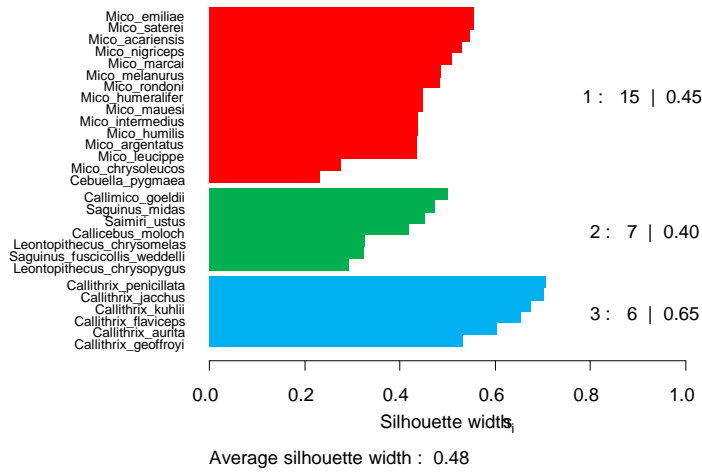
Clade Correspondence: There are two BDC clusters of two or more taxa each. Both are monophyletic if the single most parsimonious tree shown in Figure 3 of Garbino (2015) were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

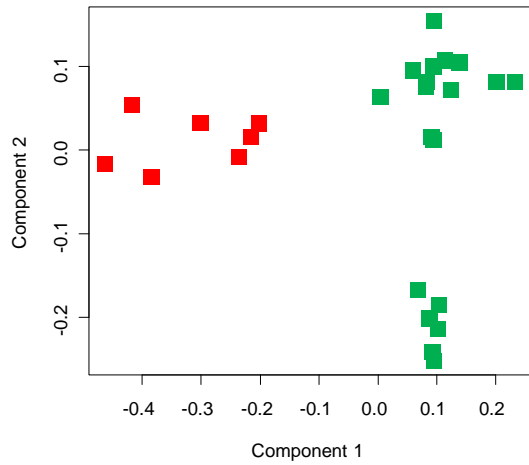
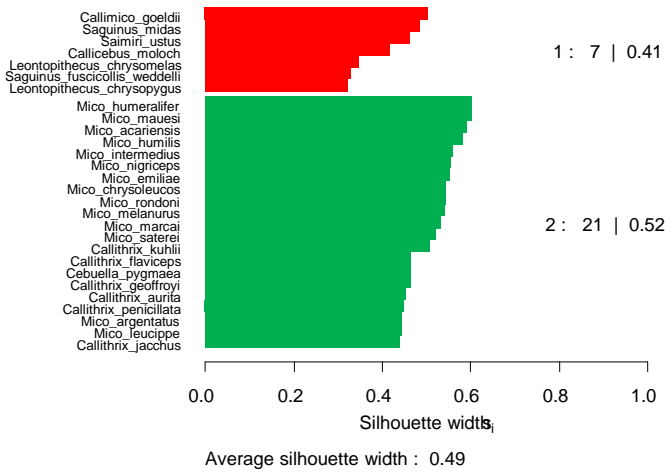


Spearman Correlation

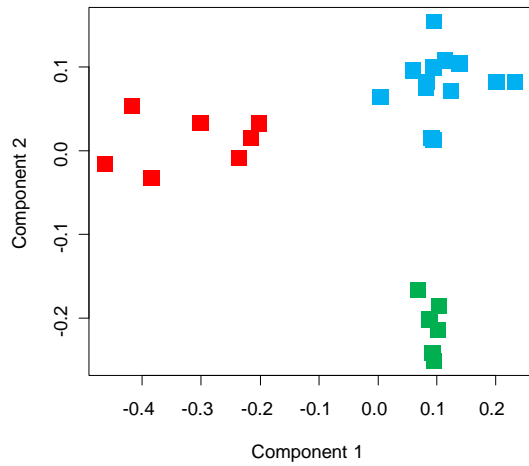
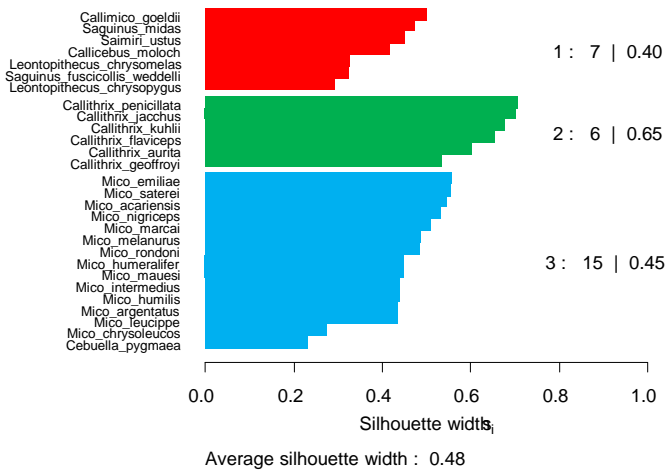


Silhouette plot, Partition Around Medoids

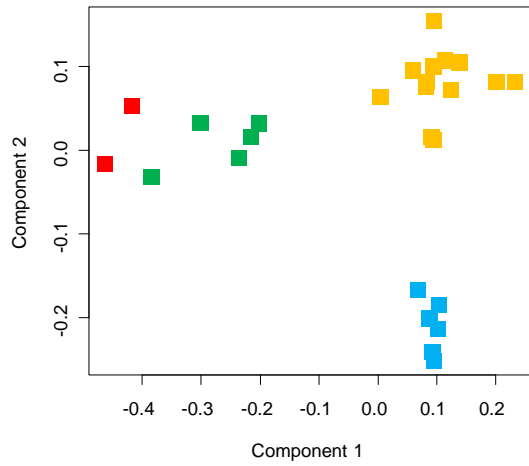
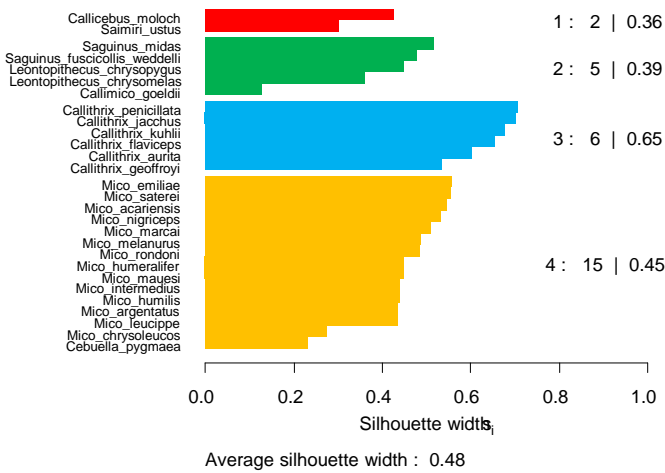
k=2



k=3

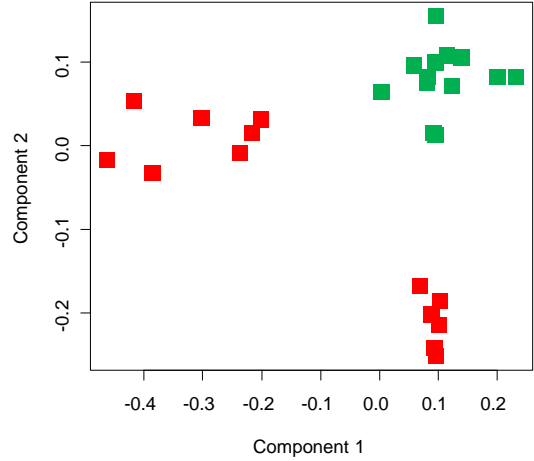
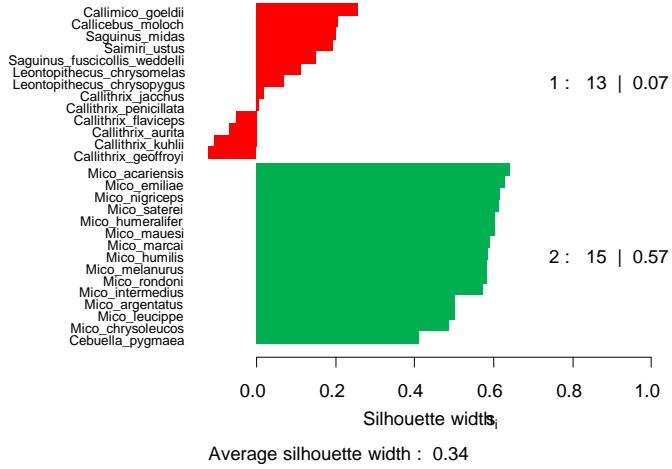


k=4

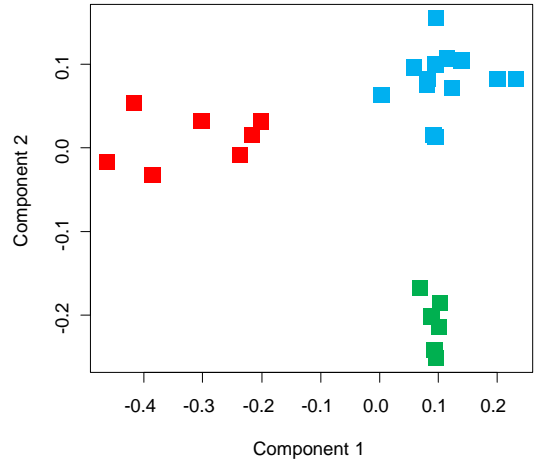
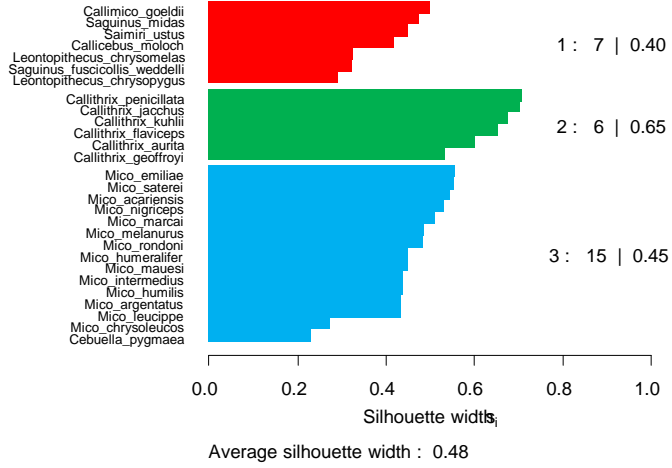


Silhouette plot, Fuzzy Analysis

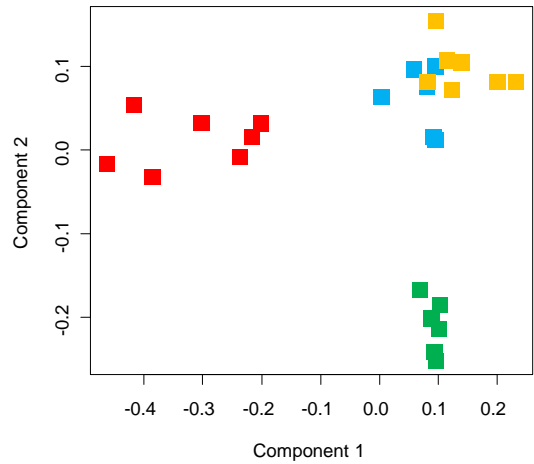
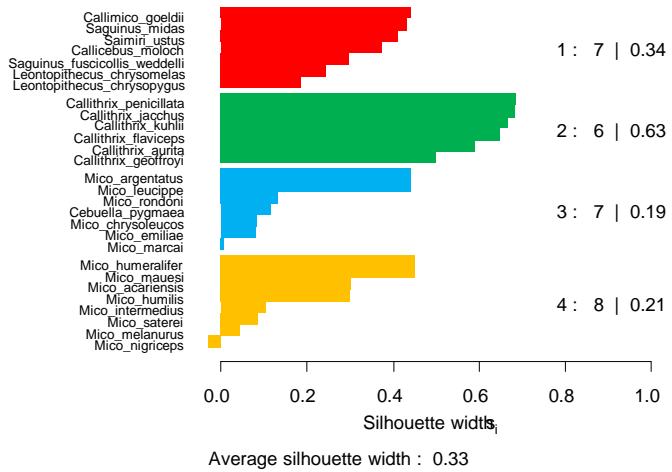
k=2



k=3



k=4



Family Cebidae

Order Primates

Schrago et al. 2013

Pearson BDC

Negative: 12

Positive: 10

Clusters: 4

Clusterability

Hopkins Statistic: 0.815

Dip test: 0.033

Dip test p-value: 0.909

Spearman BDC

Negative: 14

Positive: 19

Clusters: 2

Sparse correlation results from the Pearson BDC analysis reveals the presence of four clusters. The Spearman BDC almost doubles the instances of significant, positive correlation, thus resulting in a reduction of clusters from four to two. The Pearson BDC clusters have an average silhouette width of 0.24, with two taxa having negative silhouette widths. The Spearman BDC clusters have an average silhouette width of 0.29, with all taxa having positive silhouette widths. The cluster membership difference is 25%.

At $k=4$, the medoid partition resembles the Pearson BDC clusters. Two of the clusters are the same, and two are rearranged, resulting in a cluster membership difference of 17%. The average silhouette width of the four-cluster medoid partition is 0.33, which is substantially better than the Pearson BDC clusters. At $k=2$, the medoid partition differs from the Spearman BDC clusters only by the placement of *Saimiri boliviensis*. The two-cluster medoid partition has an average silhouette width of 0.27, which is only slightly lower than the Spearman BDC clusters.

The four-cluster fuzzy partition is identical to the medoid partition, and the two-cluster fuzzy partition is identical to the Spearman BDC clusters.

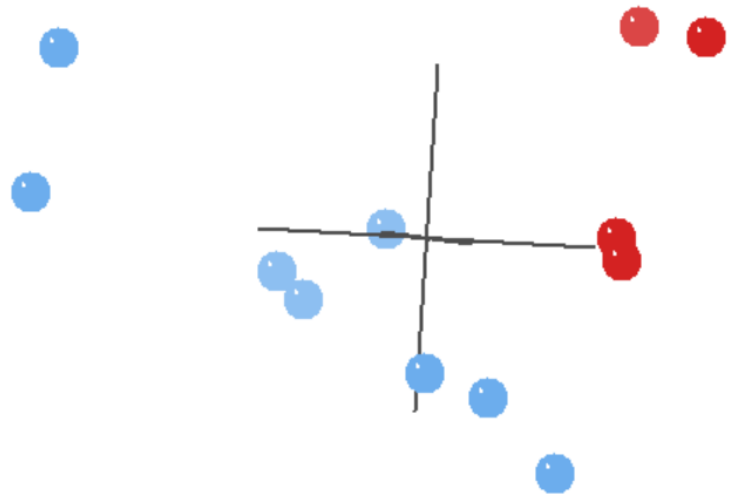
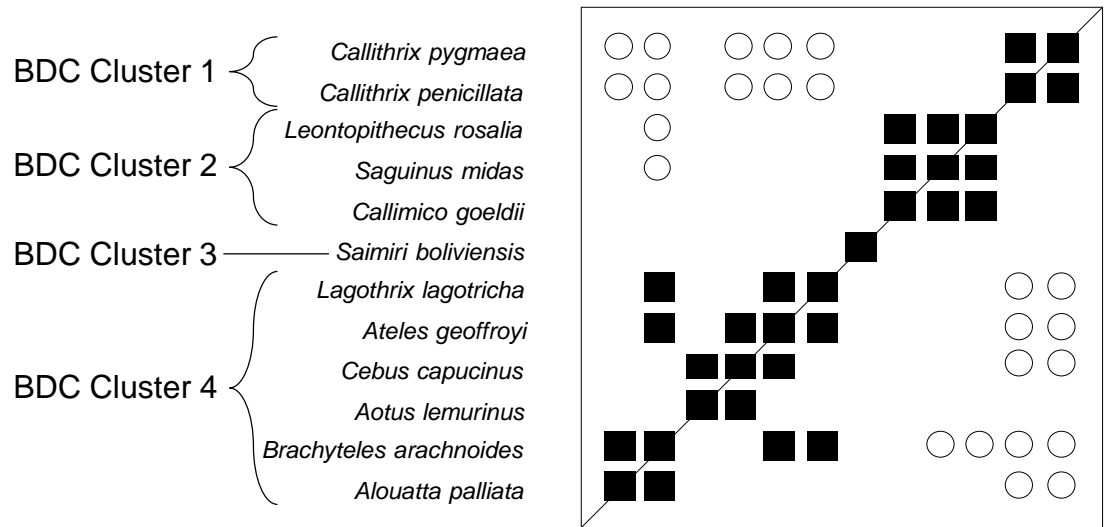
In both the medoid partitioning and the fuzzy analysis, average silhouette widths were slightly higher with a greater number of clusters.

These results suggest that there is a robust core of taxa that might be a holobaramin. This core group consists of the two species of *Callithrix*, *Leontopithecus rosalia*, *Saguinus midas*, and *Callimico goeldii*. In the Spearman BDC, they share significant, positive BDC within the group and significant, negative BDC when compared to taxa outside the group. Neither of these trends are evident in the Pearson BDC results. In addition, the existence of this cluster is supported in the medoid partitioning and fuzzy analysis at $k=2$. This of course raises questions, since the analysis of Garbino's (2015) characters for the same family revealed a robust discontinuity between *Callithrix* and a cluster containing *Leontopithecus*, *Saguinus*, and *Callimico*. Nevertheless, given the evidence from this dataset alone, we find weak evidence for a holobaramin.

Original conclusion: Inconclusive

Updated conclusion: HB?

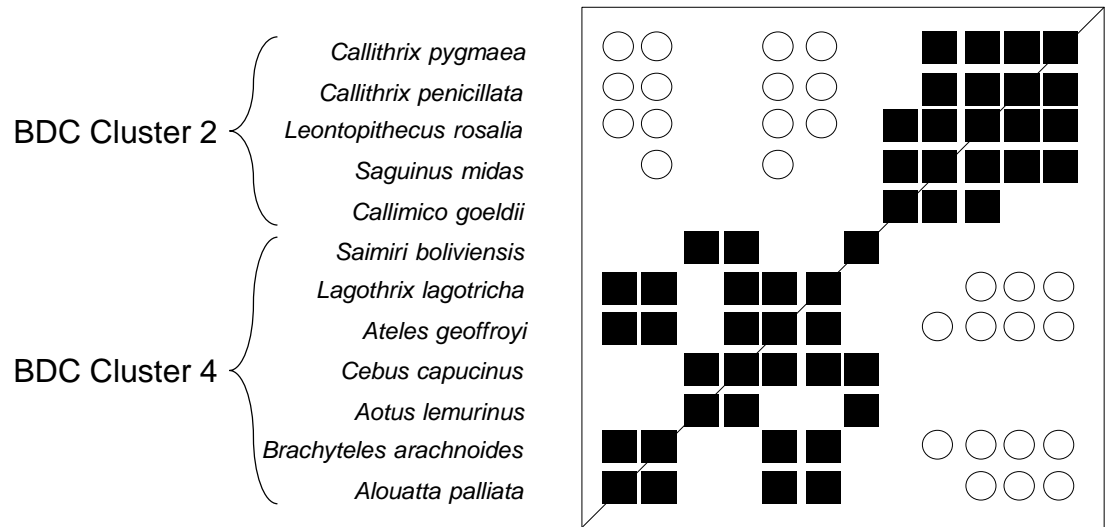
Characters: Craniodental



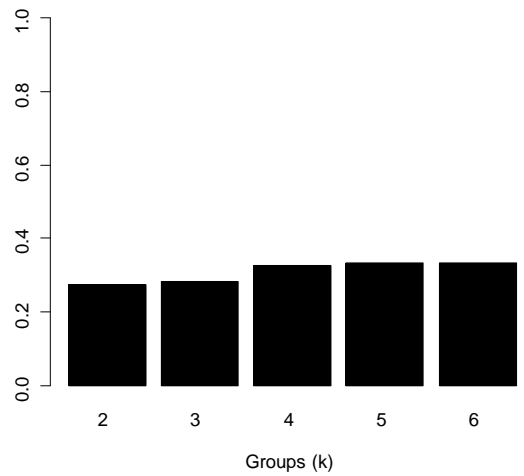
Order Primates
Family Cebidae

Published taxa	31
Published characters	268
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	12
Characters used for calculations	238
Median bootstrap value	97
F ₉₀	0.61
Stress of 3D MDS	0.19
k _{min}	9
Conclusion	Inc

Notes: BDC results are poor with few significant correlations. MDS reveals a diffuse cluster of taxa. There is no clear evidence of discontinuity.



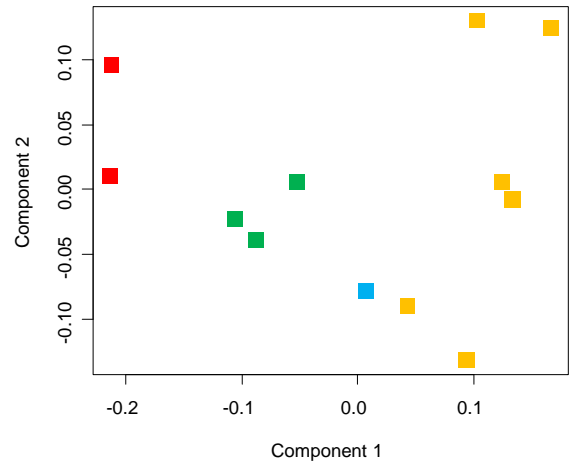
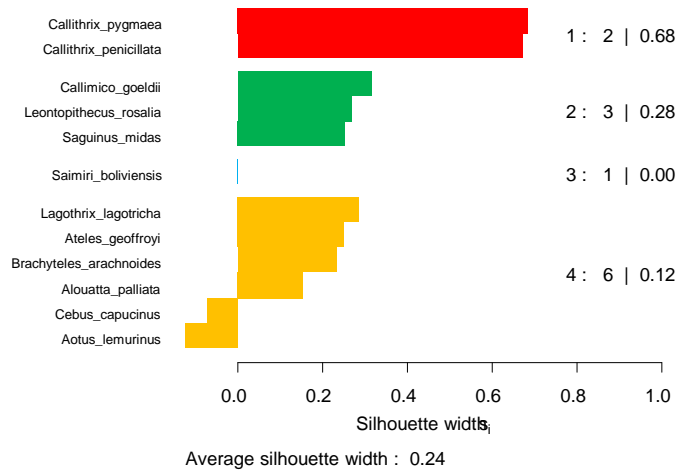
Average Silhouette Widths, Partion Around Medoids



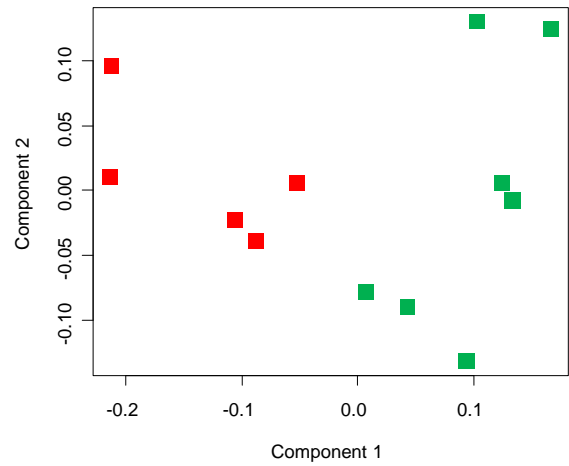
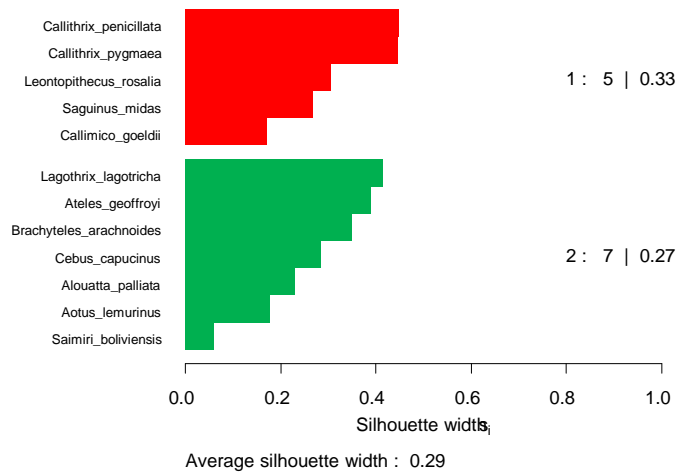
Clade Correspondence: Three of the four BDC clusters are not singletons. None of them are monophyletic in any phylogeny depicted in Schrago et al. (2013).

Silhouette plot, BDC partitions

Pearson Correlation

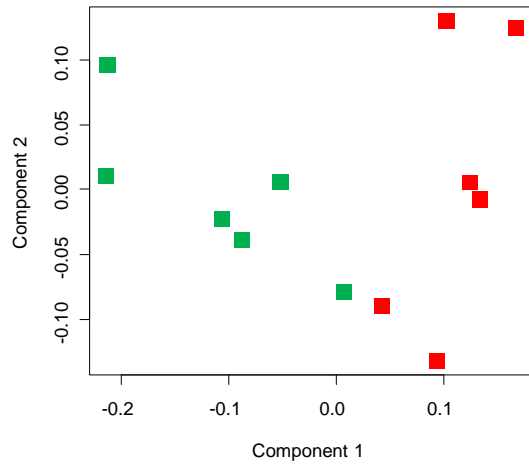
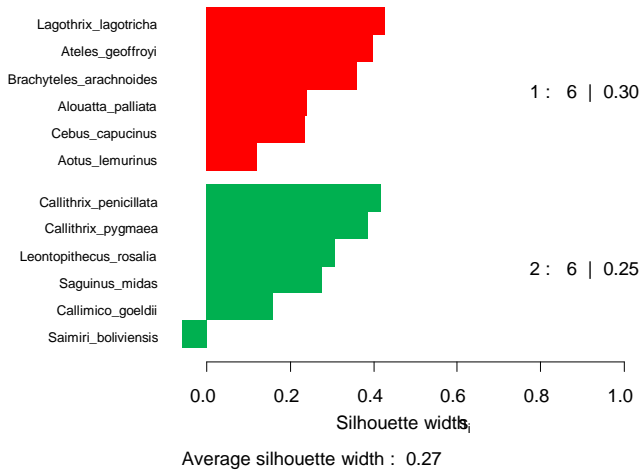


Spearman Correlation

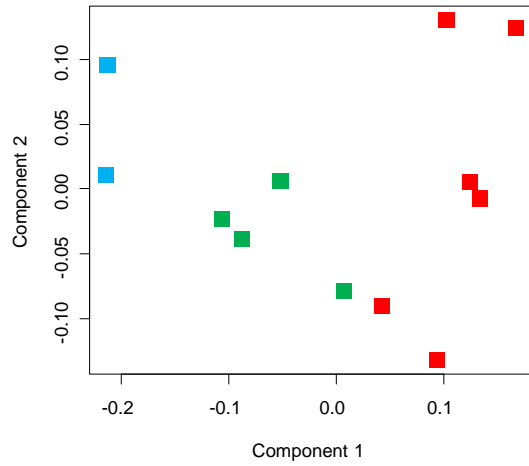
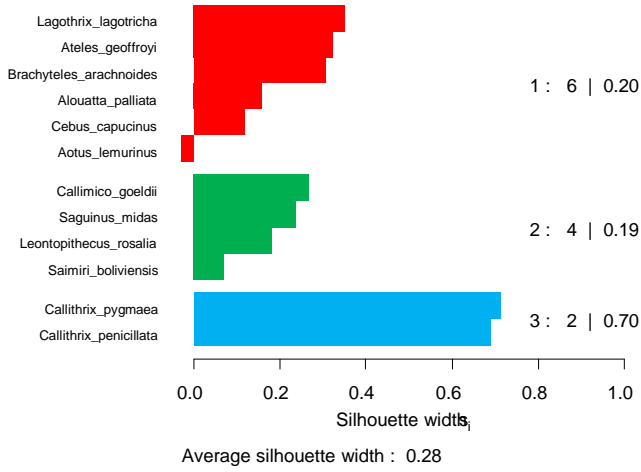


Silhouette plot, Partition Around Medoids

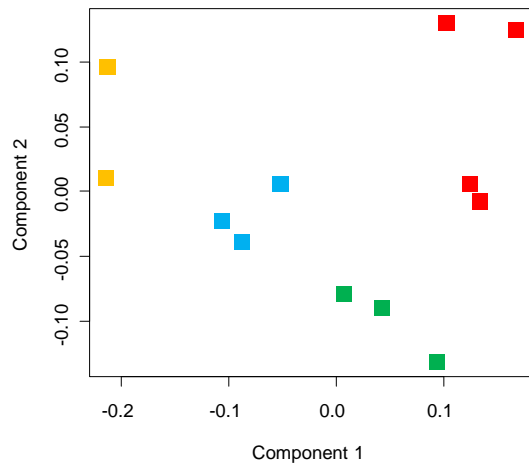
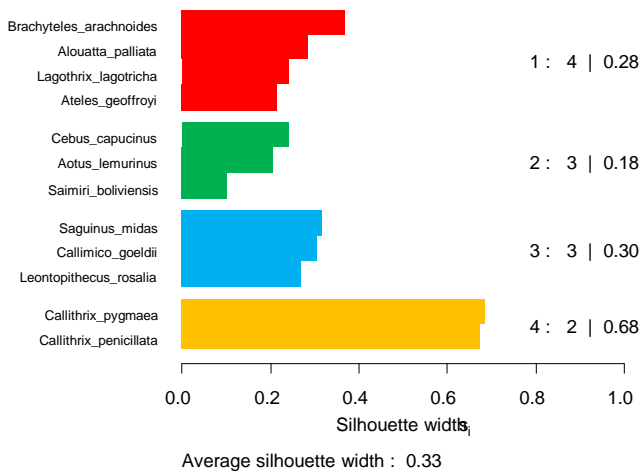
k=2



k=3

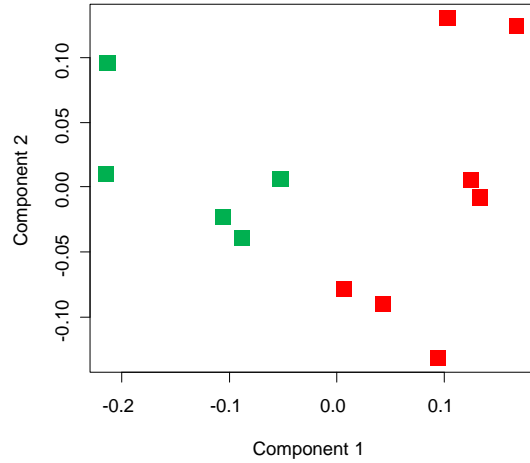
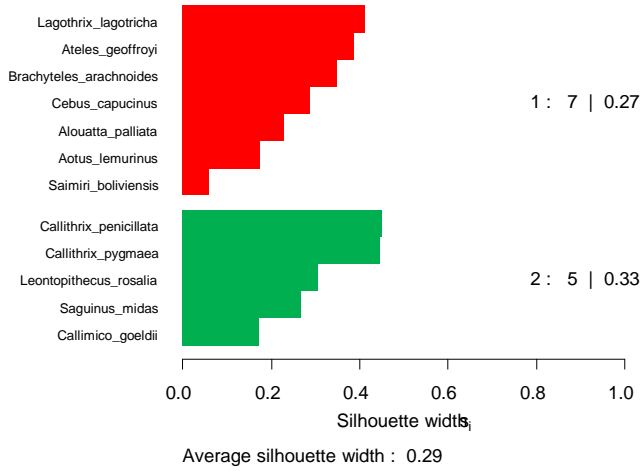


k=4

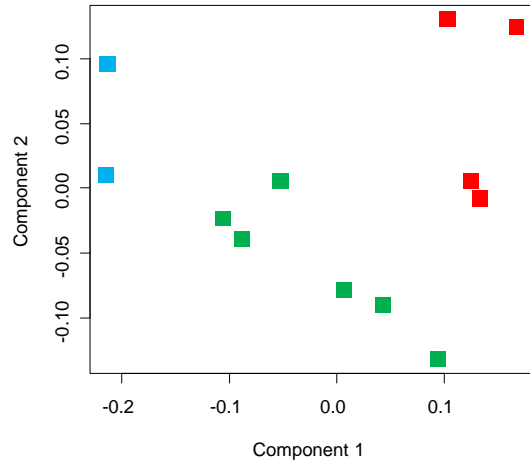
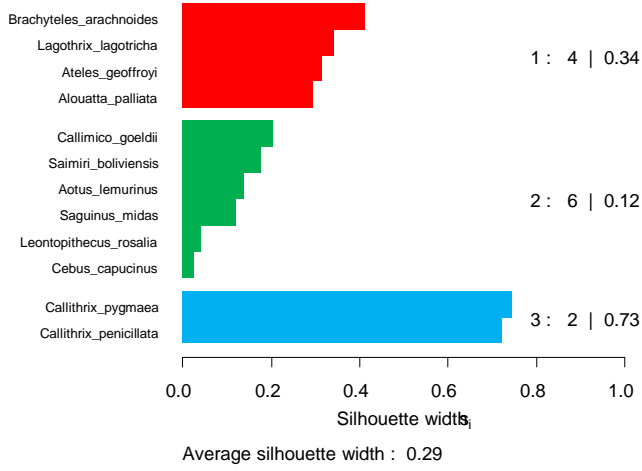


Silhouette plot, Fuzzy Analysis

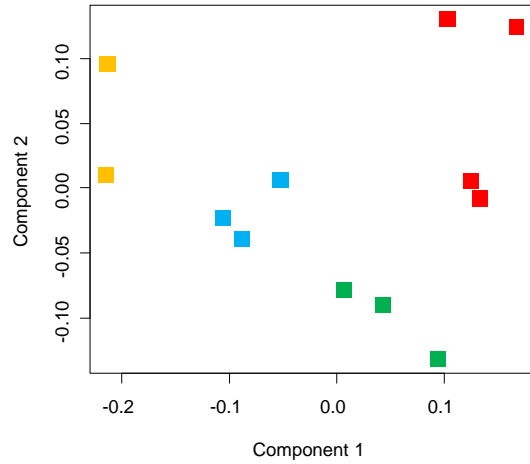
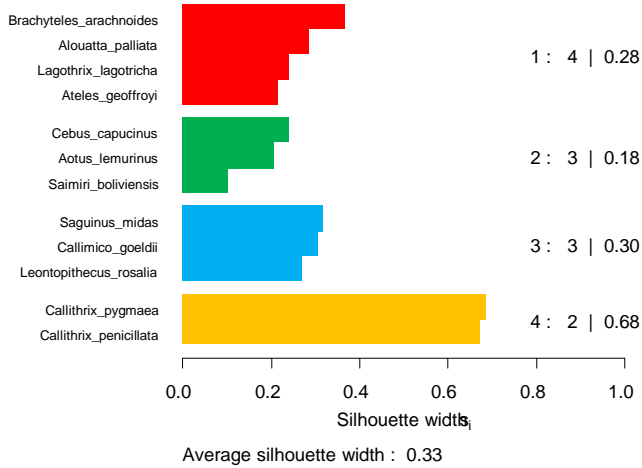
k=2



k=3



k=4



Family Orycteropodidae

Order Tubilidentata

Lehmann 2009

Pearson BDC

Negative: 10

Positive: 12

Clusters: 5

Clusterability

Hopkins Statistic: 0.703

Dip test: 0.039

Dip test p-value: 0.666

Spearman BDC

Negative: 12

Positive: 13

Clusters: 5

The results of the Spearman BDC are nearly identical to the Pearson BDC, and they both give the same five-cluster partition. This partition has an average silhouette width of 0.43.

The five-cluster medoid partition resembles the BDC clusters, with a cluster membership difference of 17%. The five-cluster medoid partition has an average silhouette width of 0.44, which is quite close to the BDC clusters.

The five-cluster fuzzy partition has an average silhouette width of 0.41 and is less similar to the BDC clusters, with a cluster membership difference of 25%.

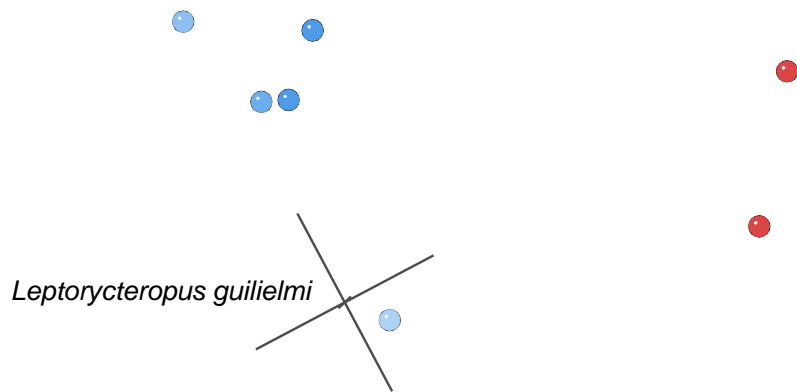
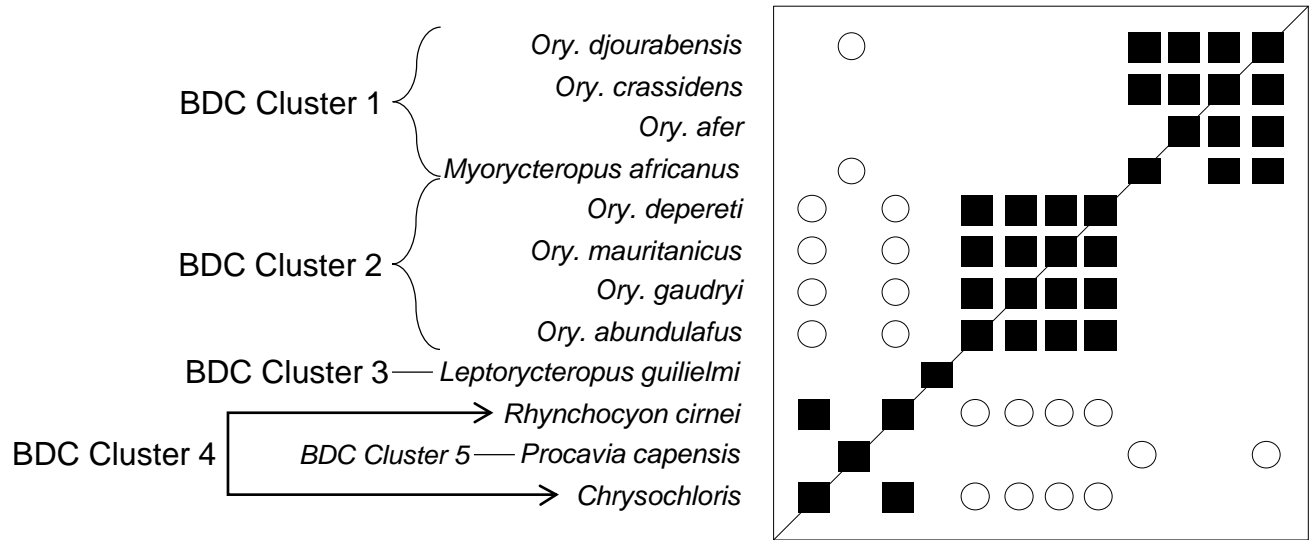
The highest average silhouette widths are observed for three-cluster partitions in both fuzzy analysis and medoid partitioning. These three-cluster partitions are very similar, differing only in the position of *Leptorycteropus guilielmi* (cluster membership difference: 8%). The average silhouette widths are 0.5 for the three-cluster medoid partition and 0.52 for the three-cluster fuzzy partition.

These results once again reveal a lack of consistency between the different methods, highlighting the uncertainty of any conclusions. Therefore, the original judgment that these results are inconclusive is confirmed.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

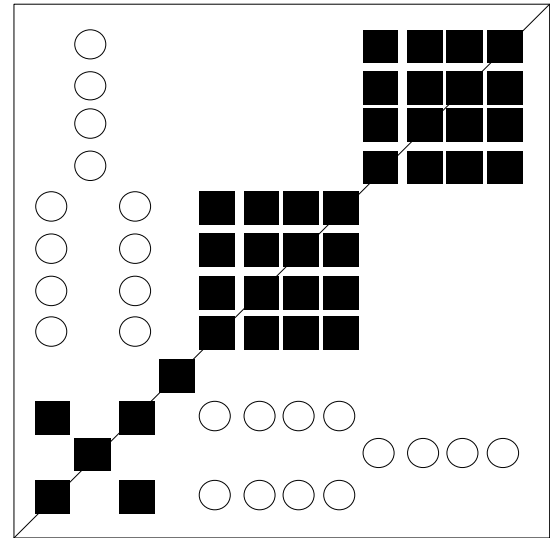
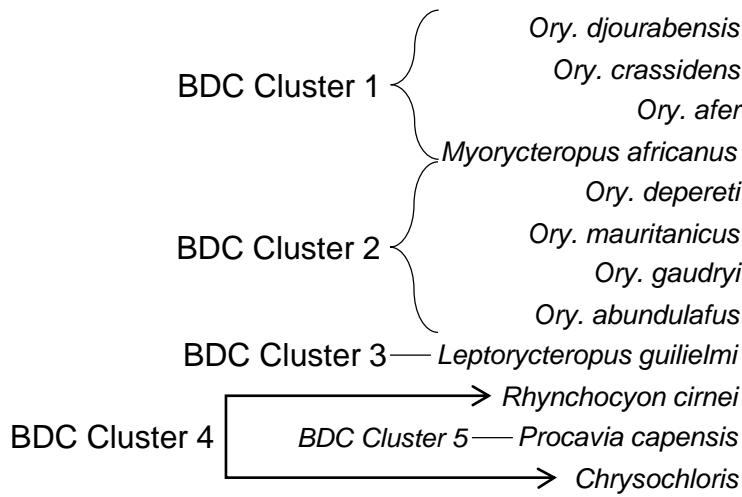
Characters: Craniodental and postcranial



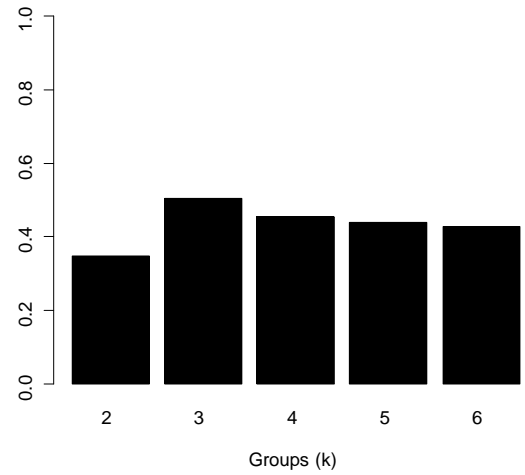
Order Tubulidentata
Family Orycteropodidae

Published taxa	12
Published characters	39
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	12
Characters used for calculations	32
Median bootstrap value	89.5
F ₉₀	0.47
Stress of 3D MDS	0.13
k _{min}	3
Conclusion	Inc

Notes: BDC results reveal two groups of orycteropids with sporadic negative BDC with outgroup taxa. MDS reveals a highly diffuse group of orycteropids that are separated from the outgroup. There is little conclusive evidence of discontinuity or continuity among the orycteropids.



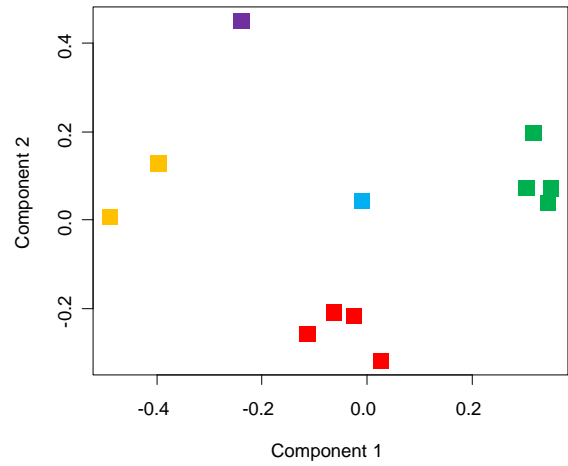
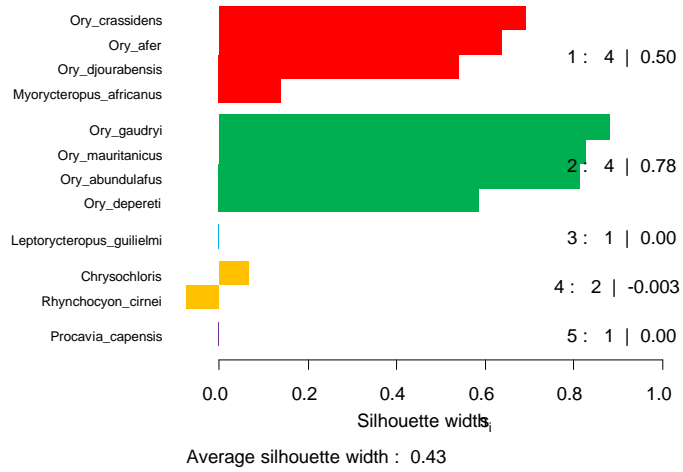
Average Silhouette Widths, Partition Around Medoids



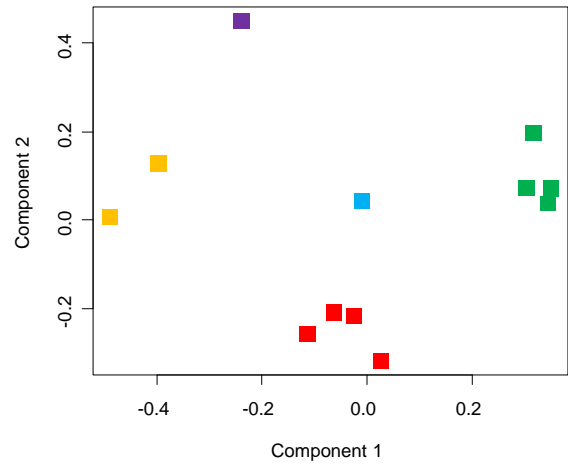
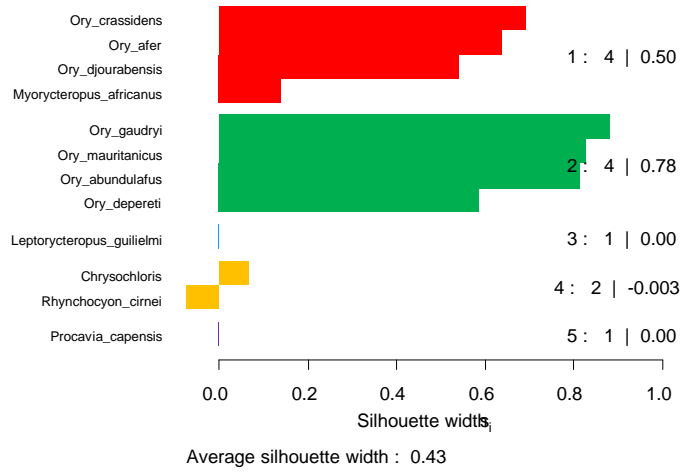
Clade Correspondence: Of the five BDC clusters, clusters 1, 2, and 4 have more than one taxon each. In the phylogeny in Figure 4 of Lehmann (2009), only cluster 2 is monophyletic. Clusters 1 and 4 are both paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

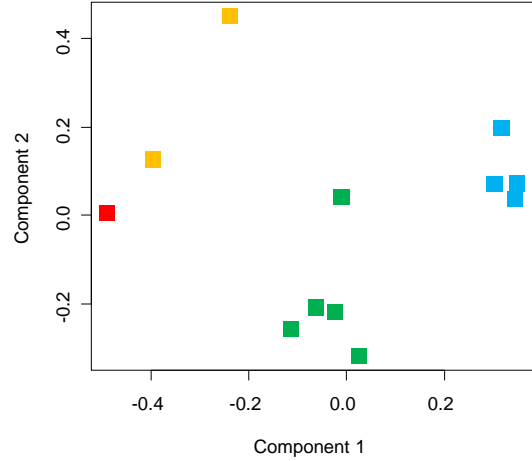
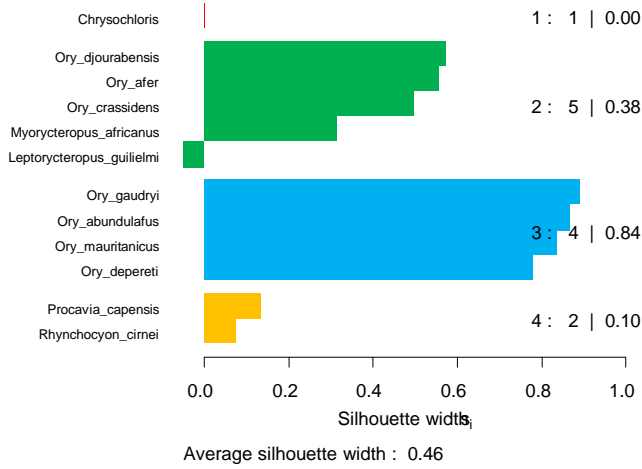


Spearman Correlation

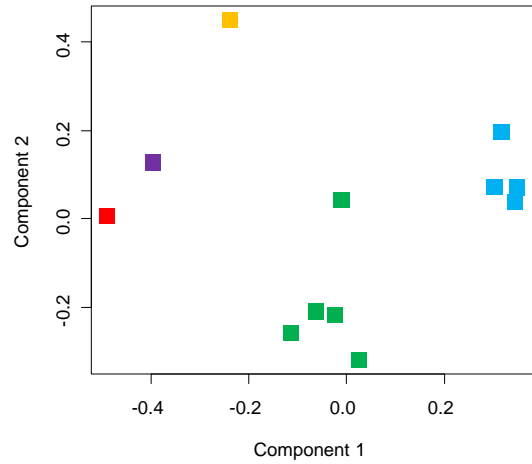
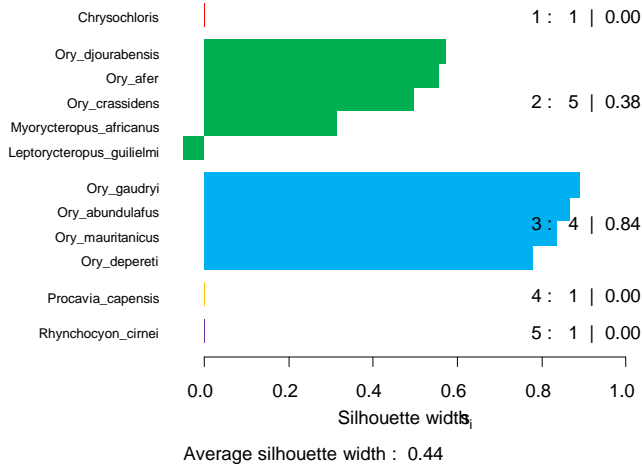


Silhouette plot, Partition Around Medoids

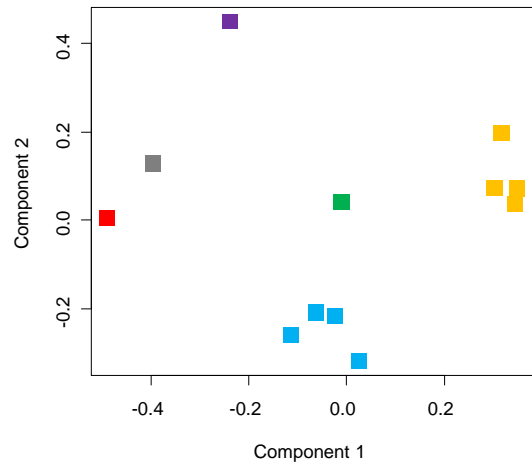
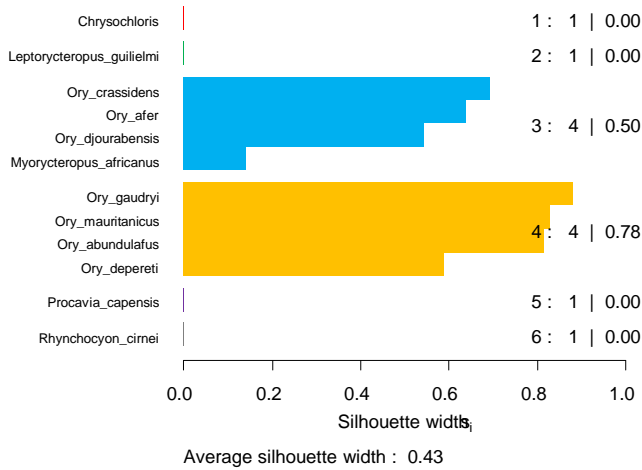
k=4



k=5

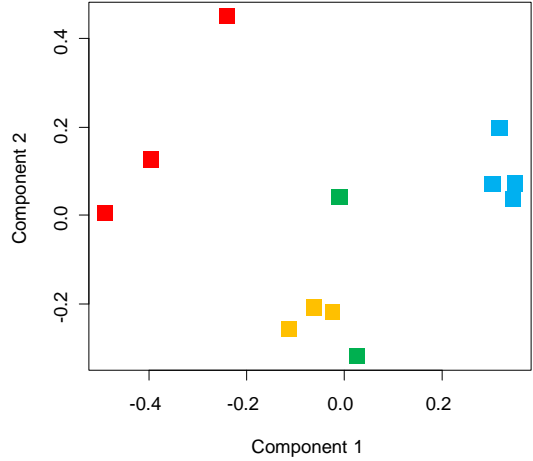
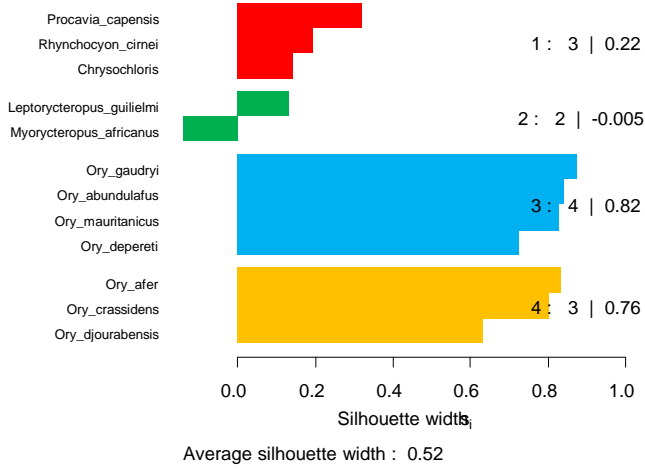


k=6

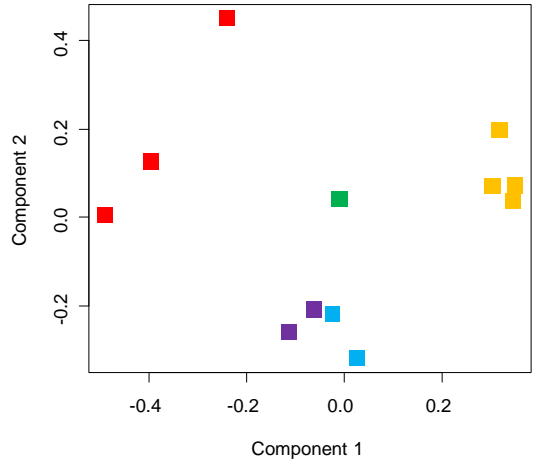
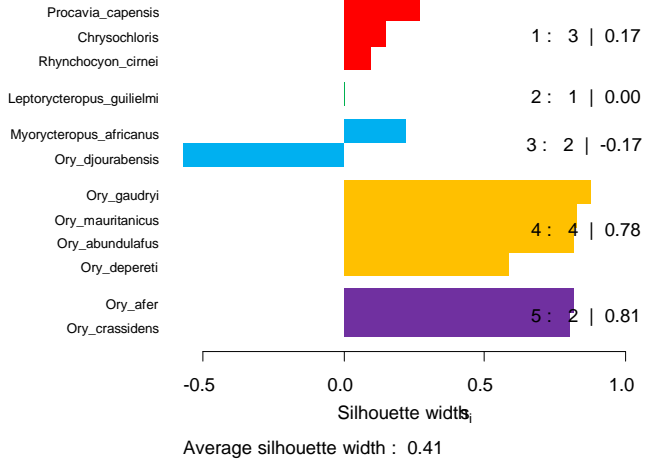


Silhouette plot, Fuzzy Analysis

k=4

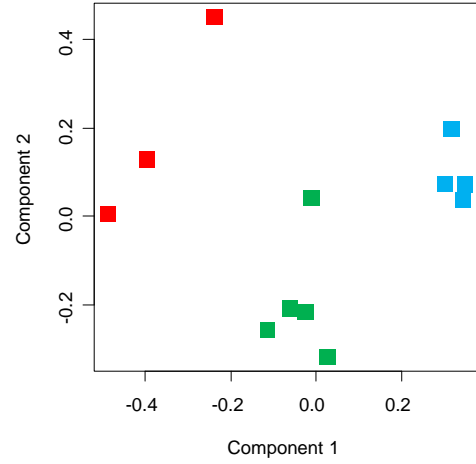
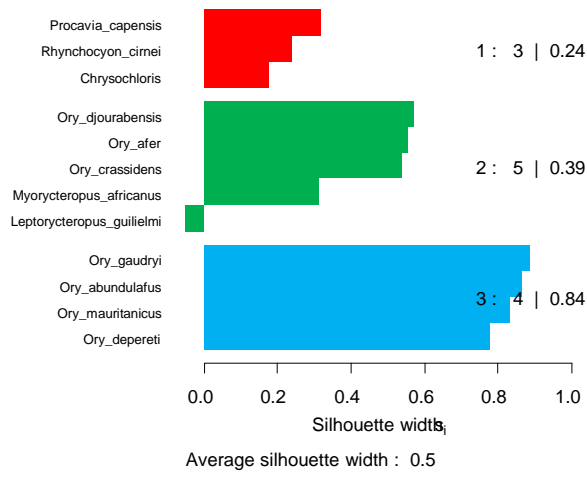


k=5

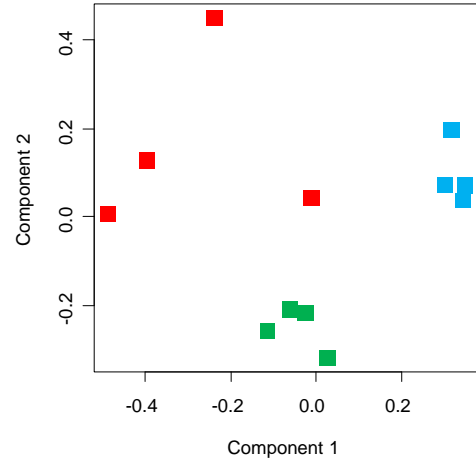
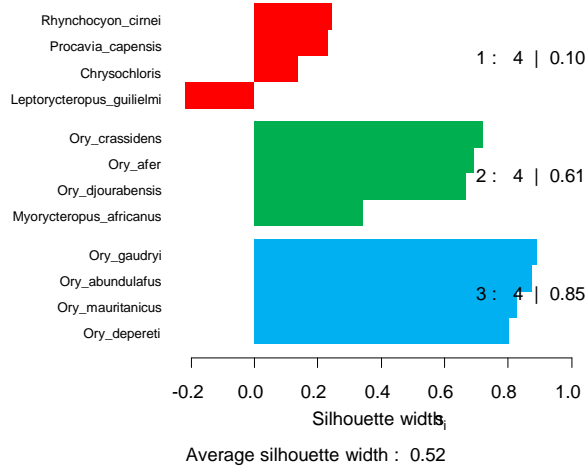


Addendum: Clustering for k=3.

Medoid Partition



Fuzzy Analysis



Family Louisinidae

Order Condylarthra

Hooker and Russell 2012

Pearson BDC

Negative: 77

Positive: 138

Clusters: 4

Clusterability

Hopkins Statistic: 0.77

Dip test: 0.019

Dip test p-value: 0.227

Spearman BDC

Negative: 75

Positive: 220

Clusters: 2

The Spearman BDC results add 82 instances of significant, positive correlation that reduces the cluster count from four in the Pearson BDC results to two. Average silhouette widths for the four-cluster Pearson BDC partition is 0.31 and for the two-cluster Spearman BDC partition is 0.24. The cluster membership difference is 48%.

The medoid partition at $k=4$ has an average silhouette width of 0.29 and closely resembles the four-cluster Pearson BDC results, with a cluster membership difference of only 9%. At $k=2$, the medoid partition differs from the two-cluster Spearman BDC partition by only one taxon (*Dipavali*), which makes the cluster membership difference 3%. The average silhouette width for the two-cluster medoid partition is 0.24.

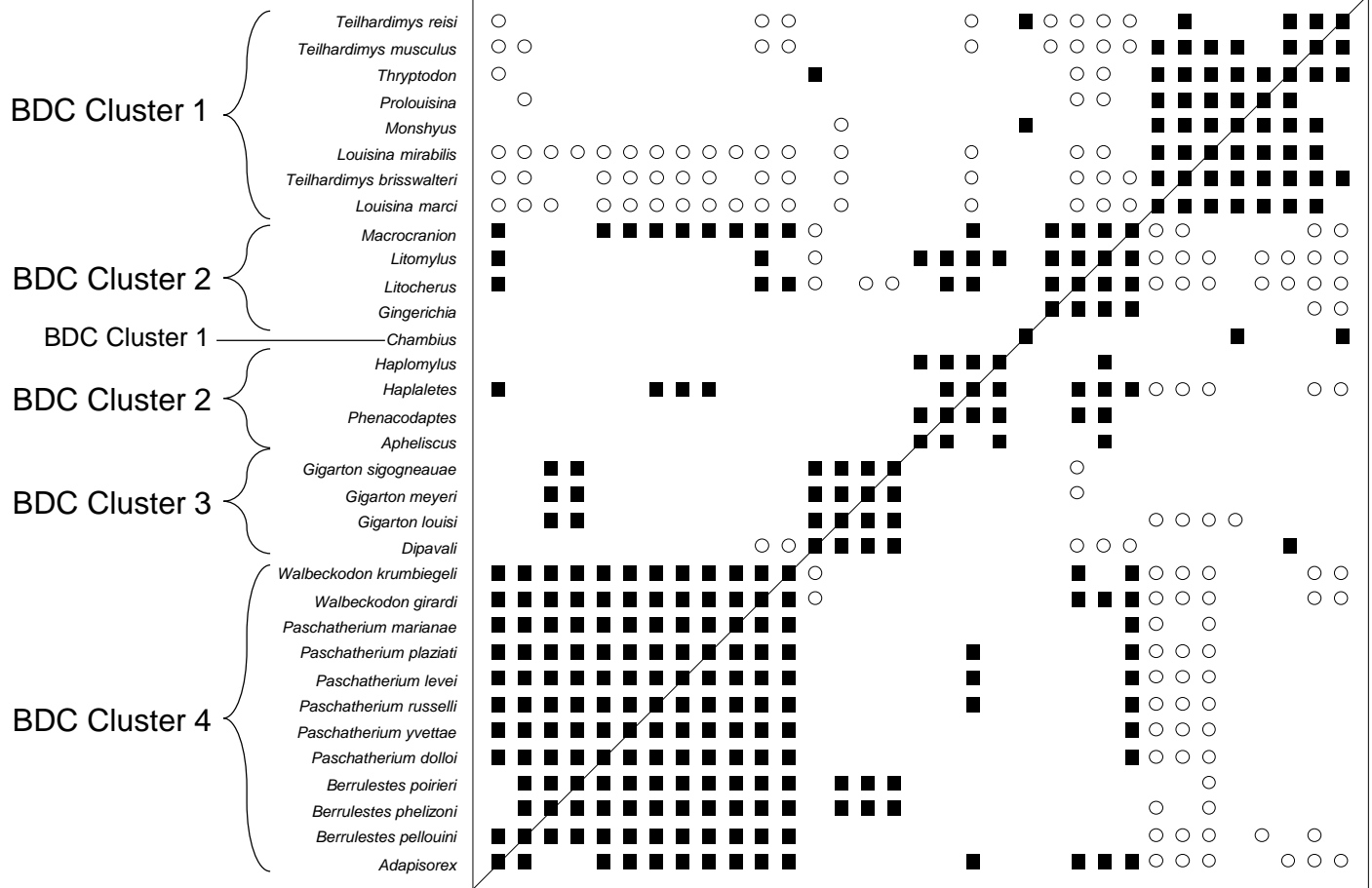
Fuzzy analysis failed at four clusters, but at two clusters, the partition still resembles that of the Spearman BDC clusters. The cluster membership difference is 21%, and the average silhouette width for the fuzzy partition is 0.2.

The original results were uninterpretable, and these results are not much better. They do suggest a possible clustering of two groups of taxa that very roughly correspond to outgroup and ingroup taxa, but the results are too inconsistent to be certain. These results are also inconclusive.

Original conclusion: Inconclusive

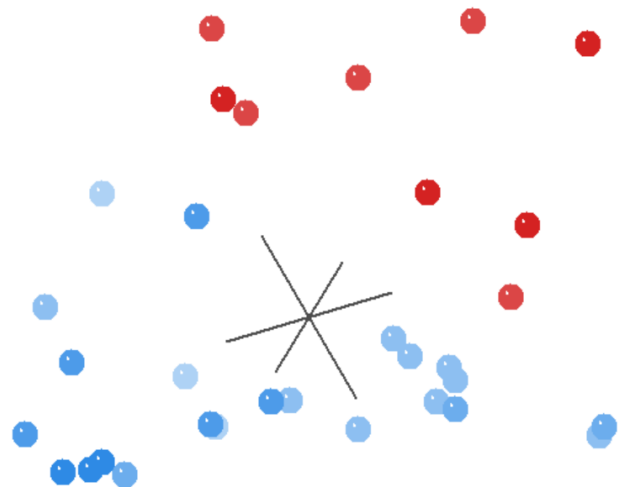
Updated conclusion: Inconclusive

Characters: Craniodental and postcranial

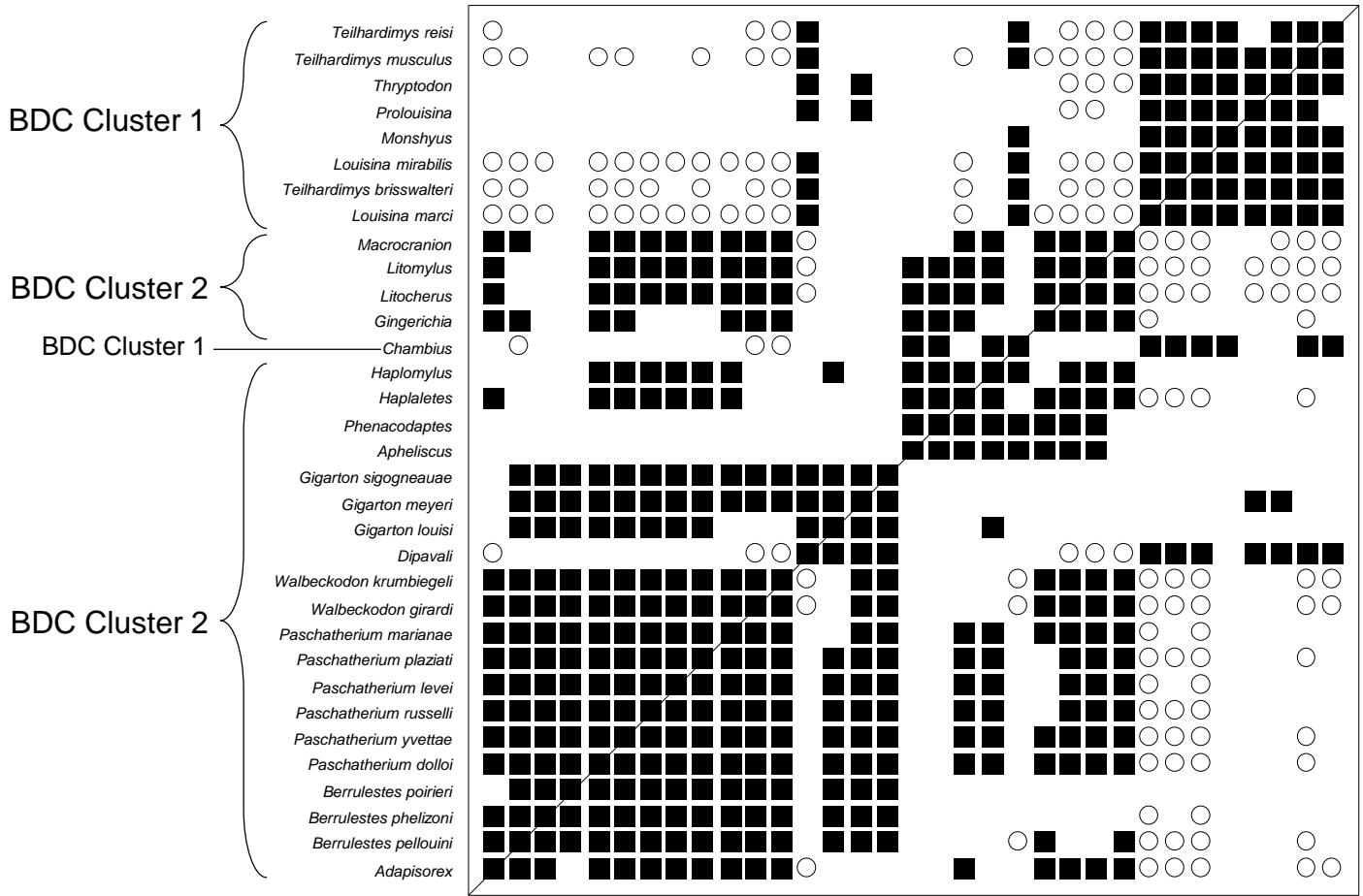


Order Condylarthra
Family Louisinidae

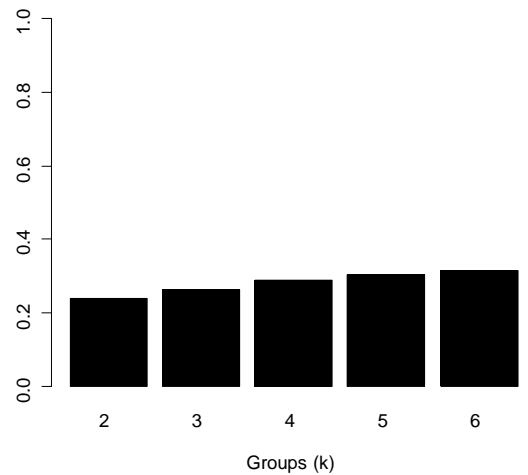
Published taxa	37
Published characters	89
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	33
Characters used for calculations	65
Median bootstrap value	79
F ₉₀	0.19
Stress of 3D MDS	0.14
k _{min}	5
Conclusion	Inc



Notes: BDC implies discontinuity within Louisinidae, but no clustering evident in MDS



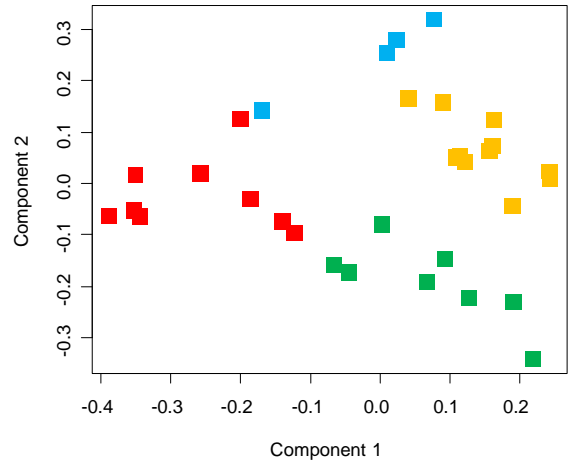
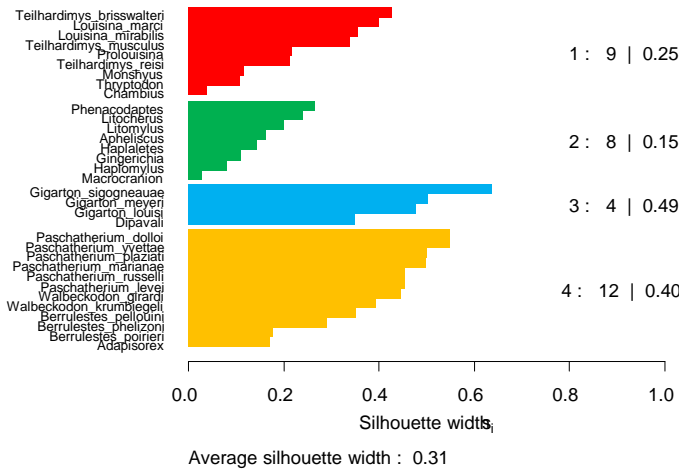
Average Silhouette Widths, Partion Around Medoids



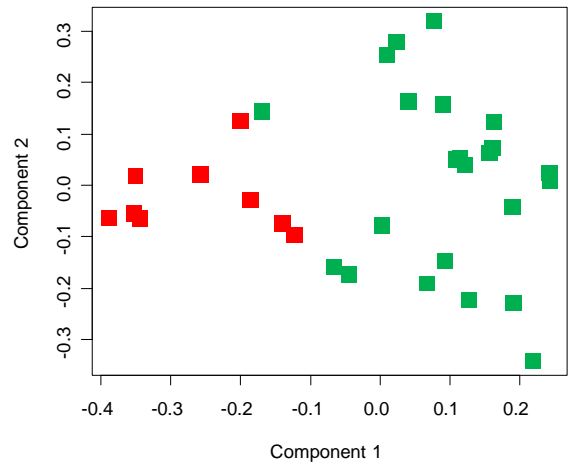
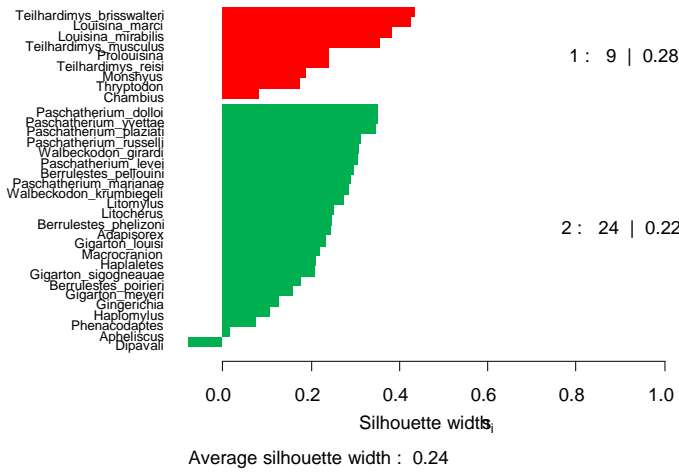
Clade Correspondence: All four BDC clusters contain more than one taxon each. Only cluster 3 appears as a clade in Hooker and Russell's (2012) most parsimonious phylogeny, shown in Figure 29 of their paper. Cluster 1 is polyphyletic. Cluster 2 is paraphyletic with one taxon (*Chambius*) of Cluster 1. Cluster 4 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

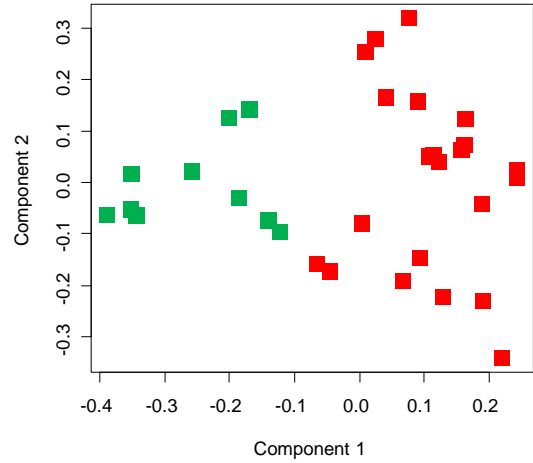
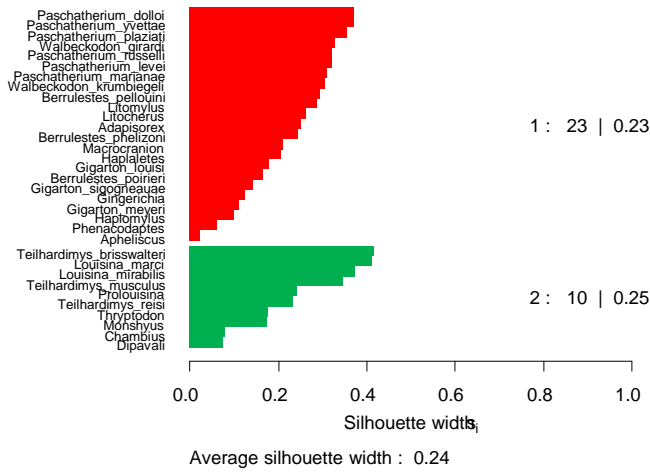


Spearman Correlation

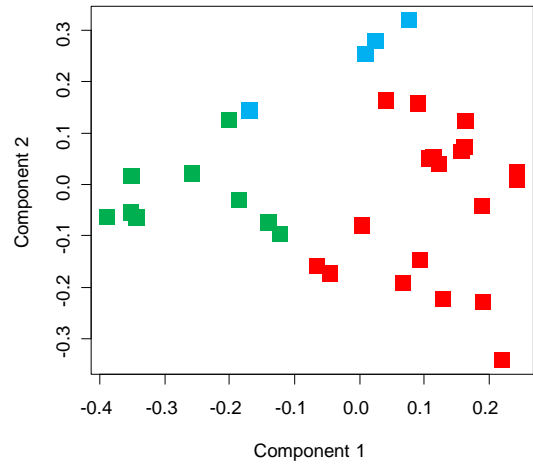
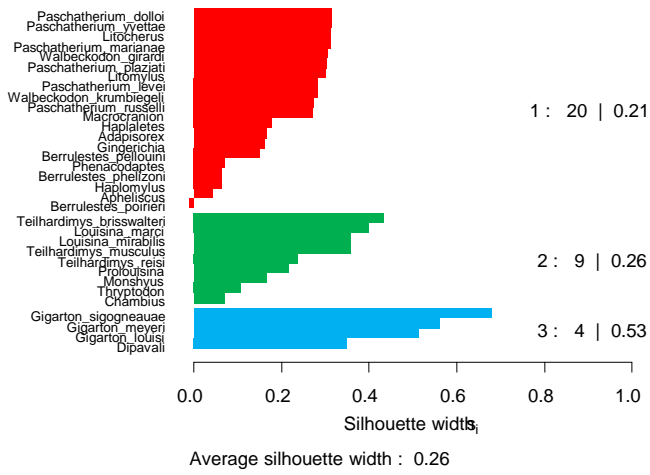


Silhouette plot, Partition Around Medoids

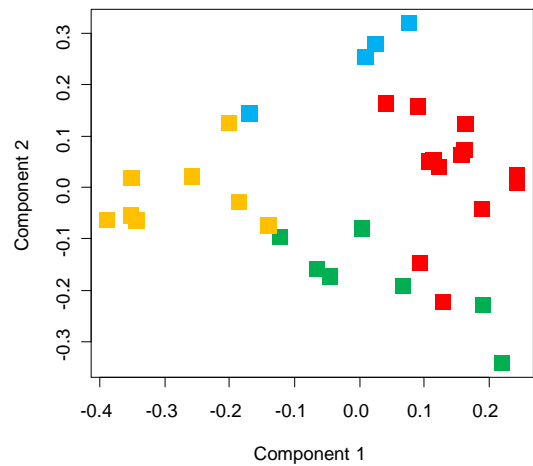
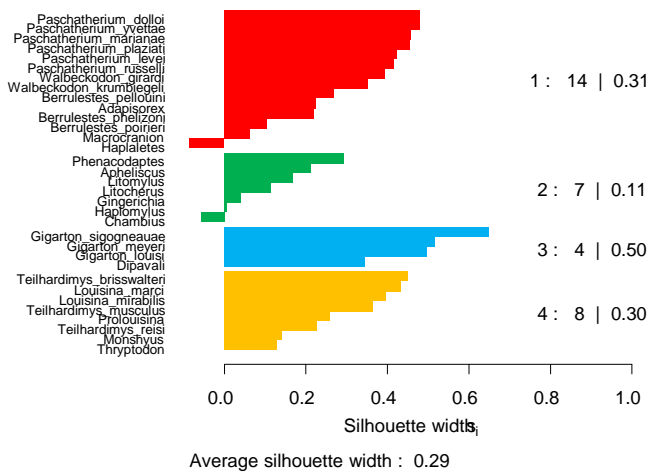
k=2



k=3

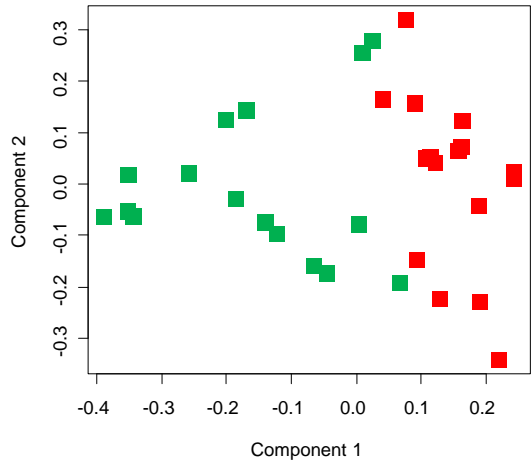
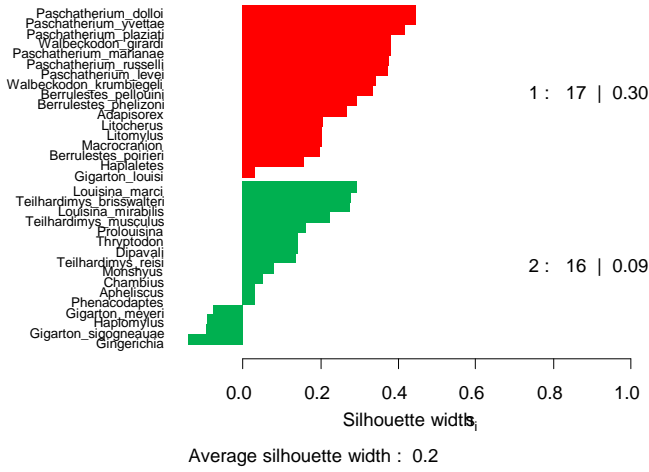


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Hyopsodontidae

Order Condylarthra

Williamson and Weil 2011

Pearson BDC

Negative: 72

Positive: 122

Clusters: 4

Clusterability

Hopkins Statistic: 0.731

Dip test: 0.019

Dip test p-value: 0.555

Spearman BDC

Negative: 69

Positive: 144

Clusters: 2

Spearman BDC adds 22 instances of significant, positive correlation, which reduces the cluster count from four in the Pearson BDC results to two in the Spearman BDC results. Because the combined clusters were mostly small, the cluster membership difference is only 9%. Average silhouette widths were 0.22 for the Pearson BDC partition and 0.36 for the Spearman BDC partition.

The four-cluster medoid partition does not match the Pearson BDC clusters. The cluster membership difference is 48%, and the average silhouette width for the four-cluster medoid partition is 0.19. The two-cluster medoid partition differs from the Spearman BDC partition by a single taxon, *Haplaletes disceptatrix*.

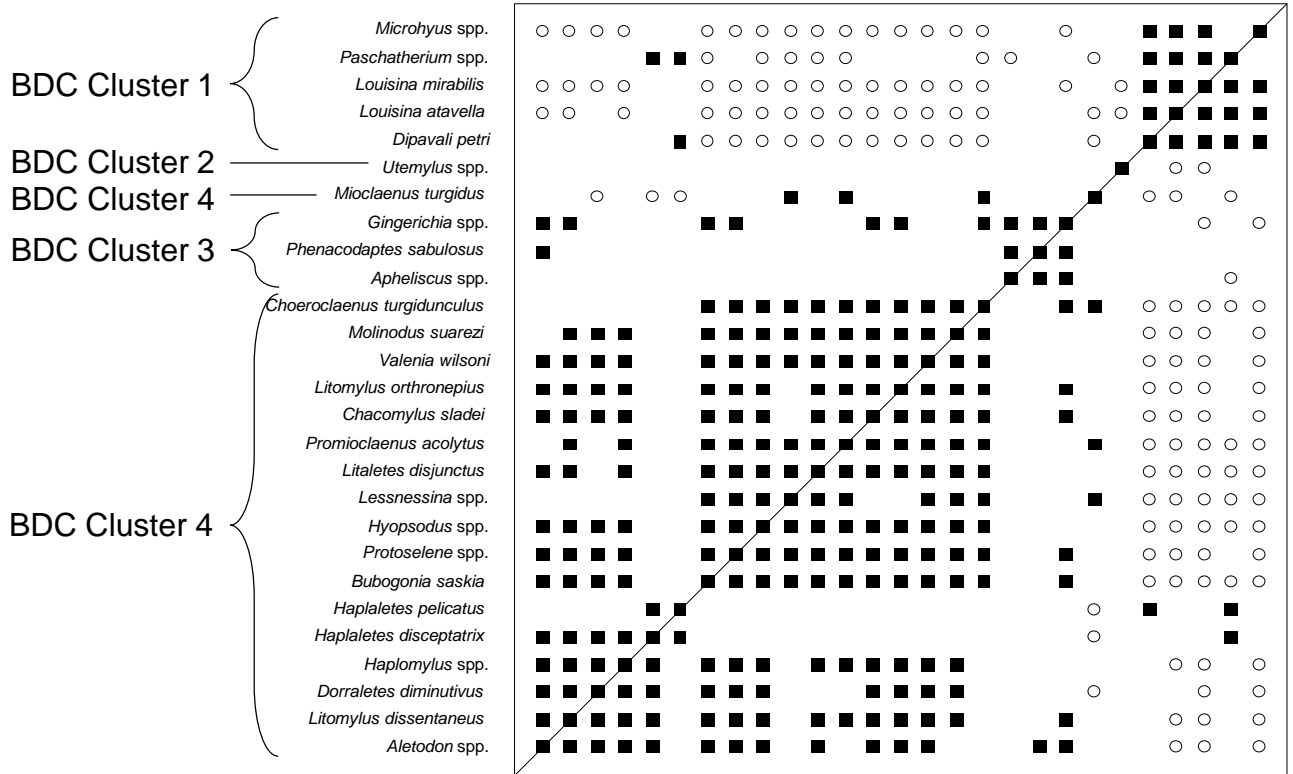
Fuzzy analysis failed at $k=4$, but the two-cluster fuzzy partition resembles the Spearman BDC partition, with a cluster membership difference of 22%. The two-cluster fuzzy partition has an average silhouette width of 0.26.

Here again, we find some very general consistency between the Spearman BDC, medoid partition, and fuzzy analysis, but that consistency does not translate to a division between the 19 ingroup and eight outgroup taxa. This lack of consistency confirms the original judgment of inconclusive.

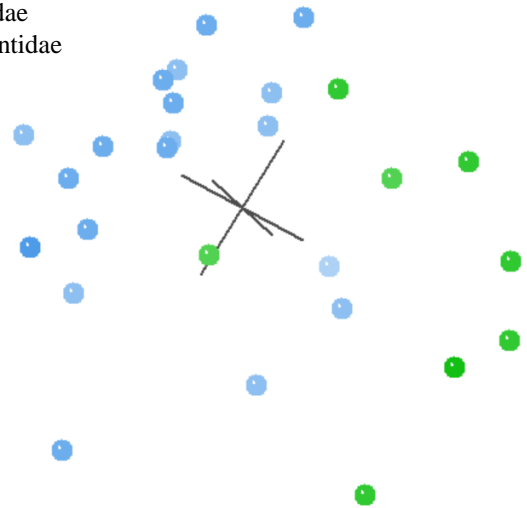
Original conclusion: Inconclusive

Updated conclusion: Inconclusive

Characters: Dental and postcranial



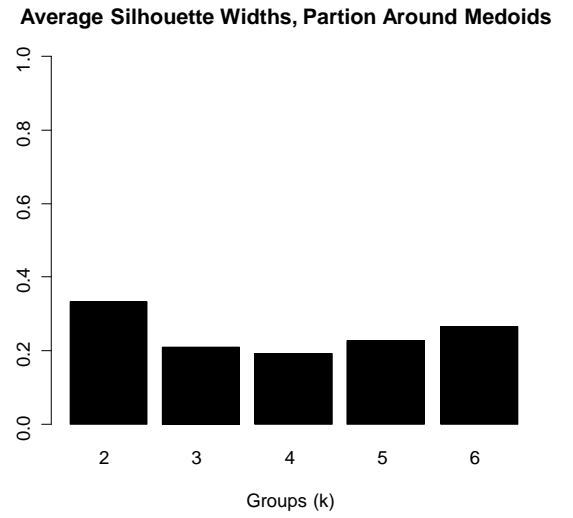
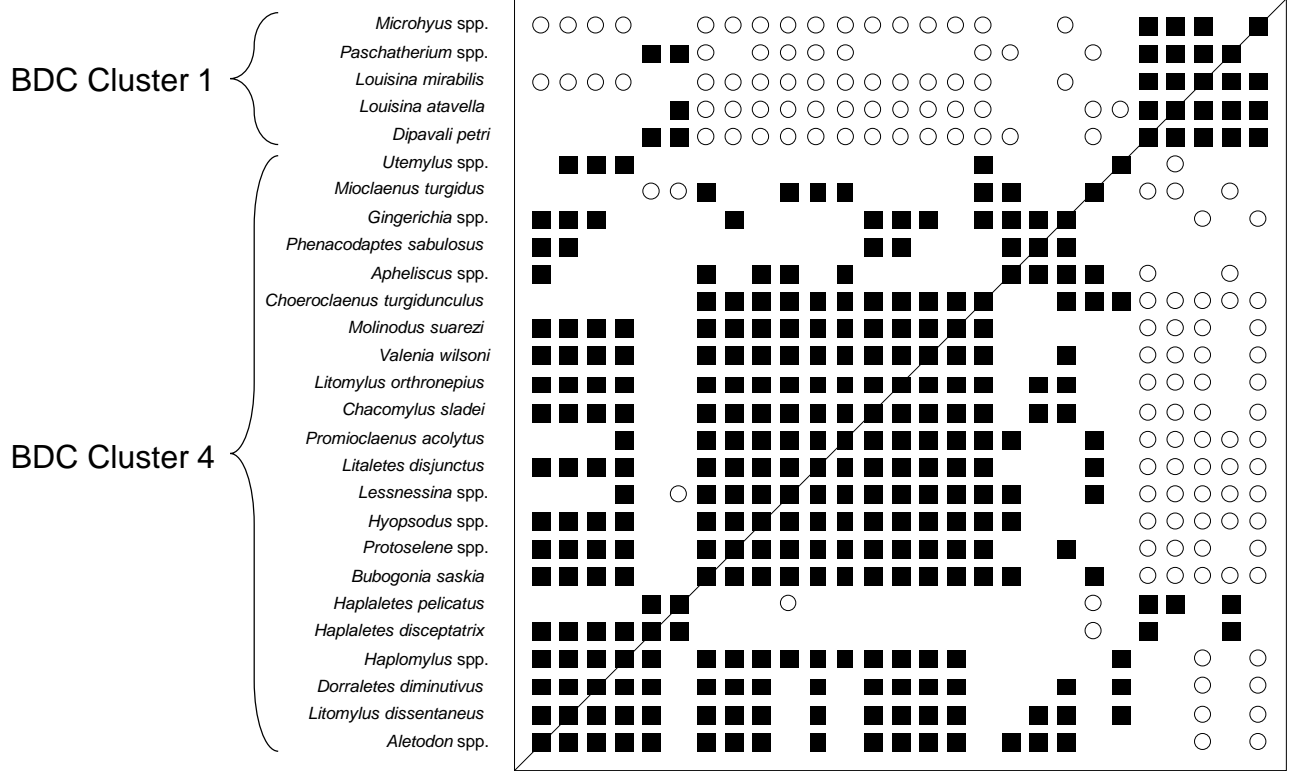
Green: Louisinidae
Blue: Hyopsodontidae



Order Condylarthra
Family Hyopsodontidae

Published taxa	30
Published characters	59
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	27
Characters used for calculations	44
Median bootstrap value	78
F ₉₀	0.22
Stress of 3D MDS	0.22
k _{min}	8
Conclusion	Inc

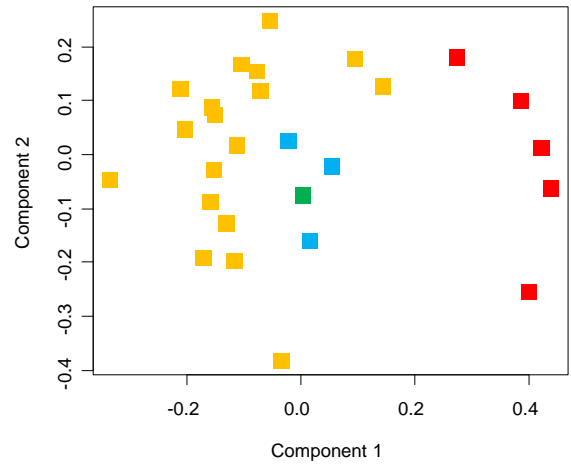
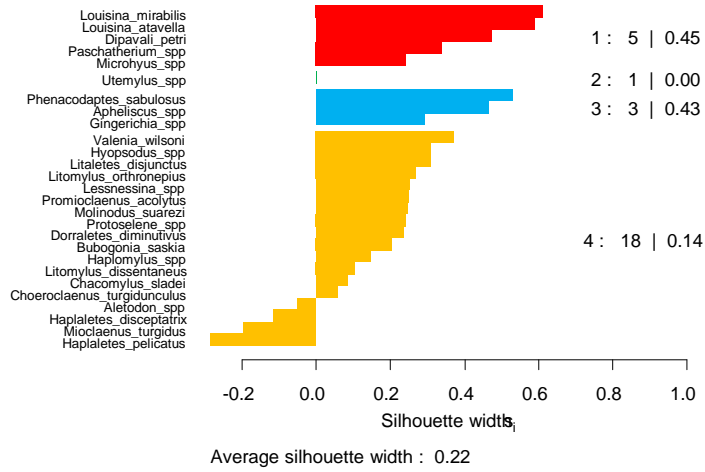
Notes: BDC reveals two groups of taxa, but MDS shows a diffuse cluster. Clear discontinuity is not evident.



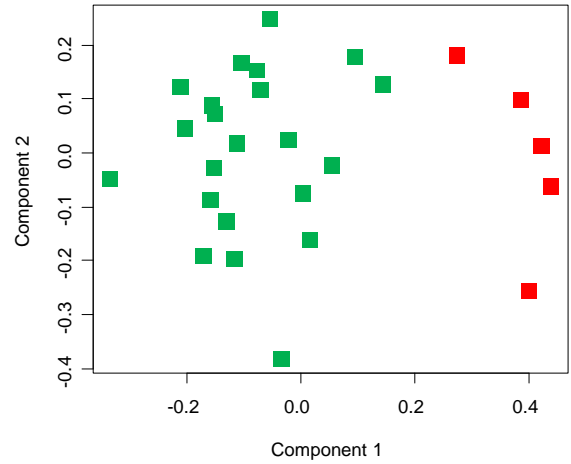
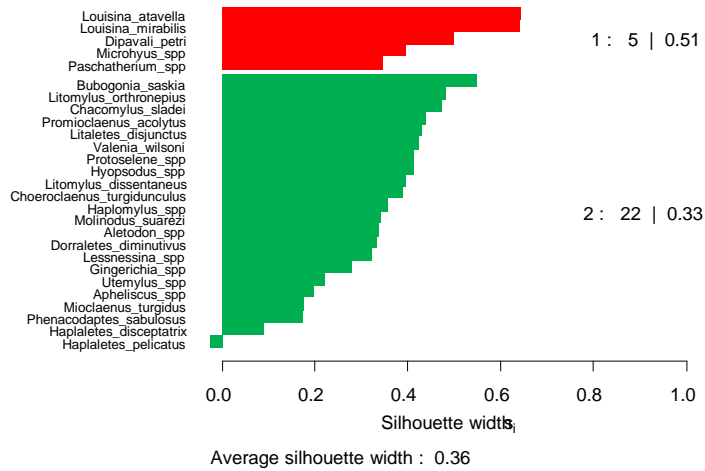
Clade Correspondence: Three of the four BDC clusters contain more than one taxon each. In the phylogeny in Figure 6 of Williamson and Weil (2011), only Clusters 1 and 3 appear as clades. The large cluster 4 is paraphyletic with all remaining clusters.

Silhouette plot, BDC partitions

Pearson Correlation

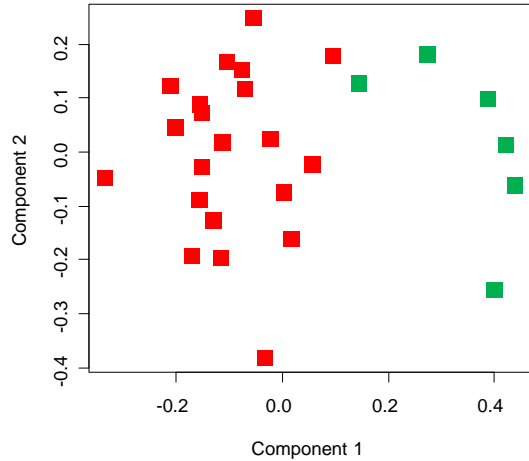
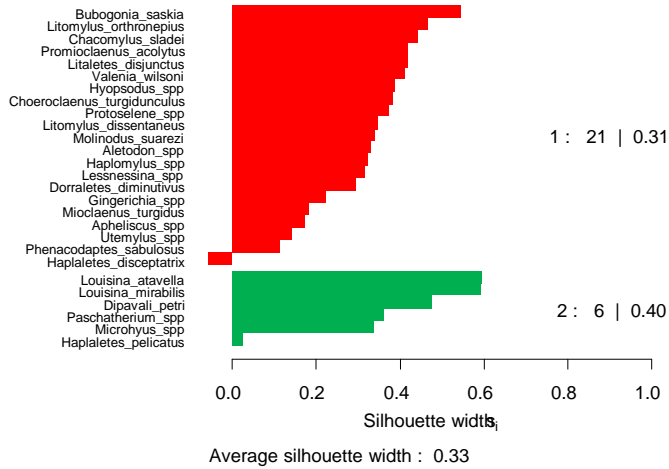


Spearman Correlation

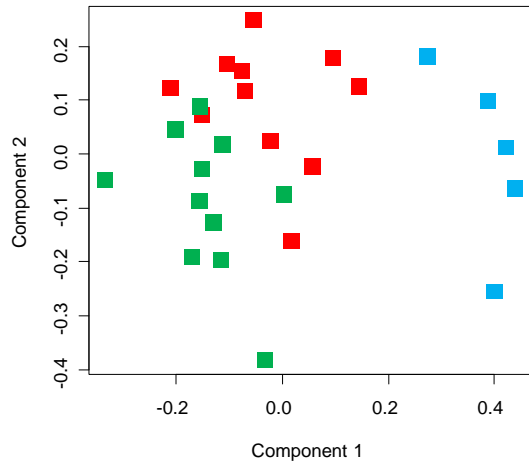
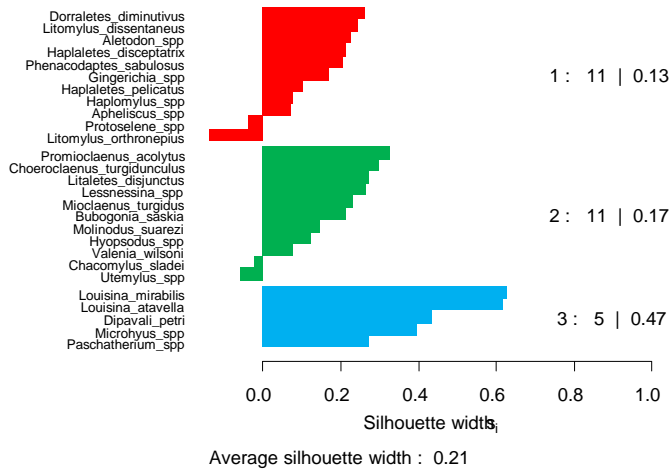


Silhouette plot, Partition Around Medoids

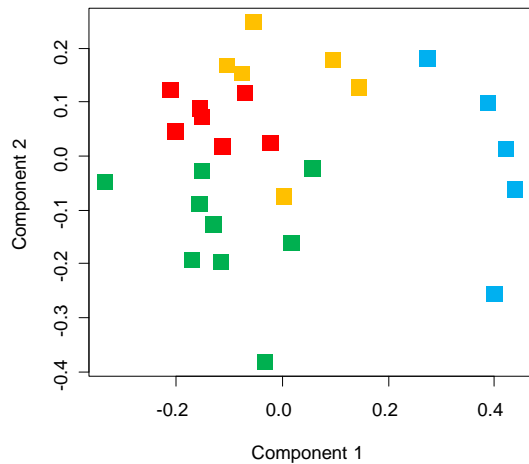
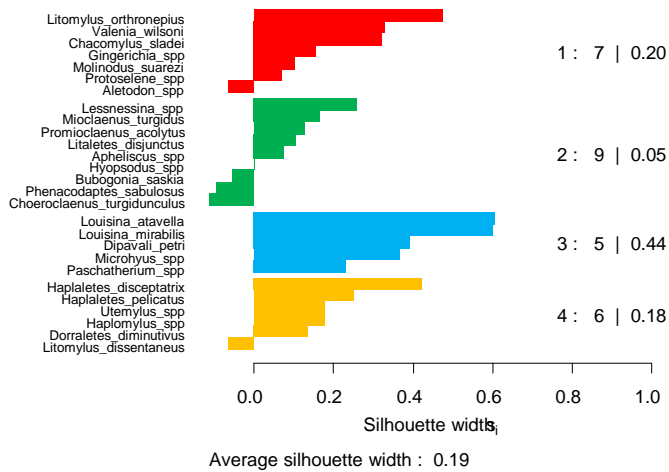
k=2



k=3

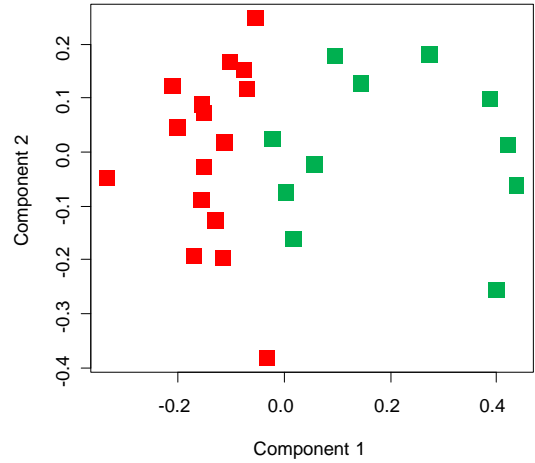
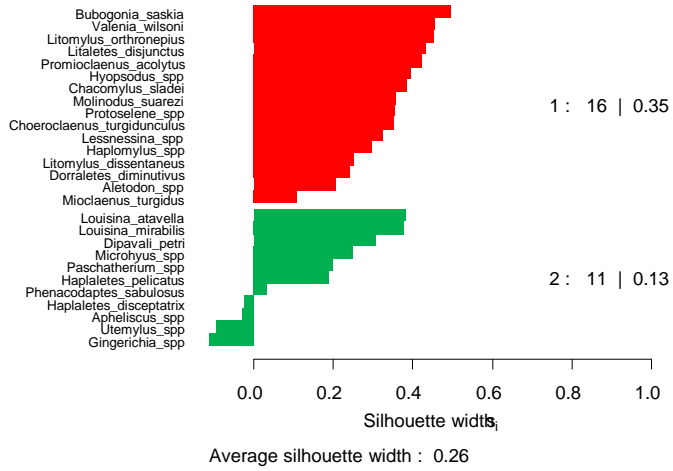


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Didolodontidae

Order Condylarthra
Gelfo and Siegé 2011

Pearson BDC
Negative: 30
Positive: 56
Clusters: 3

Clusterability
Hopkins Statistic: 0.777
Dip test: 0.047
Dip test p-value: 0.004

Spearman BDC
Negative: 21
Positive: 74
Clusters: 2

Three clusters are evident in the Pearson BDC results, with two consisting entirely of outgroup taxa. The Spearman BDC results are very similar, but a singleton outgroup cluster *Protungulatum donnae* is joined to the ingroup cluster. The Spearman BDC partition has an average silhouette width of 0.42, and the Pearson BDC clusters have an average silhouette width of 0.38. The cluster membership difference is only 5%.

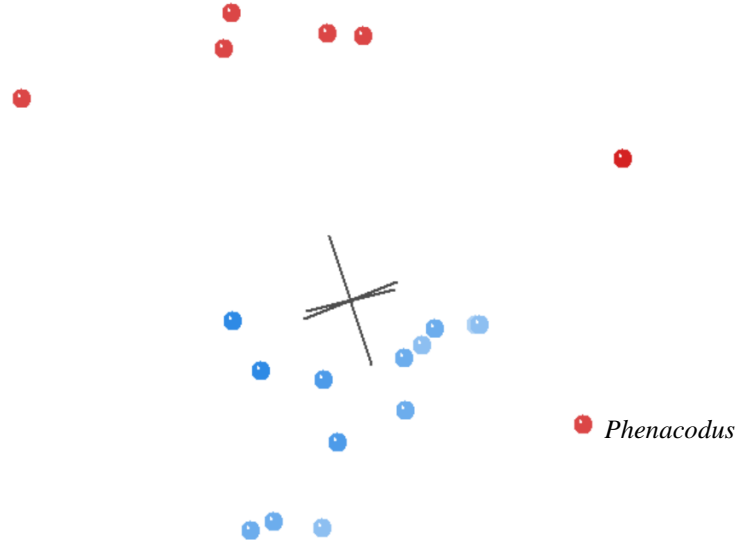
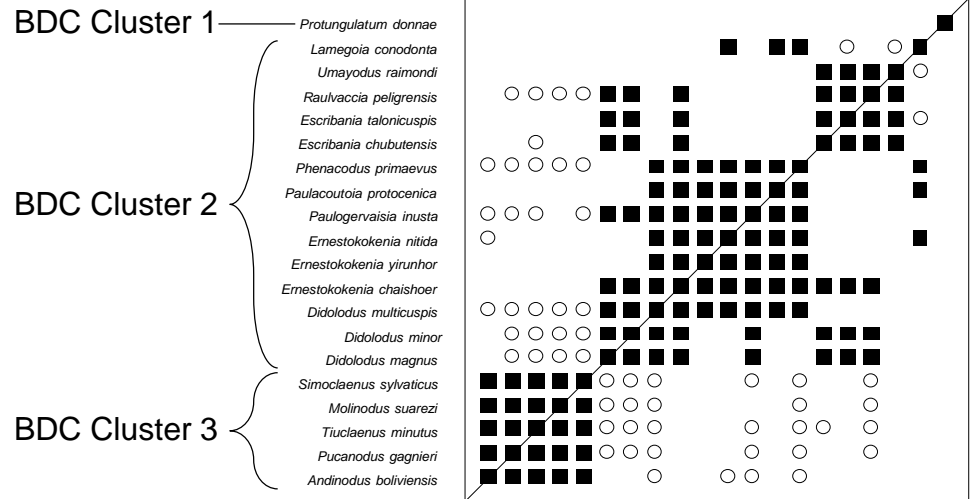
Medoid partitioning at k=2 exactly matches the Spearman BDC partition. The three-cluster medoid partition differs considerably from the Pearson BDC clusters, with a cluster membership difference of 35%.

Fuzzy analysis at k=2 differs from the Spearman BDC partition by a single taxon, *Protungulatum donnae*. Three-cluster fuzzy analysis also poorly matches the Pearson BDC partition, with a cluster membership difference of 35%. The average silhouette width of the three-cluster fuzzy partition is 0.41.

The original analysis Didolodontidae + *Phenacodus* as a likely holobaramin. These results generally reinforce the original analysis. The Spearman BDC partition reveals even more significant, positive BDC uniting the group, and there remains significant, negative correlation between the clusters that implies the presence of discontinuity. The medoid partition agrees exactly with the Spearman BDC results, and the fuzzy partition only renders a question on the position of the outgroup *Protungulatum*, which might be a part of the didolodontid holobaramin. Hence, while the general conclusion that Didolodontidae is a holobaramin is made more sure, there remains an uncertainty about the position of *Protungulatum*.

Original conclusion: HB?
Updated conclusion: HB?

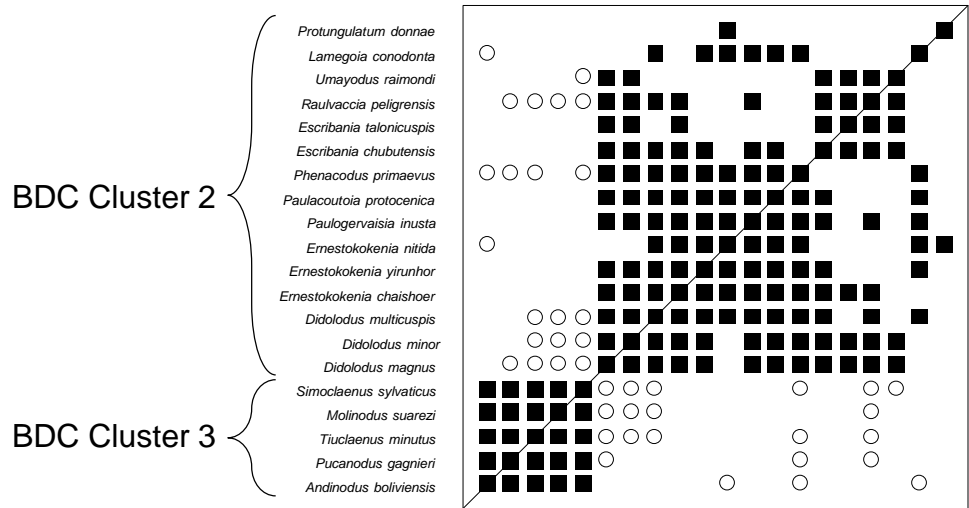
Characters: Dental



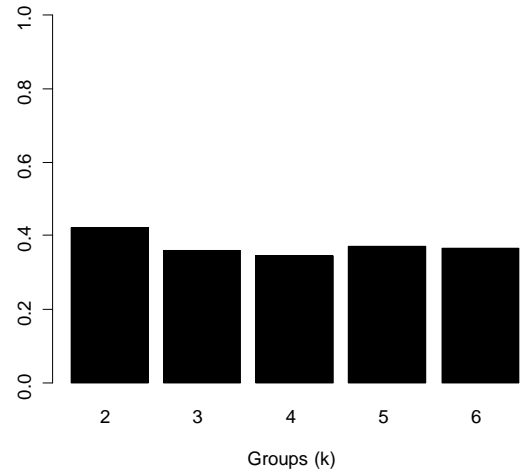
Order Condylarthra
Family Didolodontidae

Published taxa	20
Published characters	41
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	20
Characters used for calculations	25
Median bootstrap value	74
F ₉₀	0.13
Stress of 3D MDS	0.2
k _{min}	5
Conclusion	HB?

Notes: Didolodontidae is well separated from the outgroup in both BDC and MDS results. *Phenacodus* is also part of the Dipolodontidae in both analyses. Didolodontidae + *Phenacodus* is likely a holobaramin.



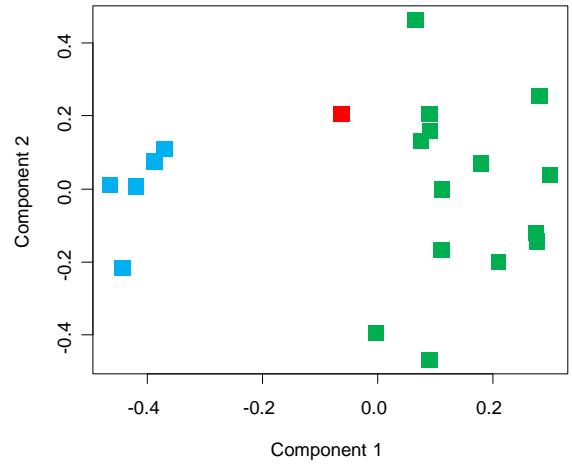
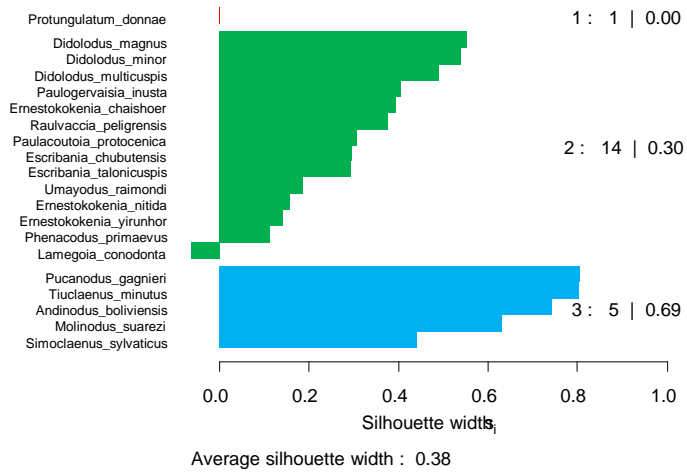
Average Silhouette Widths, Partion Around Medoids



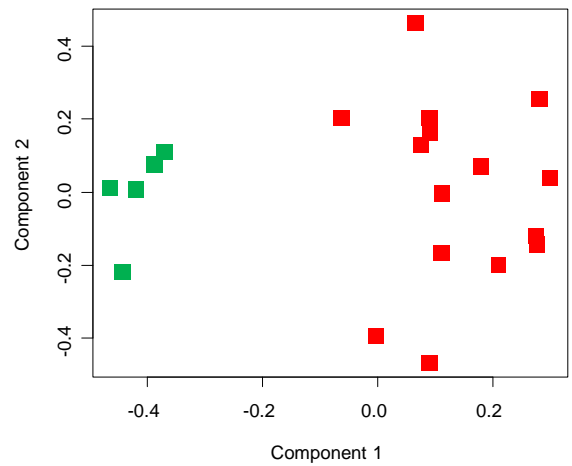
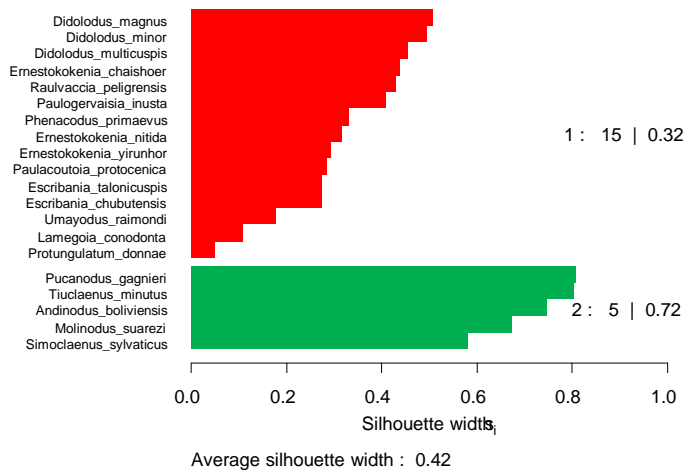
Clade Correspondence: In the BDC results, clusters 2 and 3 (of three total clusters) contain two or more taxa each. In the phylogeny depicted in Figure 4 of Gelfo and Sigé (2011), cluster 3 is a small clade, but cluster 2 is paraphyletic with cluster 3.

Silhouette plot, BDC partitions

Pearson Correlation

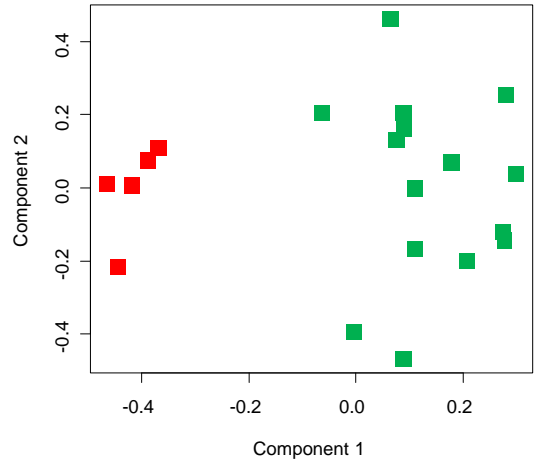
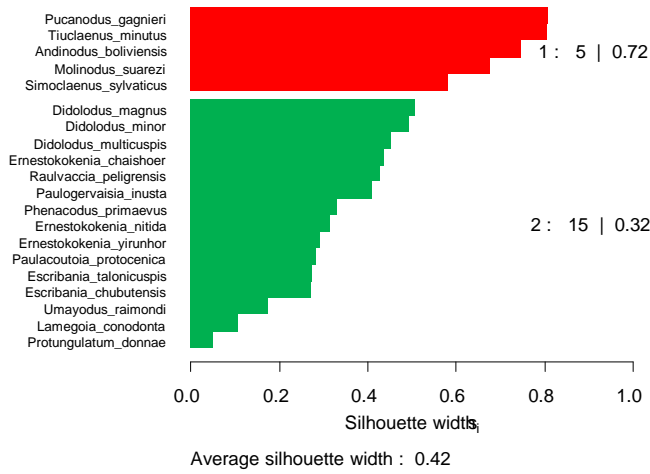


Spearman Correlation

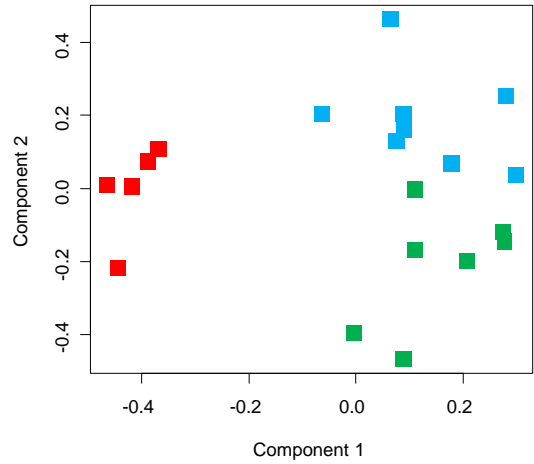
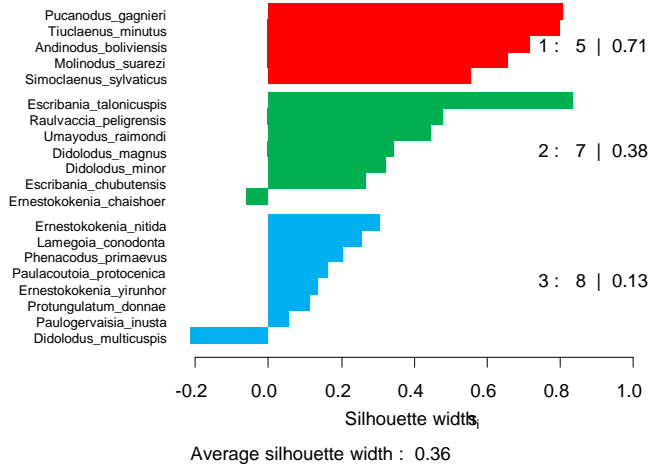


Silhouette plot, Partition Around Medoids

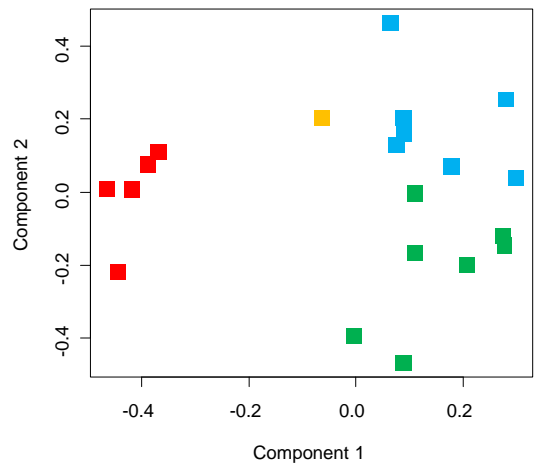
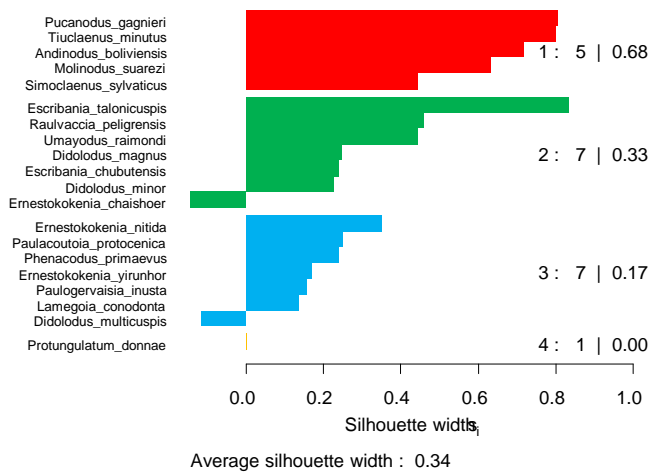
k=2



k=3

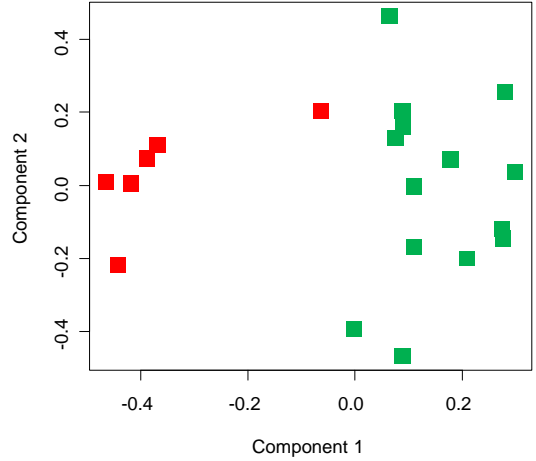
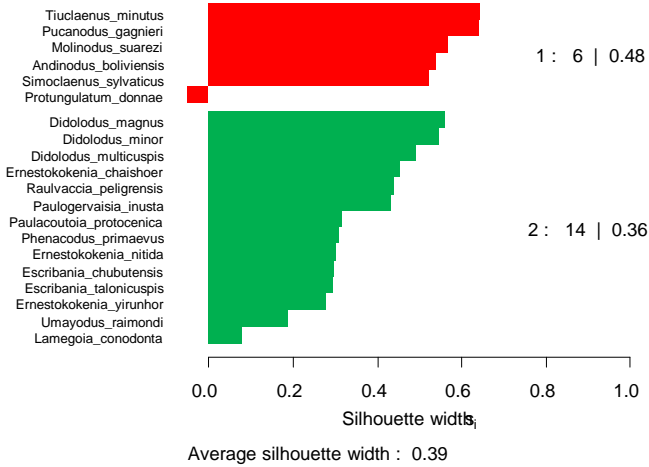


k=4

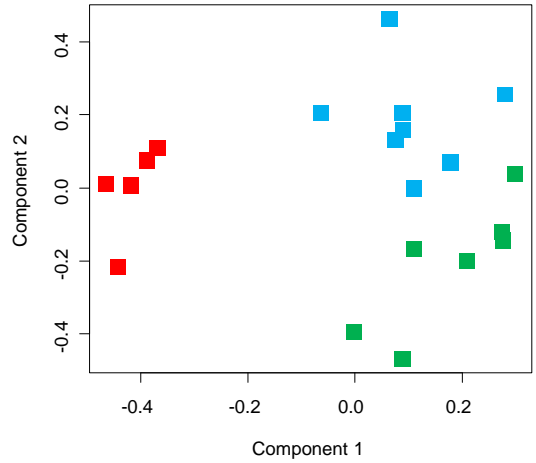
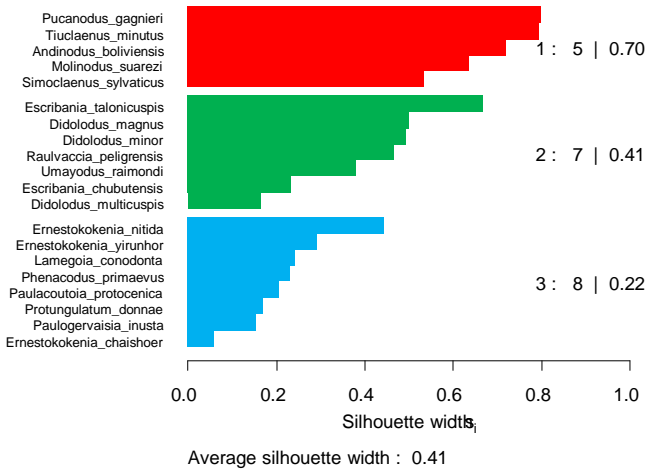


Silhouette plot, Fuzzy Analysis

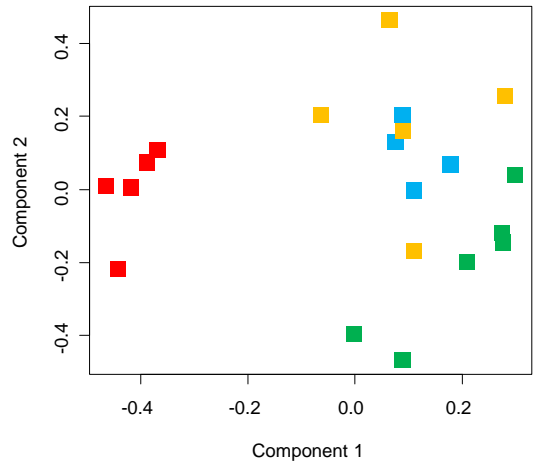
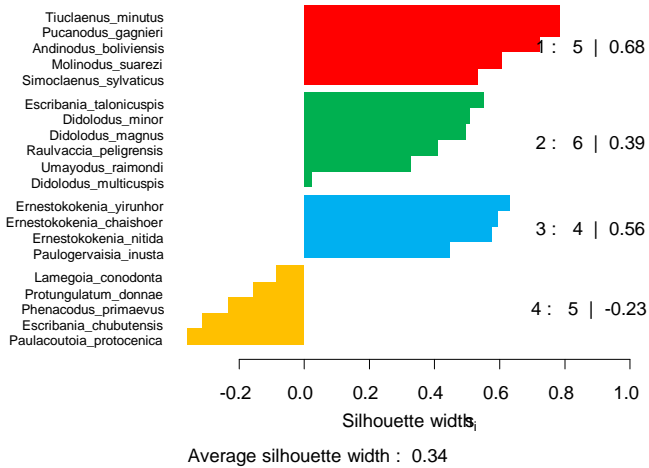
k=2



k=3



k=4



Family Suidae

Order Artiodactyla

Orliac et al. 2010

Pearson BDC

Negative: 137

Positive: 210

Clusters: 4

Spearman BDC

Negative: 104

Positive: 269

Clusters: 2

Clusterability

Hopkins Statistic: 0.856

Dip test: 0.014

Dip test p-value: 0.628

The Spearman BDC adds 59 instances of significant, positive BDC to the Pearson BDC results, thereby reducing the number of clusters from four to two. The generally negative correlation observed between the Spearman BDC clusters is also observed in the Pearson BDC results, leading the original analysis to be interpreted as a single suid holobarmin. Average silhouette widths were 0.4 for the four-cluster Pearson BDC partition and 0.34 for the two-cluster Spearman BDC partition. The cluster membership difference is 28%.

The medoid partition at $k=4$ has an average silhouette width of 0.42 and resembles the Pearson BDC clusters, with a cluster membership difference of 17%. The two-cluster medoid partition matches the Spearman BDC clusters exactly.

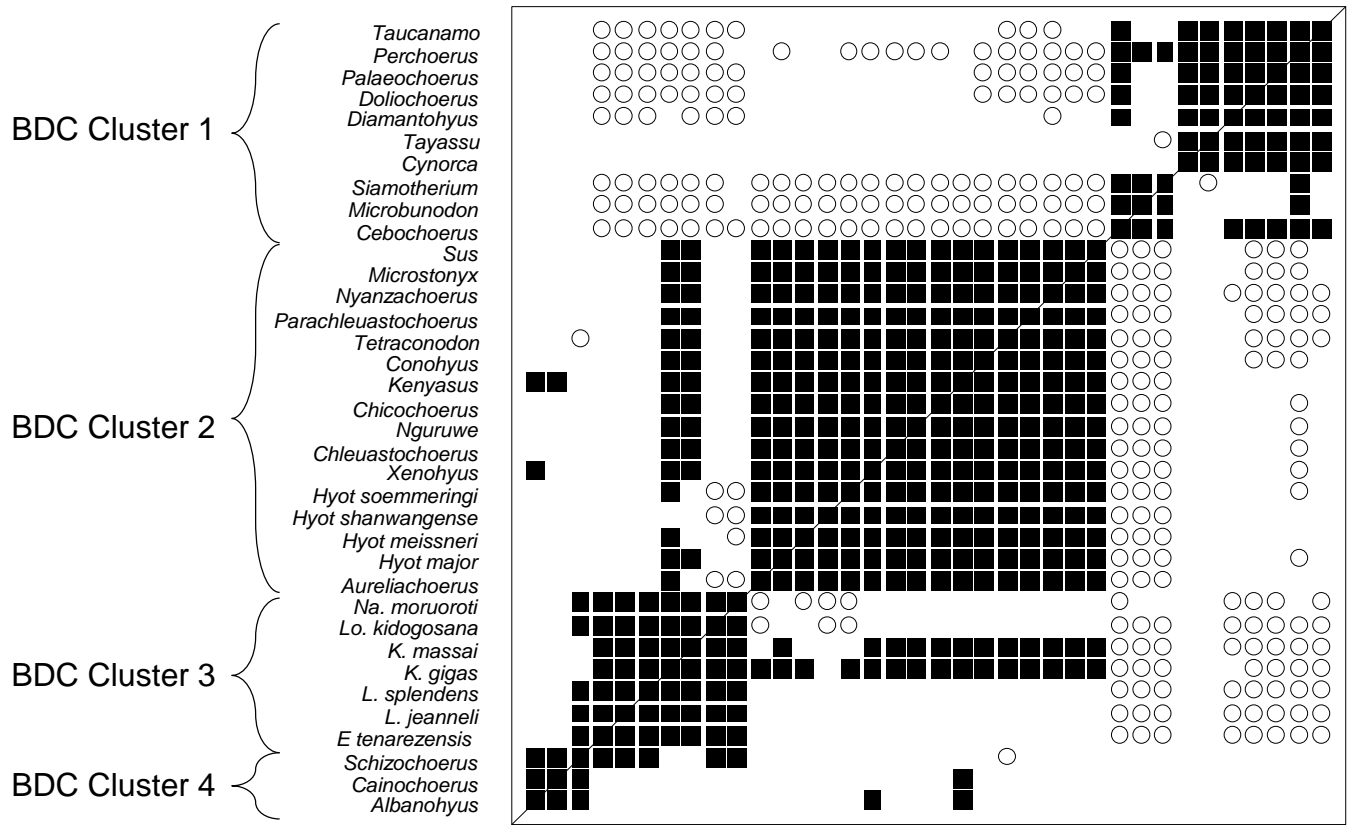
The two-cluster fuzzy partition rearranges the clusters substantially, but the average silhouette width is only 0.29. There are six taxa with negative silhouette widths. Fuzzy analysis failed at $k=4$.

These results present a partial confirmation of the original analysis. The clusters identified in the Spearman BDC and the two-cluster medoid partition correspond to the suids and the outgroup taxa. Although the two-cluster fuzzy analysis does not confirm this partition, the average silhouette width was worse (0.29 vs. 0.34). Additional uncertainty is evident in the presence of significant, positive correlation between two outgroup taxa (*Tayassu* and *Cynorca*) and five different suids of genera *Hyt* and *Aureliachoerus*. We may conclude based on these results that Suidae is a possible holobarmin.

Original conclusion: HB

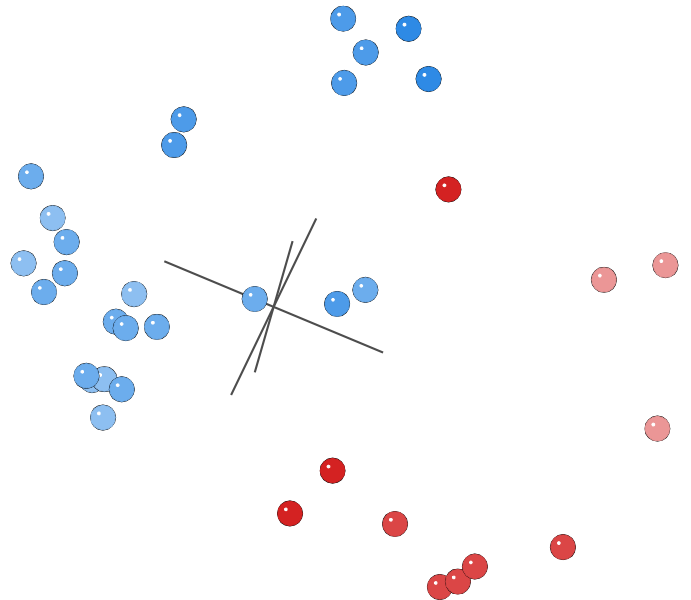
Updated conclusion: HB?

Characters: Dental

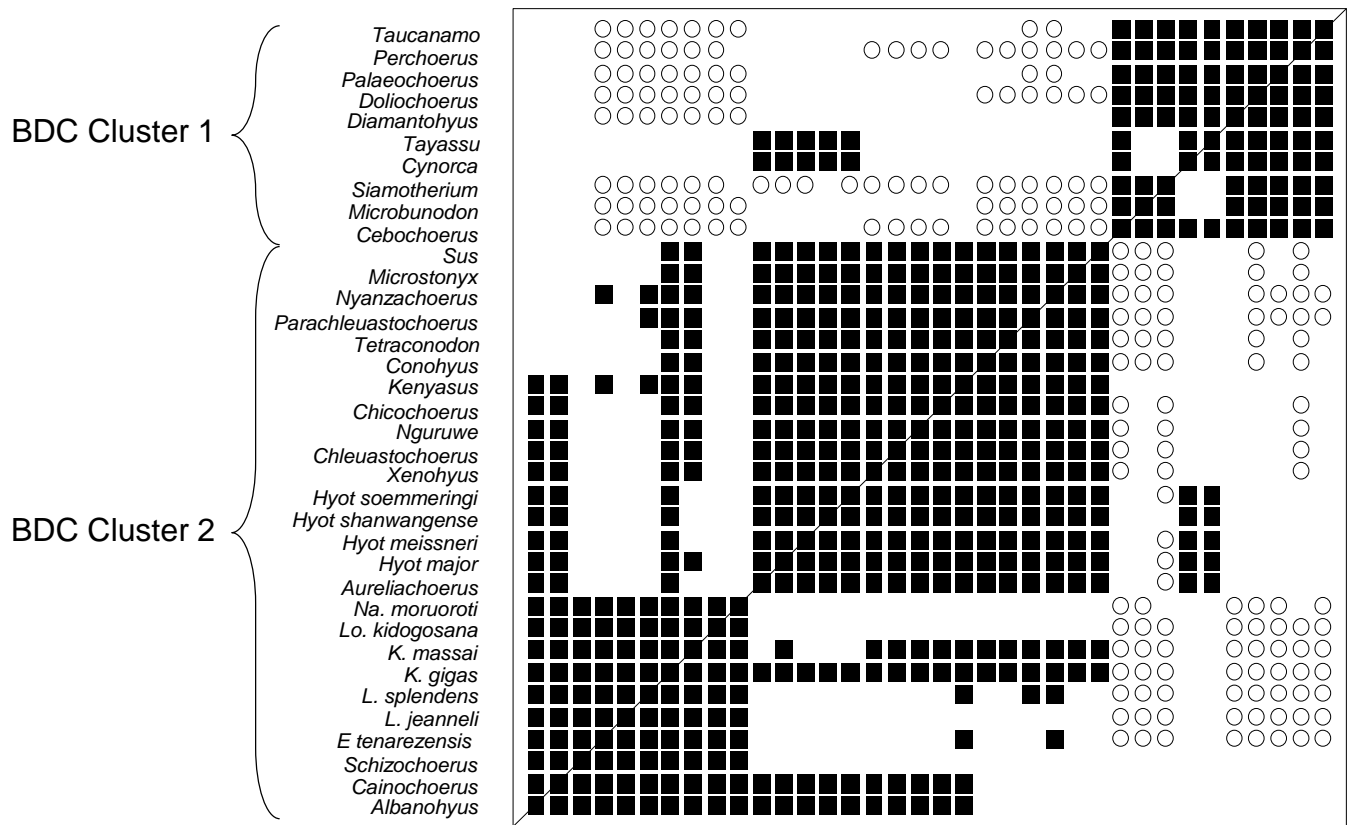


Order Artiodactyla
Family Suidae

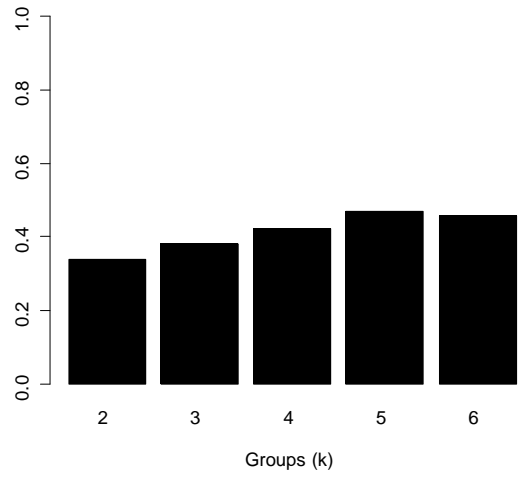
Published taxa	41
Published characters	125
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	36
Characters used for calculations	87
Median bootstrap value	79
F ₉₀	0.28
Stress of 3D MDS	0.2
k _{min}	8
Conclusion	HB



Notes: BDC supports recognizing Suidae as a holobaramin. MDS is less clear, but the suids are definitely separated from the outgroup taxa.



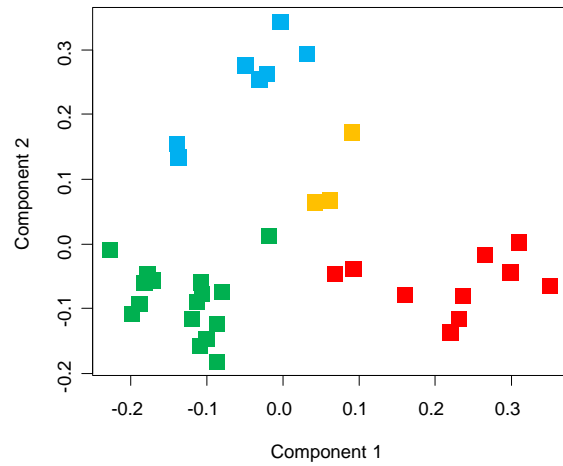
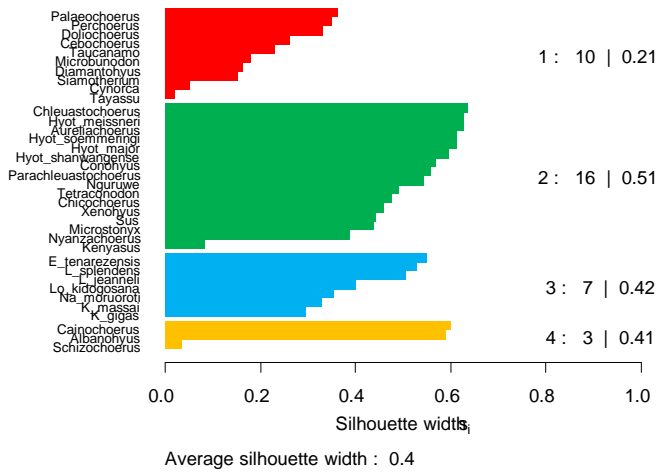
Average Silhouette Widths, Partion Around Medoids



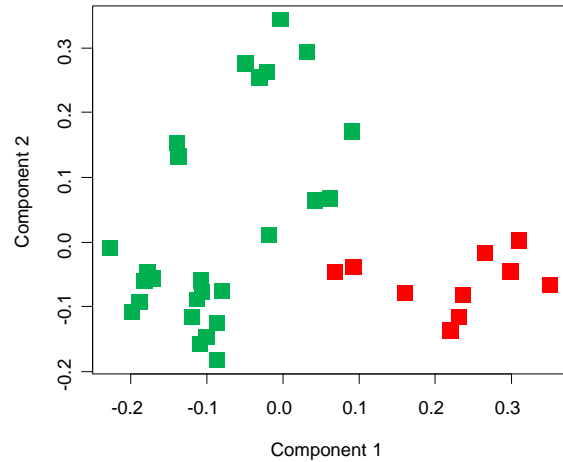
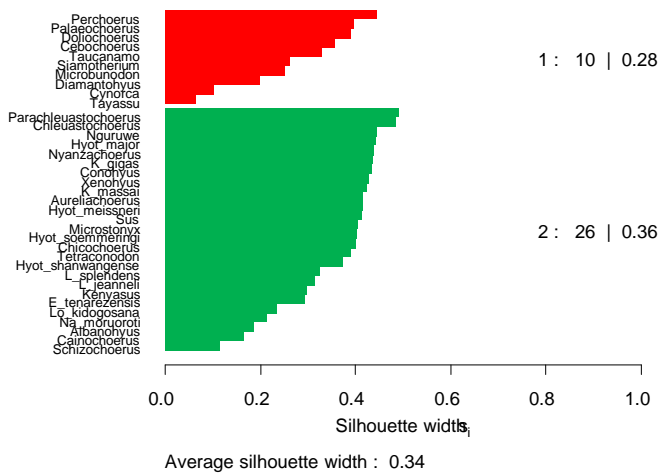
Clade Correspondence: All four clusters in the BDC results contain two or more taxa each. In the strict consensus tree shown in Figure 1 of Orliac et al. (2010), cluster 4 is polyphyletic. Cluster 3 is monophyletic. Cluster 1 is monophyletic (if the tree were drawn unrooted). Cluster 2 is paraphyletic with part of cluster 4.

Silhouette plot, BDC partitions

Pearson Correlation

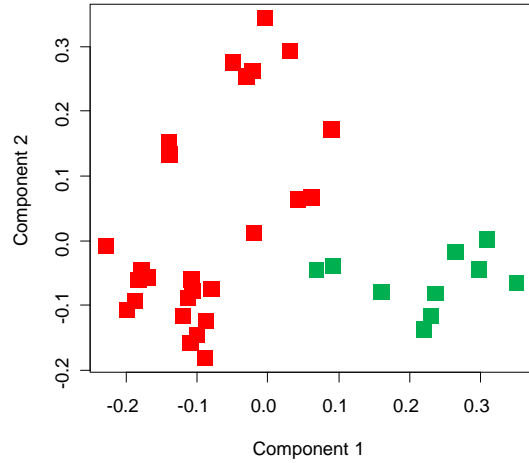
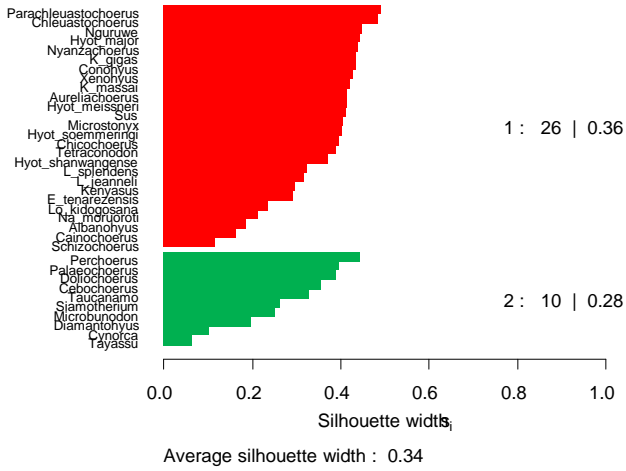


Spearman Correlation

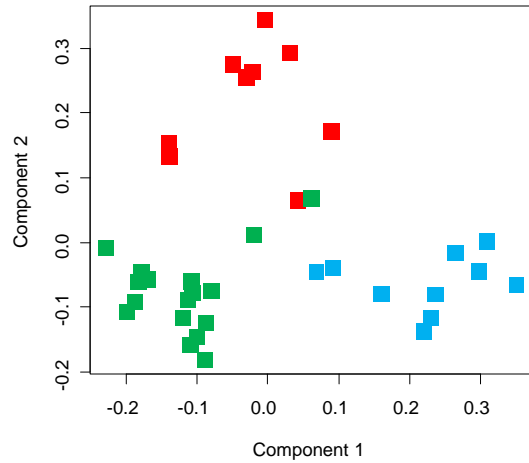
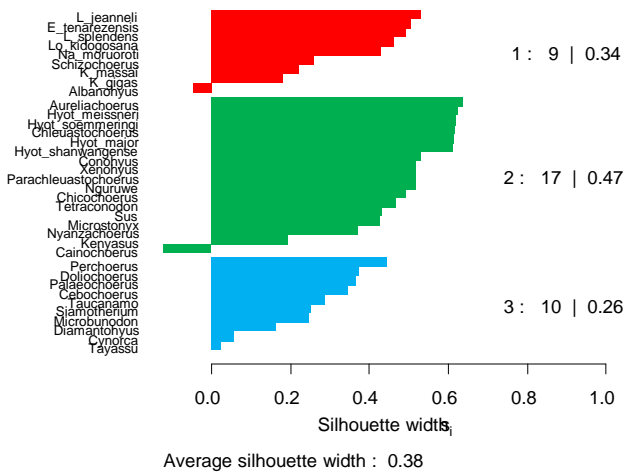


Silhouette plot, Partition Around Medoids

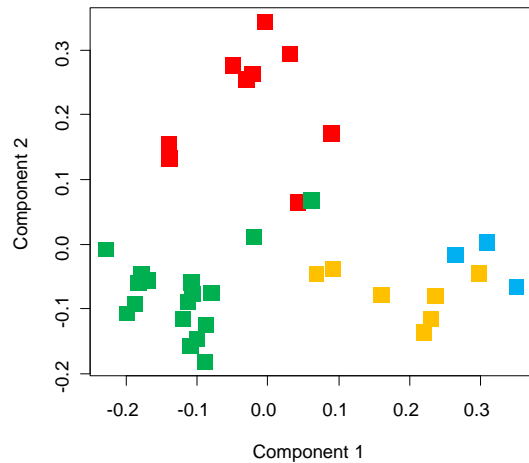
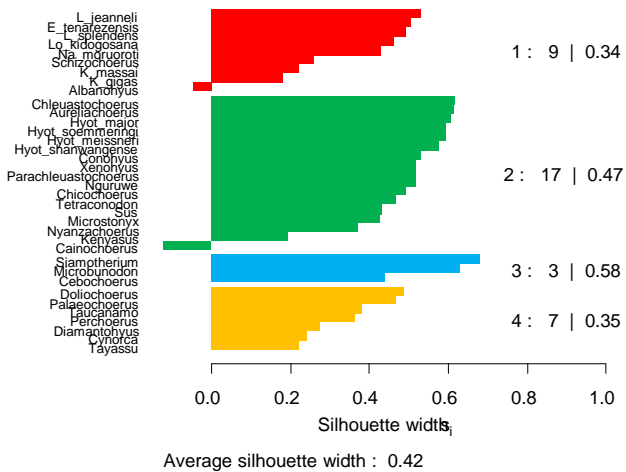
k=2



k=3

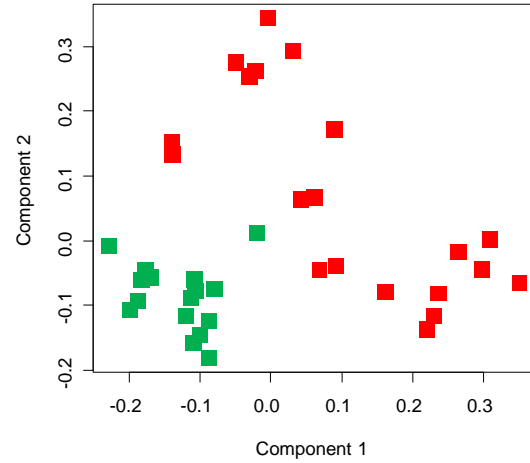
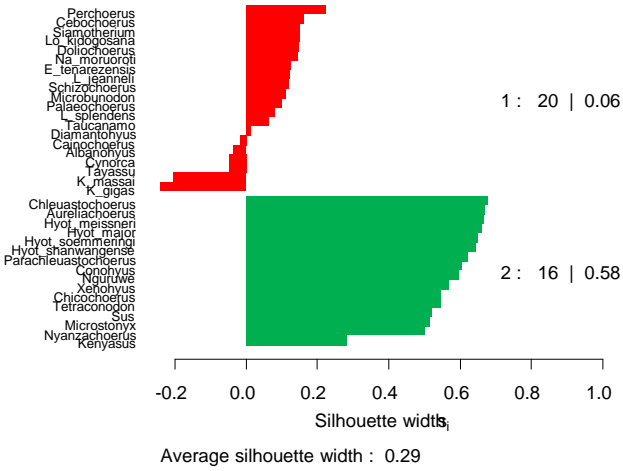


k=4

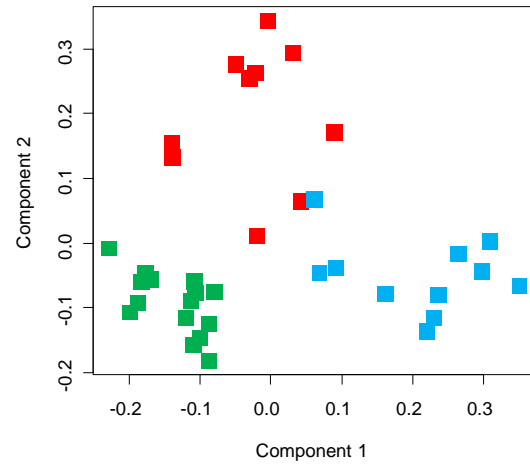
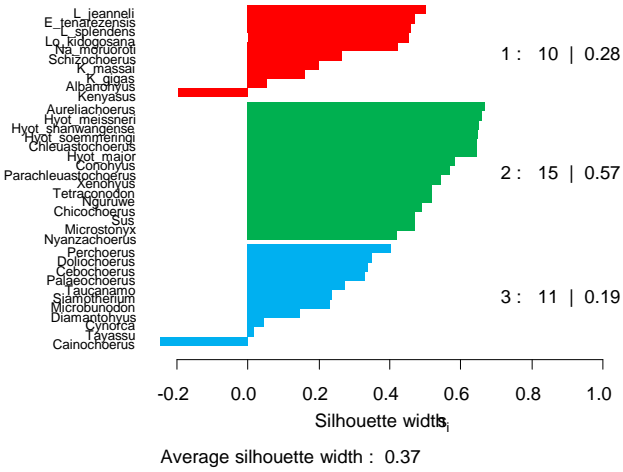


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Hippopotamidae

Order Artiodactyla
Boisserie et al. 2010

Pearson BDC
Negative: 71
Positive: 83
Clusters: 3

Clusterability
Hopkins Statistic: 0.792
Dip test: 0.013
Dip test p-value: 0.991

Spearman BDC
Negative: 84
Positive: 114
Clusters: 2

The original Pearson BDC partitioned the taxa into one ingroup cluster and two outgroup clusters. Spearman BDC added 31 instances of significant, positive correlation, resulting in the combining of the ingroup cluster with one of the outgroup clusters. The average silhouette width was 0.36 for the three-cluster Pearson BDC partition and 0.33 for the two-cluster Spearman BDC partition. The cluster membership difference was 29%.

The two-cluster medoid partition is identical to the Spearman BDC clusters. The three-cluster medoid partition differs from the Pearson BDC clusters by two taxa, which gives a cluster membership difference of only 8%. The three-cluster medoid partition has an average silhouette width of 0.37.

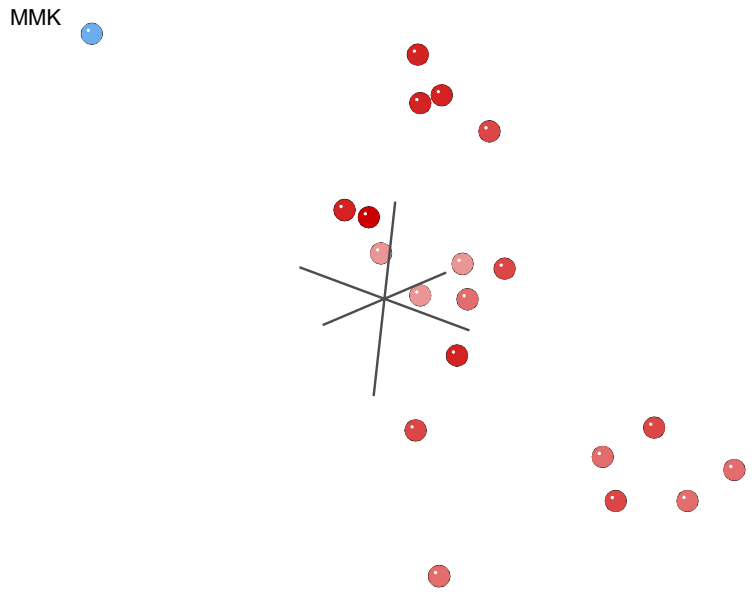
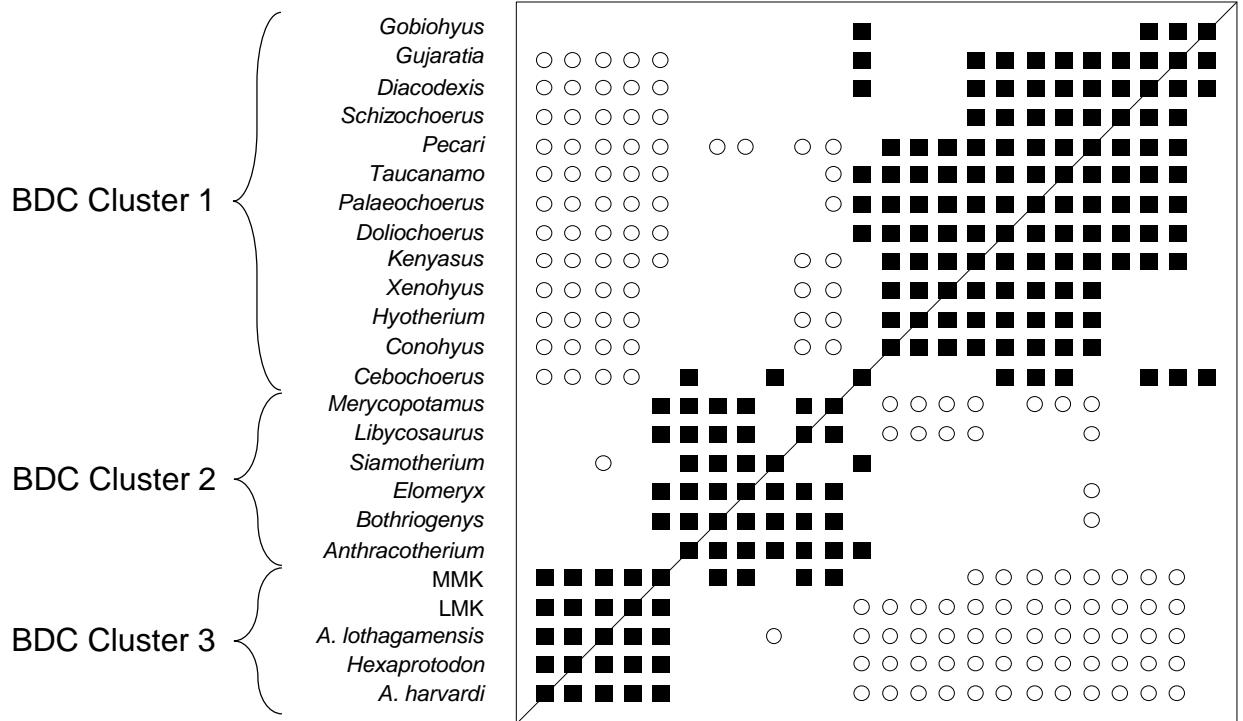
Fuzzy analysis at $k=3$ matches the three-cluster medoid partition exactly. The two-cluster fuzzy partition has an average silhouette width of 0.34 and differs from the Spearman BDC clusters by only two taxa.

Based on the original results, the cluster of five hippopotamids was classified as a tentative holobaramin, based in part on a lack of significant, negative correlation with other members the superfamily Hippopotamoidea. Here we find that this holobaramin might also include the taxa of the superfamily Hippopotamoidea. The Spearman BDC and two-cluster medoid partition support this. Fuzzy analysis generally agrees but raises the possibility that two hippopotamoids, *Gobiohyus* and *Cebochoerus*, might not belong to this holobaramin. These results therefore support an expanded holobaramin with questions remaining about some of the taxa.

Original conclusion: HB?
Updated conclusion: HB?

Boisserie, J.R., F. Lihoreau, M. Orliac, R.E. Fisher, E.M. Weston, and S. Ducrocq. 2010. Morphology and phylogenetic relationships of the earliest known hippopotamids (Cetartiodactyla, Hippopotamidae, Kenyapotaminae). *Zoological Journal of the Linnean Society* 158:325-366.

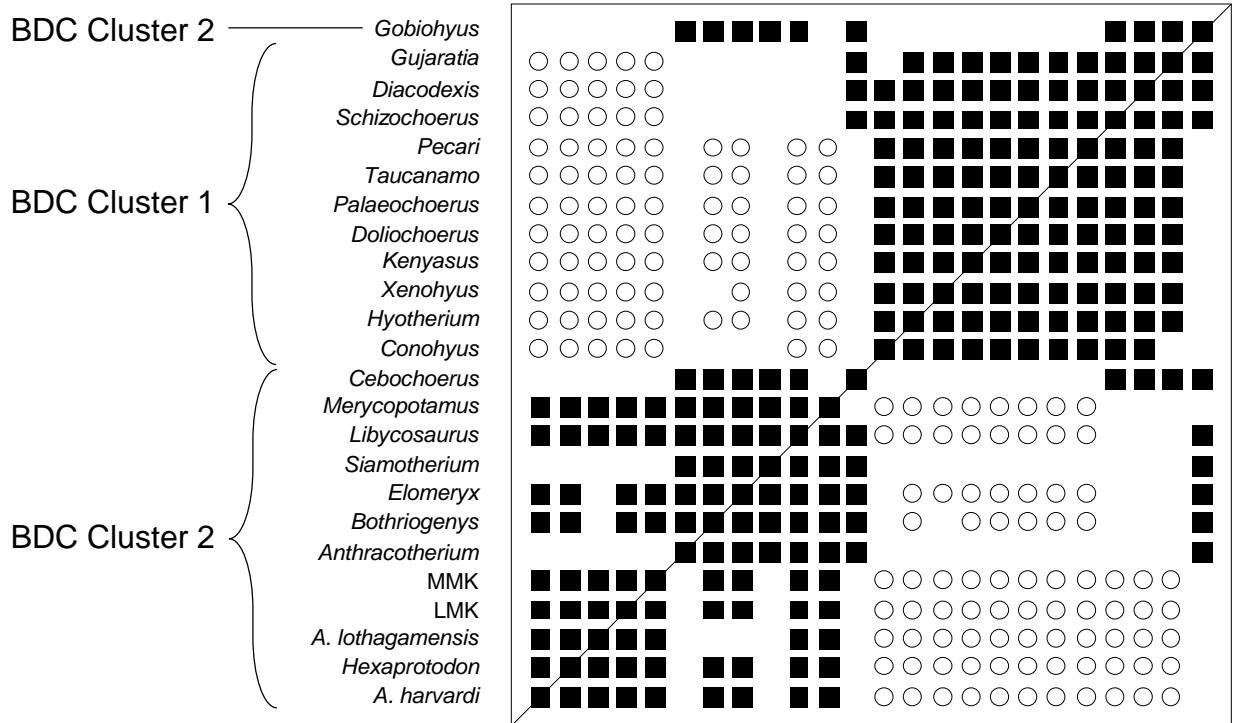
Characters: Craniodental and postcranial



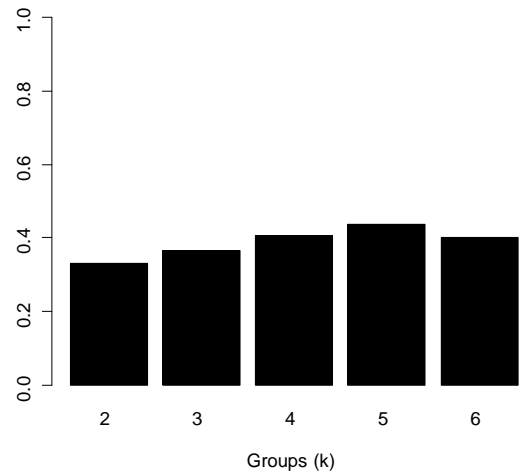
Order Artiodactyla
Family Hippopotamidae

Published taxa	24
Published characters	87
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	24
Characters used for calculations	81
Median bootstrap value	84
F ₉₀	0.38
Stress of 3D MDS	0.16
k _{min}	7
Conclusion	HB?

Notes: Both MDS and BDC reveal a distinct cluster of hippopotamids separate from other taxa. In the BDC results, the composite taxon “Middle Miocene Kenyapotamines” (MMK) shares significant, positive BDC with four outgroup taxa, but the correlations all have low bootstrap values. The MDS results reveal MMK well separated from the outgroup taxa. Thus, Hippopotamidae is probably a holobaramin.



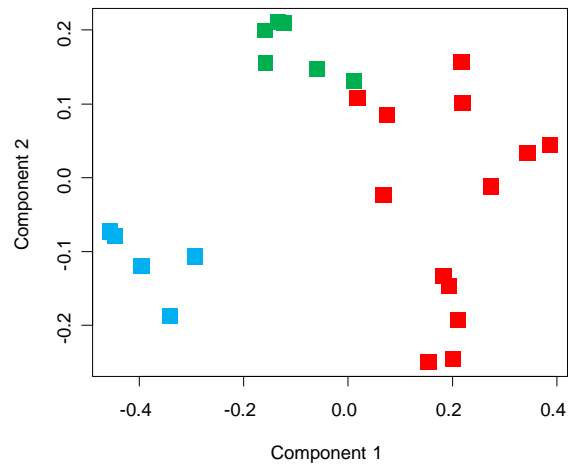
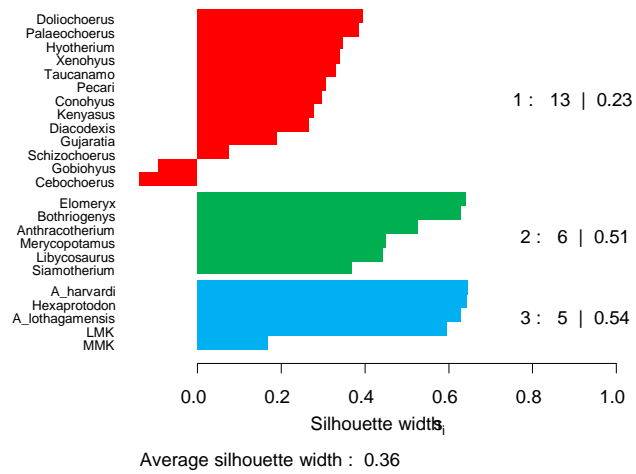
Average Silhouette Widths, Partion Around Medoids



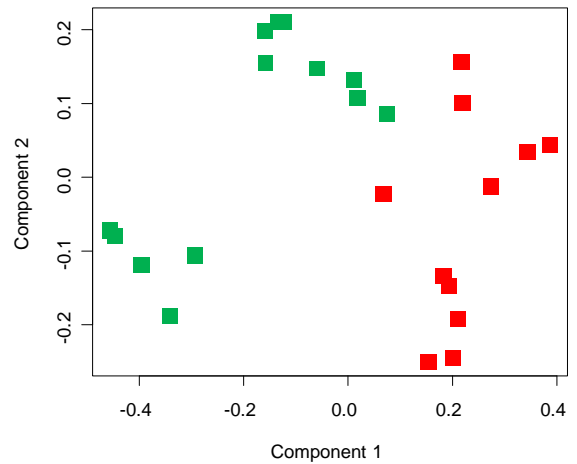
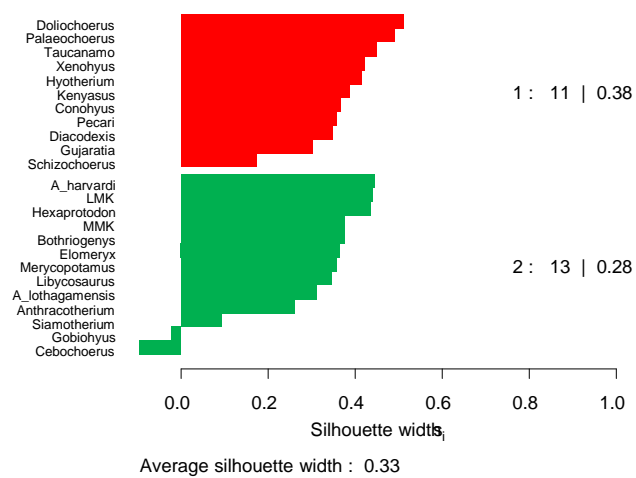
Clade Correspondence: The BDC results reveal three large clusters of at least five taxa or more. In the strict consensus tree shown in Figure 9 of Boisserie et al. (2009), clusters 3 and 1 are monophyletic, if the tree were drawn unrooted. Cluster 2 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

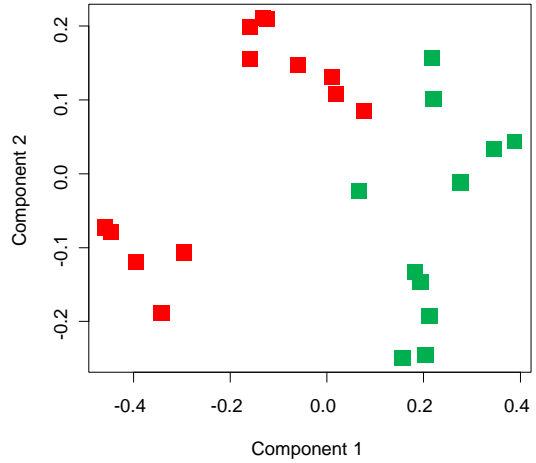
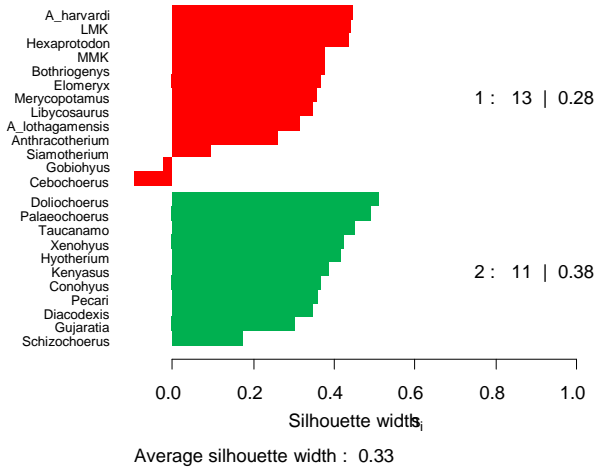


Spearman Correlation

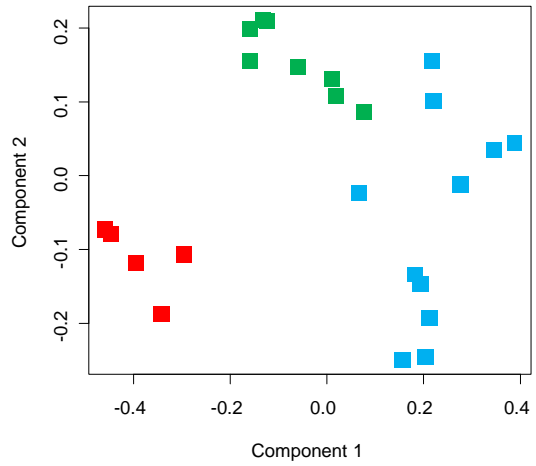
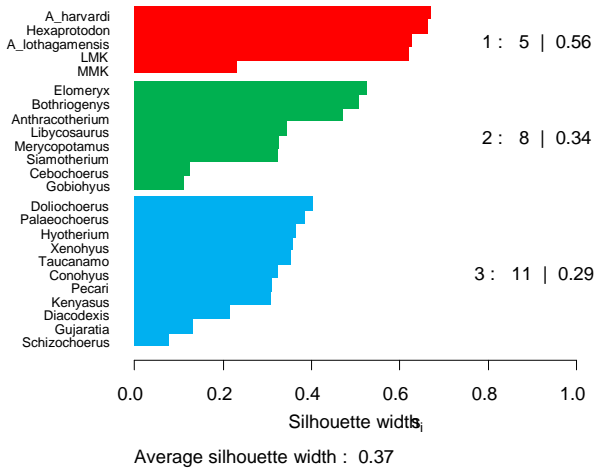


Silhouette plot, Partition Around Medoids

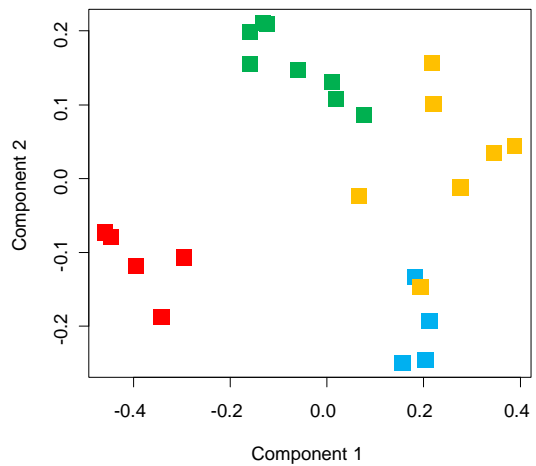
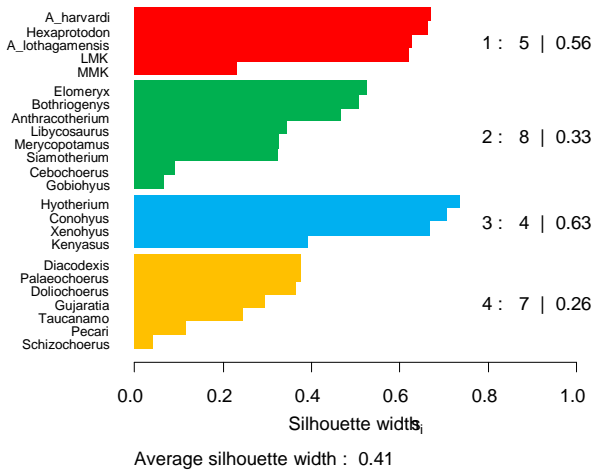
k=2



k=3

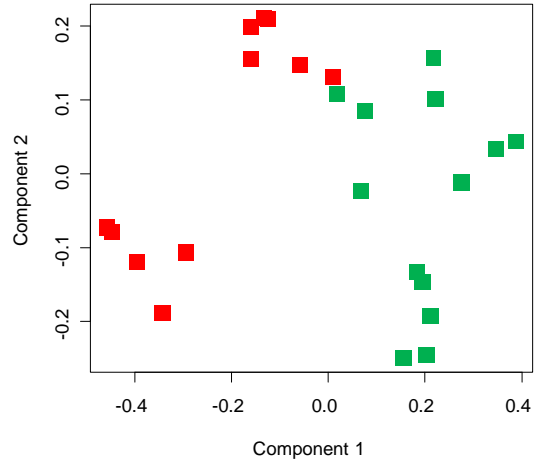
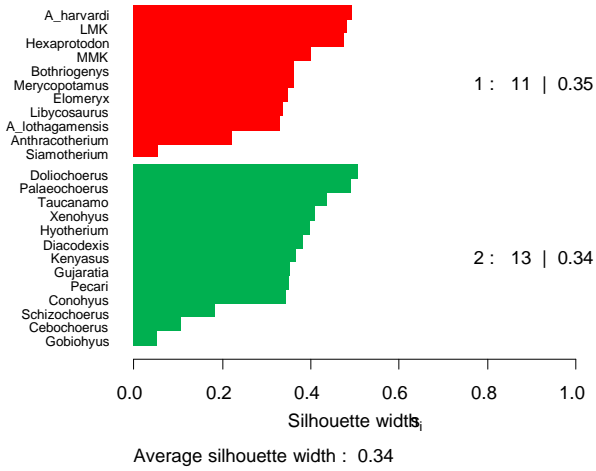


k=4

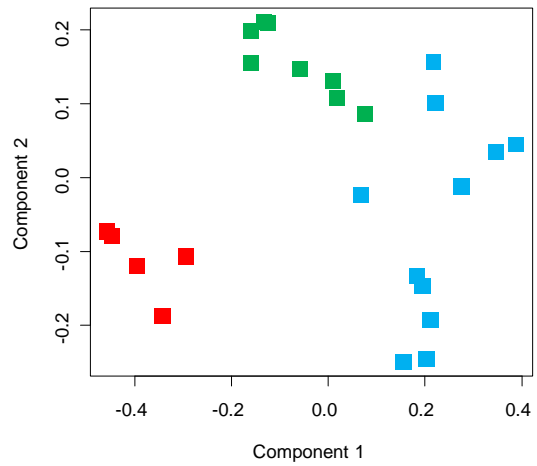
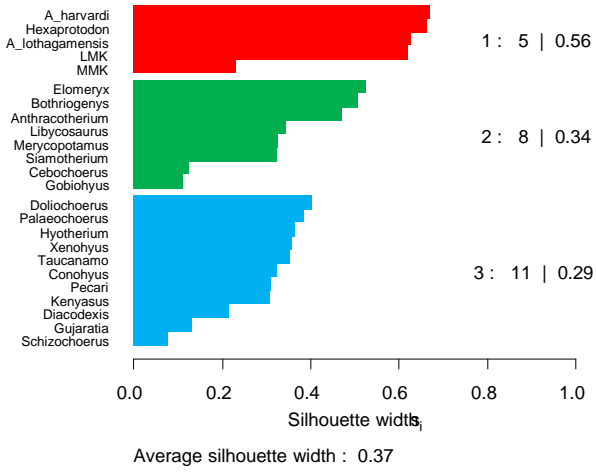


Silhouette plot, Fuzzy Analysis

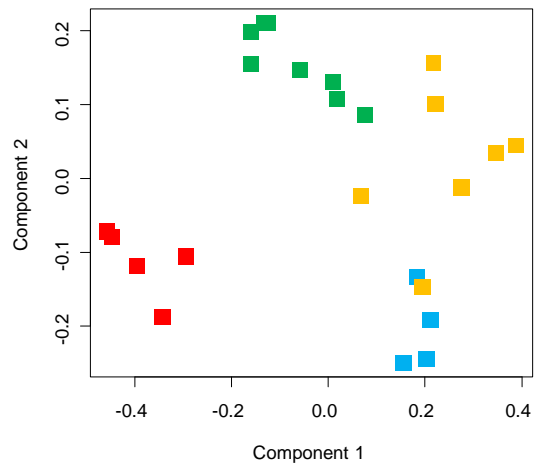
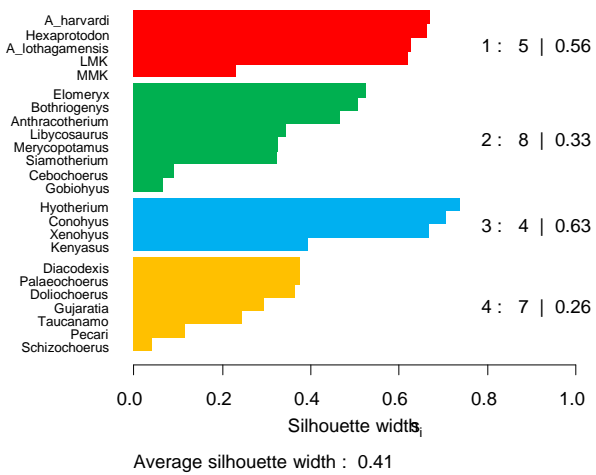
k=2



k=3



k=4



Family Anthracotheriidae

Order Artiodactyla

Rincon et al. 2013

Pearson BDC

Negative: 101

Positive: 136

Clusters: 2

Spearman BDC

Negative: 102

Positive: 164

Clusters: 2

Clusterability

Hopkins Statistic: 0.853

Dip test: 0.019

Dip test p-value: 0.391

Spearman BDC adds 28 instances of significant, positive correlation to the Pearson BDC, but the clustering partition remains the same. There are two groups of taxa that are separated by more than 100 instances of significant, negative BDC in both the Spearman and Pearson results. The average silhouette width for this partition is 0.39.

The two-cluster medoid partition has an average silhouette width of 0.34 and differs from the BDC clusters by three taxa (cluster membership difference: 14%). The two-cluster fuzzy partition matches the BDC clusters exactly.

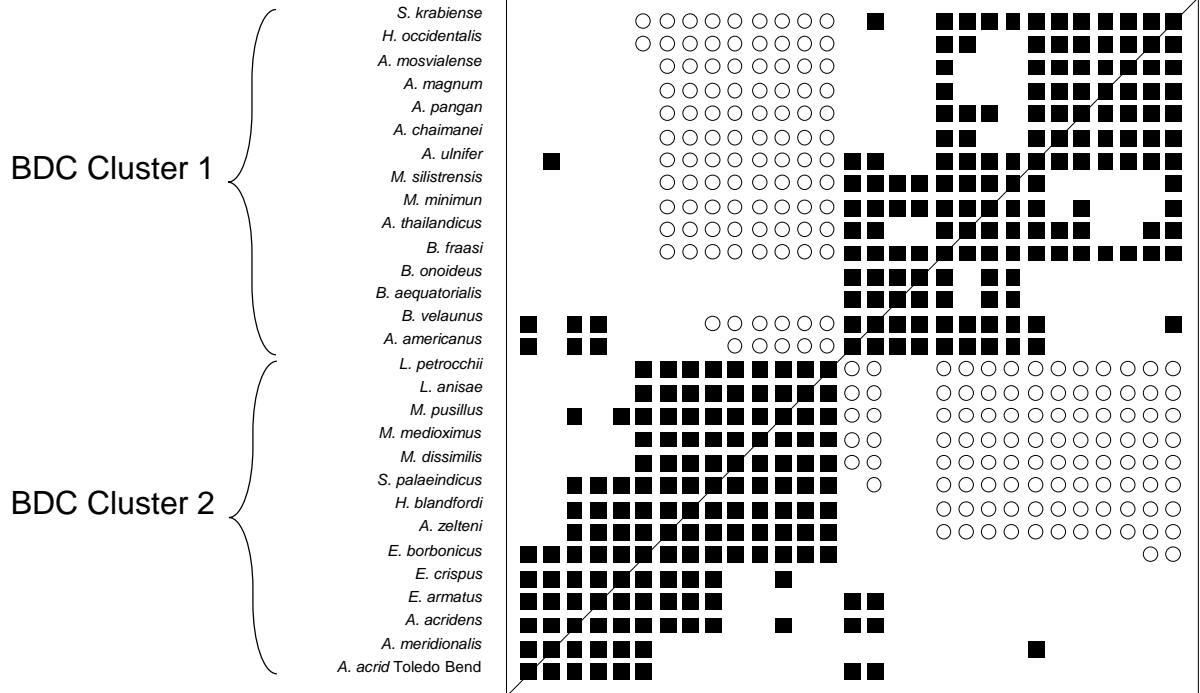
Despite what appears to be good evidence of discontinuity, the original judgment was that these results were inconclusive because there was no evidence of discontinuity. In 3D multidimensional scaling, we find that the taxa form two lines that are approximately orthogonal, resulting in an irregular tetrahedral shape. These shapes are known for producing spurious clustering patterns. These results do not change that original judgment.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

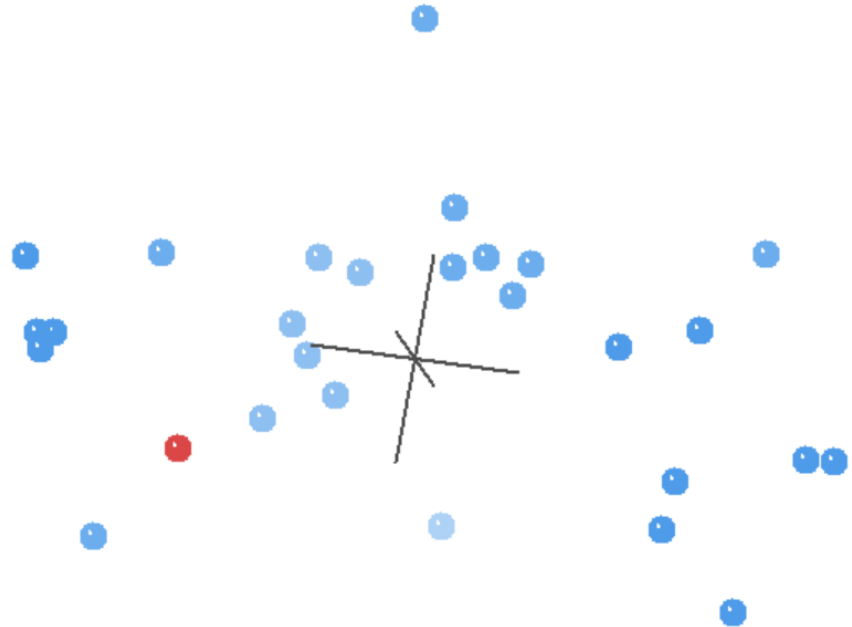
Rincon, A.F., J.I. Bloch, B.J. MacFadden, and C.A. Jaramillo. 2013. First central American record of Anthracotheriidae (Mammalia, Bothriodontinae) from the early Miocene of Panama. *Journal of Vertebrate Paleontology* 33:421-433.

Characters: Craniodental

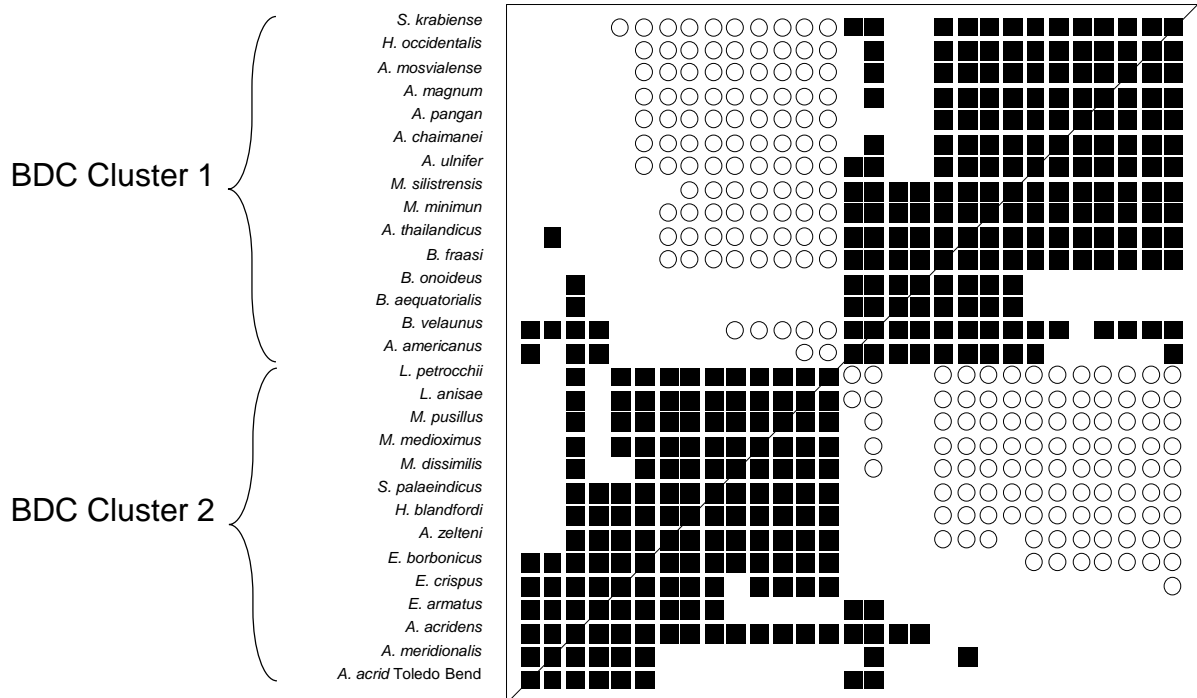


Order Artiodactyla
Family Anthracotheriidae

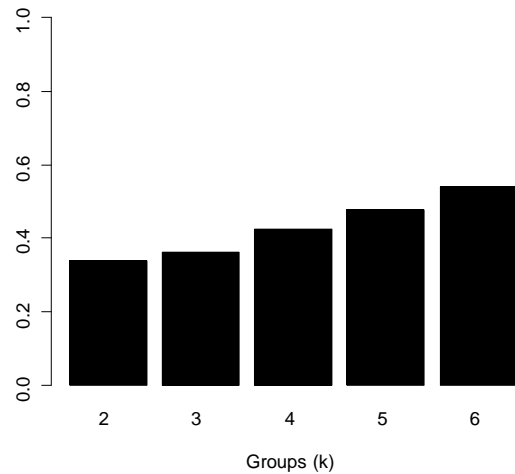
Published taxa	29
Published characters	51
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	29
Characters used for calculations	41
Median bootstrap value	73
F ₉₀	0.28
Stress of 3D MDS	0.15
k _{min}	4
Conclusion	Inc



Notes: No evidence of discontinuity.



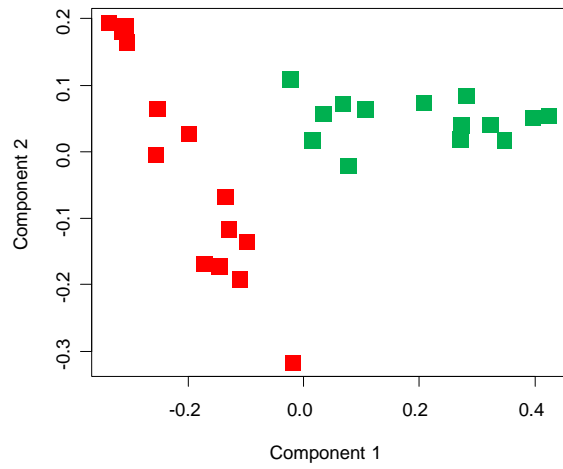
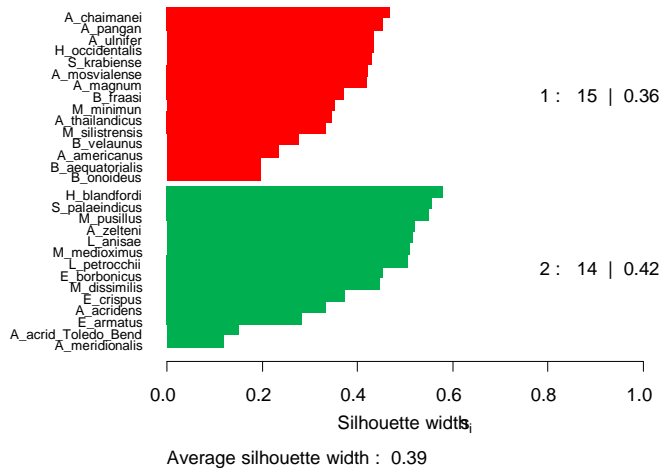
Average Silhouette Widths, Partion Around Medoids



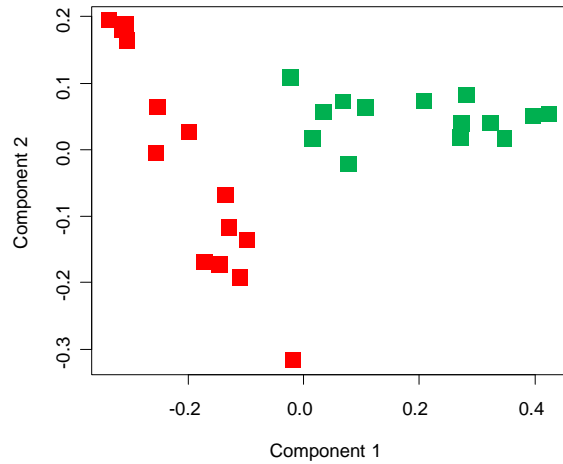
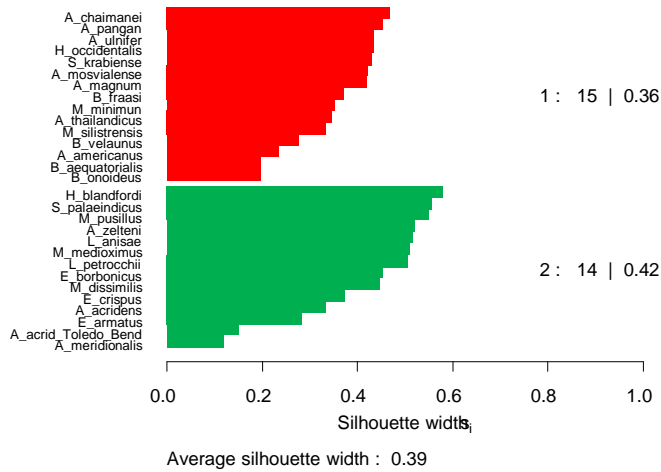
Clade Correspondence: Both BDC clusters contain more than one taxon each. In the phylogenetic tree shown in Figure 7 of Rincon et al. (2013), both clusters appear as clades if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

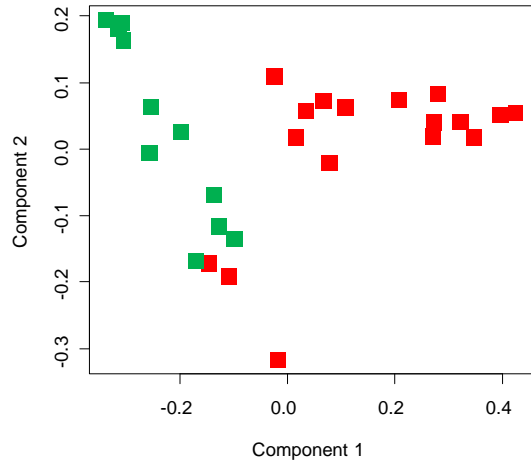
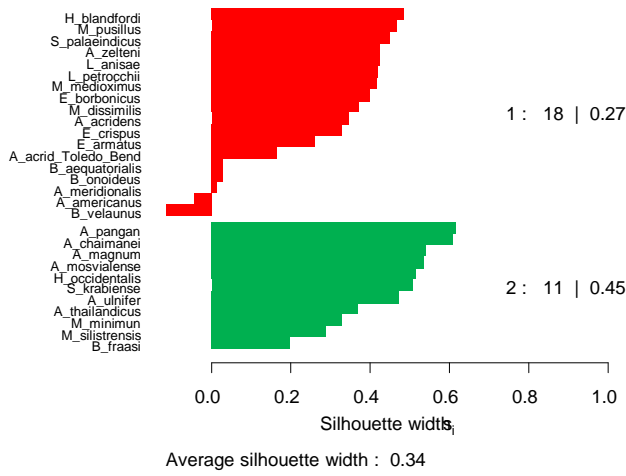


Spearman Correlation

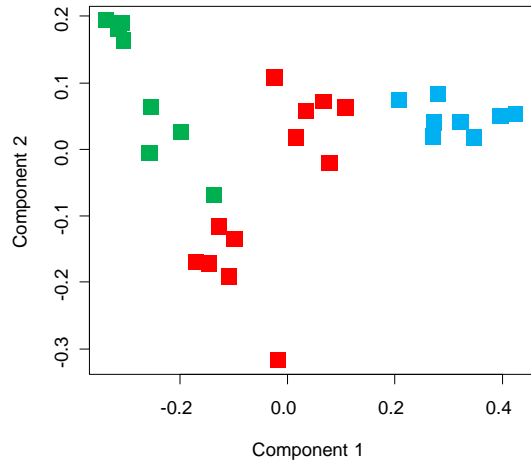
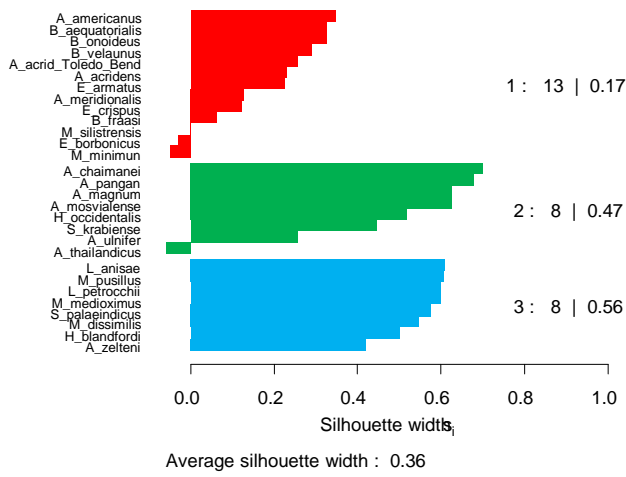


Silhouette plot, Partition Around Medoids

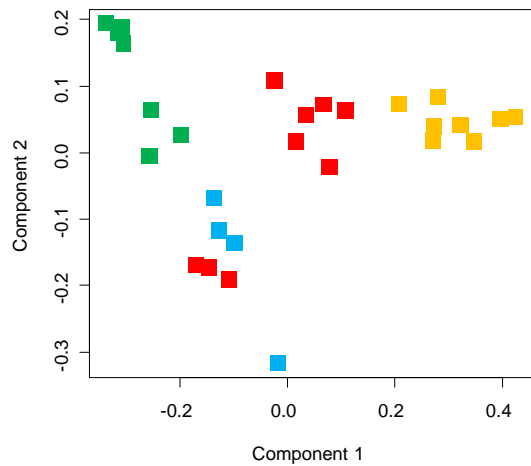
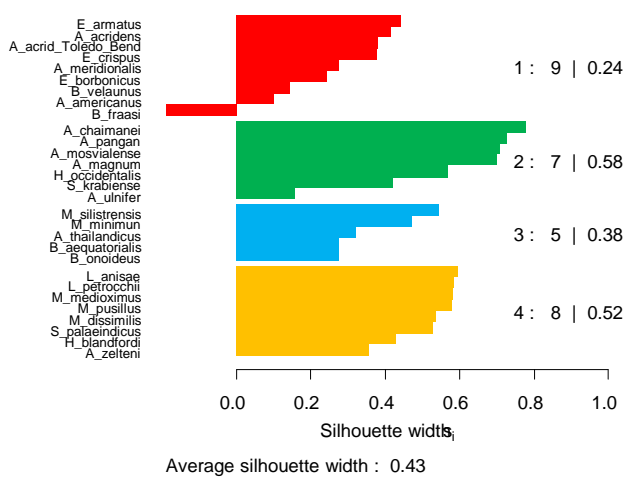
k=2



k=3

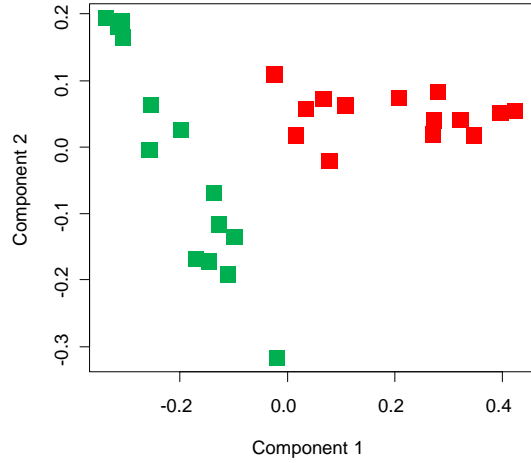
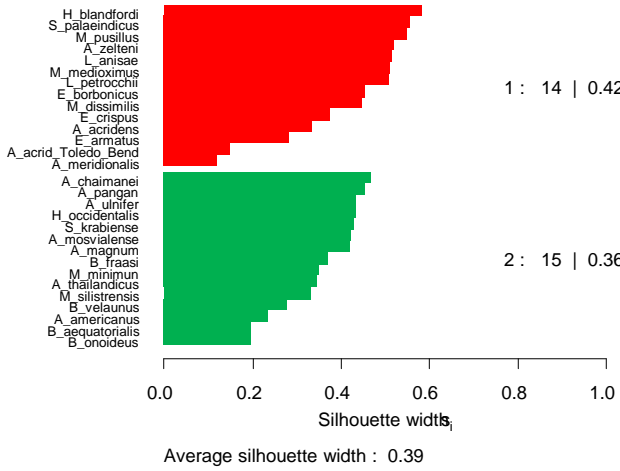


k=4

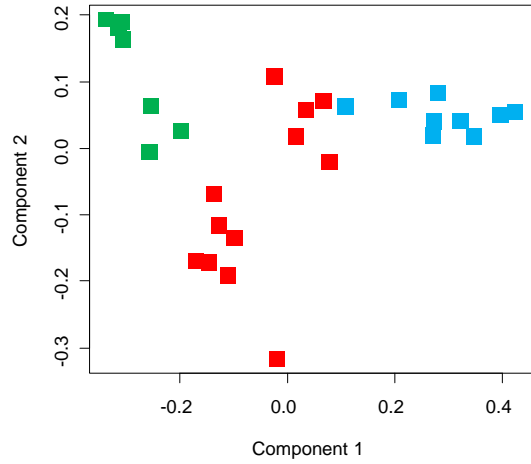
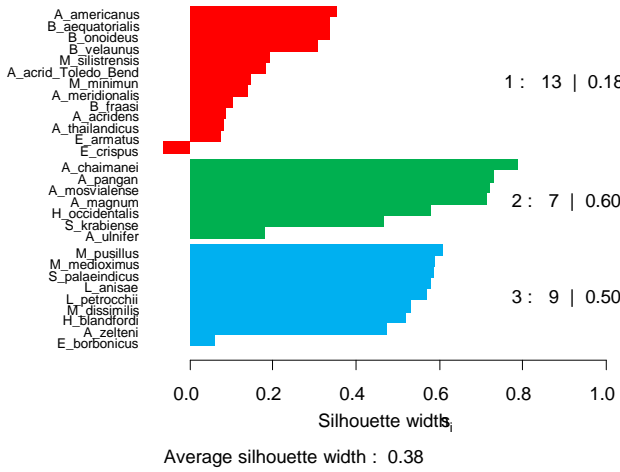


Silhouette plot, Fuzzy Analysis

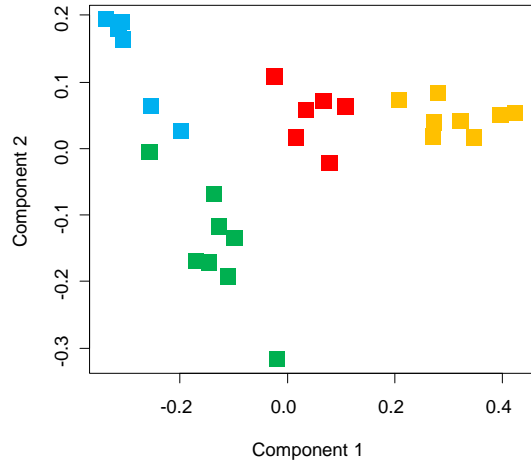
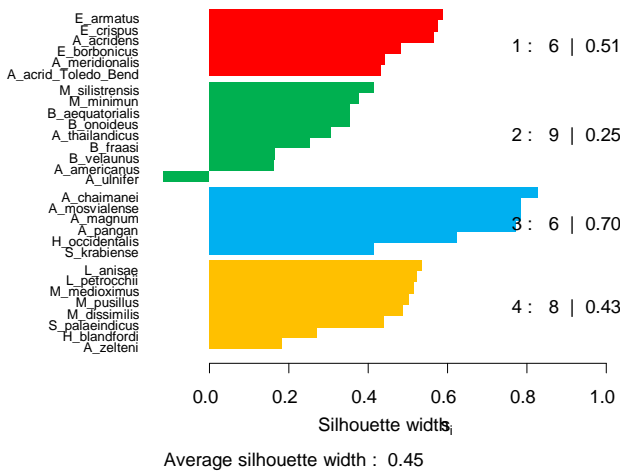
k=2



k=3



k=4



Family Camelidae

Order Artiodactyla

Scherer 2013

Pearson BDC

Negative: 66

Positive: 127

Clusters: 3

Spearman BDC

Negative: 55

Positive: 133

Clusters: 3

Clusterability

Hopkins Statistic: 0.843

Dip test: 0.026

Dip test p-value: 0.175

The Spearman BDC reveals only six additional instances of significant, positive correlation, thus resulting in the same cluster partition as in the Pearson BDC results. The three BDC clusters have an average silhouette width of 0.52.

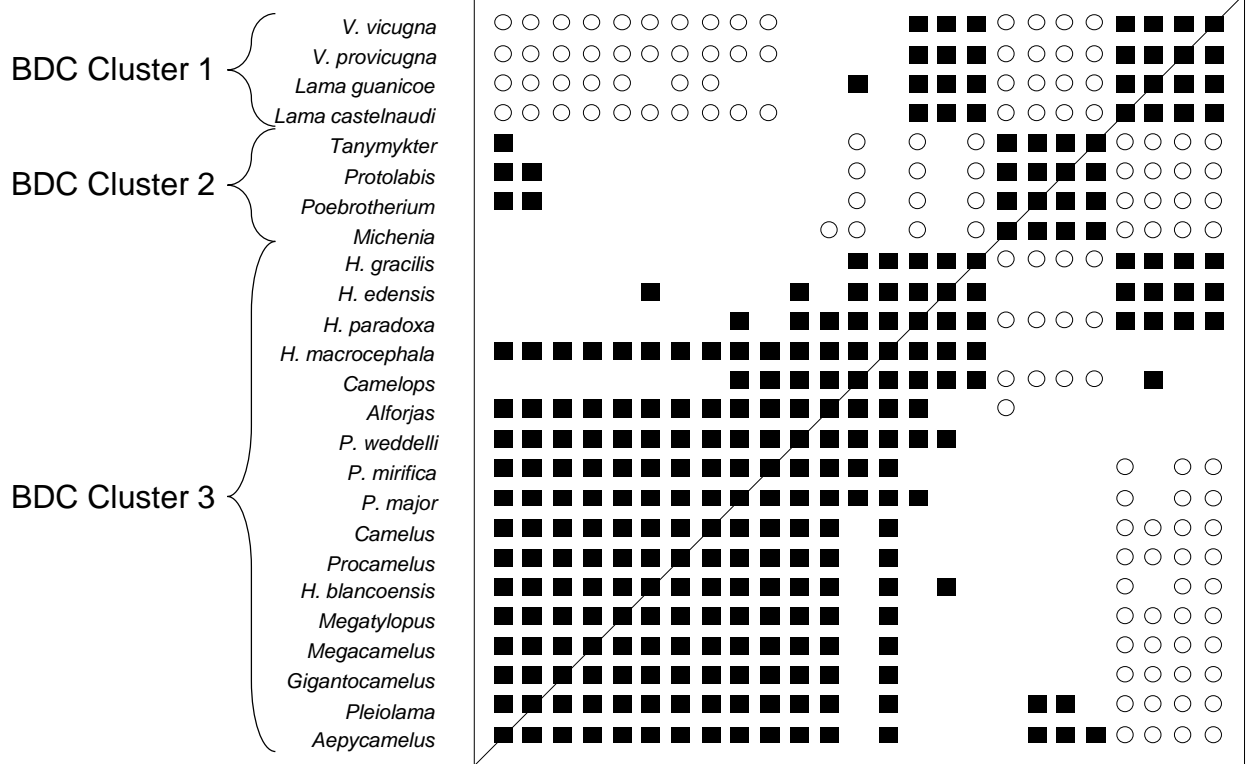
The three-cluster medoid partition has an average silhouette width of 0.52 and agrees only moderately with the BDC clusters (cluster membership difference: 28%). Similarly, the three-cluster fuzzy partition has an average silhouette width of 0.54 but matches the BDC clusters slightly better (cluster membership difference: 16%).

The original judgment was that the camelids formed a holobaramin that was discontinuous with basal members *Tanymycter*, *Protolabis*, *Poebrotherium*, and *Michenia*. There is limited evidence that that may in fact be the correct conclusion. These four taxa form a cluster in every medoid partition tested (k=2, 3, 4) and in the fuzzy analyses for k=3 and k=4. The two-cluster fuzzy partition does not support the division between basal camelids and the rest of the camels. Given the lack of consistency in these results, we are justified in refraining from a definite conclusion at this time.

Original conclusion: HB?

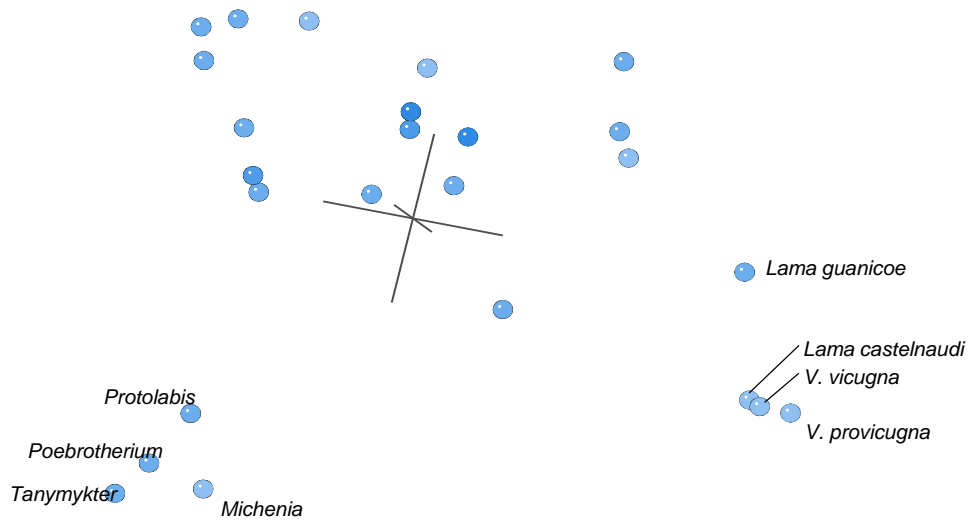
Updated conclusion: Inconclusive

Characters: Craniodental and postcranial

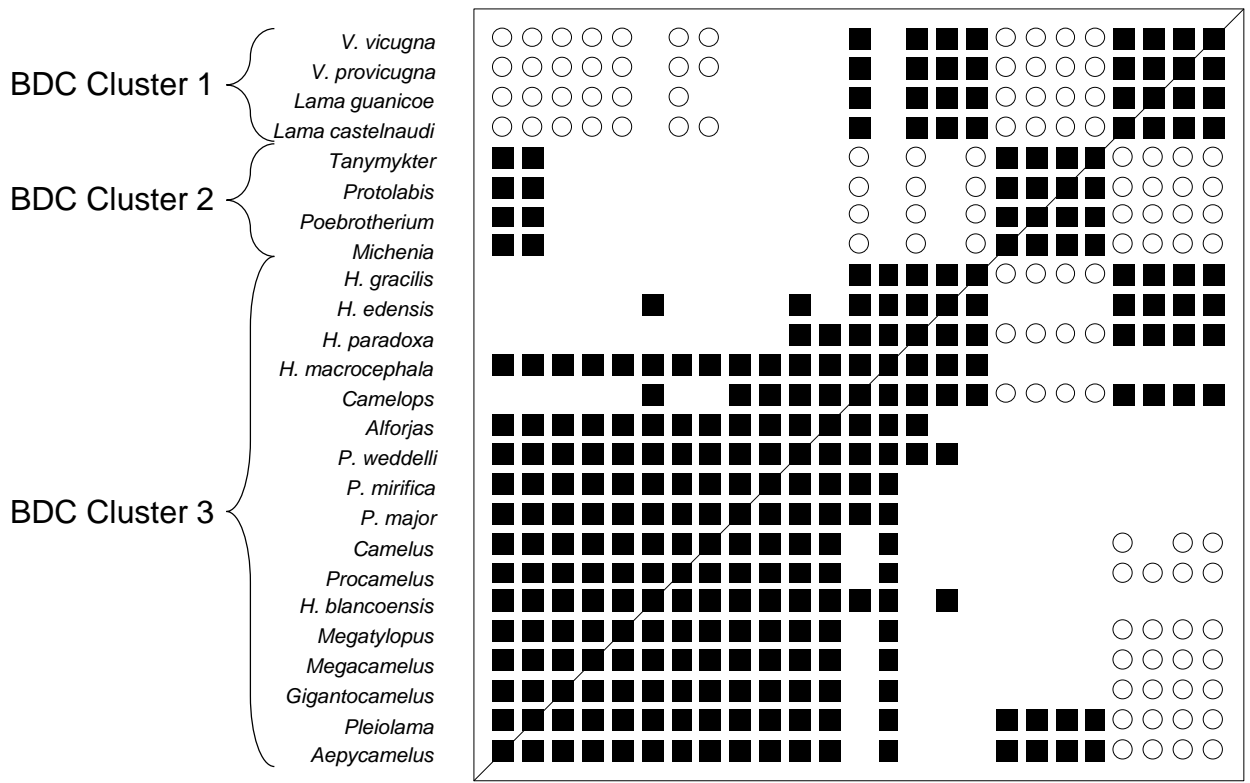


Order Artiodactyla
Family Camelidae

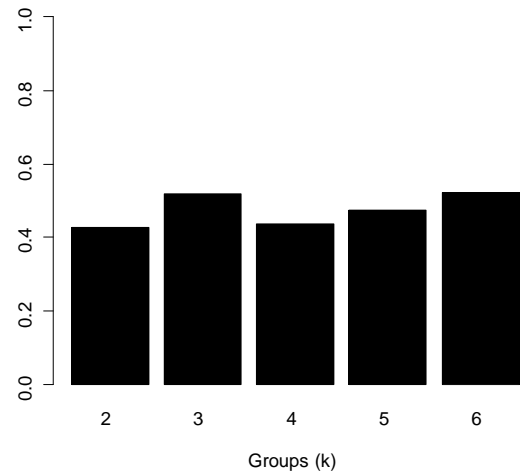
Published taxa	25
Published characters	35
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	25
Characters used for calculations	25
Median bootstrap value	71
F ₉₀	0.23
Stress of 3D MDS	0.14
k _{min}	3
Conclusion	HB?



Notes: Somewhat ambiguous BDC, with significant, negative BDC between basal camelids *Protolabis*, *Poebrotherium*, *Tanymykteer*, and *Michenia* and the rest of the camelids. MDS reveals clearer evidence of discontinuity, suggesting provisionally that Camelidae *sensu stricto* (excluding basal camelids) is a holobaramin.



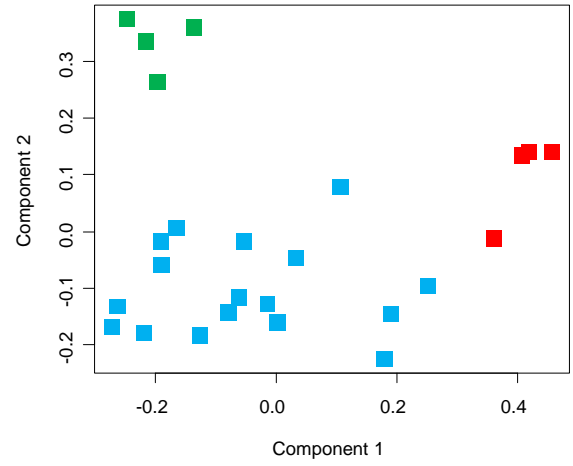
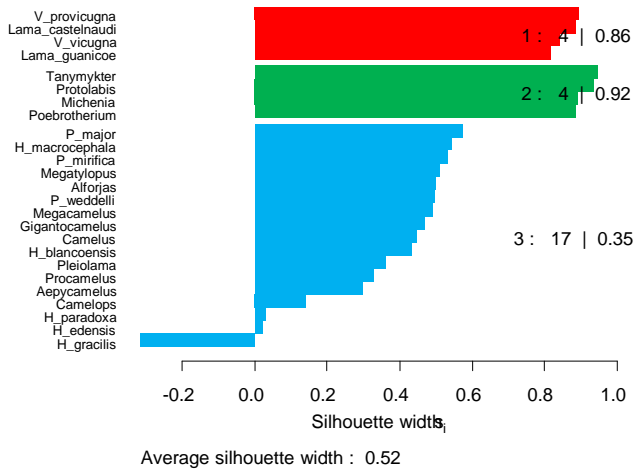
Average Silhouette Widths, Partion Around Medoids



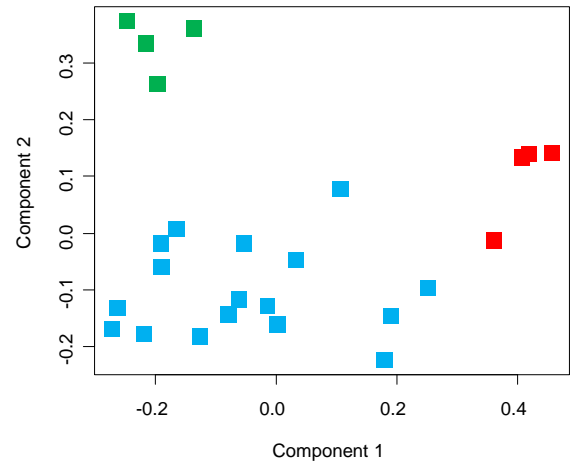
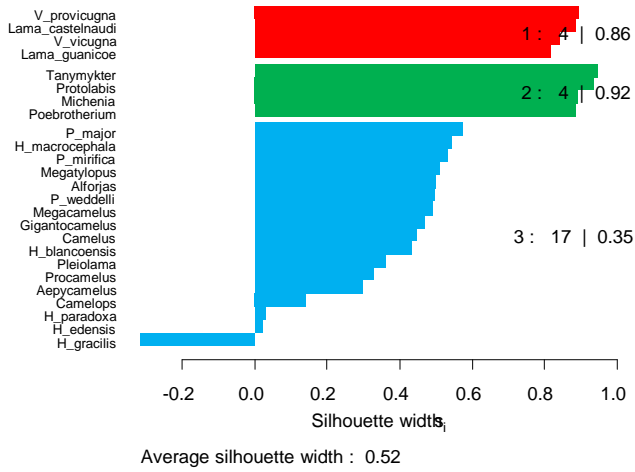
Clade Correspondence: All three BDC clusters contain at least two taxa each. In the phylogeny in Figure 1 of Scherer (2013), clusters 1 and 2 are monophyletic if the tree were drawn unrooted, but cluster 3 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

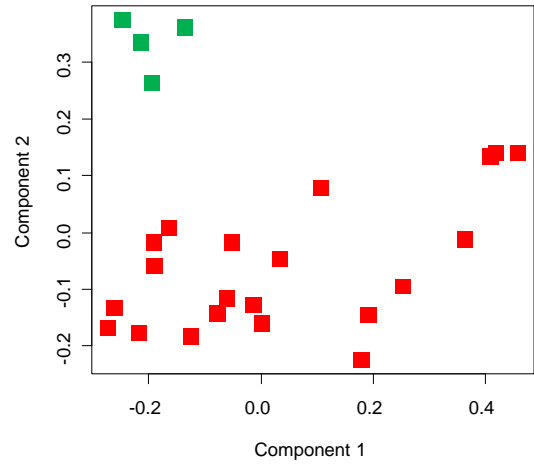
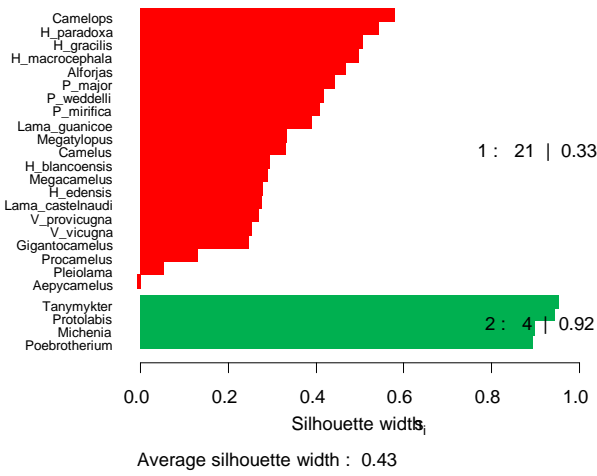


Spearman Correlation

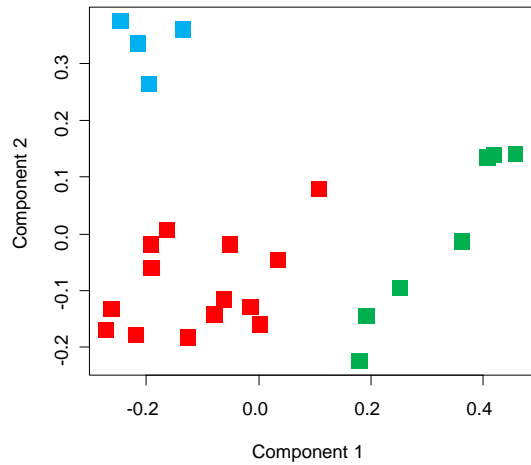
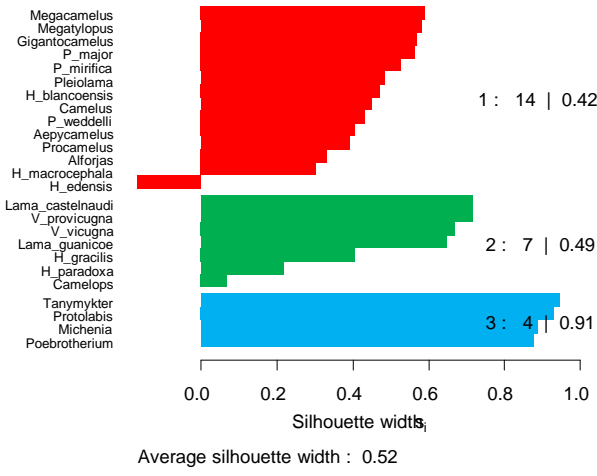


Silhouette plot, Partition Around Medoids

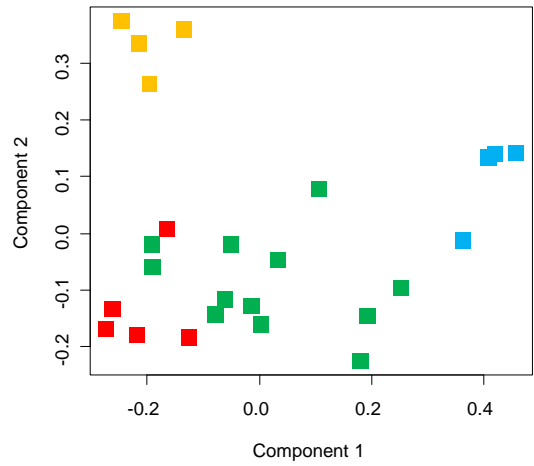
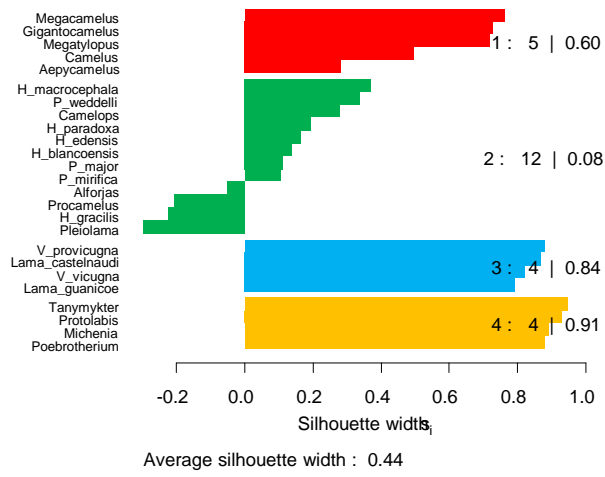
k=2



k=3

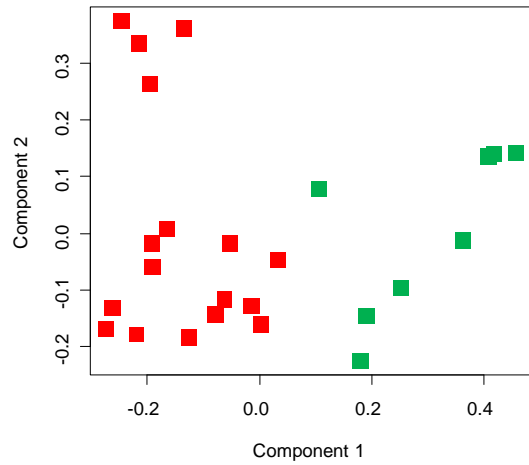
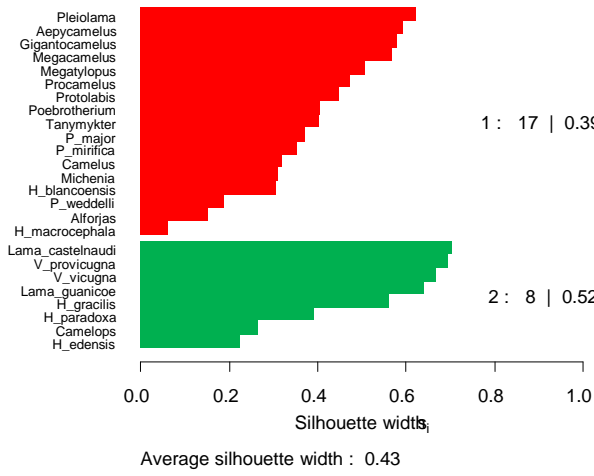


k=4

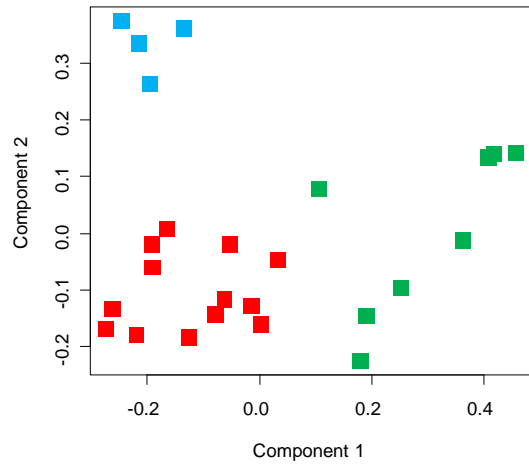
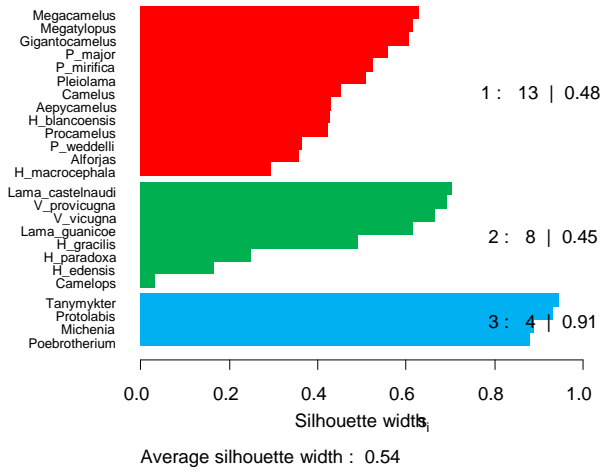


Silhouette plot, Fuzzy Analysis

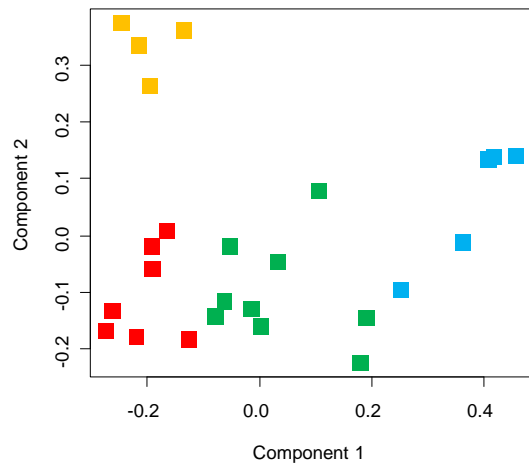
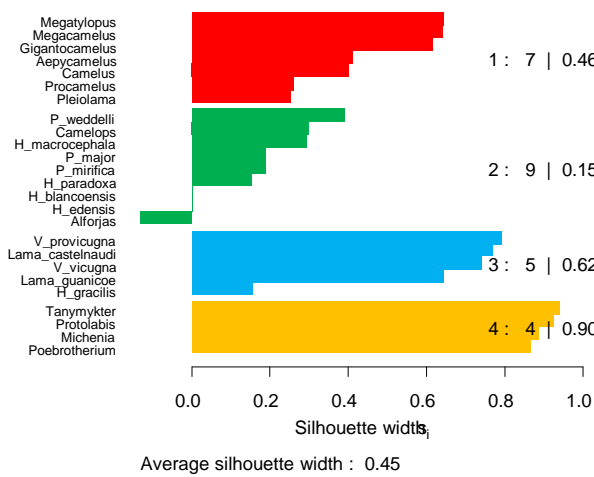
k=2



k=3



k=4



Family Moschidae

Order Artiodactyla

Sanchez et al. 2010

Pearson BDC

Negative: 4

Positive: 13

Clusters: 3

Clusterability

Hopkins Statistic: 0.779

Dip test: 0.041

Dip test p-value: 0.846

Spearman BDC

Negative: 4

Positive: 17

Clusters: 2

The Spearman BDC adds only four instances of significant, positive correlation to the Pearson BDC results, causing a singleton cluster (*Amphitragulus*) to join a larger cluster of outgroup taxa. The sparse four instances of significant, negative correlation were unchanged. The three-cluster Pearson BDC partition has an average silhouette width of 0.41. The two-cluster Spearman BDC partition has an average silhouette width of 0.41 also. The cluster membership difference is only 10%.

The three-cluster medoid partition has an average silhouette width of 0.31 and differs from the Pearson BDC clusters by only one taxon (cluster membership difference: 10%). The two-cluster medoid partition has an average silhouette width of 0.32 and differs from the Spearman BDC clusters by only one taxon (cluster membership difference: 10%). In both cases of medoid partitioning, the differing taxon was the ingroup *Micromeryx*, and in both cases, the resulting silhouette width for *Micromeryx* was substantially negative (-0.46 for k=2 and -0.35 for k=3).

The three-cluster fuzzy partition agreed exactly with the Pearson BDC clusters, and the two-cluster fuzzy partition agreed exactly with the Spearman BDC clusters.

The original analysis placed the Moschidae in a monobaramin due to lack of evidence of discontinuity. The new results generally confirm this. Given the poor silhouette widths, we may reasonably discount the medoid partitioning, but the fuzzy analysis fully confirms the existence of the clusters from the BDC results. The original judgment is confirmed.

Original conclusion: MB

Updated conclusion: MB

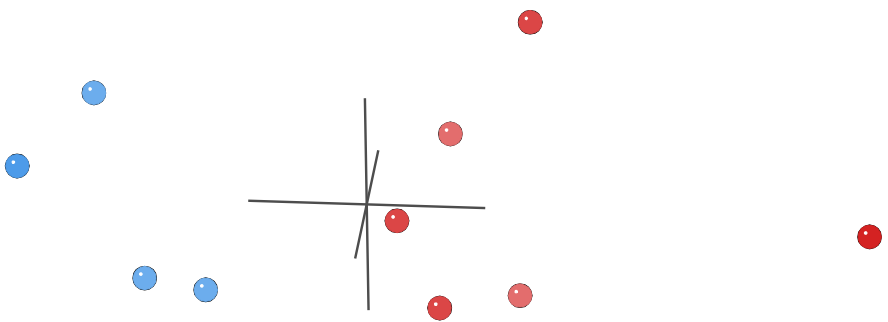
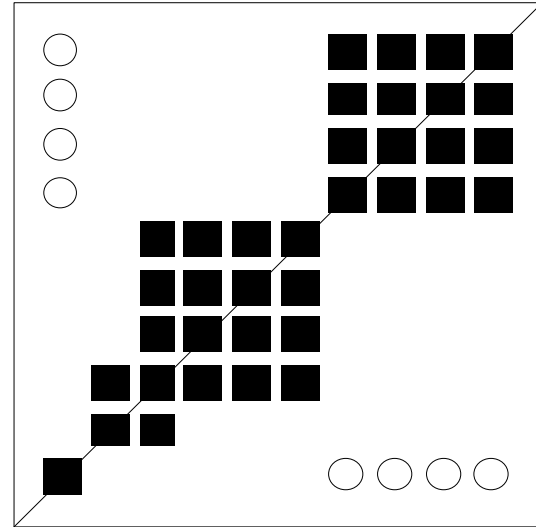
Sanchez, I.M., M.S. Domingo, and J. Morales. 2010. The genus *Hispanomeryx* (Mammalia, Ruminantia, Moschidae) and its bearing on musk deer phylogeny and systematics. *Palaeontology* 53:1023-1047.

Characters: Craniodental and postcranial

BDC Cluster 1 { *Moschus*
M. grandeavus
Micromeryx
Hispanomeryx

BDC Cluster 2 { *Orangemeryx*
Sperrgebietomeryx
Namibiomeryx
Dremotherium
Blastomeryx

BDC Cluster 3 — *Amphitragulus*



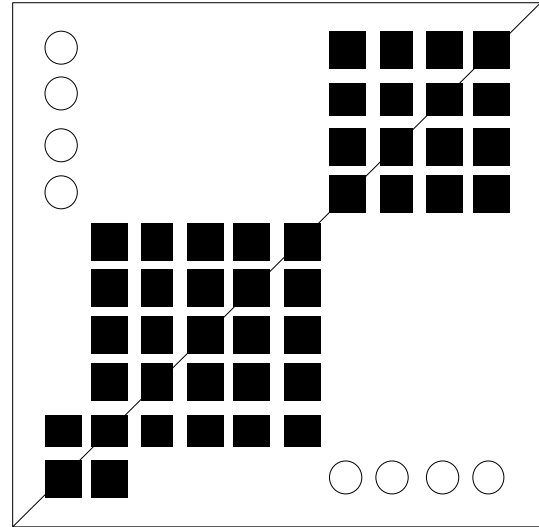
Order Artiodactyla
 Family Moschidae

Published taxa	10
Published characters	71
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	10
Characters used for calculations	40
Median bootstrap value	86
F ₉₀	0.38
Stress of 3D MDS	0.08
k _{min}	4
Conclusion	MB

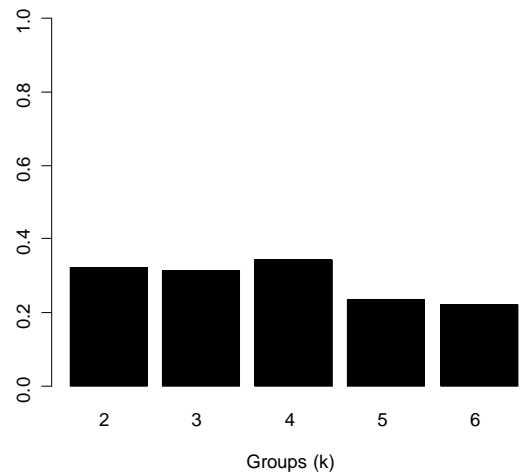
Notes: Moschidae is a definite cluster in the BDC results, but there is little significant, negative BDC. MDS shows Moschidae adjacent to outgroup taxa. Moschidae is a monobaramin.

BDC Cluster 1 {
Moschus
M. grandeavus
Micromeryx
Hispanomeryx

BDC Cluster 2 {
Orangemeryx
Sperrgebietomeryx
Namibiomeryx
Dremotherium
Blastomeryx
Amphitragulus



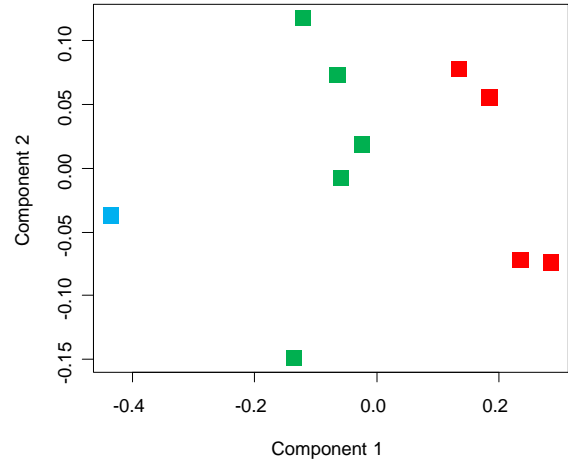
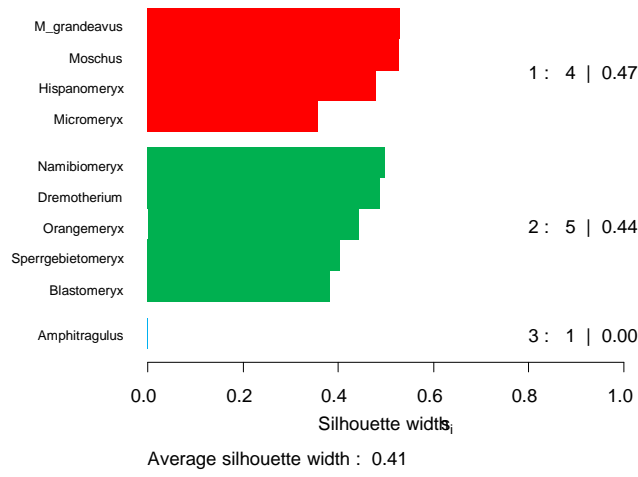
Average Silhouette Widths, Partion Around Medoids



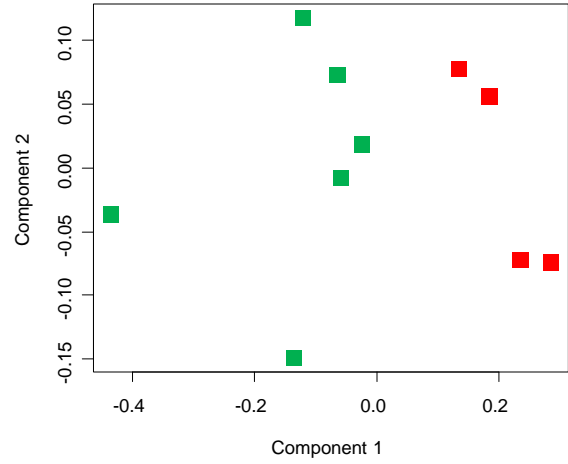
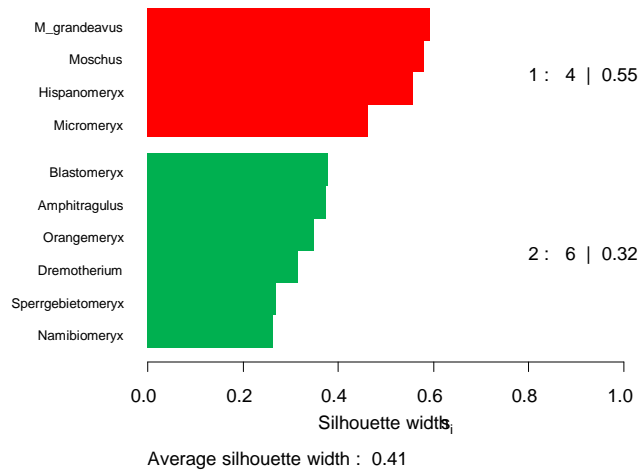
Clade Correspondence: Of the three BDC clusters, only cluster 3 is a singleton. Only cluster 1 is a clade in the phylogenies of Figure 10 of Sanchez et al. (2010).

Silhouette plot, BDC partitions

Pearson Correlation

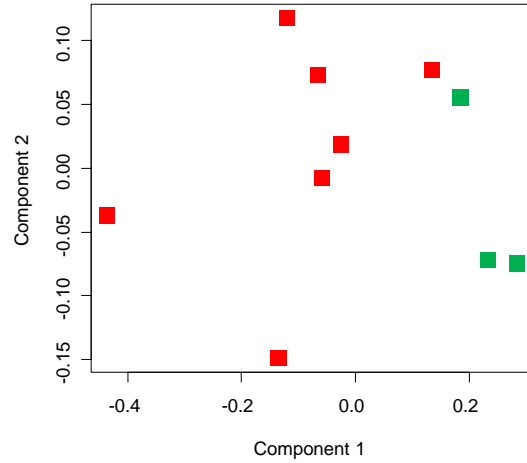
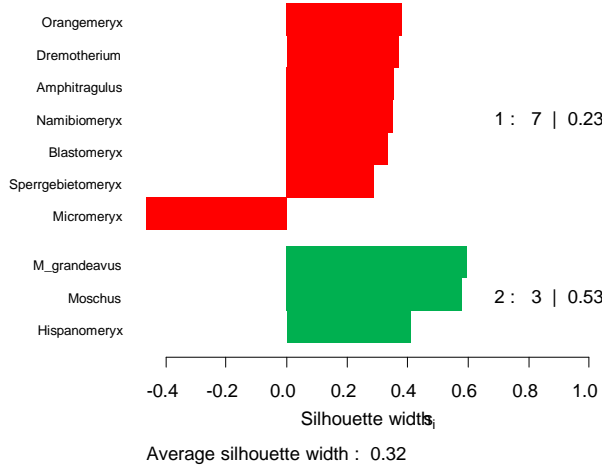


Spearman Correlation

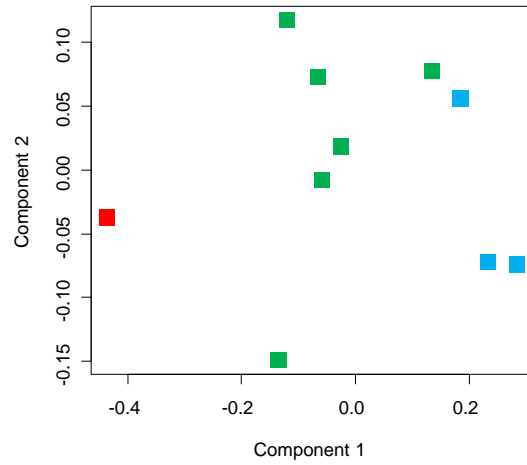
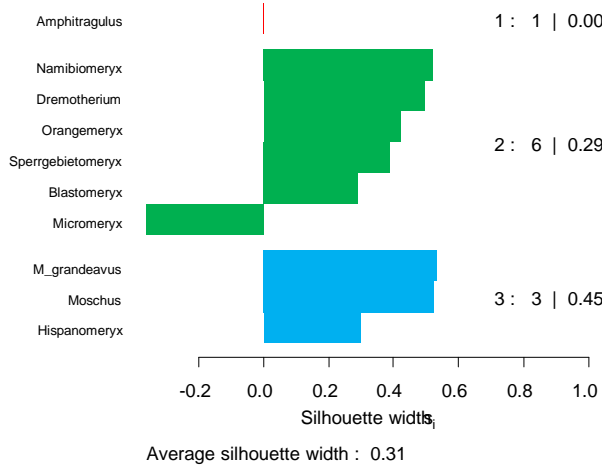


Silhouette plot, Partition Around Medoids

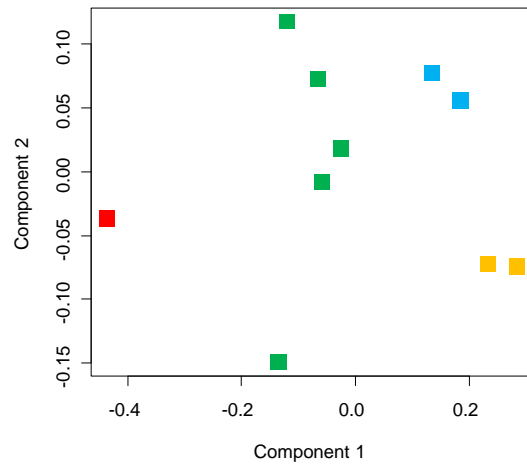
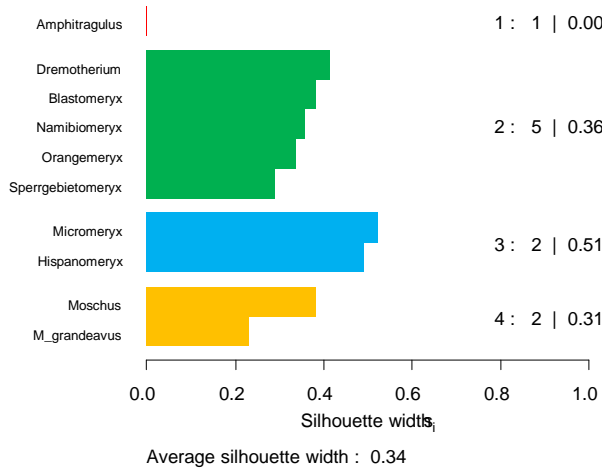
k=2



k=3

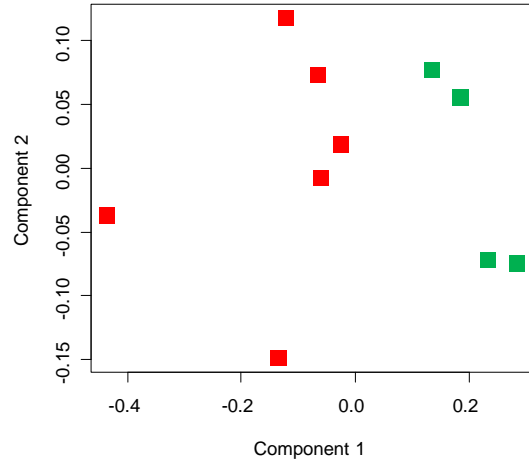
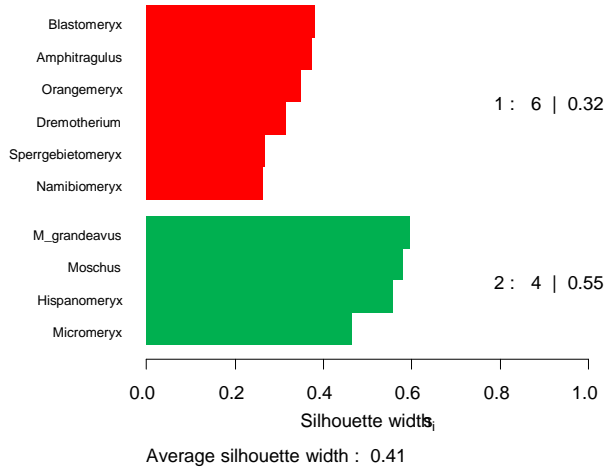


k=4

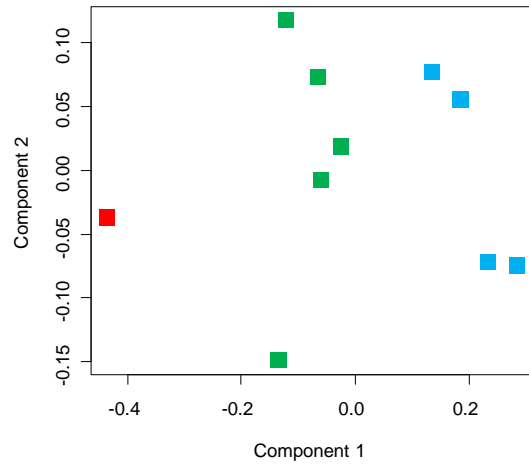
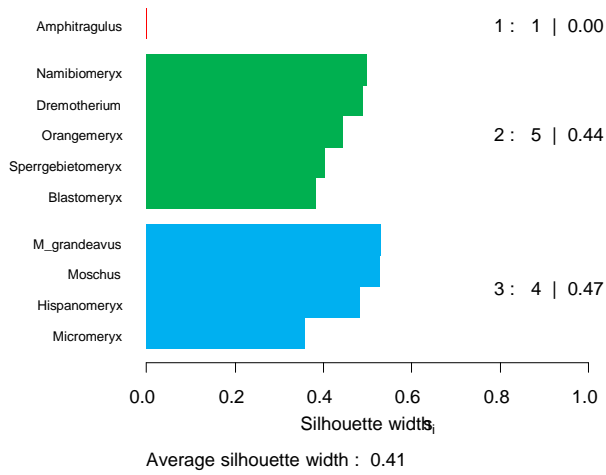


Silhouette plot, Fuzzy Analysis

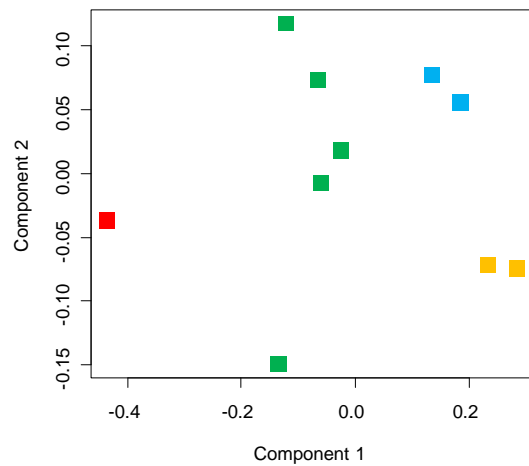
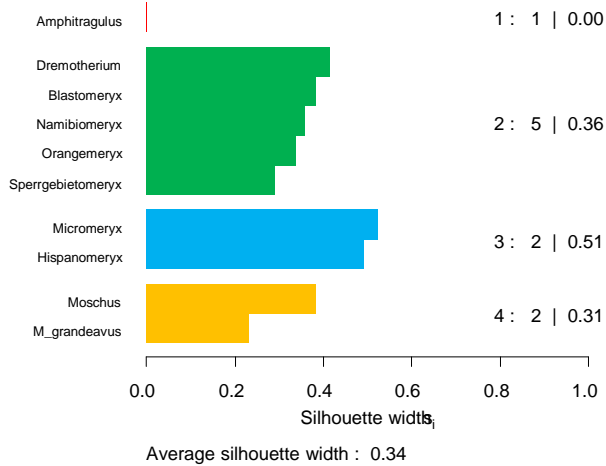
k=2



k=3



k=4



Family Cervidae

Order Artiodactyla

Lister et al. 2005

Pearson BDC

Negative: 3

Positive: 5

Clusters: 5

Clusterability

Hopkins Statistic: 0.63

Dip test: 0.041

Dip test p-value: 0.846

Spearman BDC

Negative: 4

Positive: 9

Clusters: 5

Spearman BDC exhibited an entirely different arrangement of significant, positive correlation than observed in the Pearson BDC results. Thus, though the number of clusters remains, their membership is rearranged (cluster membership difference: 20%). Average silhouette widths are 0.3 for the Pearson BDC clusters and 0.24 for the Spearman BDC clusters.

The five-cluster medoid partition has an average silhouette width of 0.27 and matches neither the Spearman nor the Pearson BDC clusters. The five-cluster medoid partition differs by two taxa from the Pearson BDC clusters and by two taxa from the Spearman BDC clusters.

Fuzzy analysis failed at $k=5$.

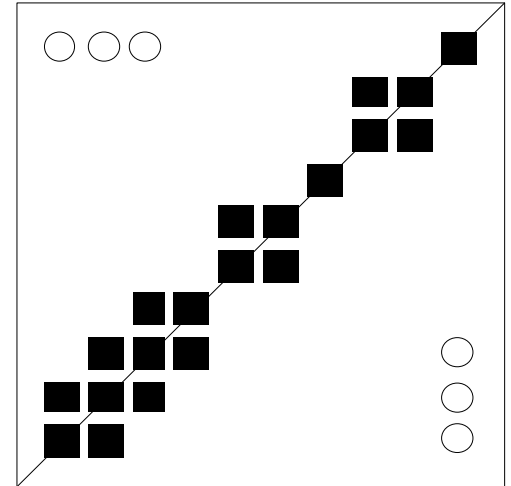
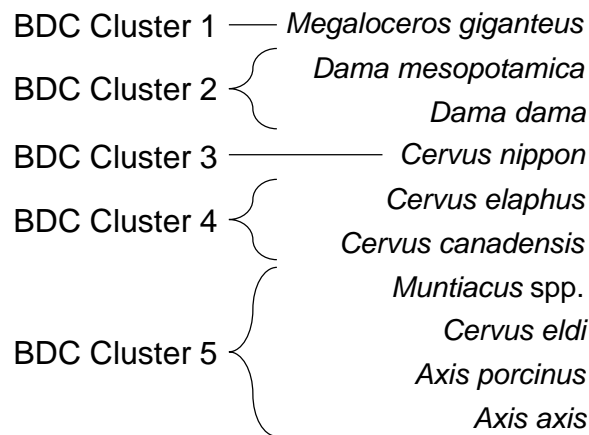
The high number of clusters and lack of consistency from these new results reinforces the original judgment that these analyses are inconclusive.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

Lister, A.M., C.J. Edwards, D.A.W. Nock, M. Bunce, I.A. Van Pijlen, D.G. Bradley, M.G. Thomas, and I. Barnes. 2005. The phylogenetic position of the 'giant deer' *Megaloceros giganteus*. *Nature* 438:850-853.

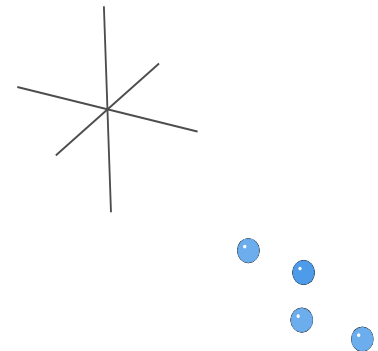
Characters: Craniodental and postcranial



Megaloceros giganteus

Cervus

Dama

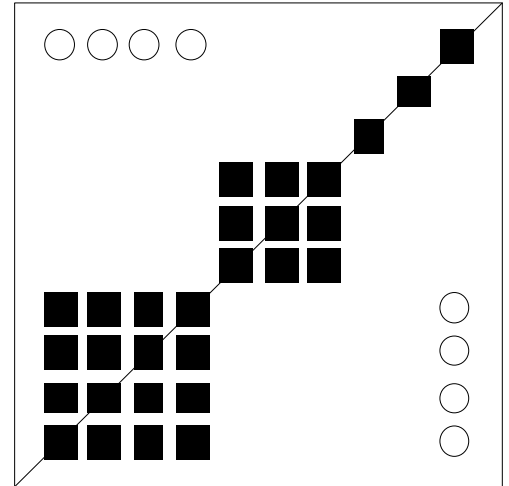


Order Artiodactyla
Family Cervidae

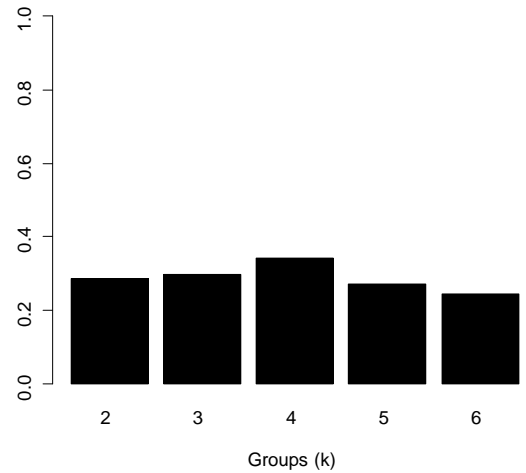
Published taxa	10
Published characters	74
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	10
Characters used for calculations	74
Median bootstrap value	100
F ₉₀	0.69
Stress of 3D MDS	0.23
k _{min}	7
Conclusion	Inc

Notes: Very few correlations in BDC, and a diffuse cluster of taxa in MDS. No clear discontinuity is evident.

- BDC Cluster 1 — *Megaloceros giganteus*
- BDC Cluster 2 — *Dama mesopotamica*
- BDC Cluster 3 — *Dama dama*
- BDC Cluster 4 { *Cervus nippon*
Cervus elaphus
Cervus canadensis
- BDC Cluster 5 { *Muntiacus spp.*
Cervus eldi
Axis porcinus
Axis axis



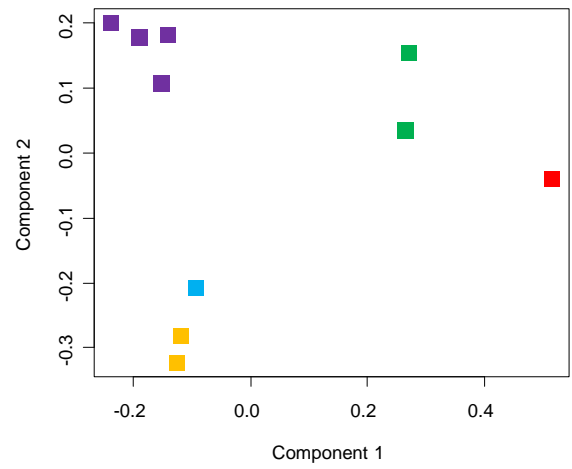
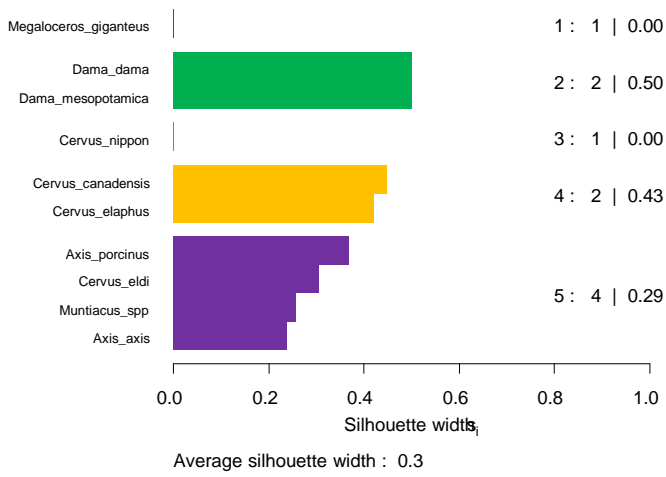
Average Silhouette Widths, Partion Around Medoids



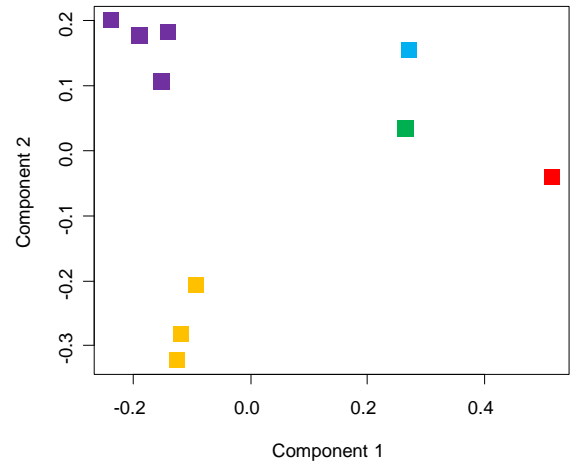
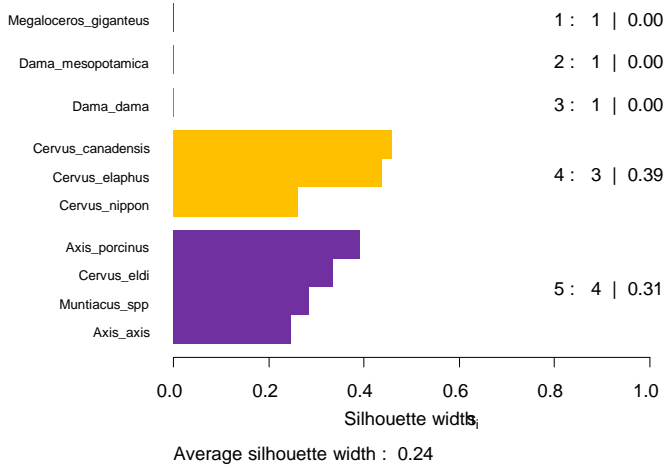
Clade Correspondence: Of the five BDC clusters, only clusters 2, 4, and 5 contain two or more taxa. In the single most parsimonious tree shown in Figure 1b of Lister et al. (2005), all three clusters are monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

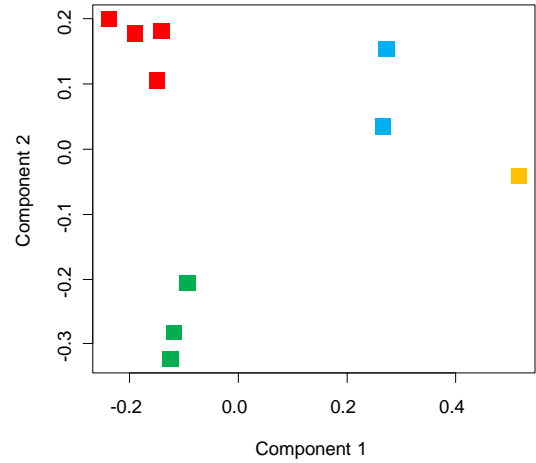
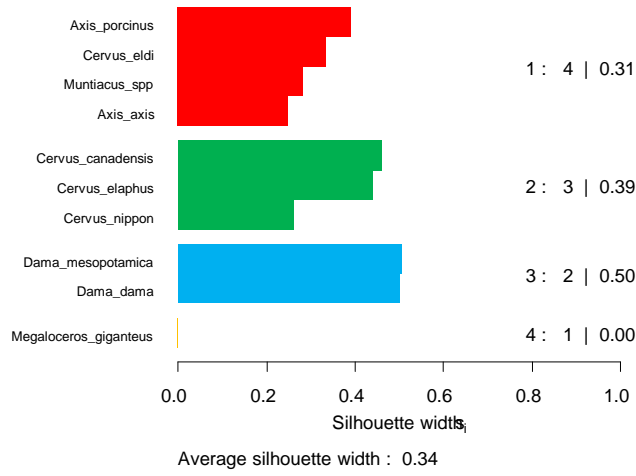


Spearman Correlation

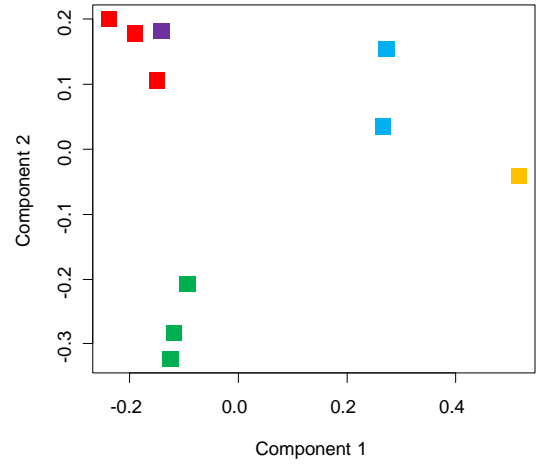
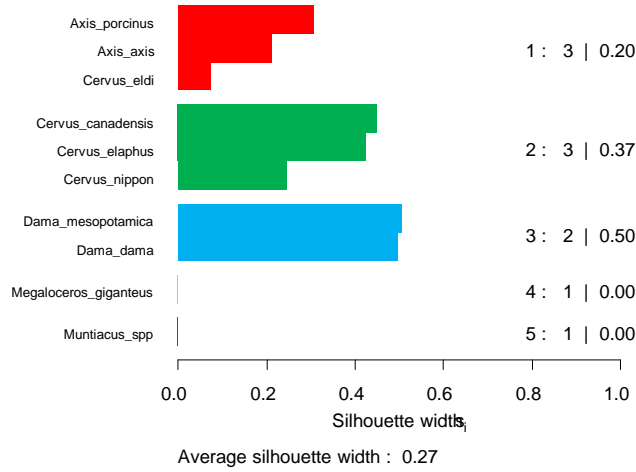


Silhouette plot, Partition Around Medoids

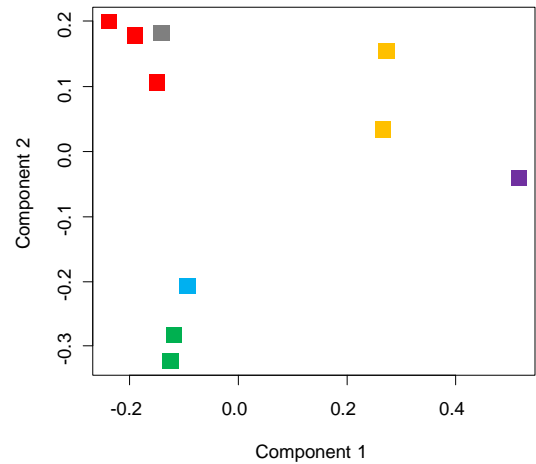
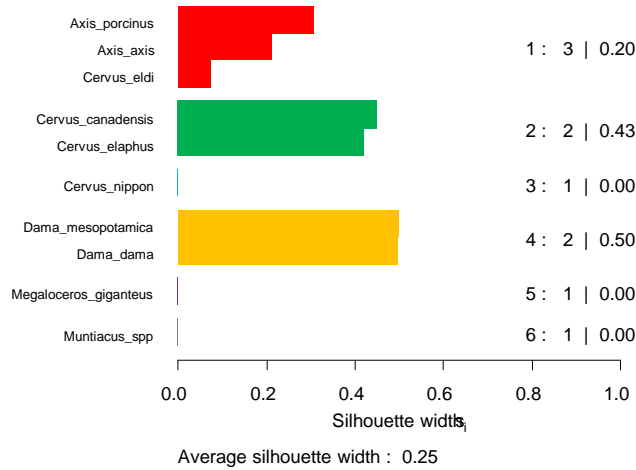
k=4



k=5

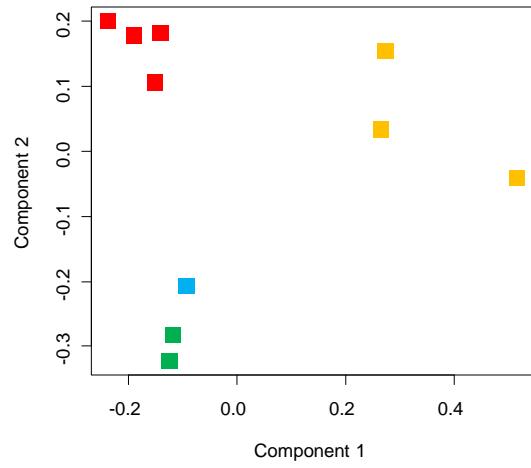
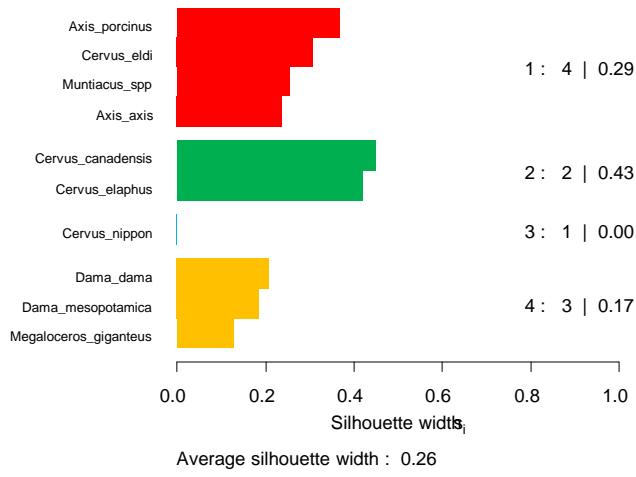


k=6



Silhouette plot, Fuzzy Analysis

k=4



Family Notohippidae

Order Notoungulata

Cerdeño and Vera 2010

Pearson BDC

Negative: 25

Positive: 58

Clusters: 3

Clusterability

Hopkins Statistic: 0.836

Dip test: 0.045

Dip test p-value: 0.014

Spearman BDC

Negative: 20

Positive: 78

Clusters: 2

Three clusters are evident in the Pearson BDC results, but only two in the Spearman BDC results. The Pearson BDC clusters have an average silhouette width of 0.45, and the Spearman BDC clusters have an average silhouette width of 0.38. The cluster membership difference is 16%.

Medoid partitioning at $k=3$ has an average silhouette width of 0.44 and is roughly consistent with the Pearson BDC clusters (cluster membership difference: 16%). At $k=2$, medoid partitioning has an average silhouette width of 0.41 and differs from the Spearman BDC clusters by three taxa (cluster membership difference: 16%).

Two-cluster fuzzy analysis produced a partition that exactly matches the Spearman BDC clusters. At $k=3$, the fuzzy partition has an average silhouette width of 0.44 and differs from the Pearson BDC clusters by a single taxon (cluster membership difference: 5%).

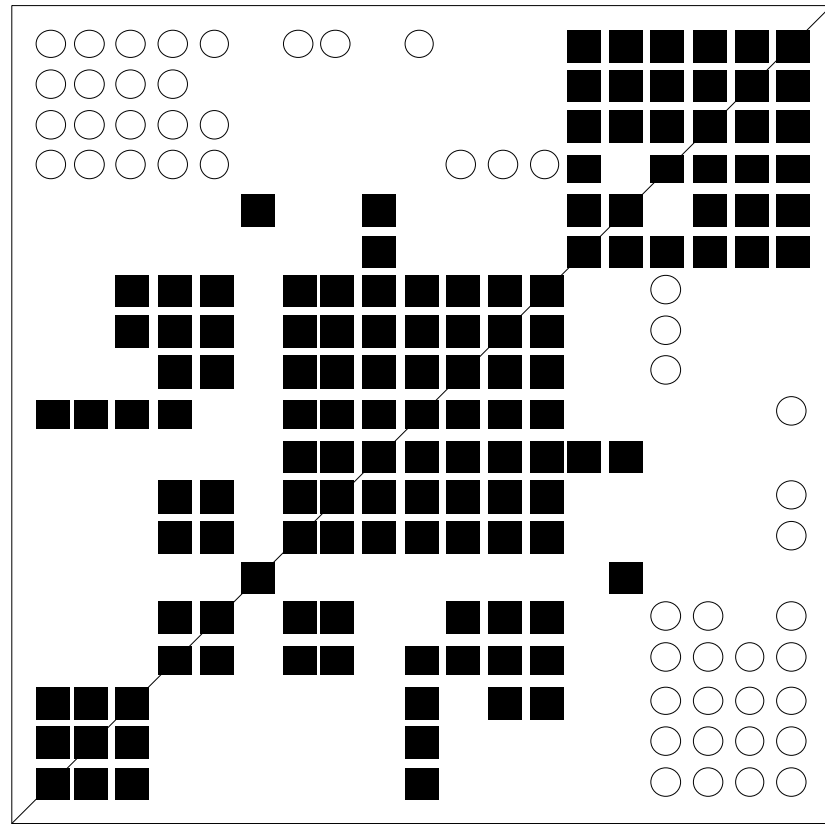
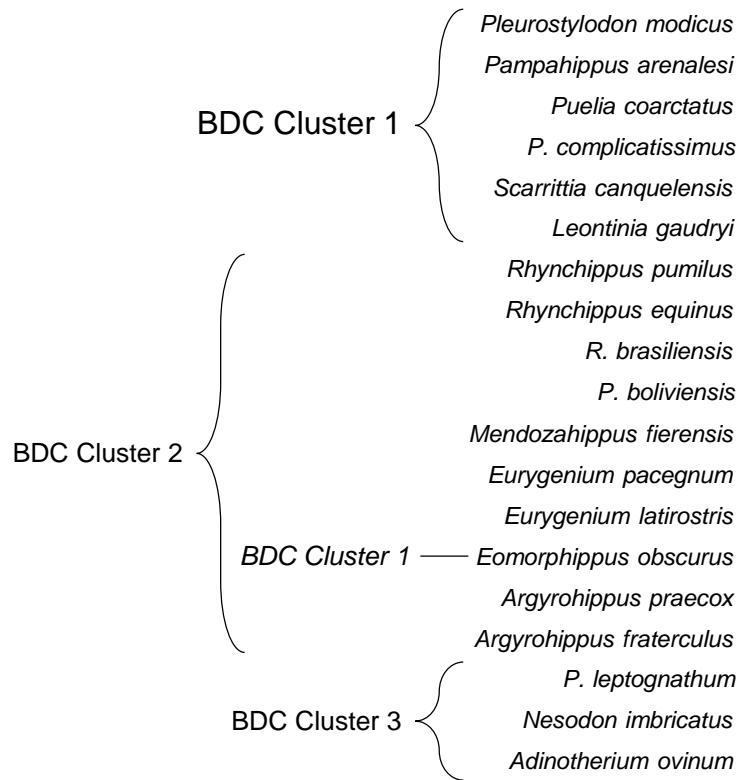
These results reinforce the original analyses. The Pearson BDC was judged to be too sparse to support the inference of either continuity within the notohippids nor discontinuity surrounding it. Here, despite similar results, the lack of consistency in the fuzzy analysis and medoid partition, together with additional instances of significant, positive BDC in the Spearman BDC results, warrant concluding that these distances do not support meaningful clustering.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

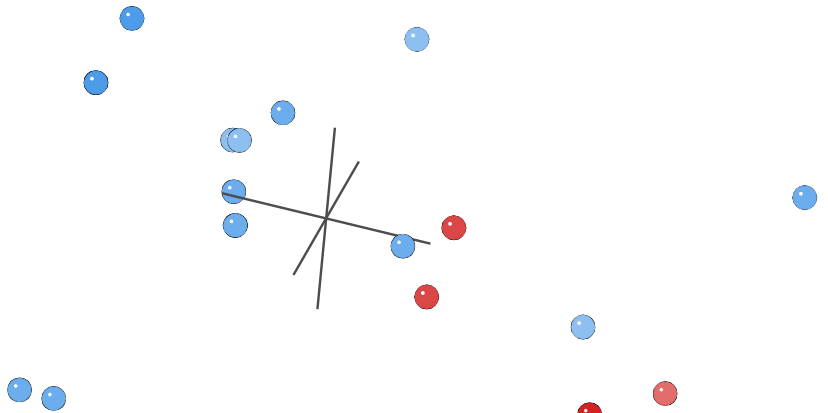
Cerdeño, E. and B. Vera. 2010. *Mendozahippus fierensis*, gen. et sp. nov., new Notohippidae (Notoungulata) from the late Oligocene of Mendoza (Argentina). *Journal of Vertebrate Paleontology* 30:1805-1817.

Characters: Craniodental and postcranial

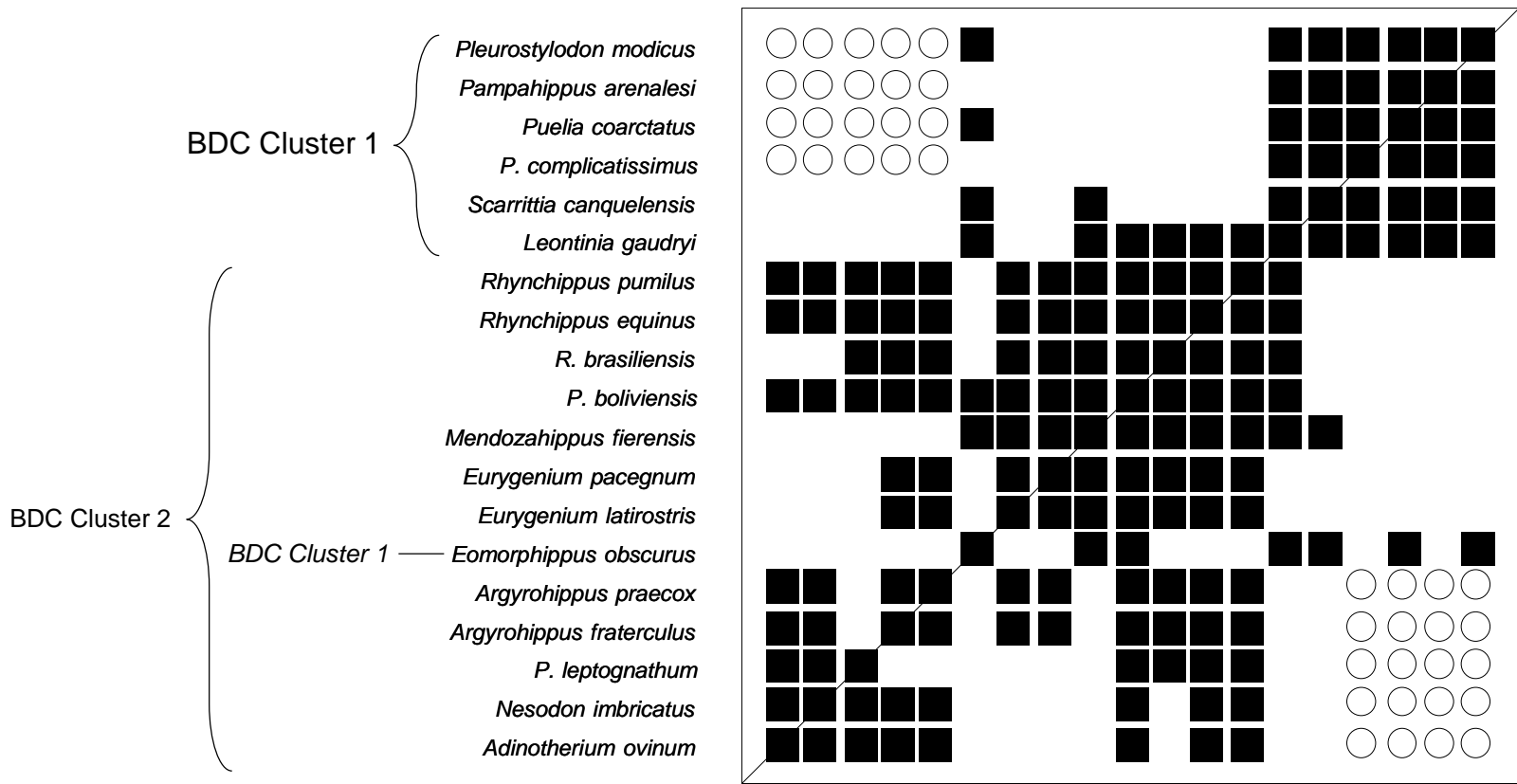


Order Notoungulata
Family Notohippidae

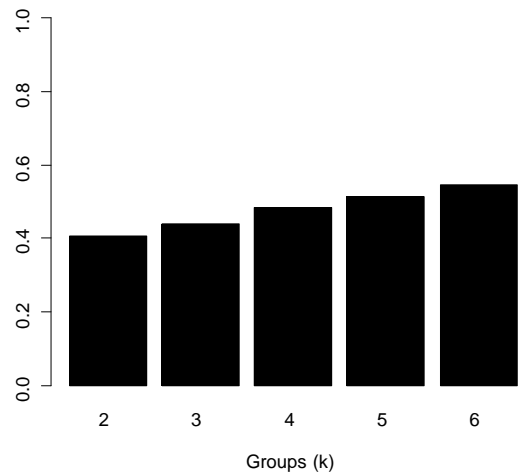
Published taxa	19
Published characters	38
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	19
Characters used for calculations	29
Median bootstrap value	73
F ₉₀	0.13
Stress of 3D MDS	0.14
k _{min}	4
Conclusion	Inc



Notes: BDC reveals two groups with substantial overlap, and MDS confirms. No clear discontinuity is evident.



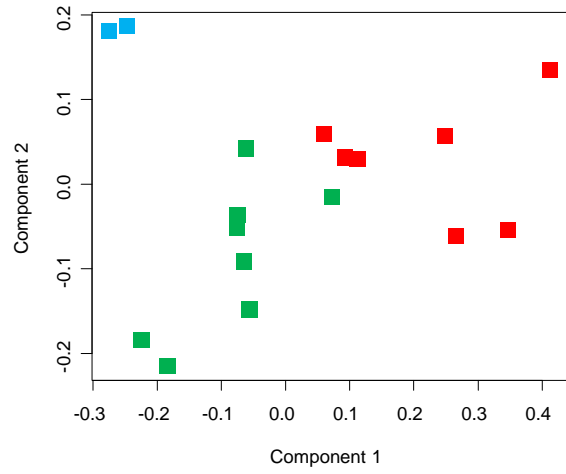
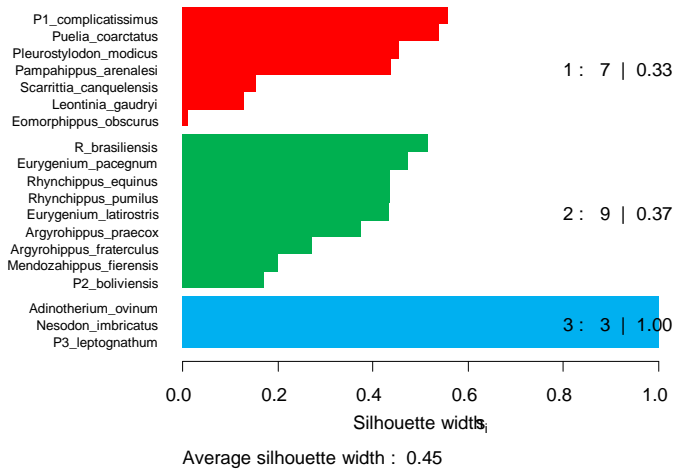
Average Silhouette Widths, Partition Around Medoids



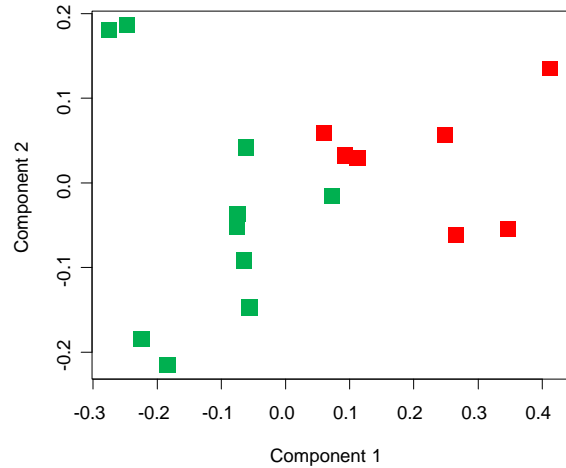
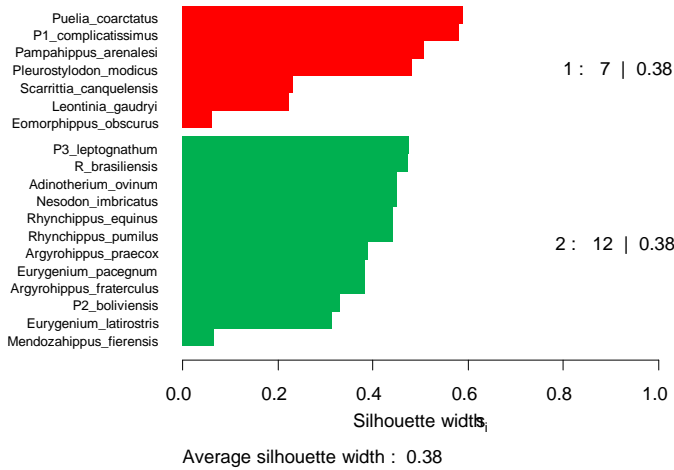
Clade Correspondence: All three BDC clusters contain more than one taxon each. In the phylogeny shown in Figure 7 of Cerdeño and Vera (2010), only cluster 3 is monophyletic.

Silhouette plot, BDC partitions

Pearson Correlation

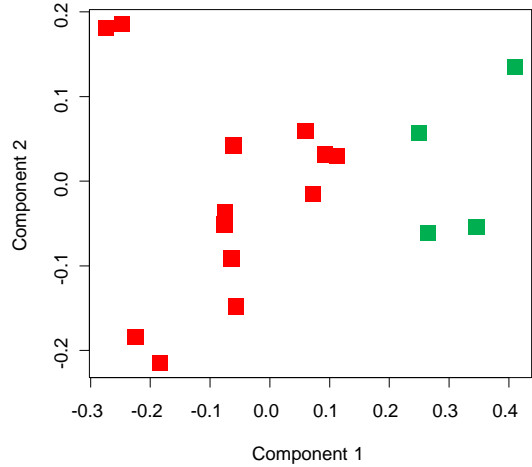
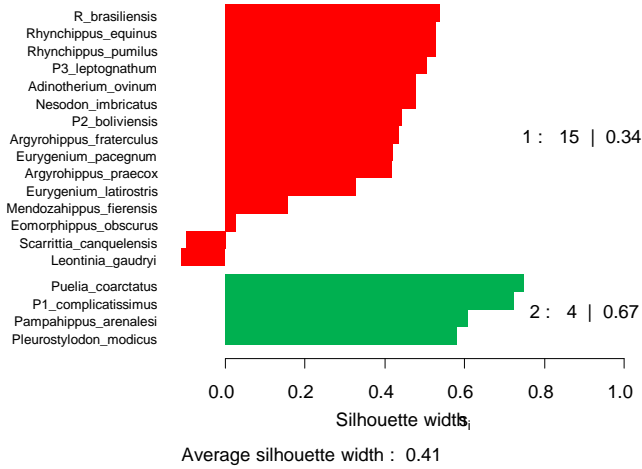


Spearman Correlation

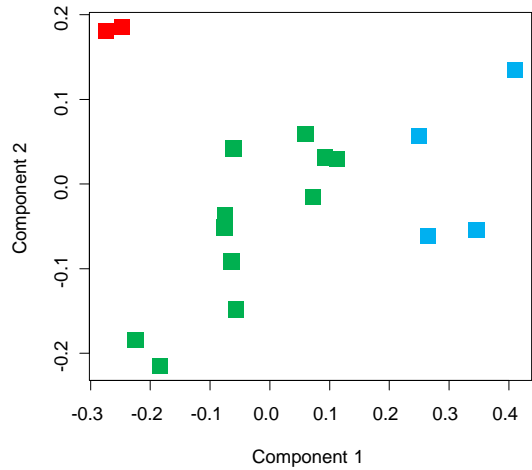
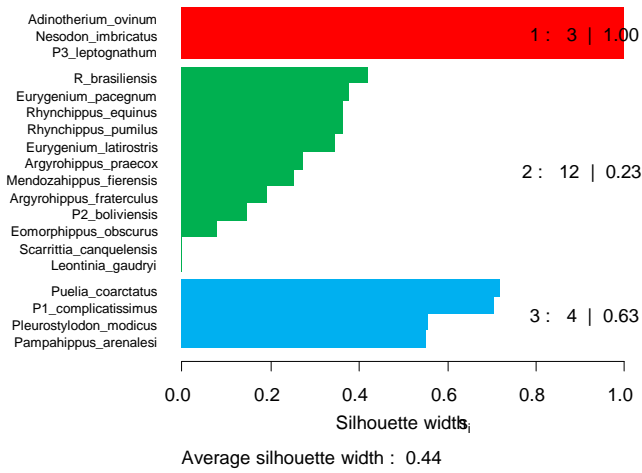


Silhouette plot, Partition Around Medoids

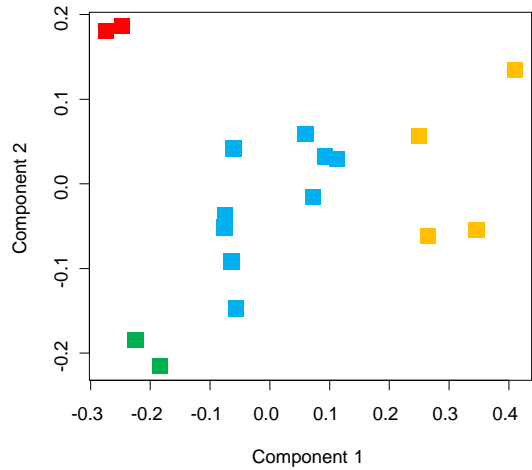
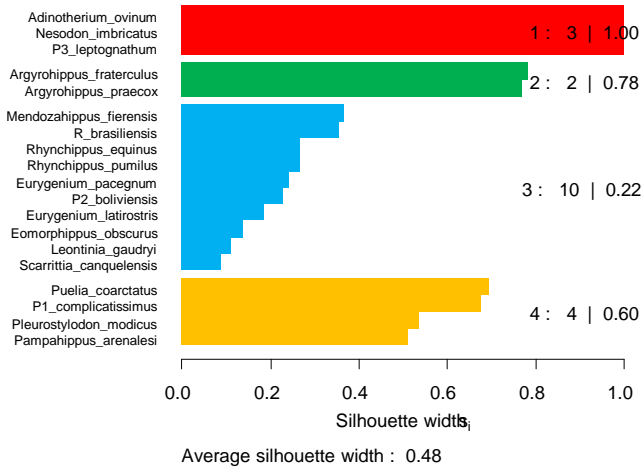
k=2



k=3

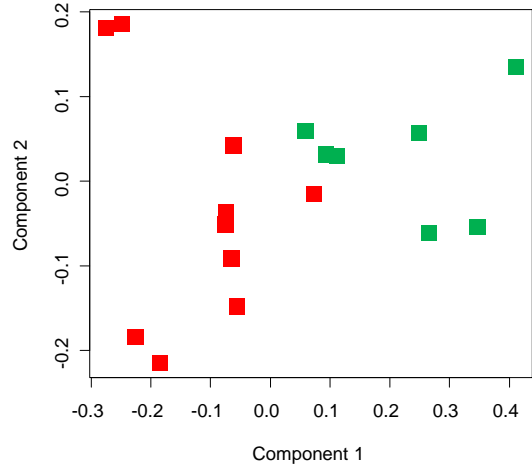
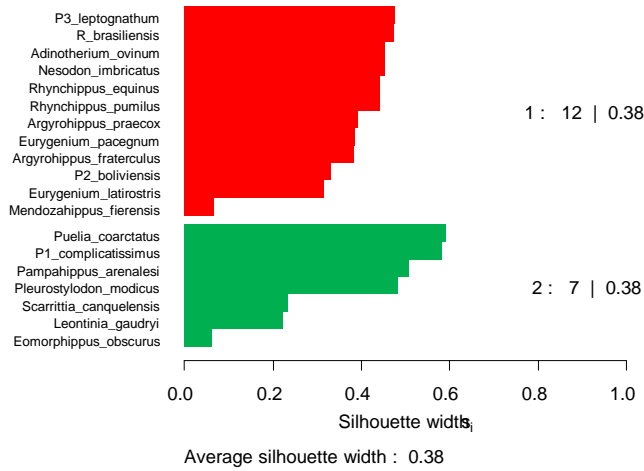


k=4

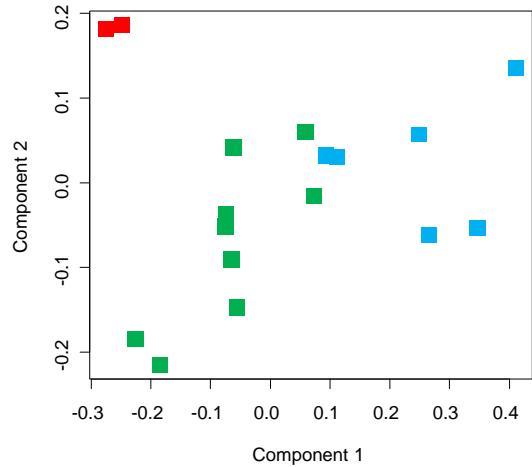
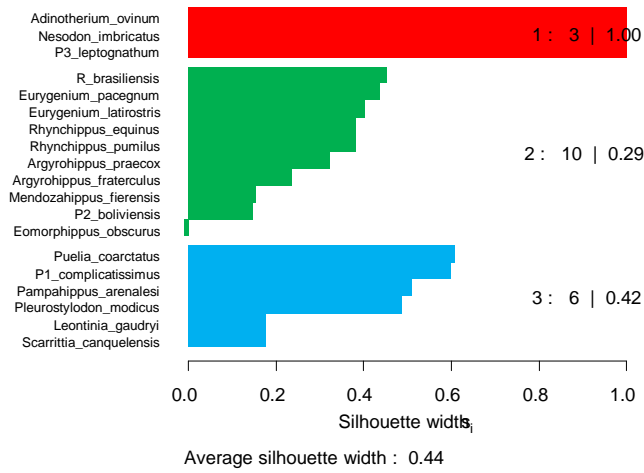


Silhouette plot, Fuzzy Analysis

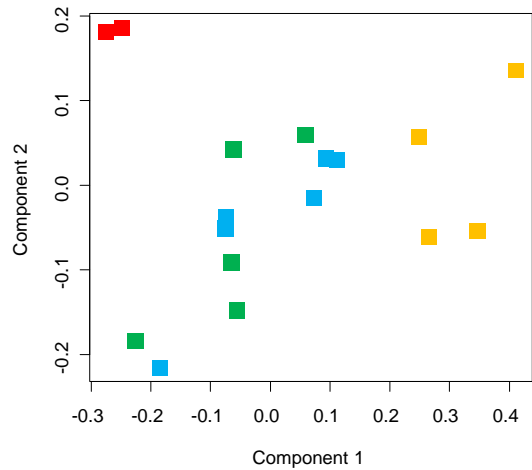
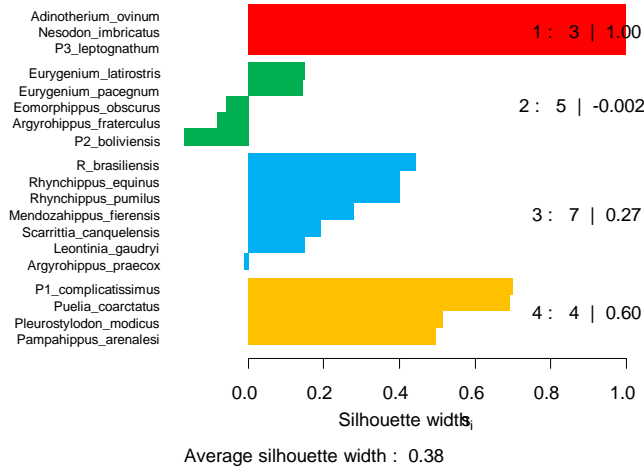
k=2



k=3



k=4



Family Leontiniidae

Order Notoungulata

Schockey et al. 2012

Pearson BDC

Negative: 149

Positive: 137

Clusters: 3

Clusterability

Hopkins Statistic: 0.883

Dip test: 0.022

Dip test p-value: 0.313

Spearman BDC

Negative: 148

Positive: 144

Clusters: 2

A rearrangement of instances of significant, positive correlation in the Spearman vs. Pearson BDC results reduces the number of clusters from three to two. The three-cluster Pearson BDC partition has an average silhouette width of 0.49, and the two-cluster Spearman BDC partition has an average silhouette width of 0.51. The cluster membership difference is 11%.

The three-cluster medoid partition has an average silhouette width of 0.43 and poorly matches the Pearson BDC results (cluster membership difference: 30%). The two-cluster medoid partition has an average silhouette width of 0.48 and differs from the Spearman BDC clusters by a single taxon.

Three-cluster fuzzy analysis has an average silhouette width of 0.42 and differs substantially from the Pearson BDC clusters (cluster membership difference: 30%). The two-cluster fuzzy partition matches the two-cluster Spearman BDC partition exactly.

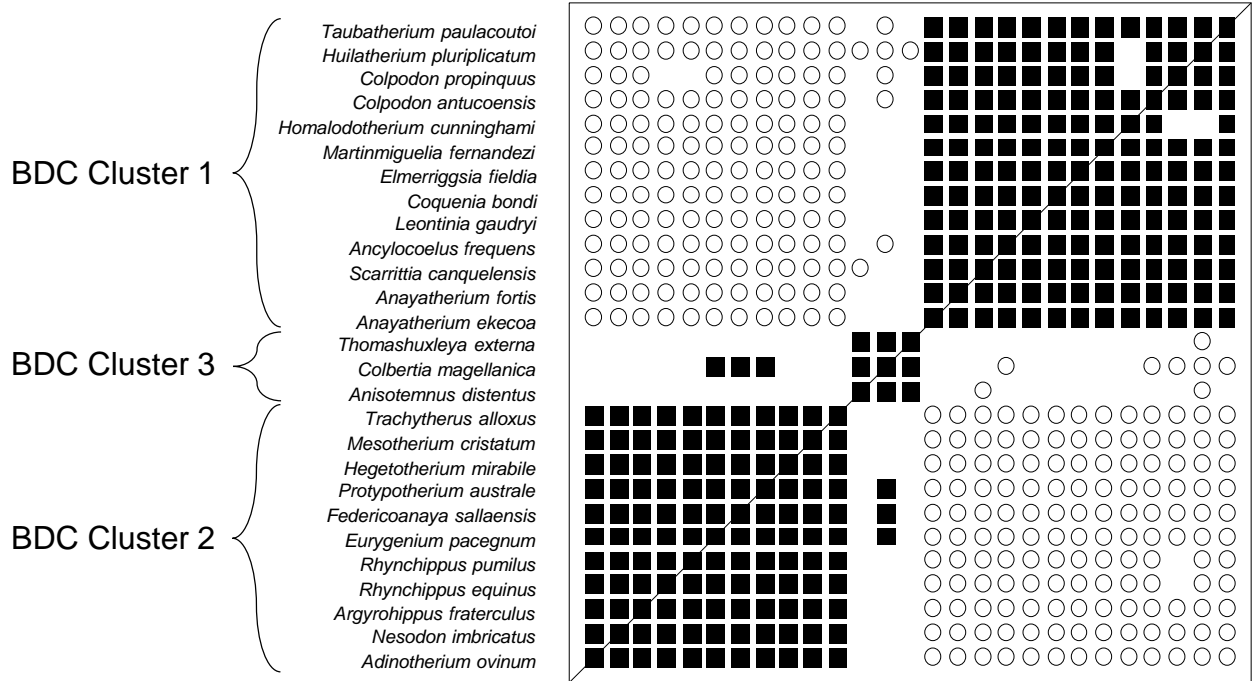
The support for two clusters in the Spearman BDC and fuzzy analysis neatly separates Leontiniidae from the outgroup taxa. Even the medoid partition differs from this division by only one taxon. Hence we may infer support for the initial judgment that Leontiniidae is a holobaramin.

Original conclusion: HB

Updated conclusion: HB

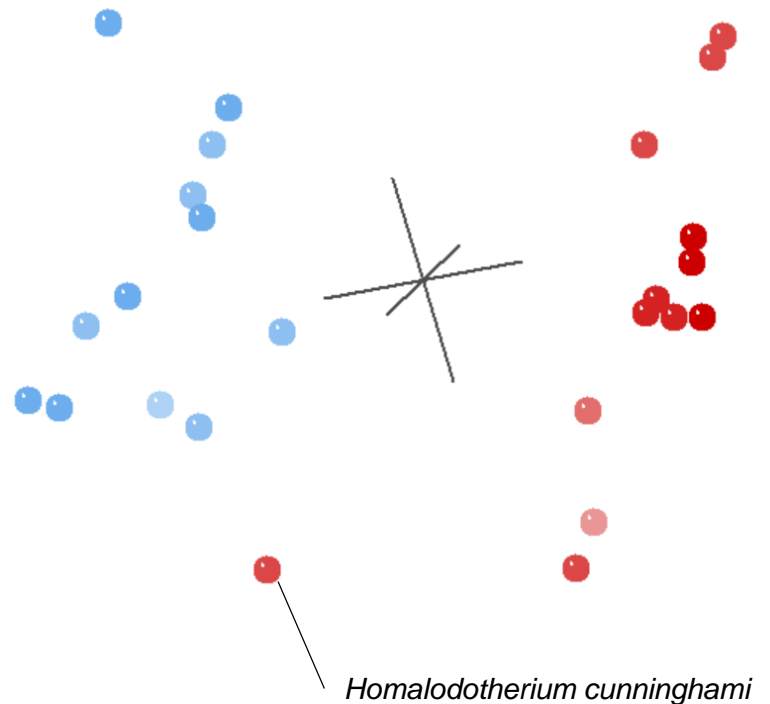
Schockey, B.J., J.J. Flynn, D.A. Croft, P. Gans, and R.A. Wyss. 2012. New leontiniid Notoungulata (Mammalia) from Chile and Argentina: comparative anatomy, character analysis, and phylogenetic hypotheses. *American Museum Novitates* 3737:1-64.

Characters: Craniodental and postcranial

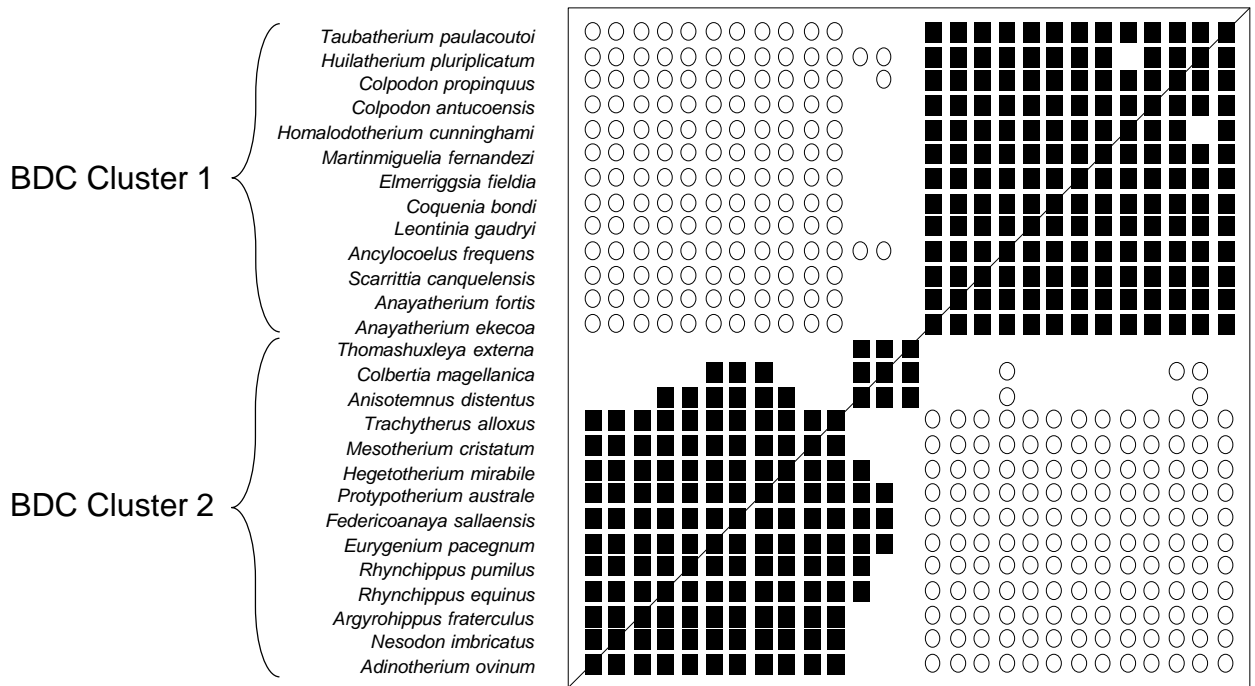


Order Notoungulata
Family Leontiniidae

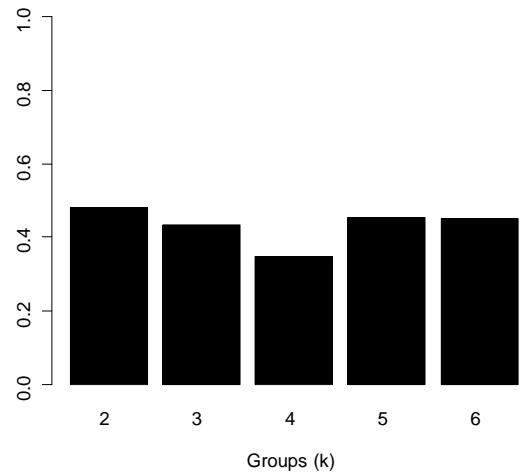
Published taxa	27
Published characters	83
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	27
Characters used for calculations	36
Median bootstrap value	90
F ₉₀	0.49
Stress of 3D MDS	0.13
k _{min}	4
Conclusion	HB



Notes: BDC and MDS reveal two groups corresponding to Leontiniidae and the outgroup. They are well separated in both analyses. Leontiniidae is likely a holobaramin.



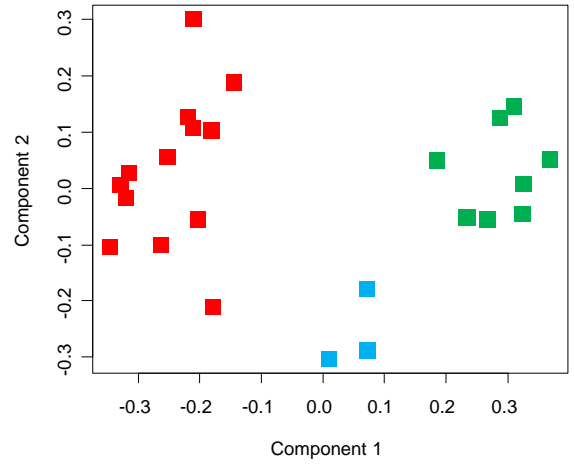
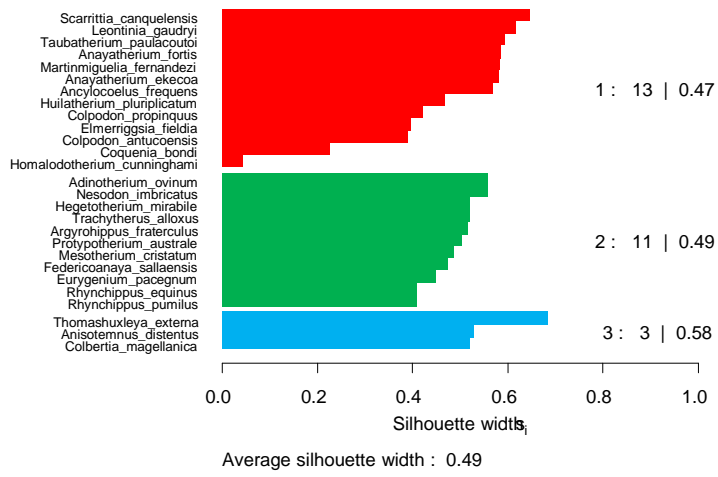
Average Silhouette Widths, Partion Around Medoids



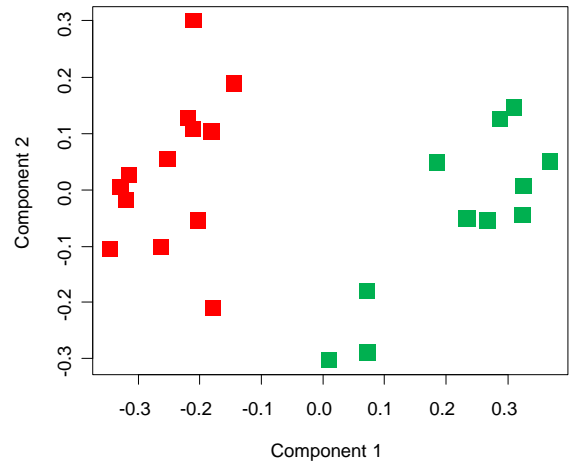
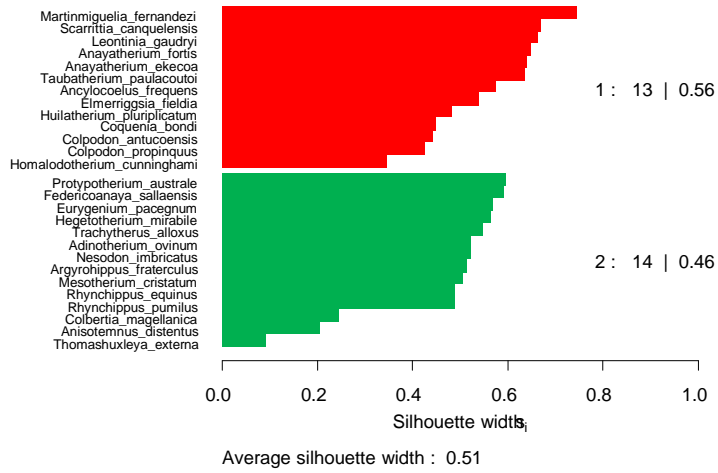
Clade Correspondence: All three BDC clusters contain more than one taxon each. Only cluster 3 is monophyletic in the majority rule consensus tree shown in Figure 13 of Schockey et al. (2012).

Silhouette plot, BDC partitions

Pearson Correlation

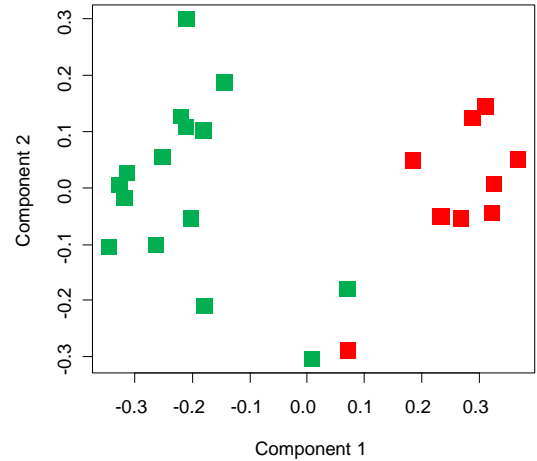
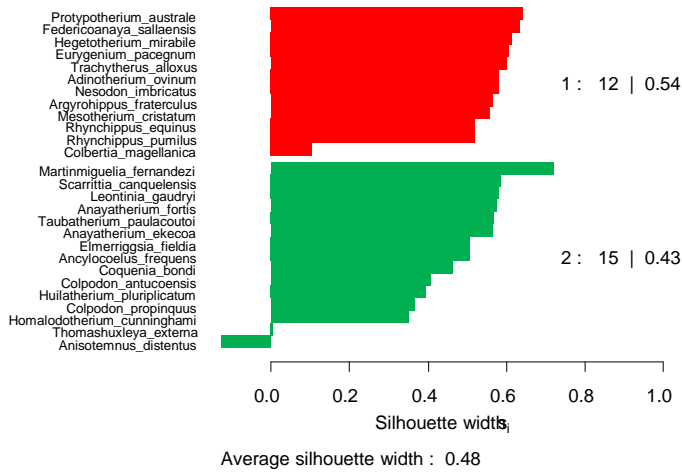


Spearman Correlation

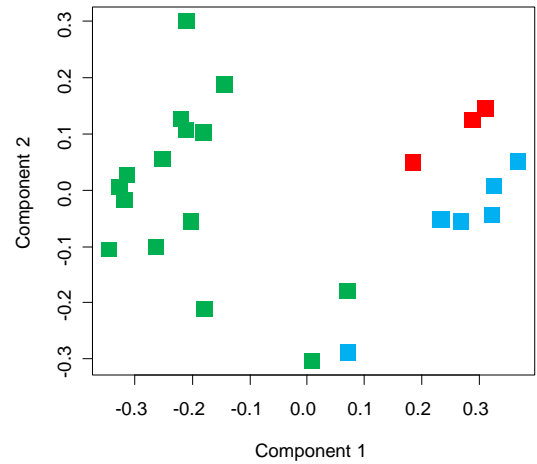
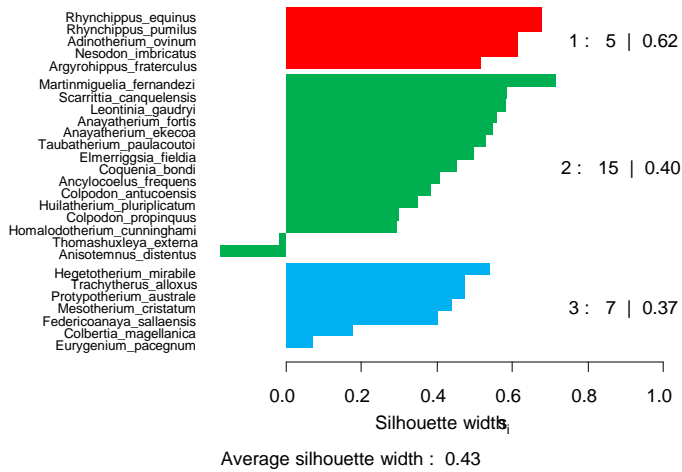


Silhouette plot, Partition Around Medoids

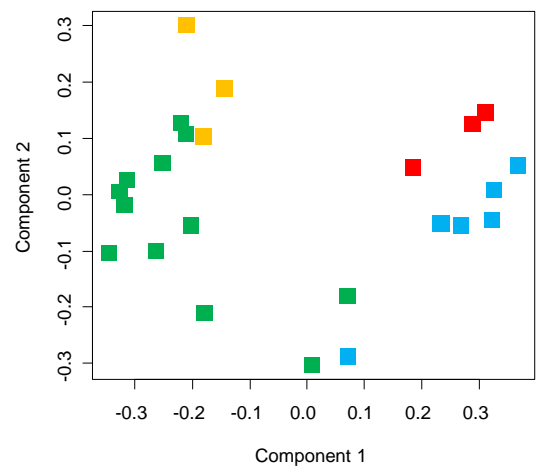
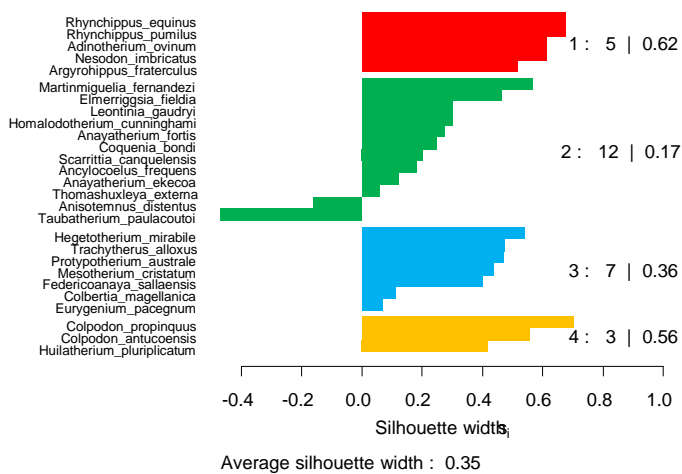
k=2



k=3

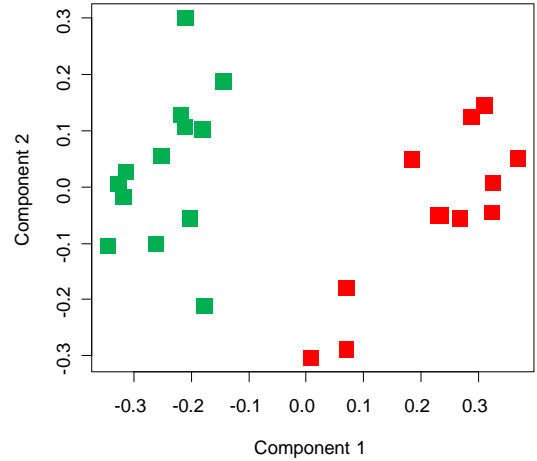
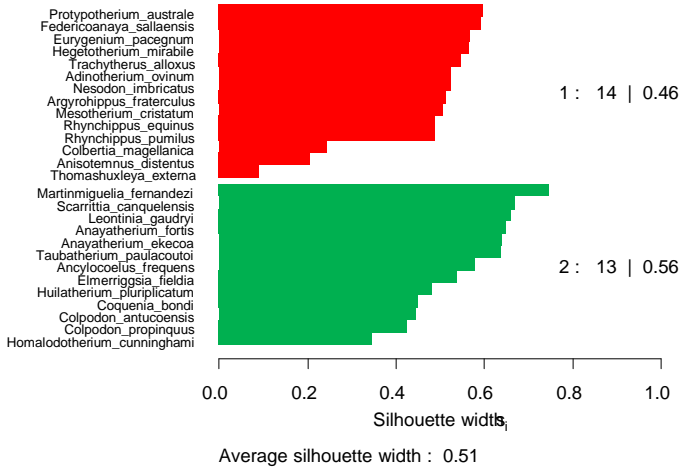


k=4

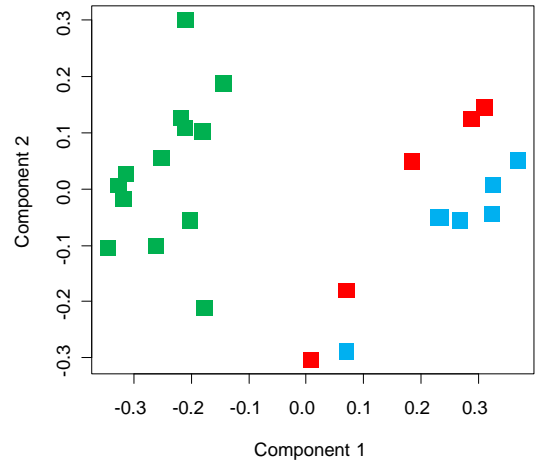
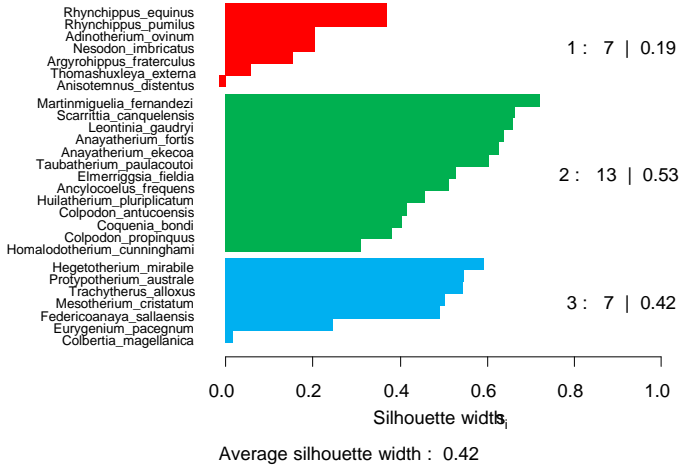


Silhouette plot, Fuzzy Analysis

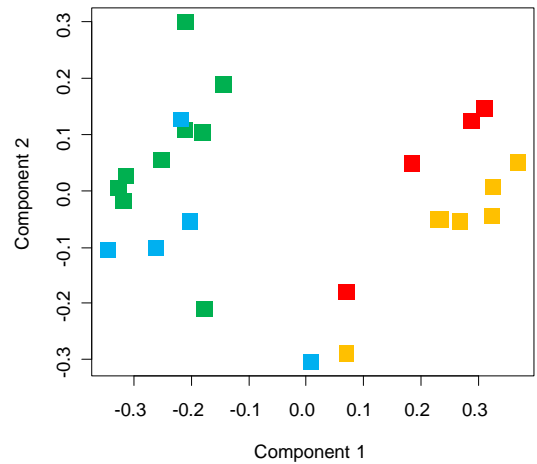
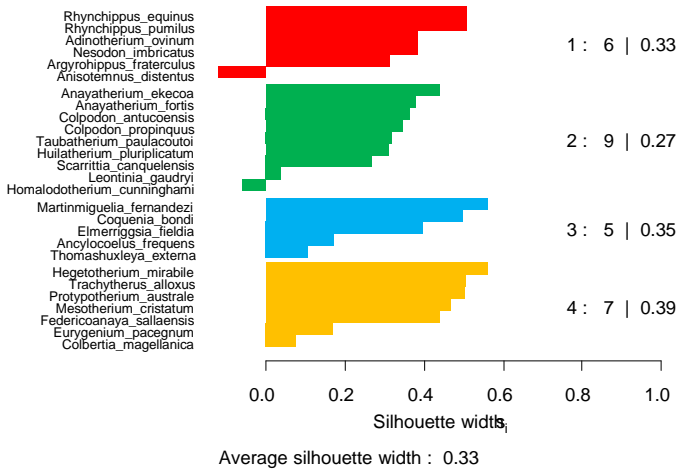
k=2



k=3



k=4



Family Toxodontidae

Order Notoungulata

Forasiepi et al. 2015

Pearson BDC

Negative: 118

Positive: 152

Clusters: 2

Spearman BDC

Negative: 112

Positive: 154

Clusters: 2

Clusterability

Hopkins Statistic: 0.815

Dip test: 0.027

Dip test p-value: 0.15

The differences between the Pearson and Spearman BDC are extremely slight. Both yield a two-cluster partition with most intracluster taxon pairs exhibiting significant, positive BDC and most intercluster taxon pairs exhibiting significant, negative BDC. The average silhouette width for this partition is 0.56. The two-cluster medoid partition and fuzzy analysis exactly match the BDC clusters.

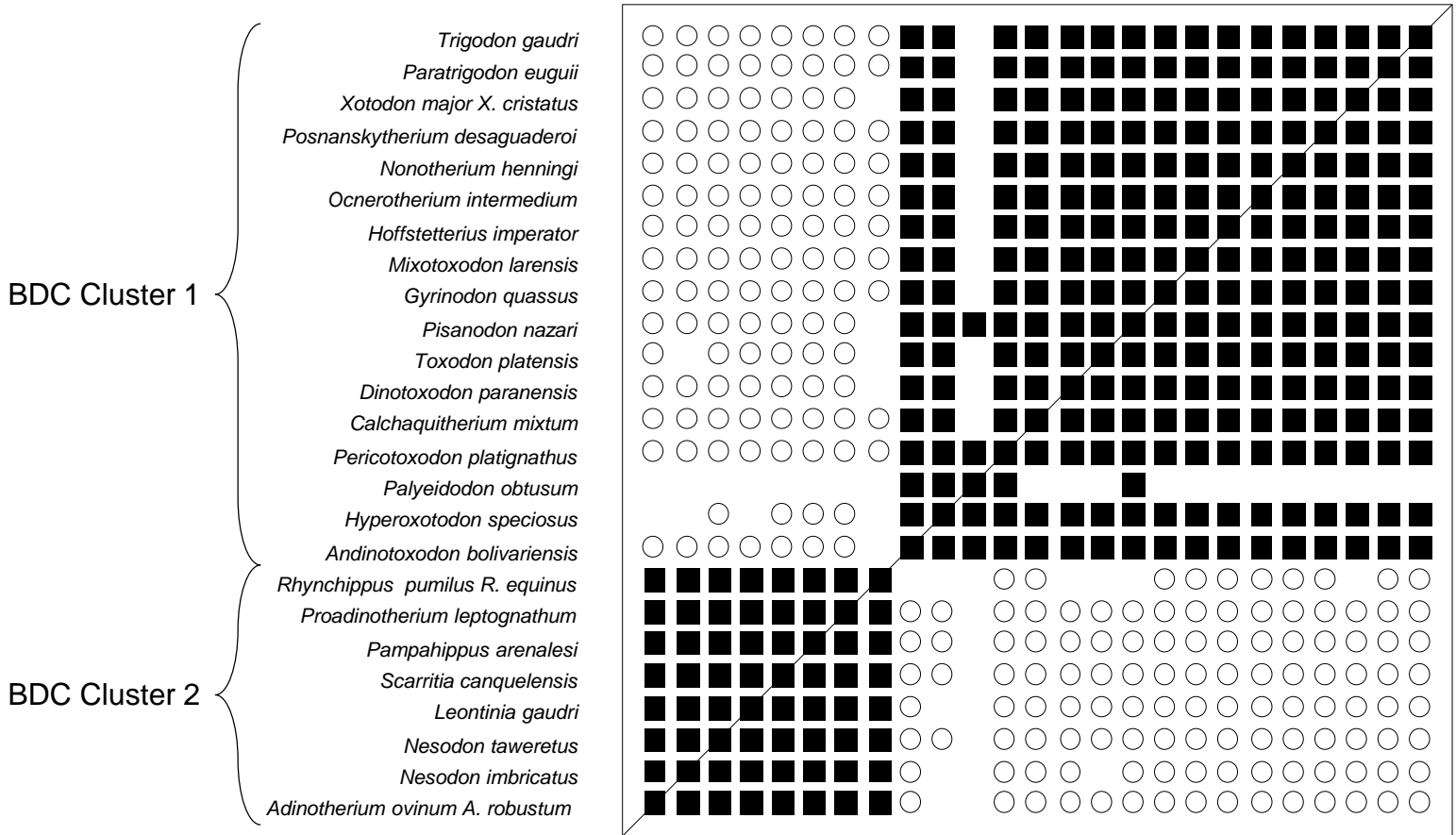
These results reinforce the original conclusion.

Original conclusion: HB

Updated conclusion: HB

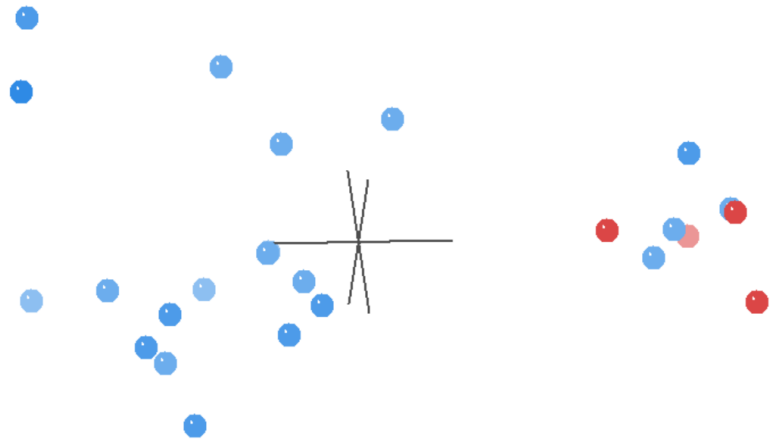
Forasiepi, A.M., E. Cerdeno, M. Bond, G.I. Schmidt, M. Naipauer, F.R. Straehl, A.G. Martinelli, A.C. Garrido, M.D. Schmitz, and J.J. Crowley. 2015. New toxodontid (Notoungulata) from the early Miocene of Mendoza, Argentina. *Paläontologische Zeitschrift* 89:611-634.

Characters: Craniodental

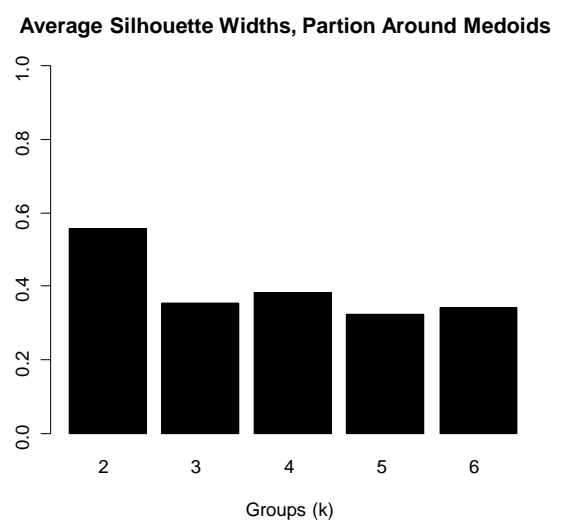
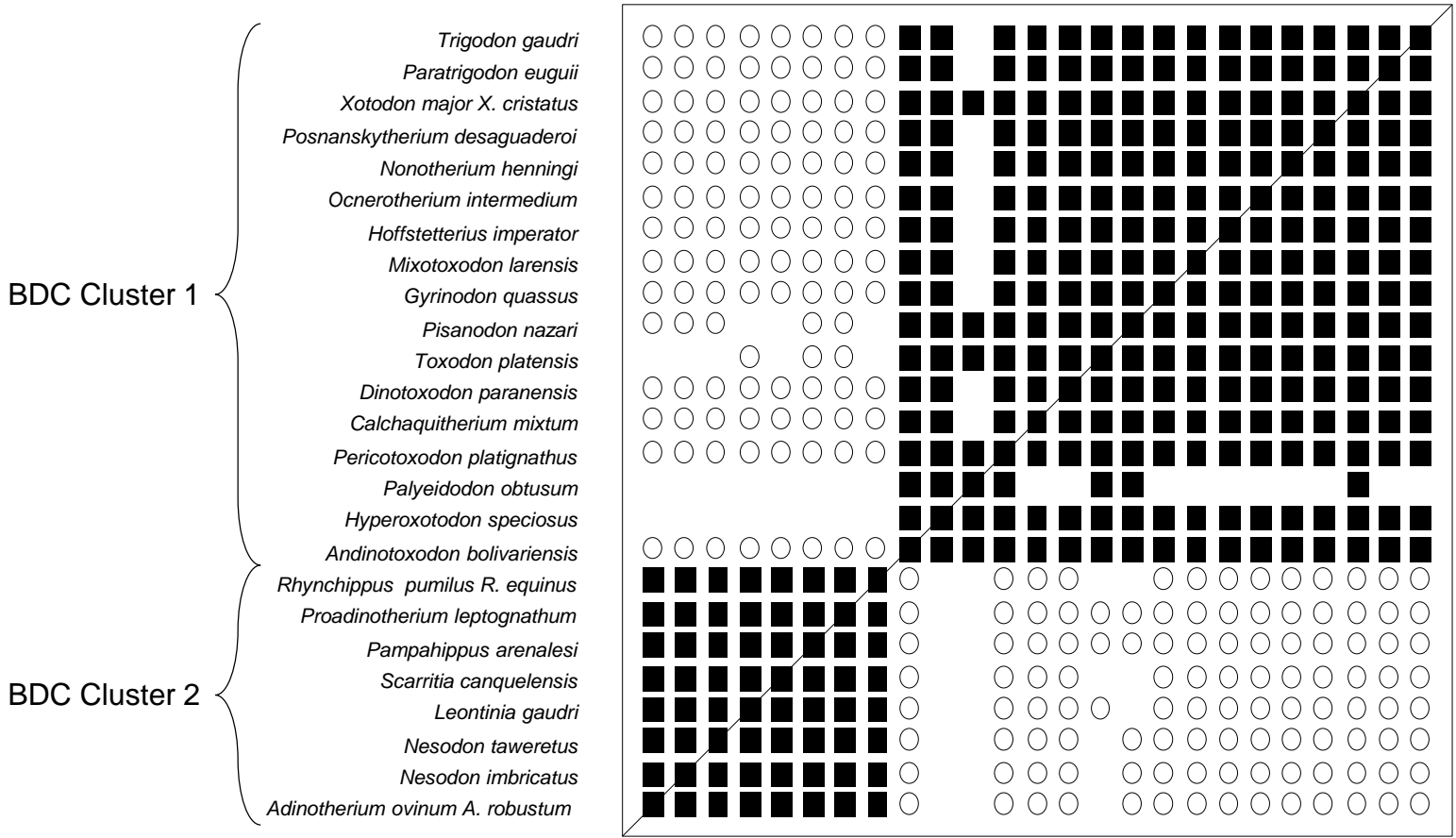


Order Notoungulata
Family Toxodontidae

Published taxa	25
Published characters	59
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	25
Characters used for calculations	33
Median bootstrap value	86
F ₉₀	0.38
Stress of 3D MDS	0.14
k _{min}	4
Conclusion	HB



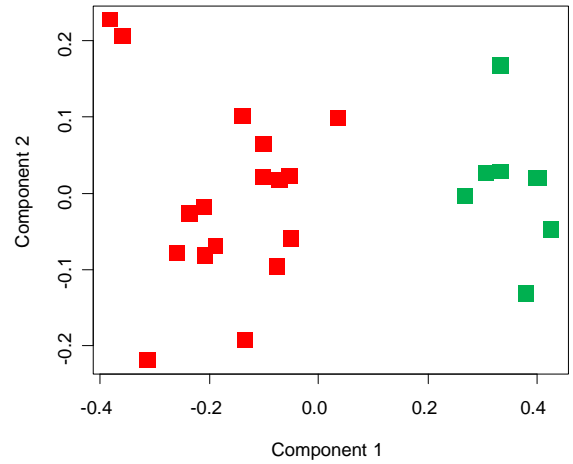
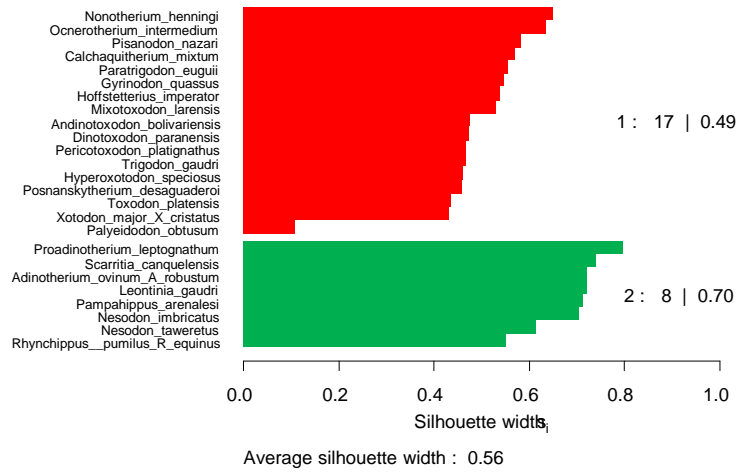
Notes: Two groups of taxa are distinguishable in the BDC and MDS results. The four outgroup taxa cluster with four basal toxodontids. Toxodontidae *sensu stricto* is a holobaramin.



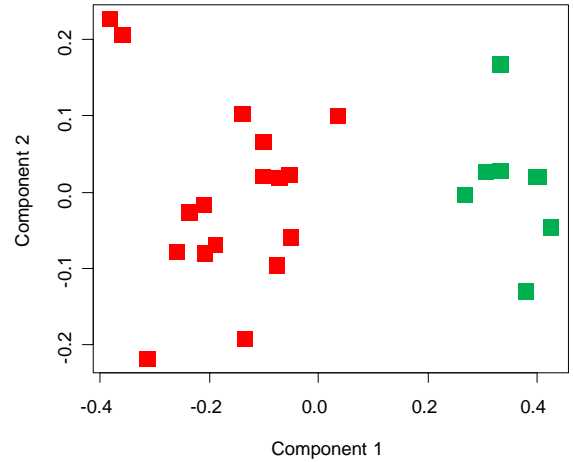
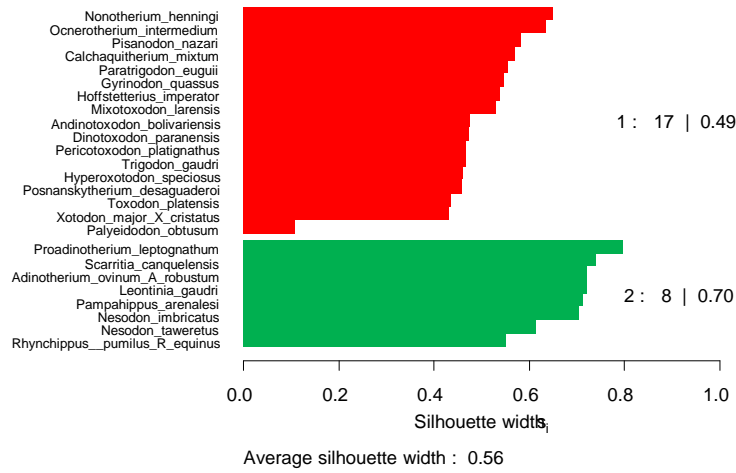
Clade Correspondence: The BDC results reveal two well defined clusters, both of which contain more than two taxa. Both are monophyletic in the published phylogeny (Forasiepi et al. 2015, Figure 11).

Silhouette plot, BDC partitions

Pearson Correlation

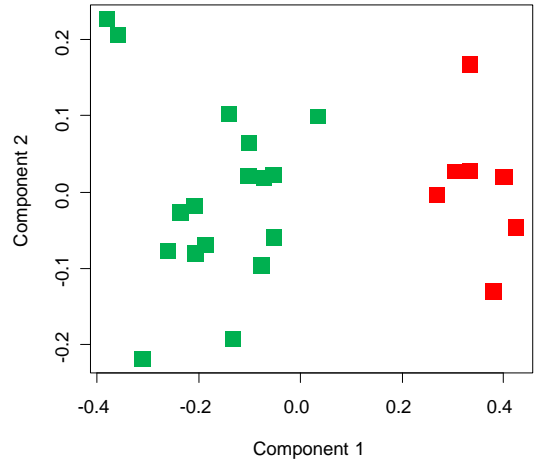
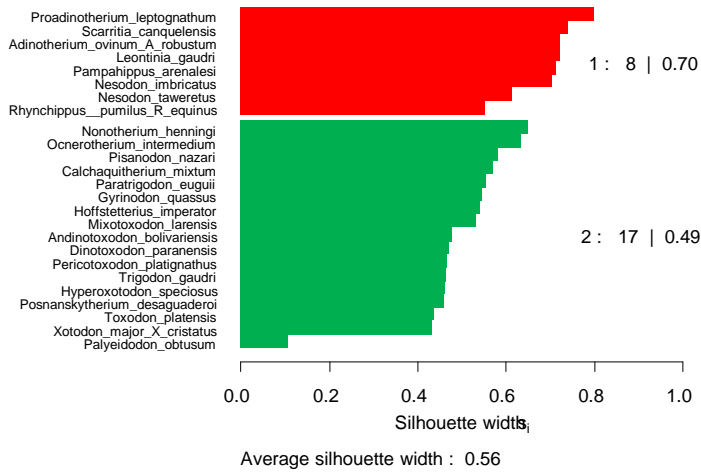


Spearman Correlation

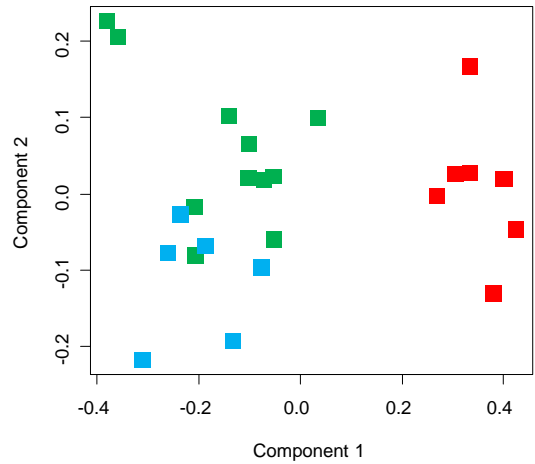
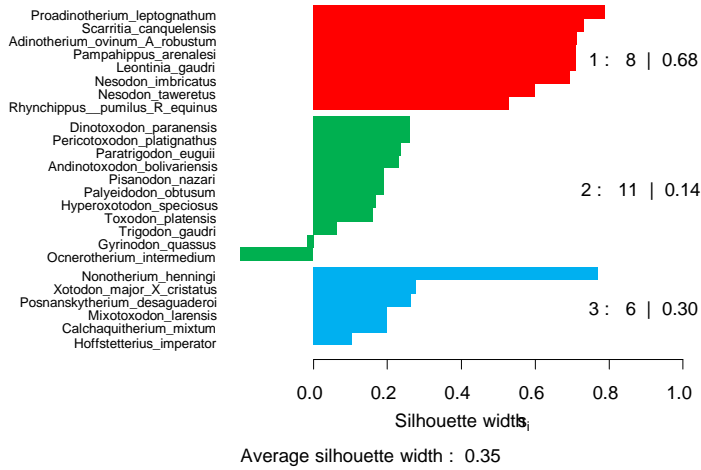


Silhouette plot, Partition Around Medoids

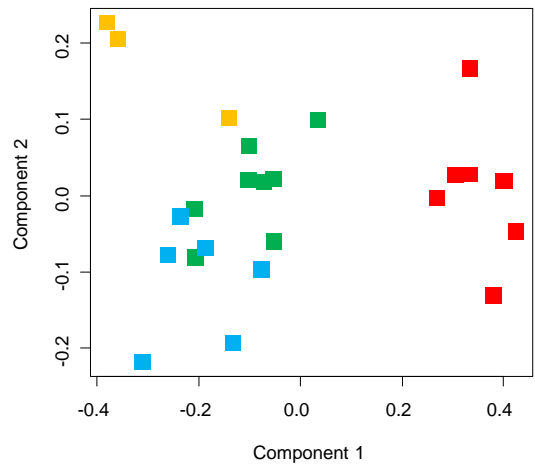
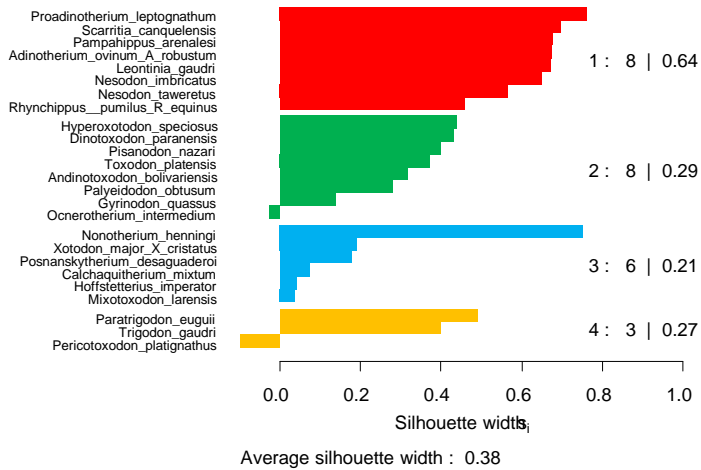
k=2



k=3

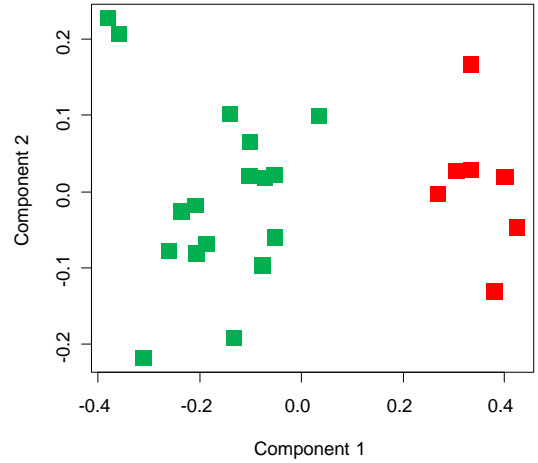
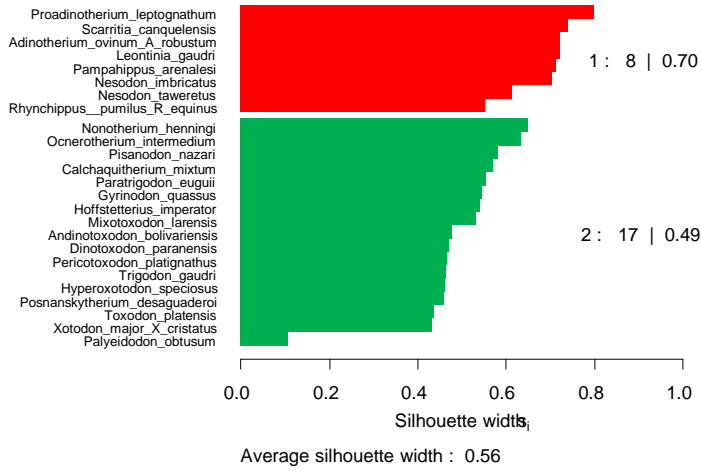


k=4

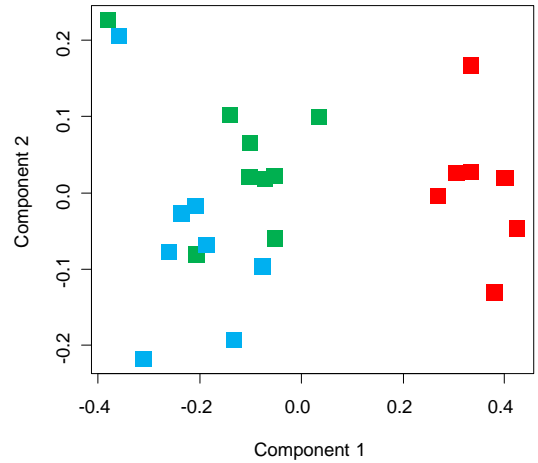
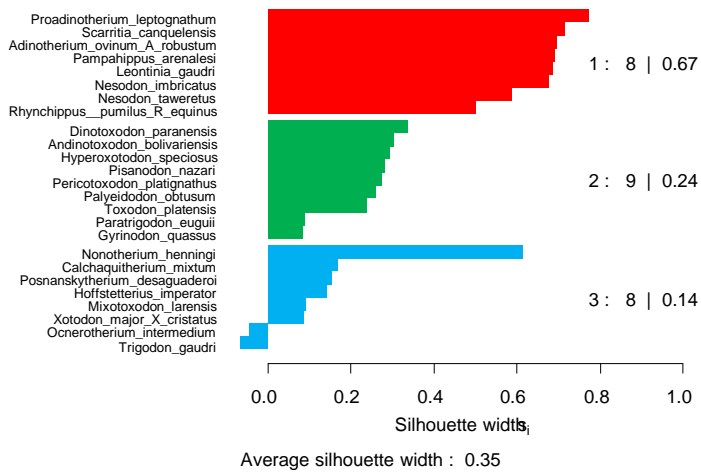


Silhouette plot, Fuzzy Analysis

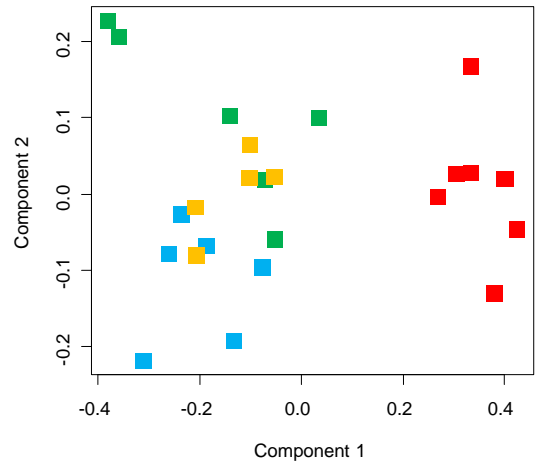
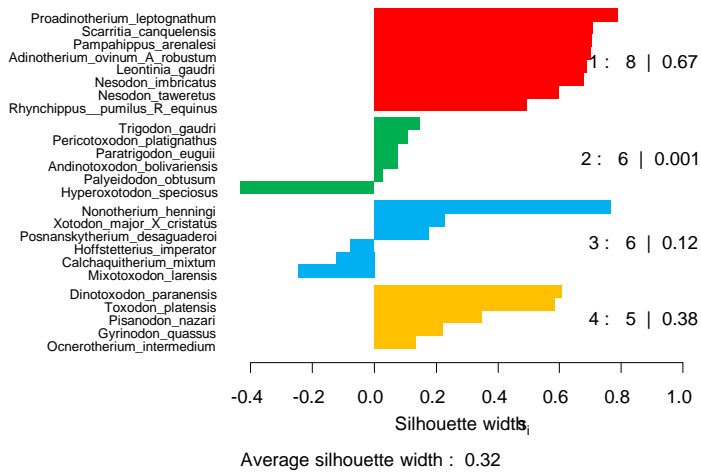
k=2



k=3



k=4



Family Interatheriidae

Order Notoungulata

Reguero et al. 2003

Pearson BDC

Negative: 21

Positive: 14

Clusters: 4

Clusterability

Hopkins Statistic: 0.815

Dip test: 0.043

Dip test p-value: 0.508

Spearman BDC

Negative: 21

Positive: 22

Clusters: 3

Spearman BDC adds eight more instances of significant, positive correlation to the Pearson BDC results. These additional correlations reduce the number of clusters from four to three. Two of the clusters in the Spearman BDC results exhibit significant, negative correlation for 21 of the 24 possible intercluster taxon pairs. Average silhouette width for the Pearson BDC clusters is 0.55 and for the Spearman BDC clusters is 0.43. The cluster membership difference is 17%.

The four-cluster medoid partition has an average silhouette width of 0.53 and differs from the Pearson BDC clusters by a single taxon *Cochilius* (cluster membership difference: 8%). The three-cluster medoid partition has an average silhouette width of 0.45 and differs from the Spearman BDC clusters by three taxa (cluster membership difference 25%). The five-cluster medoid partition has the largest average silhouette value by far, 0.7.

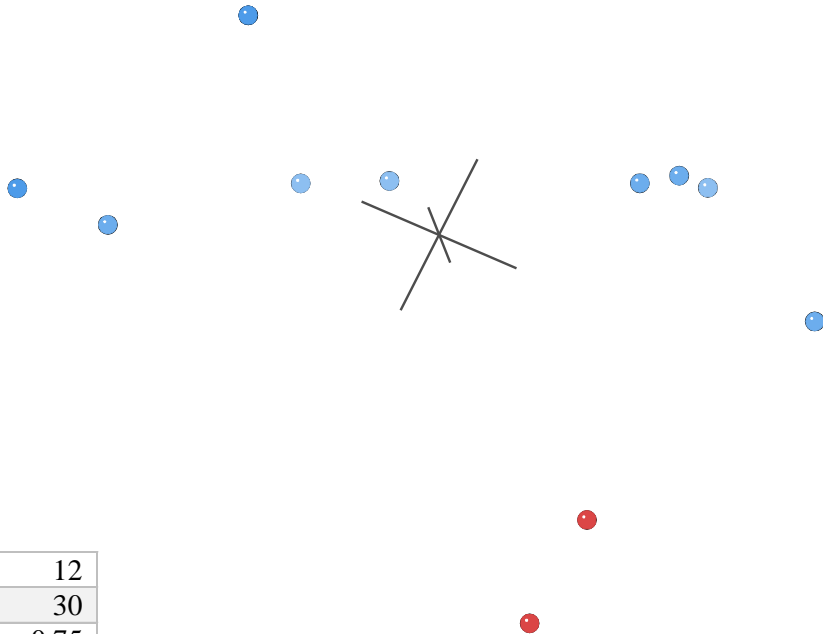
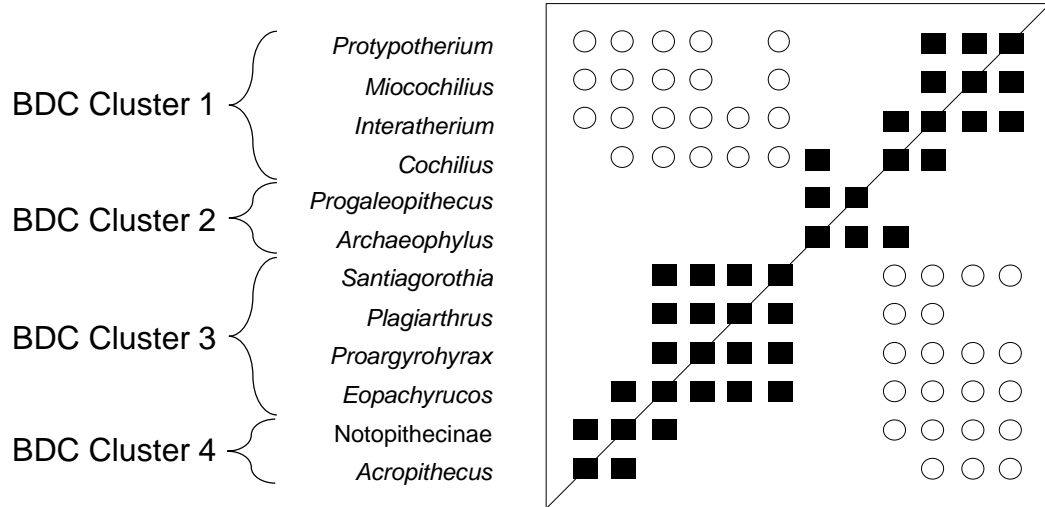
Four-cluster fuzzy partitioning has an average silhouette width of 0.58 and agrees moderately well with the Pearson BDC clustering (cluster membership difference: 17%). Three-cluster fuzzy analysis agrees exactly with the three-cluster medoid partition and thus differs by three taxa from the Spearman BDC clustering. Unlike the medoid partition, fuzzy analysis at $k=5$ produces a partition with a lower average silhouette width (0.49) than fuzzy analysis at $k=4$.

In the original analysis we refrained from drawing a conclusion because the MDS revealed a highly diffuse set of taxa with no clear clustering, despite the BDC results. These new analyses confirm that diagnosis. Different methods give an inconsistent division of taxa into clusters. Though the five-cluster medoid partition represents the best average silhouette width, that partition is not confirmed by the five-cluster fuzzy analysis. These results present too much uncertainty to warrant any conclusion.

Original conclusion: Inconclusive

Updated conclusion: Inconclusive

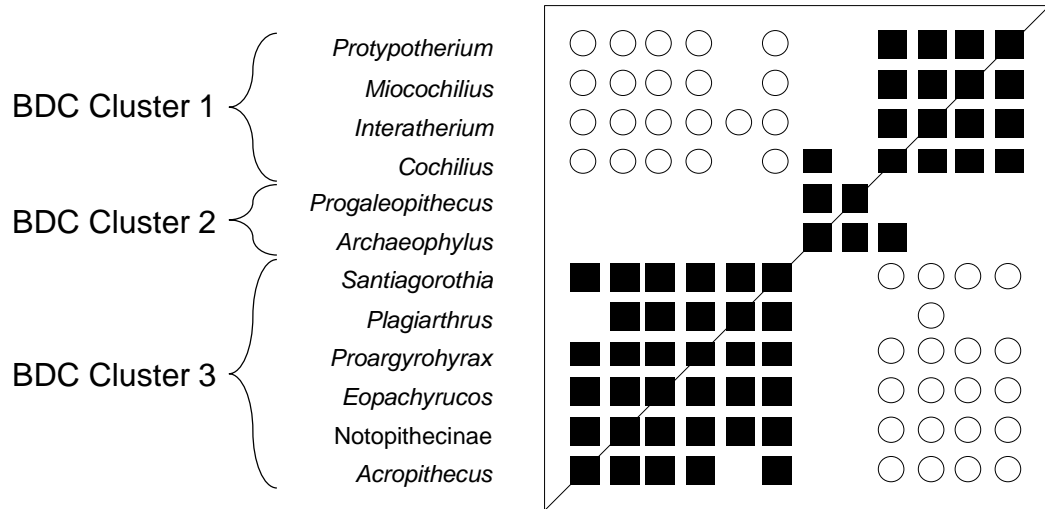
Reguero, M.A., M. Ubilla, and D. Perea. 2003. A new species of *Eopachyrucos* (Mammalia, Notoungulata, Interatheriidae) from the late Oligocene of Uruguay. *Journal of Vertebrate Paleontology* 23:445-457. Characters: Craniodental and postcranial



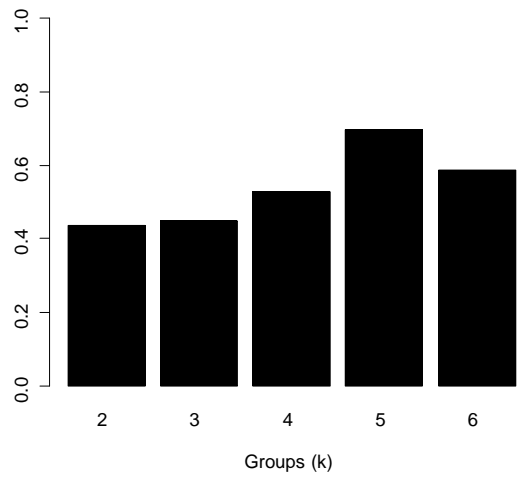
Order Notoungulata
Family Interatheriidae

Published taxa	12
Published characters	30
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	12
Characters used for calculations	26
Median bootstrap value	78.5
F ₉₀	0.23
Stress of 3D MDS	0.08
k _{min}	3
Conclusion	Inc

Notes: BDC reveals two groups with no overlap, neither of which corresponds to a named taxonomic group. The MDS does not confirm these groups but instead shows separation between the ingroup Interatheriinae and two taxa corresponding to the outgroup *Acropithecus* and the composite interatheriid subfamily Notopithecinae. These results are inconclusive.



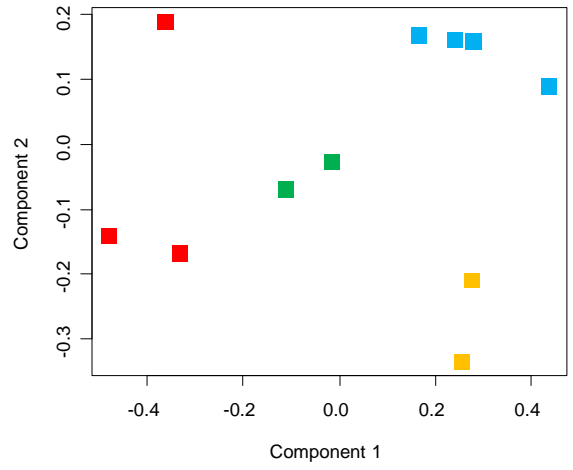
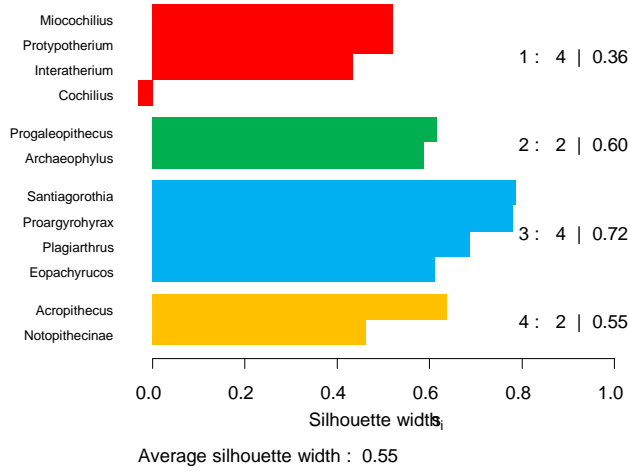
Average Silhouette Widths, Partion Around Medoids



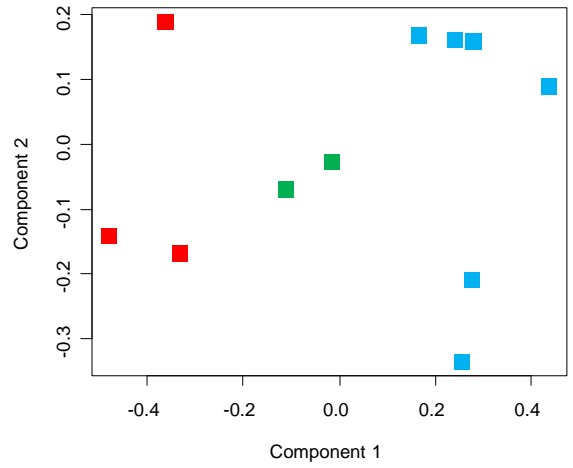
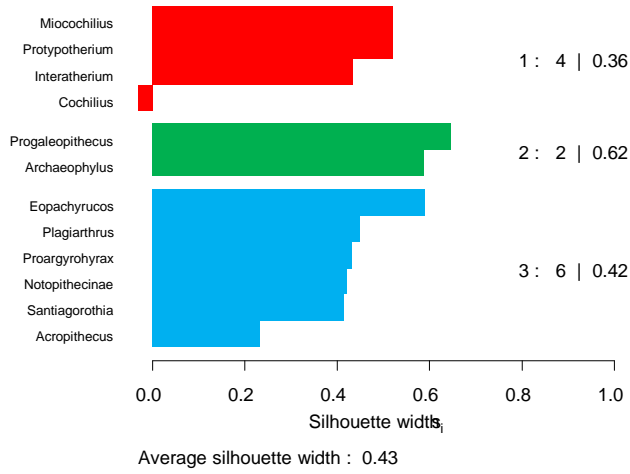
Clade Correspondence: All four BDC clusters contain at least two taxa. Only clusters 1 and 4 are monophyletic in the strict consensus tree shown in Figure 8 of Reguero et al. (2003).

Silhouette plot, BDC partitions

Pearson Correlation

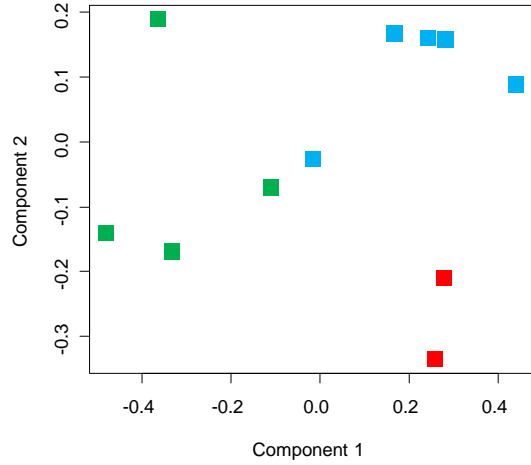
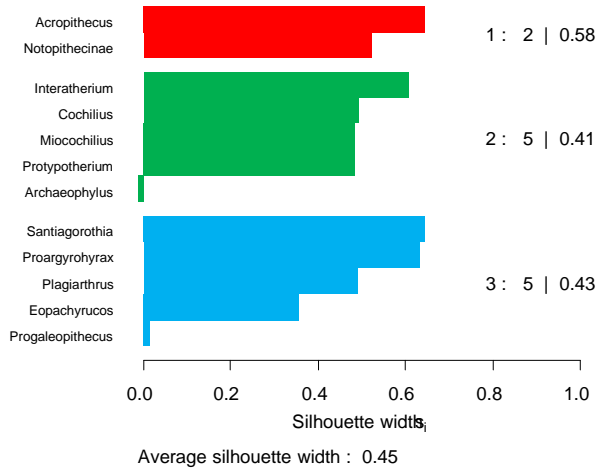


Spearman Correlation

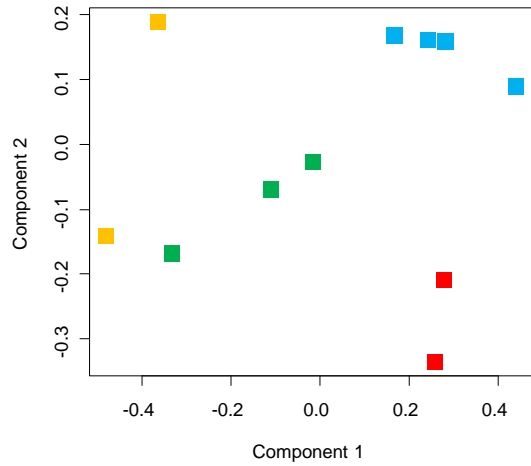
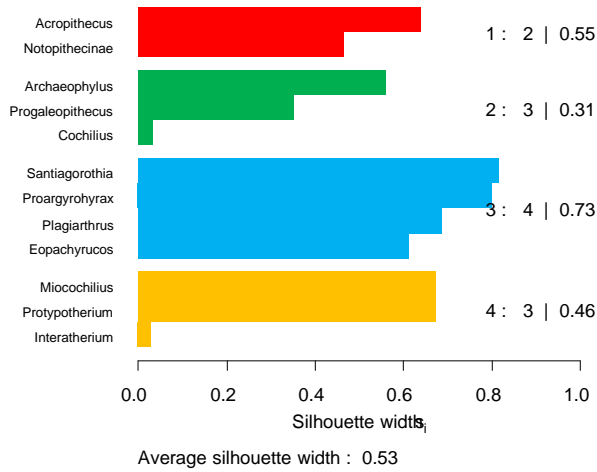


Silhouette plot, Partition Around Medoids

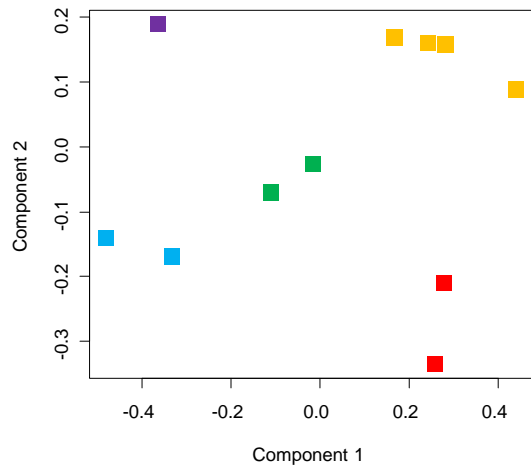
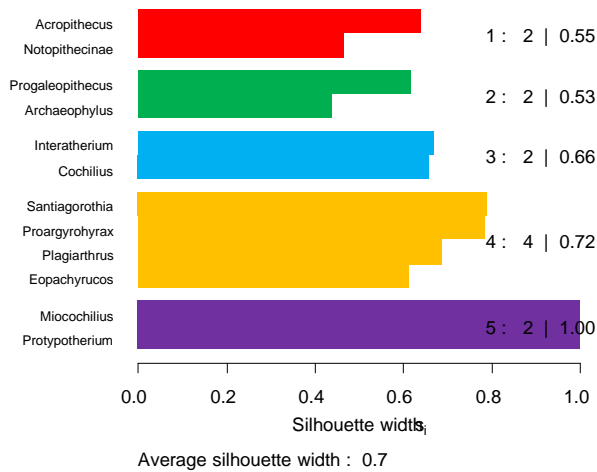
k=3



k=4

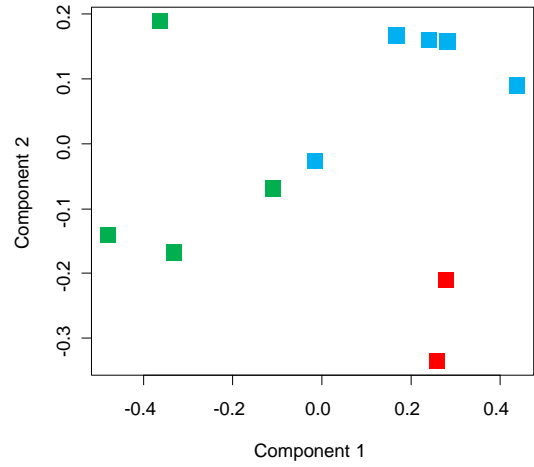
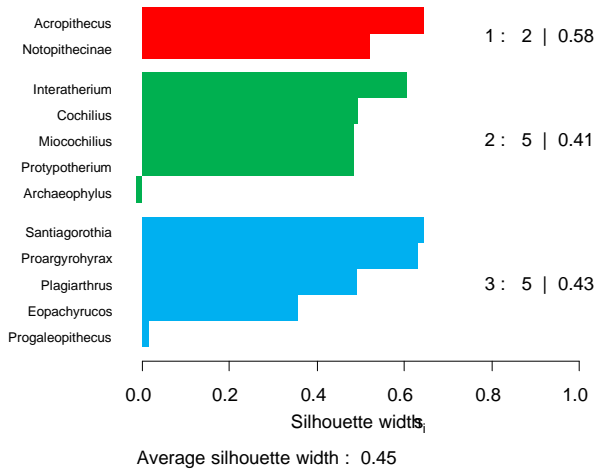


k=5

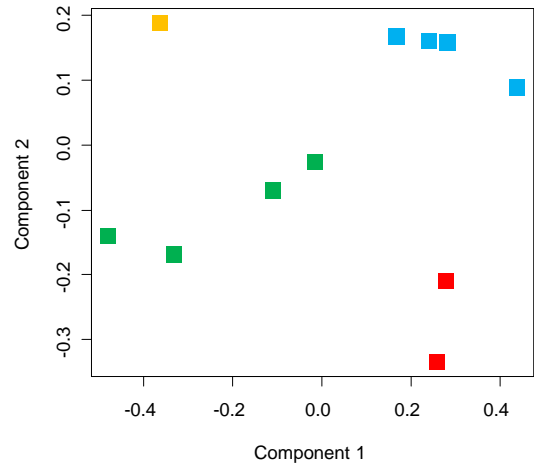
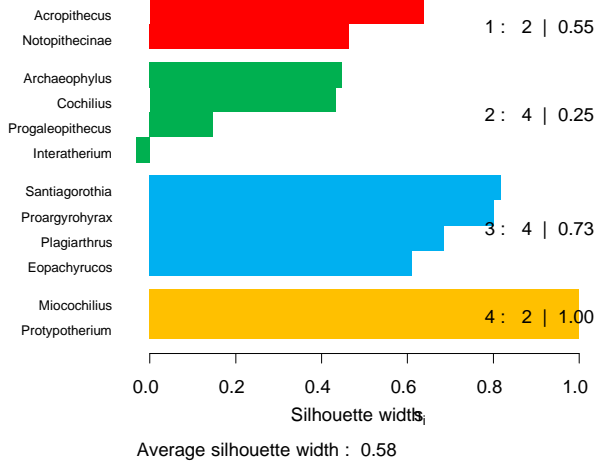


Silhouette plot, Fuzzy Analysis

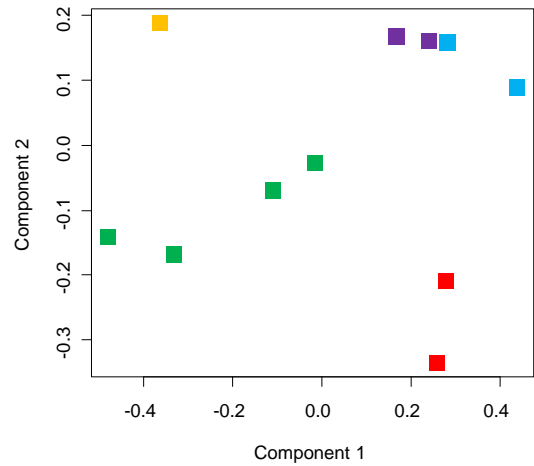
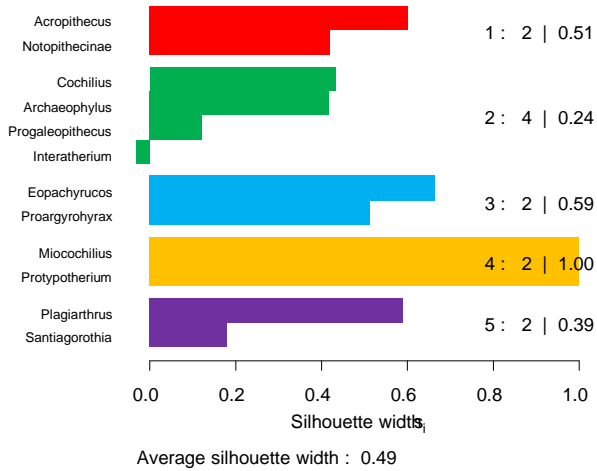
k=3



k=4



k=5



Family Interatheriidae

Order Notoungulata

Hitz et al. 2006

Pearson BDC

Negative: 60

Positive: 60

Clusters: 3

Clusterability

Hopkins Statistic: 0.838

Dip test: 0.063

Dip test p-value: 0.00032

Spearman BDC

Negative: 60

Positive: 61

Clusters: 2

The Pearson BDC results reveal three very clear clusters, for two of which, every possible intracluster taxon pair exhibits either significant, positive correlation, and every possible intercluster taxon pair exhibits significant, negative correlation. Only one taxon, *Johnbell*, has no significant correlation with any other taxa.

The Spearman BDC results are nearly identical, except that *Johnbell* now exhibits significant, positive BDC with *Santiagorothia*, placing *Johnbell* in the larger of the two other clusters. This reduces the number of BDC clusters from three to two, but the cluster membership difference is still only 6% (one taxon). The average silhouette width for the three-cluster Pearson BDC partition is 0.6 and for the two-cluster Spearman BDC partition is 0.69.

The two-cluster medoid partition agrees exactly with the Spearman BDC partition, but the three-cluster medoid partition differs substantially from the Pearson BDC partition, with a cluster membership difference of 29%. The three-cluster medoid partition has an average silhouette width of 0.35, with four taxa having negative silhouette widths.

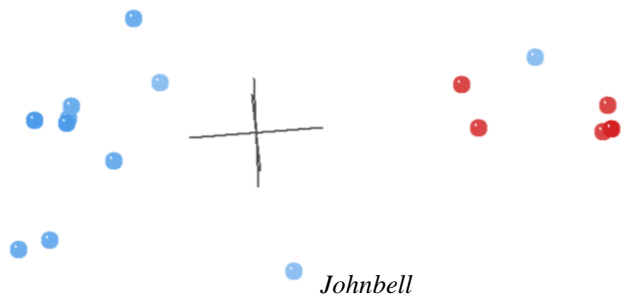
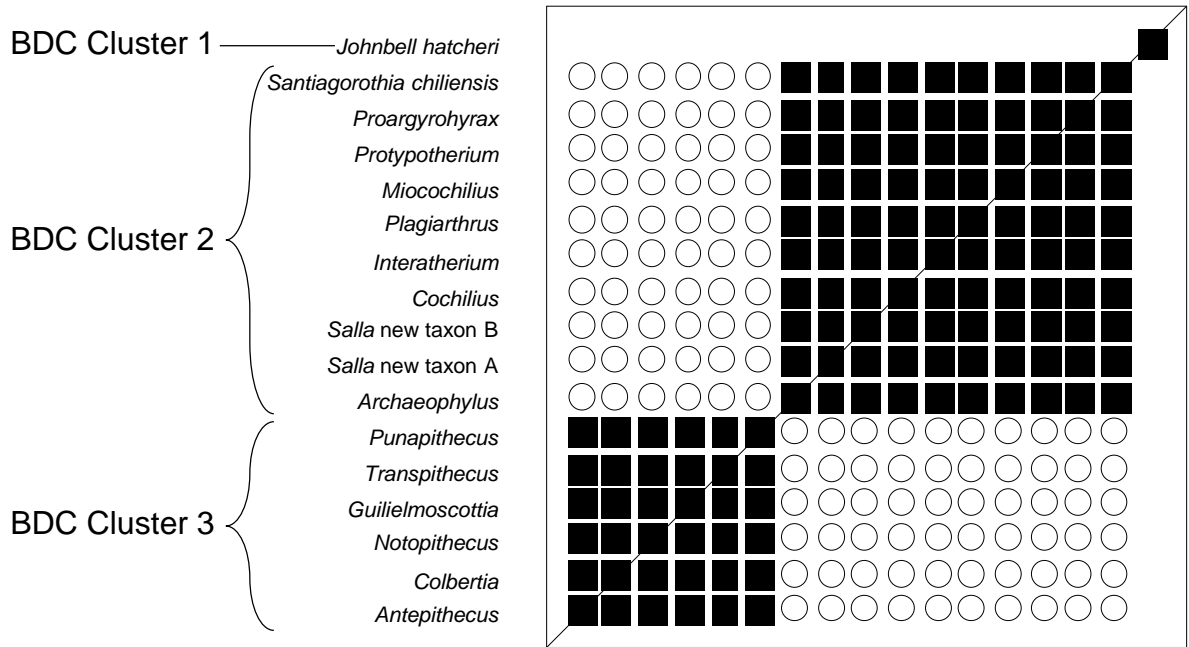
Two-cluster fuzzy partition also matches the Spearman BDC clusters exactly, but the three-cluster fuzzy analysis yields yet another partition of the taxa that differs from the Pearson BDC clusters and from the three-cluster medoid partition. The three-cluster fuzzy partition has an average silhouette width of 0.53 with only one taxon having a negative silhouette width. It differs from the Pearson BDC clusters by two taxa (cluster membership difference: 12%).

The original analysis concluded that Interatheriidae (except *Notopithecus*) was a holobaramin, but the position of *Johnbell* was uncertain. Here, the new analyses confirm this result and consistently place *Johnbell* with the interatheriids in the Spearman BDC clusters, the two-cluster medoid partition, and the two-cluster fuzzy analysis. Interatheriidae, including *Johnbell* but excluding *Notopithecus*, is a holobaramin.

Original conclusion: HB

Updated conclusion: HB

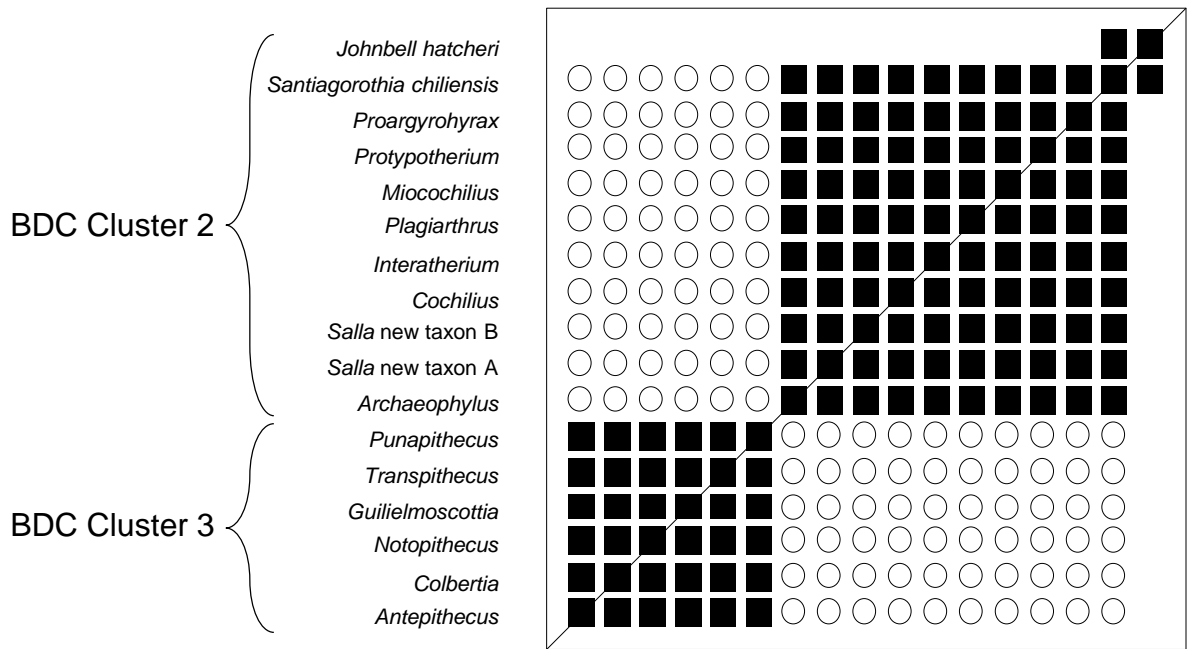
Characters: Craniodental



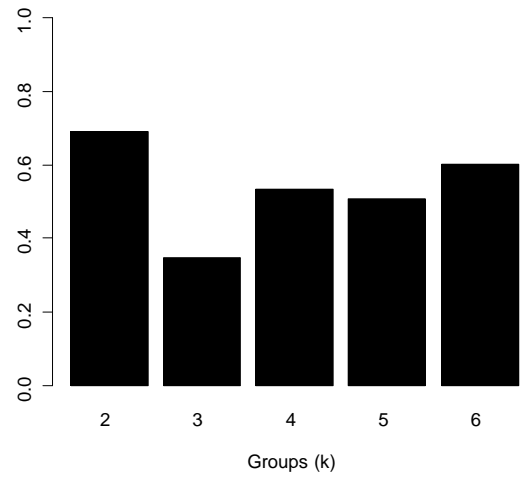
Order Notoungulata
Family Interatheriidae

Published taxa	21
Published characters	43
Character relevance	0.75
Taxic relevance	0.45
Taxa used for calculations	17
Characters used for calculations	21
Median bootstrap value	98
F ₉₀	0.76
Stress of 3D MDS	0.04
k _{min}	3
Conclusion	HB

Notes: BDC and MDS support a distinct Interatheriidae cluster. The interatheriid *Punapithecus* clusters with the outgroup, and another, *Johnbell*, shares no BDC with any other taxa. Interatheriidae *sensu stricto* could be a holobaramin.



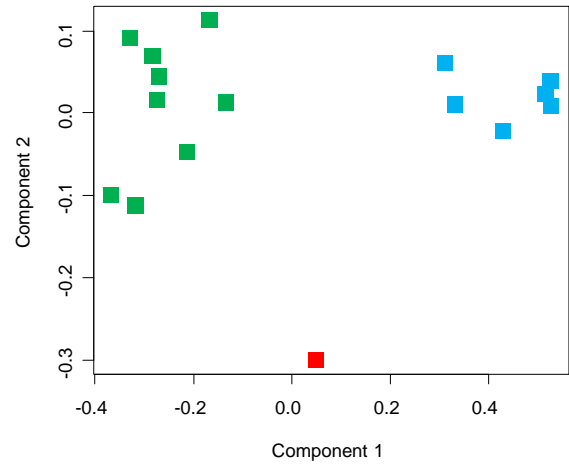
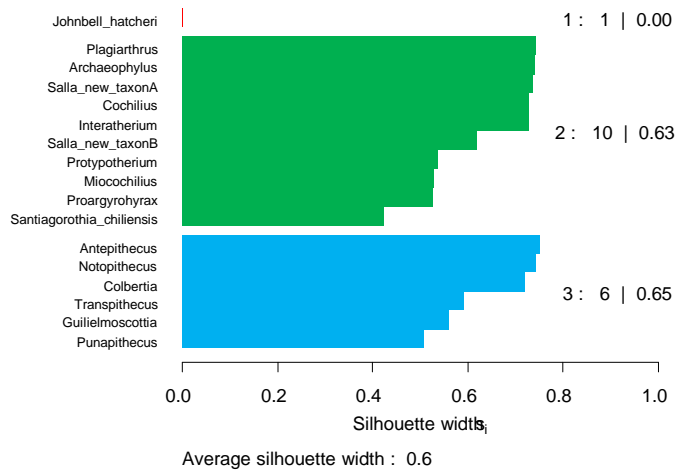
Average Silhouette Widths, Partion Around Medoids



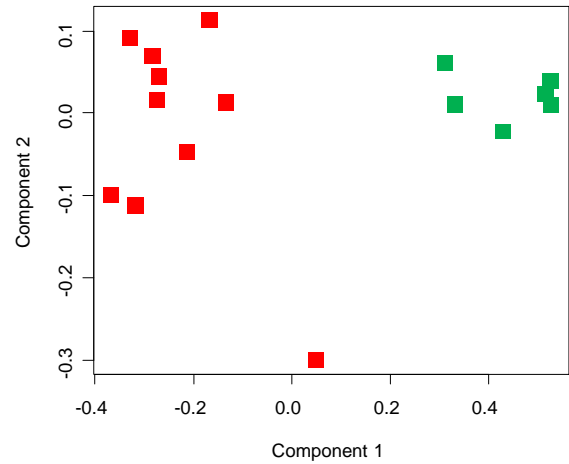
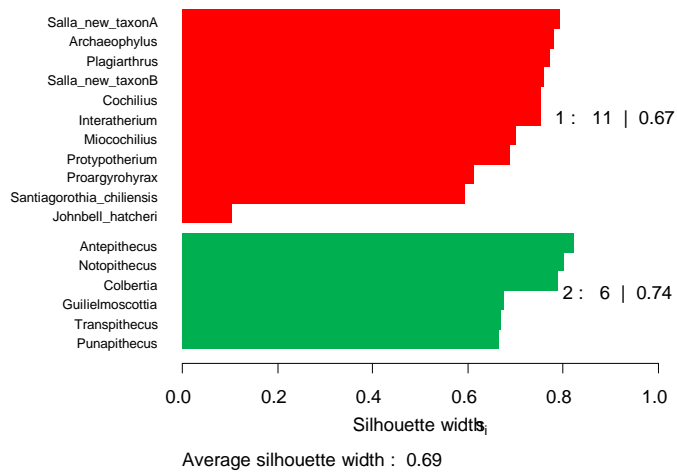
Clade Correspondence: The BDC results reveal two large clusters (numbered 2 and 3) and a singleton. Both clusters are clades in the phylogeny shown in Figure 6 of Hitz et al. (2006).

Silhouette plot, BDC partitions

Pearson Correlation

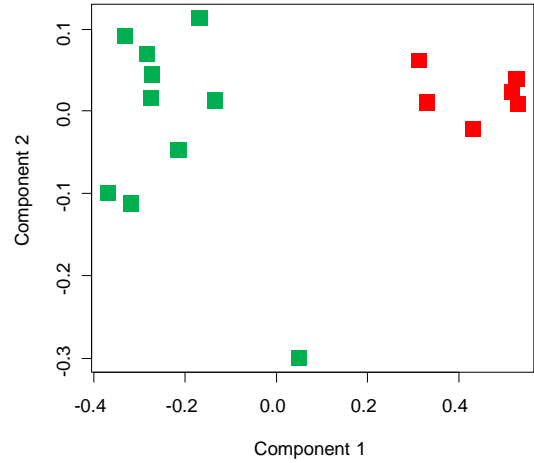
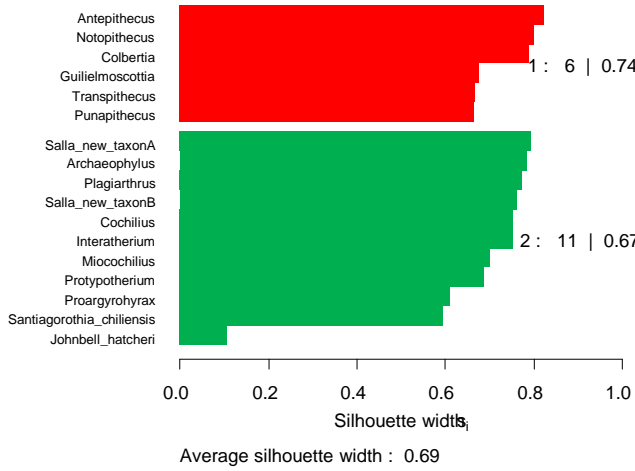


Spearman Correlation

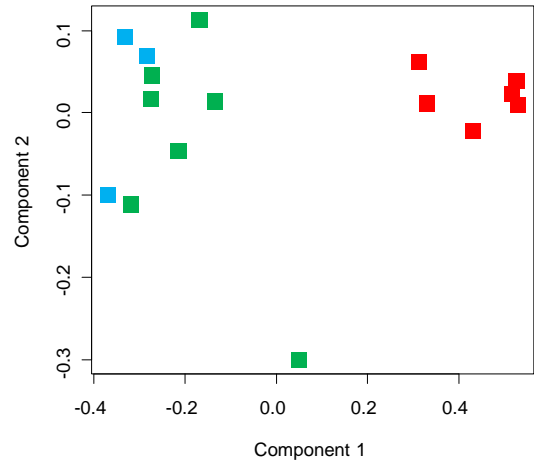
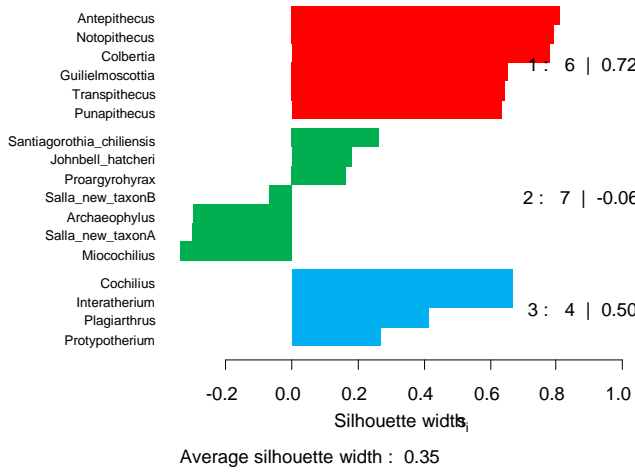


Silhouette plot, Partition Around Medoids

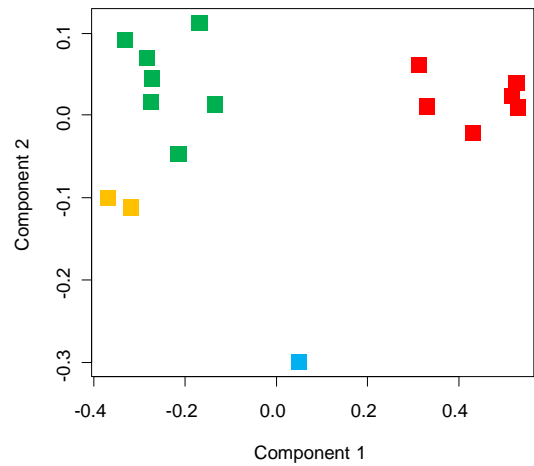
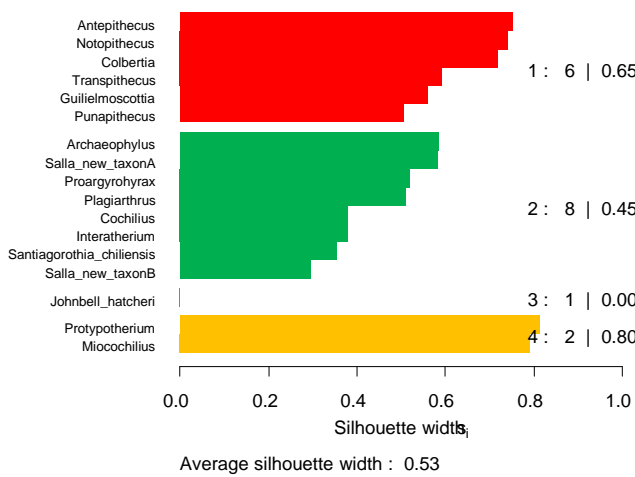
k=2



k=3

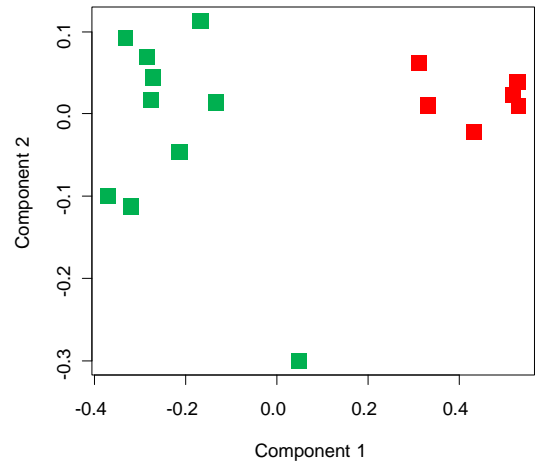
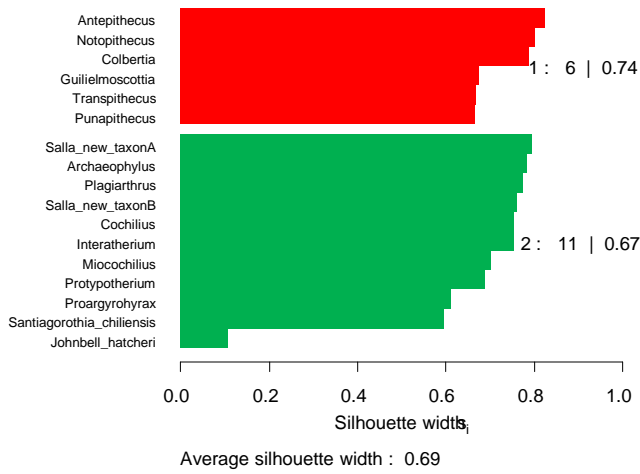


k=4

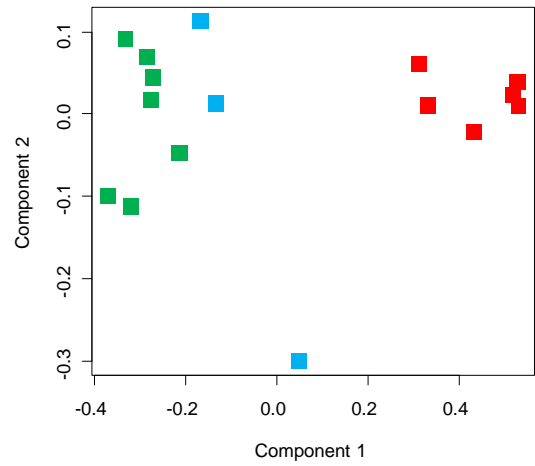
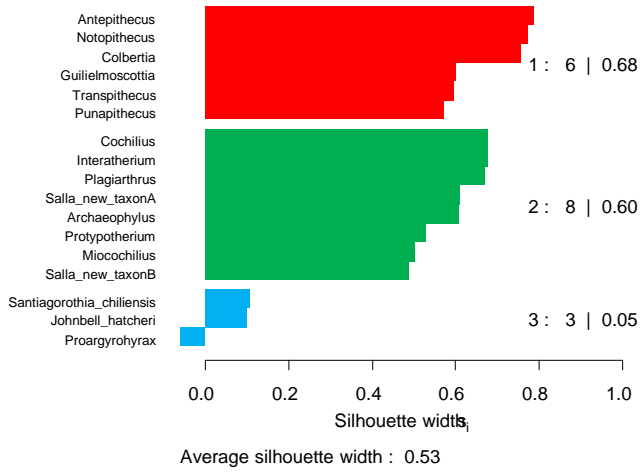


Silhouette plot, Fuzzy Analysis

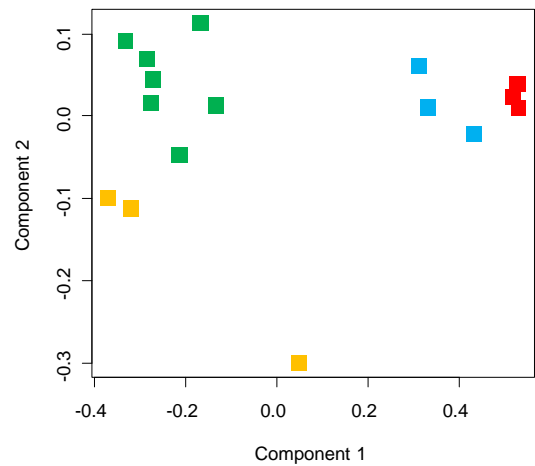
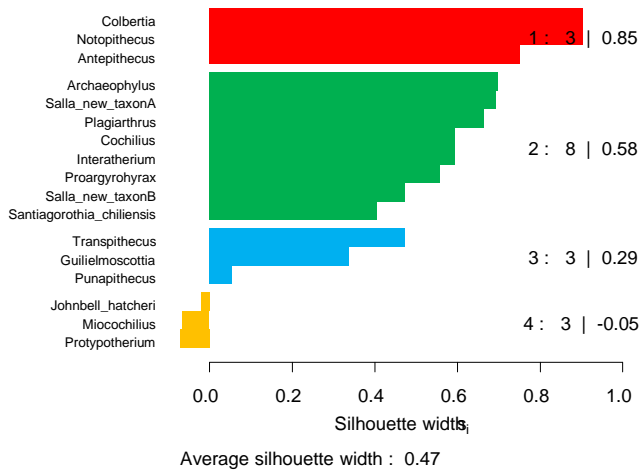
k=2



k=3



k=4



Family Hegetotheriidae

Order Notoungulata

Billet et al. 2009

Pearson BDC

Negative: 32

Positive: 30

Clusters: 2

Clusterability

Hopkins Statistic: 0.847

Dip test: 0.039

Dip test p-value: 0.543

Spearman BDC

Negative: 38

Positive: 35

Clusters: 2

The Spearman BDC results add five instances of significant, positive correlation and six instances of significant, negative correlation to the Pearson BDC results, but these correlations only serve to reinforce the original two-cluster partition of the Pearson BDC results. These clusters correspond exactly to the ingroup and outgroup taxa and have an average silhouette width of 0.61.

Two-cluster medoid partition agrees exactly with the BDC clusters, as does the two-cluster fuzzy analysis.

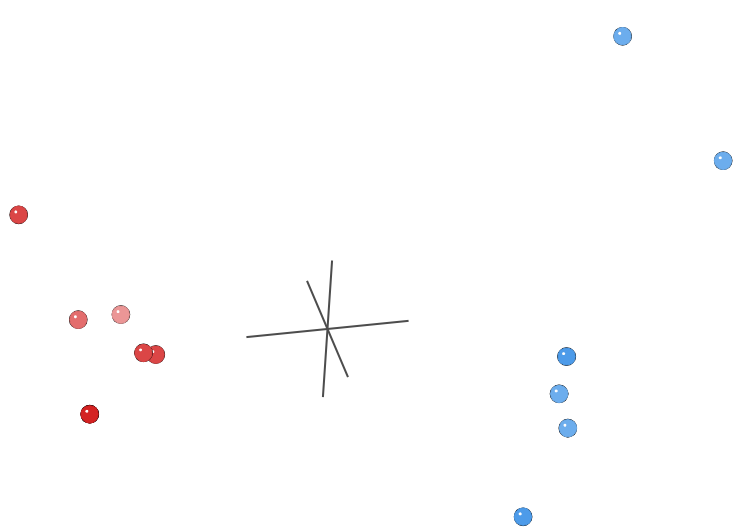
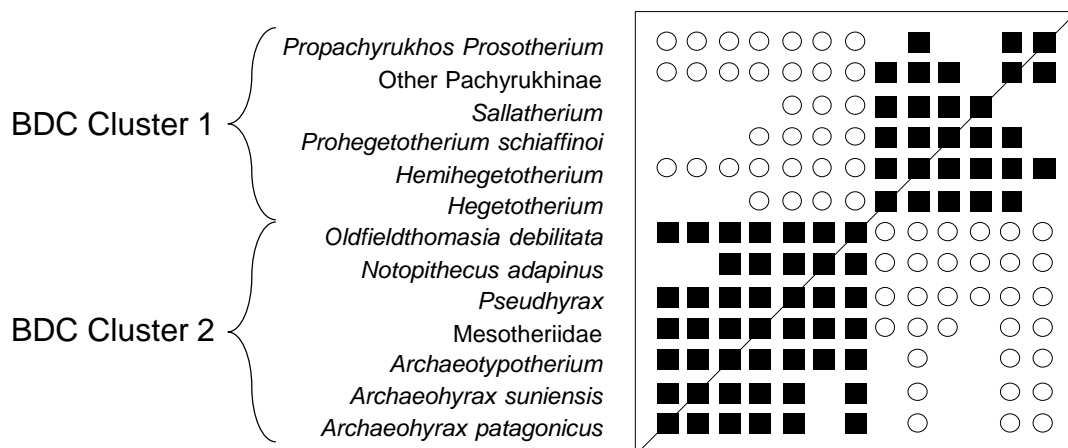
The original results are identical across all new analyses, and therefore we may simply affirm the original conclusion. Hegetotheriidae is a holobaramin.

Original conclusion: HB

Updated conclusion: HB

Billet, G., B. Patterson, and C. De Muizon. 2009. Craniodental anatomy of late Oligocene archaeohyracids (Notoungulata, Mammalia) from Bolivia and Argentina and new phylogenetic hypotheses. *Zoological Journal of the Linnean Society* 155:458-509.

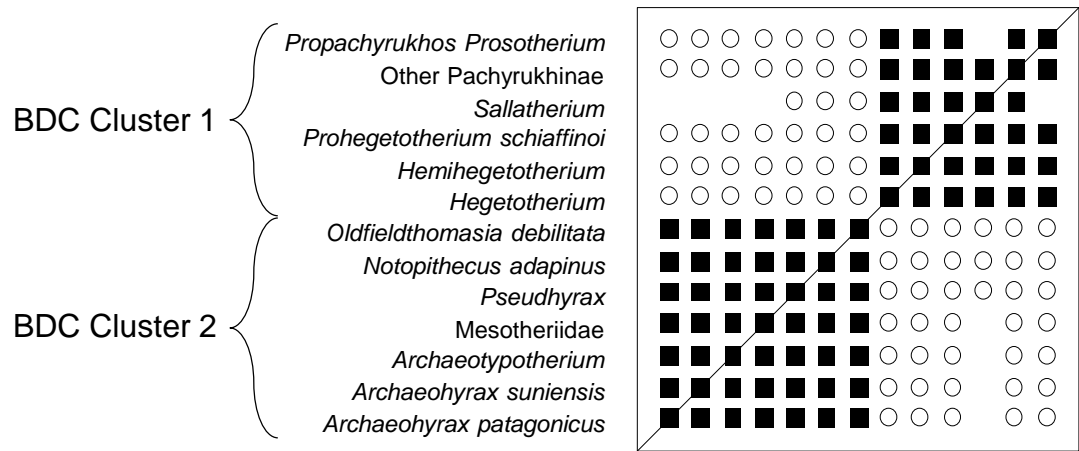
Characters: Craniodental and postcranial



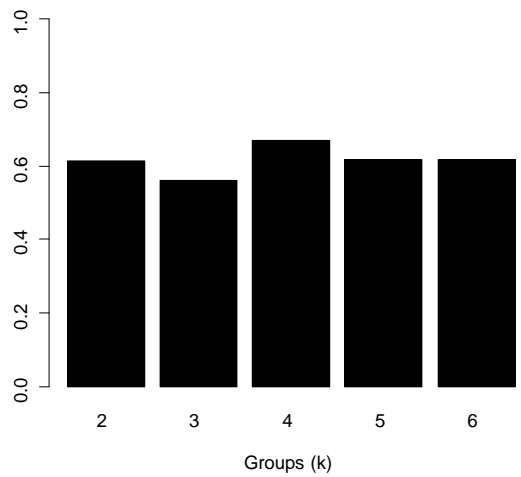
Order Notoungulata
Family Hegetotheriidae

Published taxa	15
Published characters	39
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	13
Characters used for calculations	32
Median bootstrap value	82.5
F ₉₀	0.29
Stress of 3D MDS	0.07
k _{min}	3
Conclusion	HB

Notes: Hegetotheriidae and outgroup taxa are well-separated in both BDC and MDS results. Hegetotheriidae is likely a holobaramin.



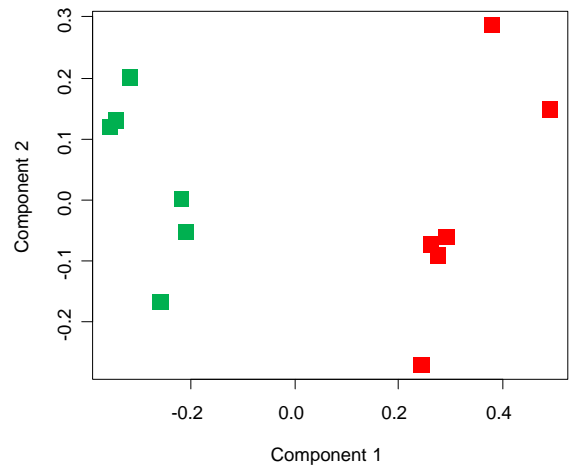
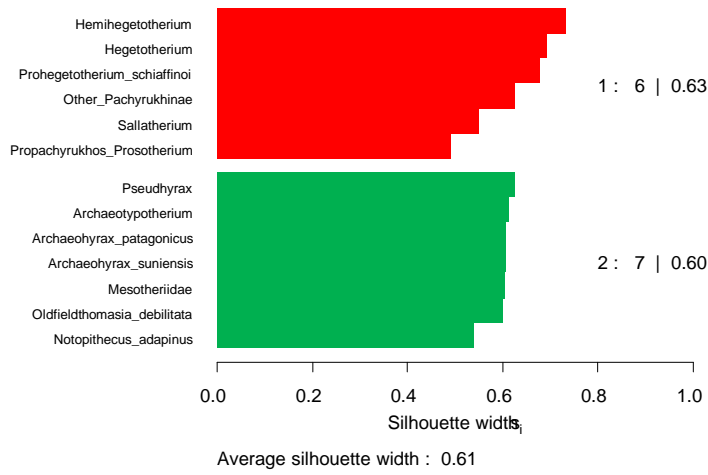
Average Silhouette Widths, Partition Around Medoids



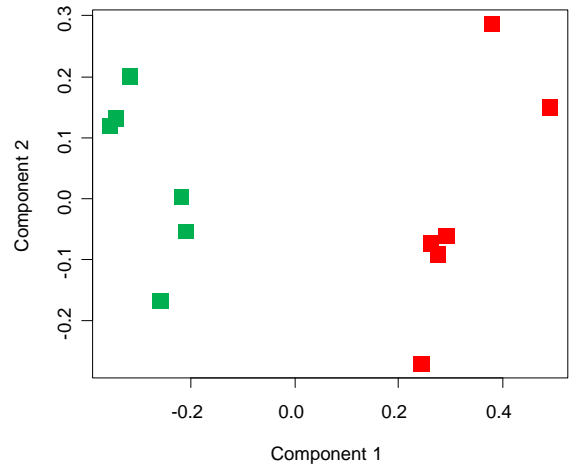
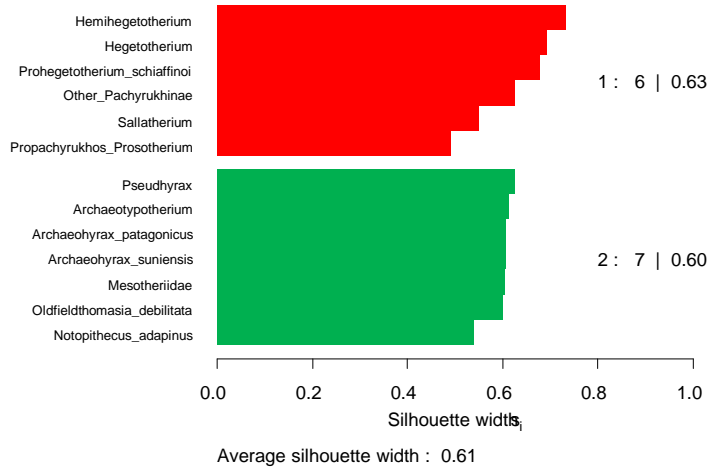
Clade Correspondence: Both BDC clusters contain more than two taxa each. Both are monophyletic in the majority rule consensus tree shown in Figure 24B of Billet et al. (2009), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

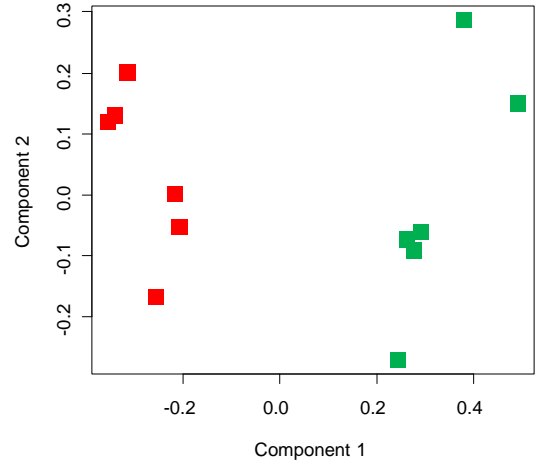
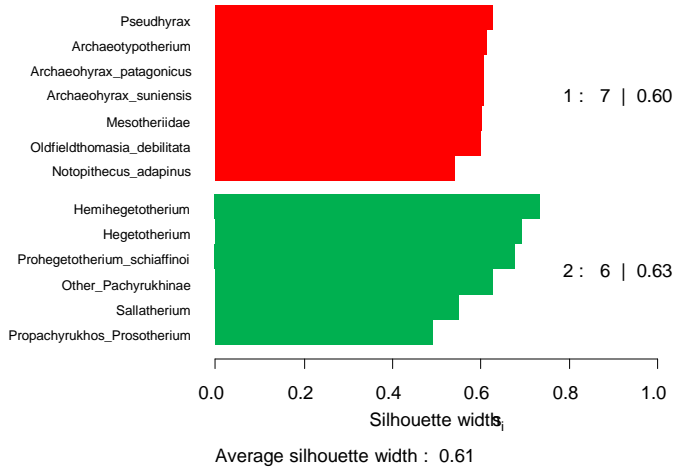


Spearman Correlation

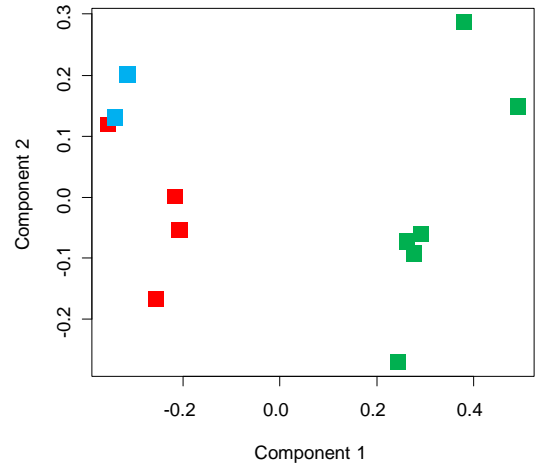
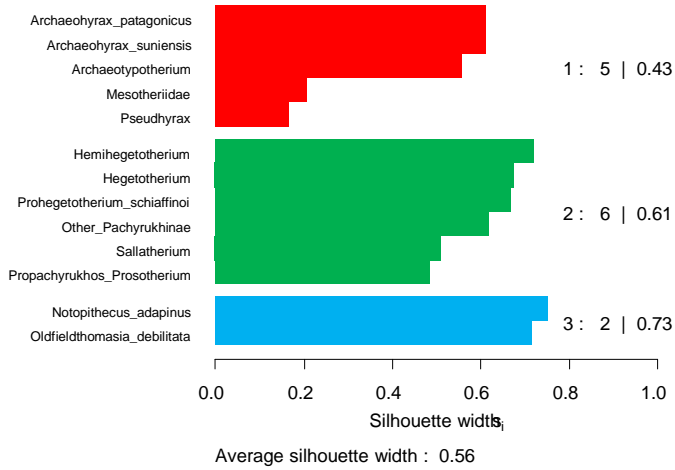


Silhouette plot, Partition Around Medoids

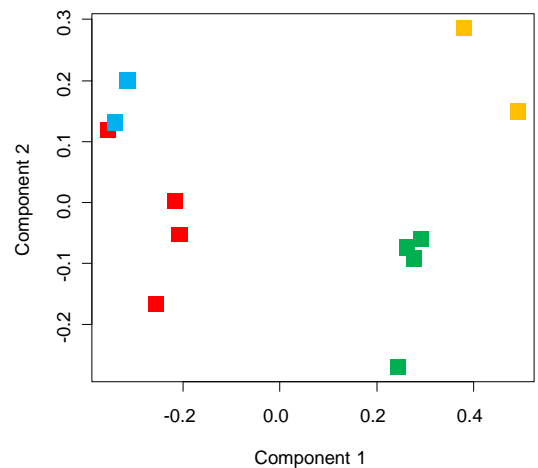
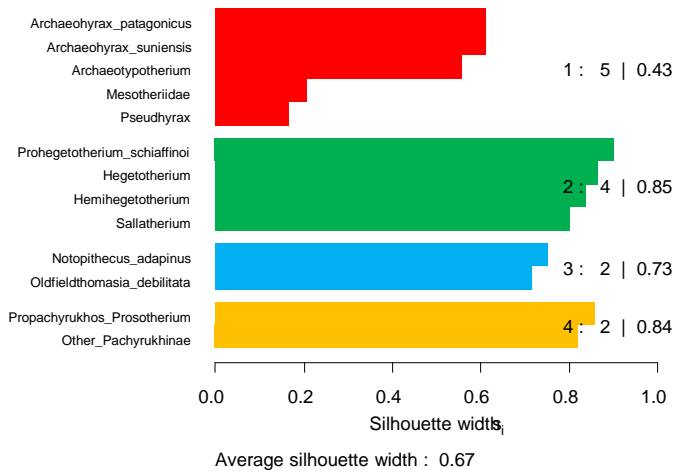
k=2



k=3

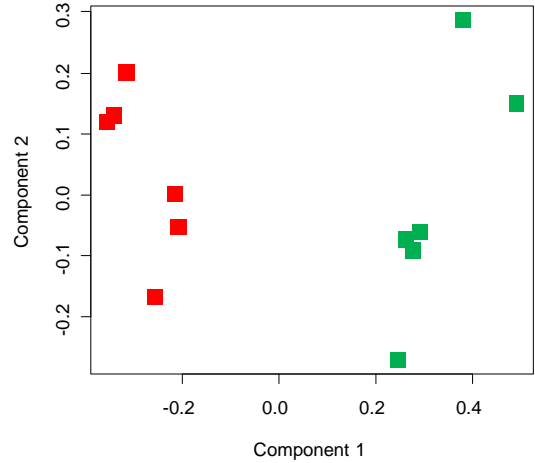
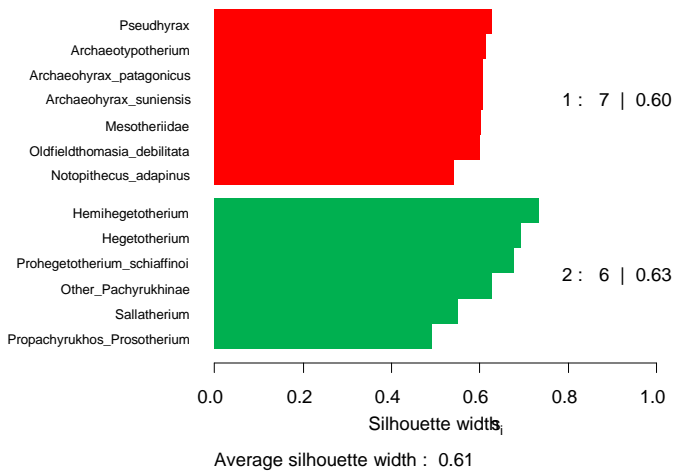


k=4

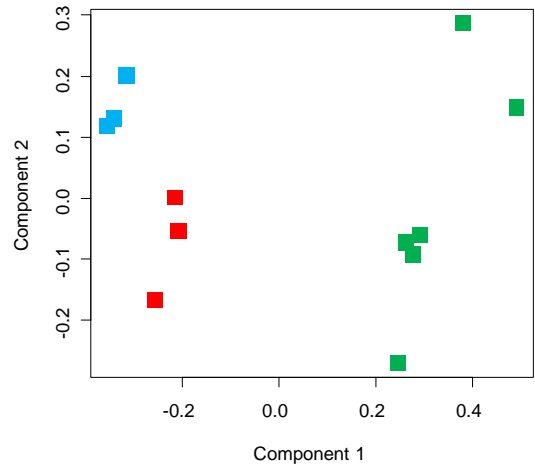
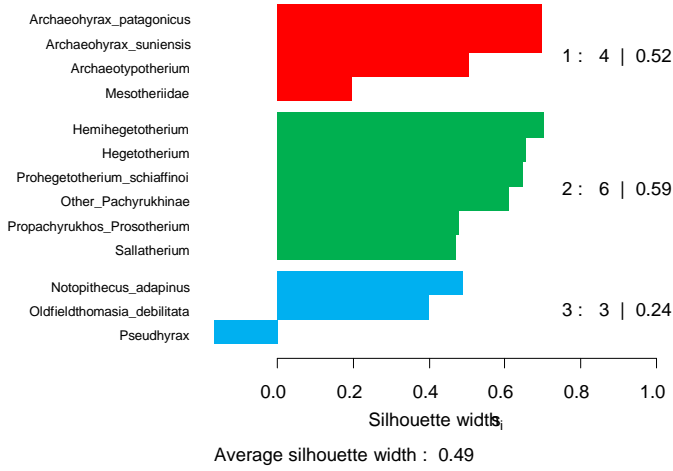


Silhouette plot, Fuzzy Analysis

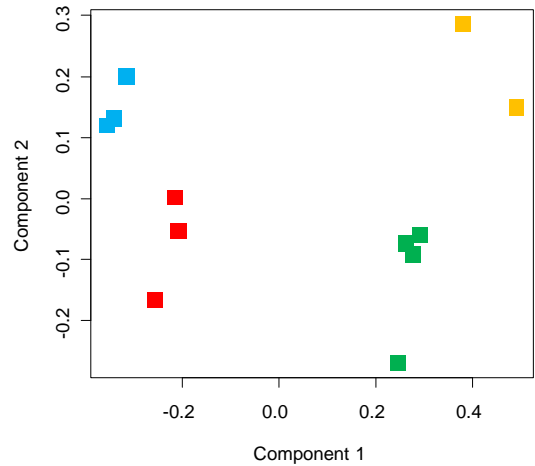
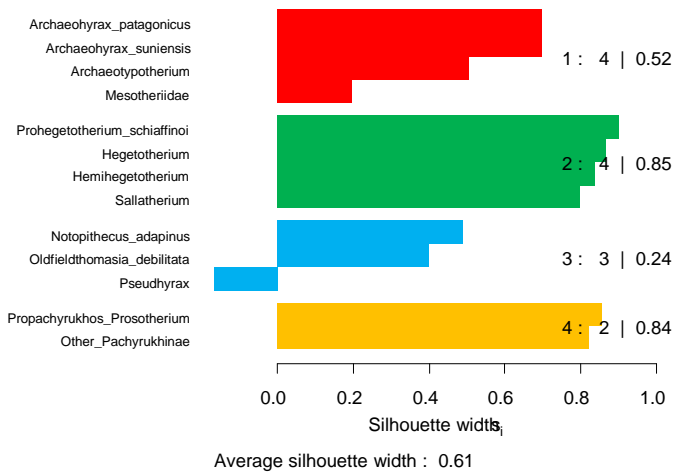
k=2



k=3



k=4



Family Astrapotheriidae

Order Astrapotheria

Vallejo-Pareja et al. 2015

Pearson BDC

Negative: 31

Positive: 29

Clusters: 3

Clusterability

Hopkins Statistic: 0.72

Dip test: 0.042

Dip test p-value: 0.381

Spearman BDC

Negative: 31

Positive: 32

Clusters: 2

Pearson BDC results reveal three groups of taxa, with one cluster corresponding to the singleton ingroup taxon *Maddenia*. Spearman BDC results add three instances of significant, positive correlation, placing *Maddenia* in the smaller cluster. Thus the number of clusters is reduced from three to two. The average silhouette width for the three-cluster Pearson BDC partition is 0.37 and for the two-cluster Spearman BDC partition is 0.52. The cluster membership difference is a single taxon (8%).

The two-cluster medoid partition agrees exactly with the Spearman BDC clustering. The three-cluster medoid partition has an average silhouette width of 0.36 and differs from the Pearson BDC partition by four taxa (cluster membership difference: 31%).

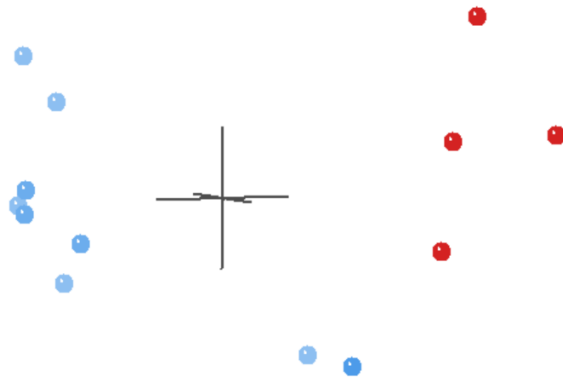
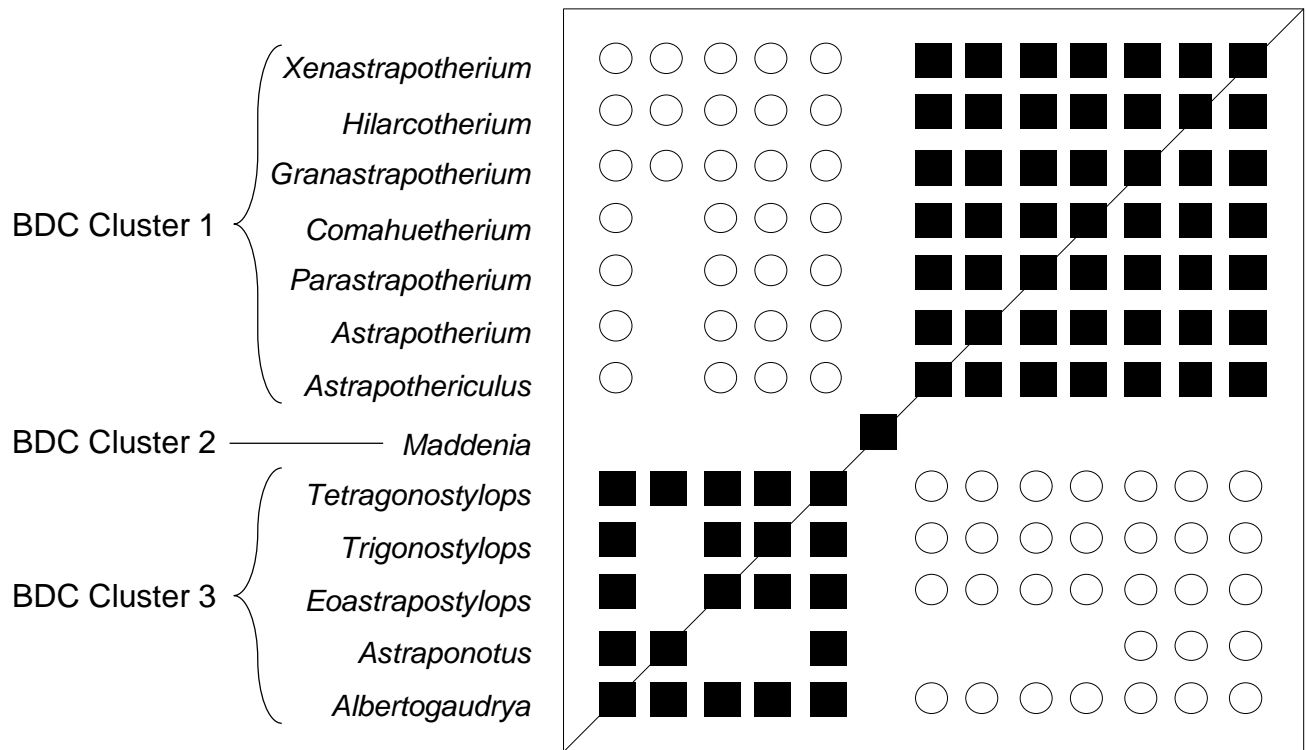
The two-cluster fuzzy analysis yields a partition that is identical to the Spearman BDC clustering and the two-cluster medoid partition. The three-cluster fuzzy partition is identical to the three-cluster medoid partition and therefore differs by four taxa with the Pearson BDC partition.

The original analysis concluded that Astrapotheriidae was a holobaramin except for two taxa. *Astraponotus*, the basal-most astrapotheriid in Vallejo-Peraja et al.'s phylogeny, grouped with the outgroup taxa, and the position of *Maddenia* was unknown. Here, the Spearman BDC results are entirely consistent with the Pearson BDC results, except that *Maddenia* groups with the outgroup taxa. This partition is supported by the two-cluster fuzzy analysis and medoid partition. Therefore the original result is confirmed, with the additional detail that *Maddenia* does not belong in the astrapotheriid holobaramin.

Original conclusion: HB

Updated conclusion: HB

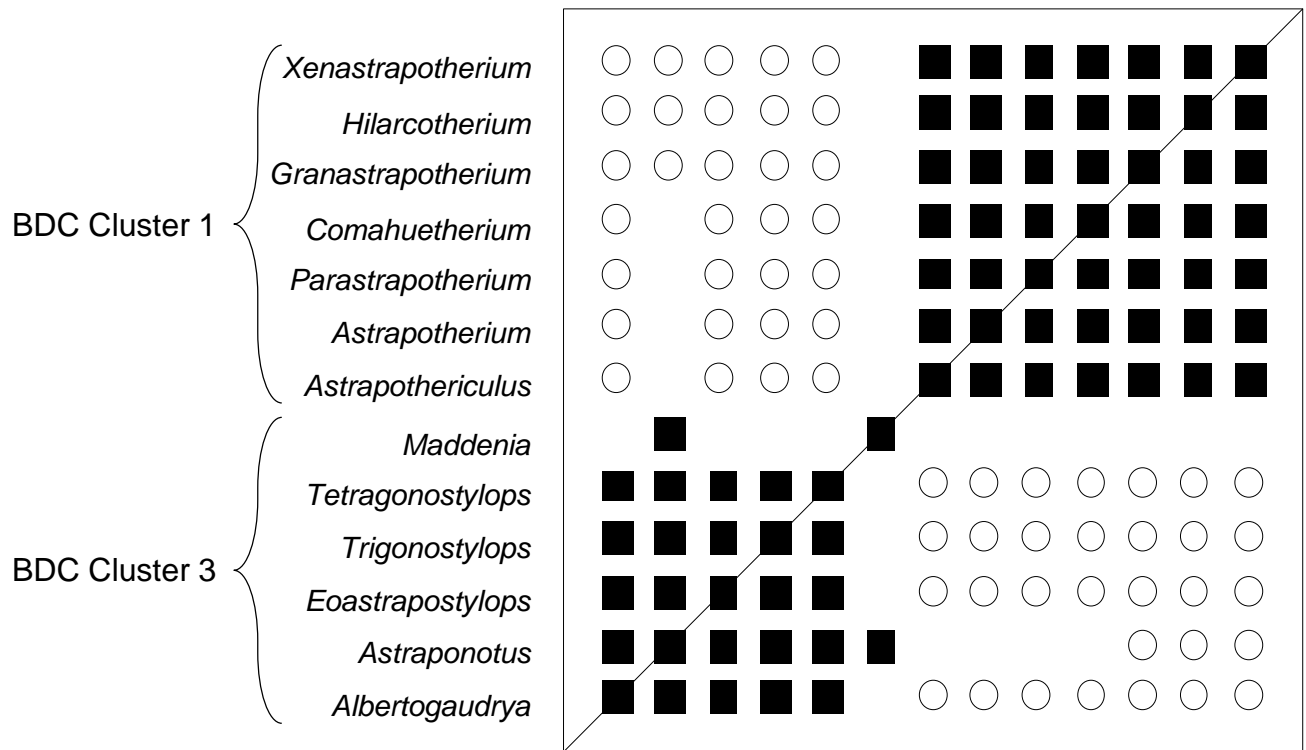
Vallejo-Pareja, M.C., J.D. Carrillo, J.W. Moreno-Bernal, M. Pardo-Jaramillo, D.F. Rodriguez-Gonzalez, and J. Muñoz-Duran. 2015. *Hilarchotherium castanedaii*, gen. et sp. nov., a new Miocene astrapothere (Mammalia, Astrapotheriidae) from the Upper Magdalena Valley, Colombia. *Journal of Vertebrate Paleontology* 35:e903960. Characters: Craniodental



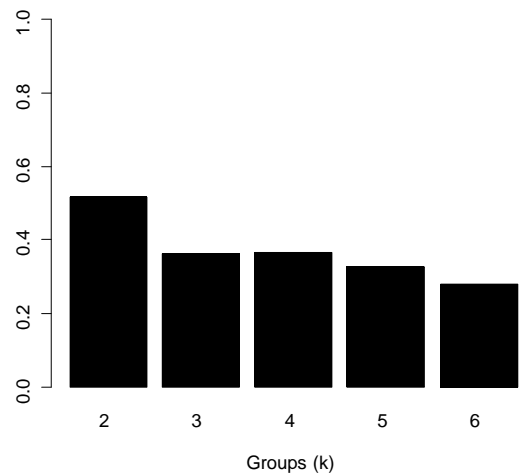
Order Astrapotheria
Family Astrapotheriidae

Published taxa	15
Published characters	64
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	13
Characters used for calculations	45
Median bootstrap value	93
F ₉₀	0.59
Stress of 3D MDS	0.09
k _{min}	5
Conclusion	HB

Notes: BDC and MDS reveal two well-separated groups. One astrapotheriid *Astraponotus* clusters with the outgroup taxa, and *Maddenia* does not cluster with either larger group. Astrapotheriidae *sensu stricto* (excluding *Astraponotus* and *Maddenia*) is probably a holobaramin.



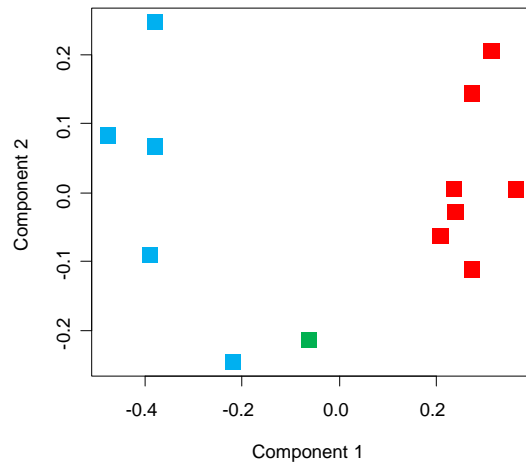
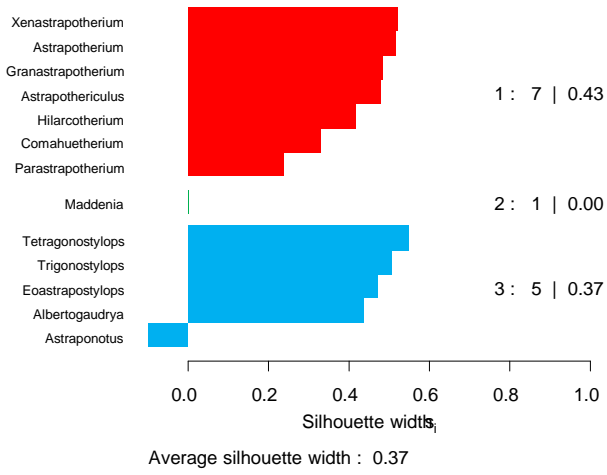
Average Silhouette Widths, Partion Around Medoids



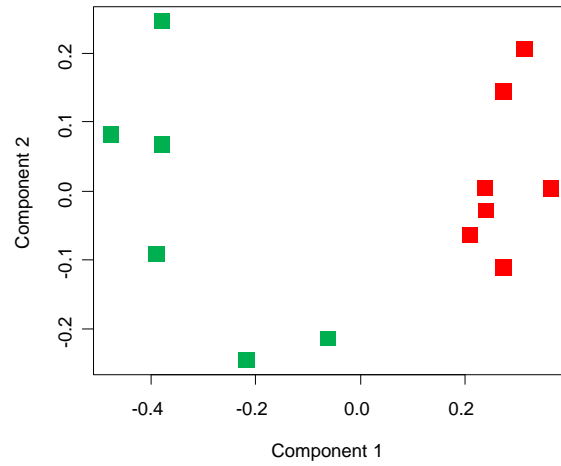
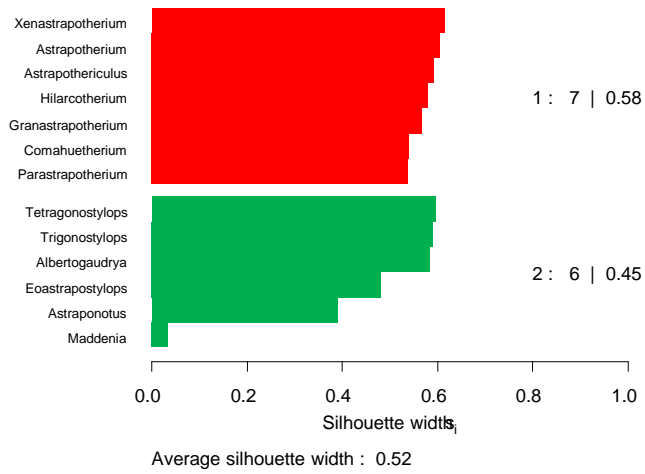
Clade Correspondence: Two of the three BDC clusters contain more than one taxon each. Both appear as clades in the majority rule consensus tree shown in Figure 6 in Vallejo-Pareja et al. (2015), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

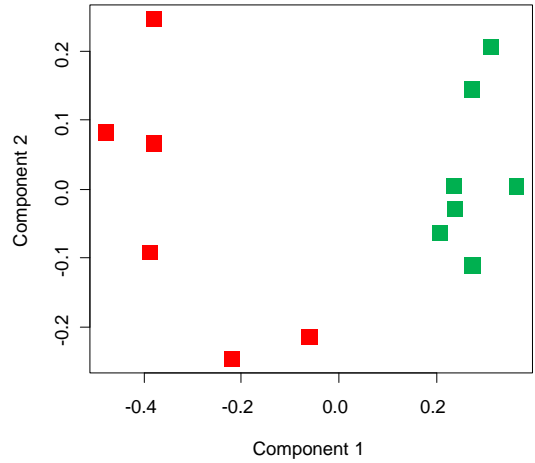
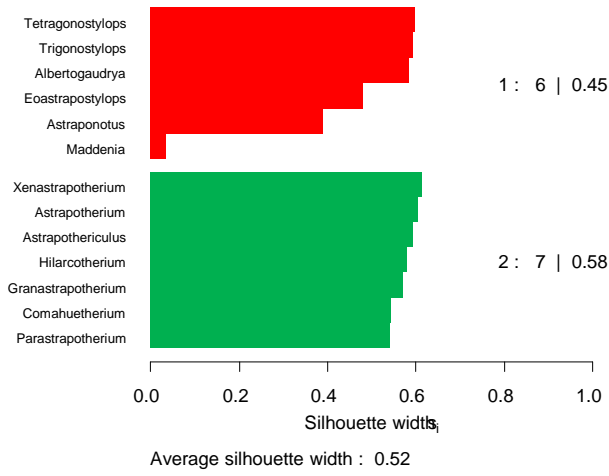


Spearman Correlation

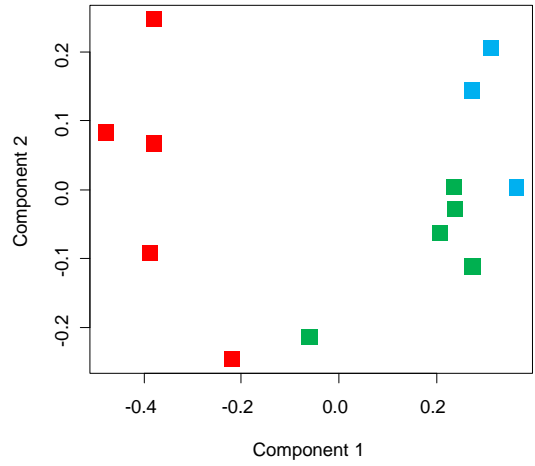
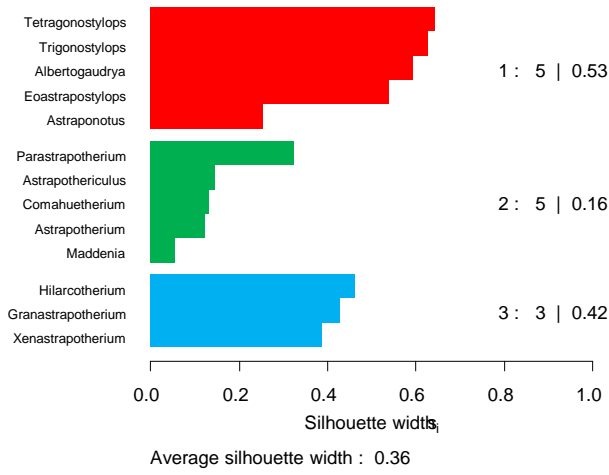


Silhouette plot, Partition Around Medoids

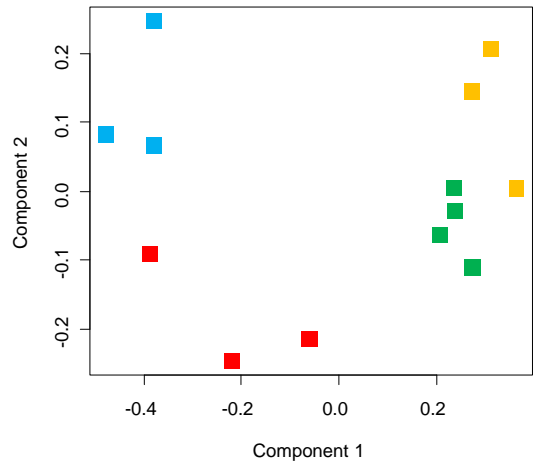
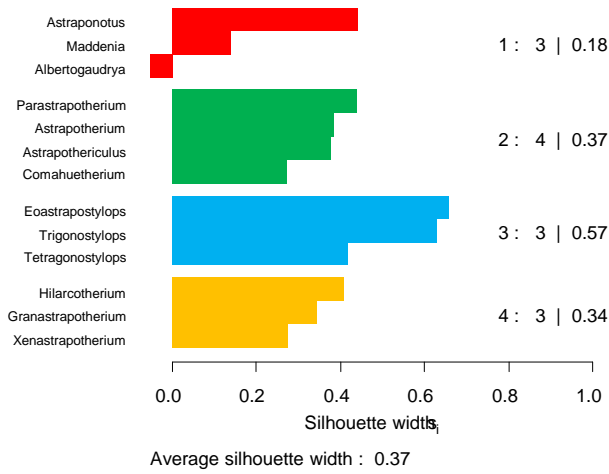
k=2



k=3

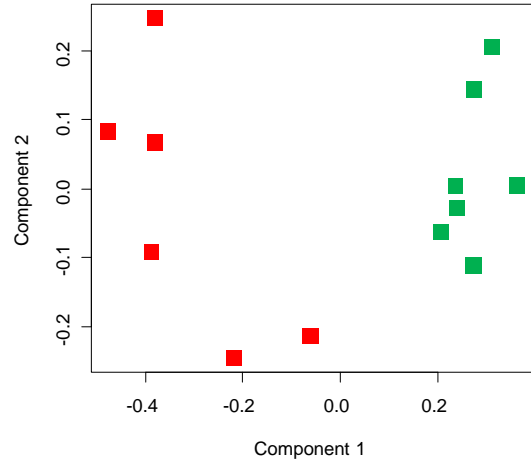
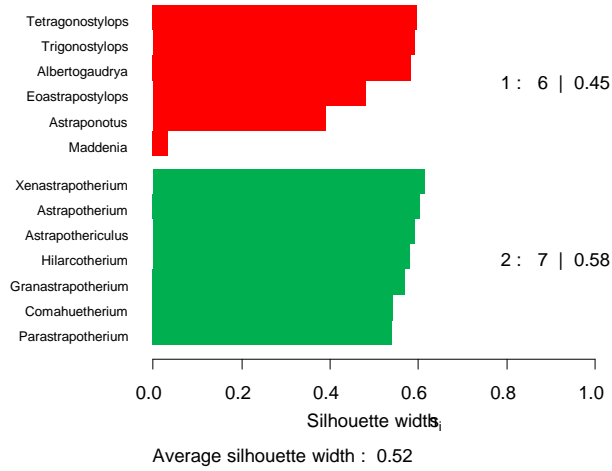


k=4

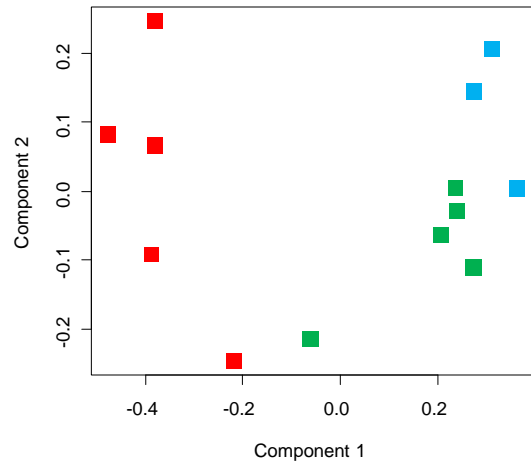
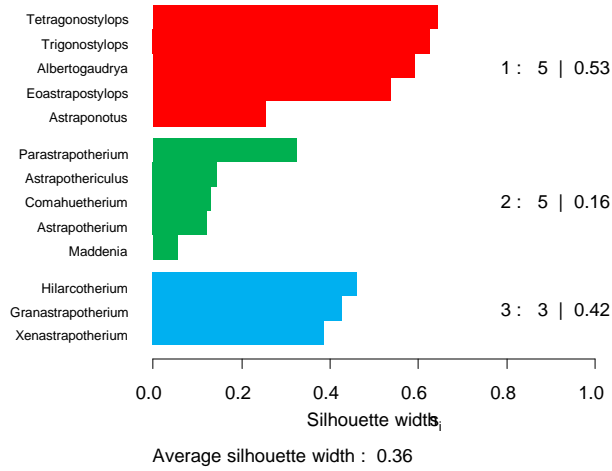


Silhouette plot, Fuzzy Analysis

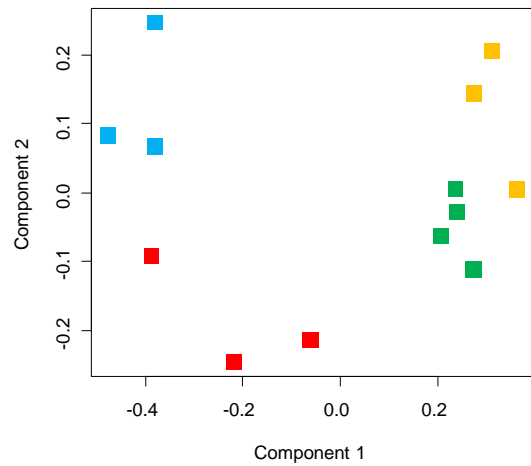
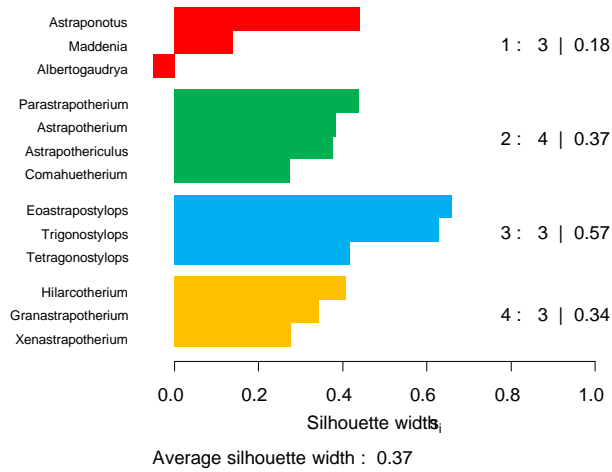
k=2



k=3



k=4



Family Carodniidae

Order Xenungulata

Antoine et al. 2015

Pearson BDC

Negative: 9

Positive: 9

Clusters: 3

Clusterability

Hopkins Statistic: 0.728

Dip test: 0.054

Dip test p-value: 0.59

Spearman BDC

Negative: 11

Positive: 11

Clusters: 3

Spearman BDC reveals two additional instances of significant, positive BDC, but the cluster partition is still the same as the original Pearson BDC partition. The three-cluster BDC partition has an average silhouette width of 0.5.

Three-cluster medoid partition has an average silhouette width of 0.53 and differs from the BDC partition by one taxon (cluster membership difference: 11%). The two-cluster medoid partition divides the taxa into ingroup and outgroup clusters and has an average silhouette width of 0.57, better than the BDC partition or the three-cluster medoid partition.

Three-cluster and two-cluster fuzzy analyses yield partitions identical to the corresponding medoid partitions.

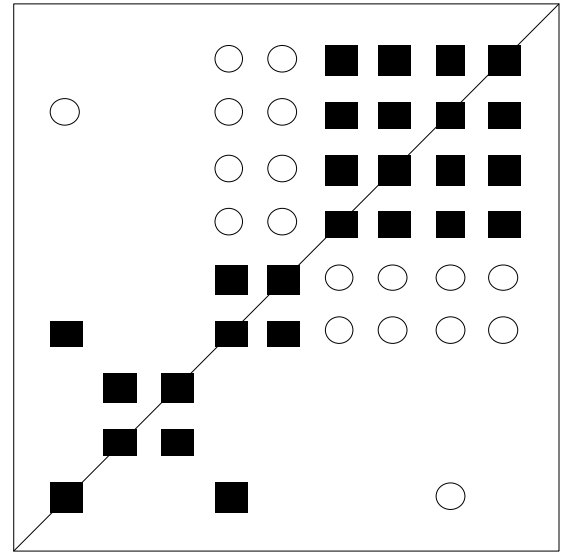
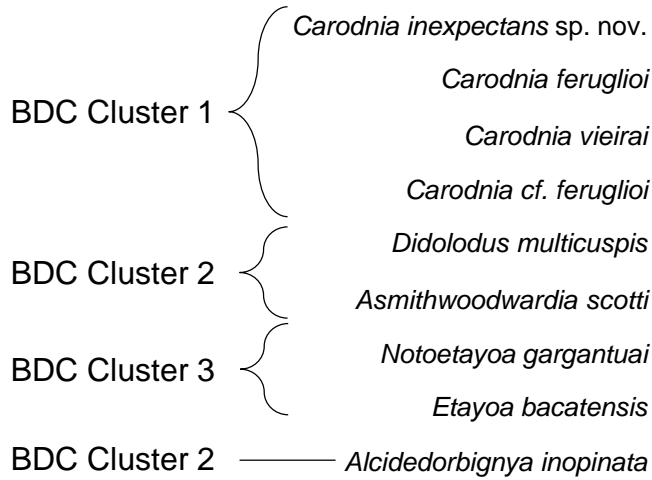
The original conclusion is here confirmed. Even though the three-cluster medoid and fuzzy partitions differ from the BDC clusters, the differences are entirely among the outgroup taxa. The carodniid cluster appears in the Spearman BDC clusters as well as the three-cluster fuzzy and medoid partitions. More importantly, the two-cluster medoid and fuzzy partitions have a higher average silhouette width than any of the three-cluster partitions and divide the taxa into ingroup and outgroup. The presence of eleven instances of significant, negative BDC between the ingroup and outgroup taxa imply that the carodniids are surrounded by a discontinuity. Carodniidae is a holobaramin.

Original conclusion: HB?

Updated conclusion: HB

Antoine, P.O., G. Billet, R. Salas-Gismondi, J.T. Lara, P. Baby, S. Brusset, and N. Espurt. 2015. A new *Carodnia* Simpson, 1935 (Mammalia, Xenungulata) from the early Eocene of Northwestern Peru and a phylogeny of xenungulates at species level. *Journal of Mammalian Evolution* 22:129-140.

Characters: Craniodental



Order Xenungulata
Family Carodniidae

Published taxa	9
Published characters	34
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	9
Characters used for calculations	28
Median bootstrap value	92.5
F ₉₀	0.53
Stress of 3D MDS	0.1
k _{min}	3
Conclusion	HB?

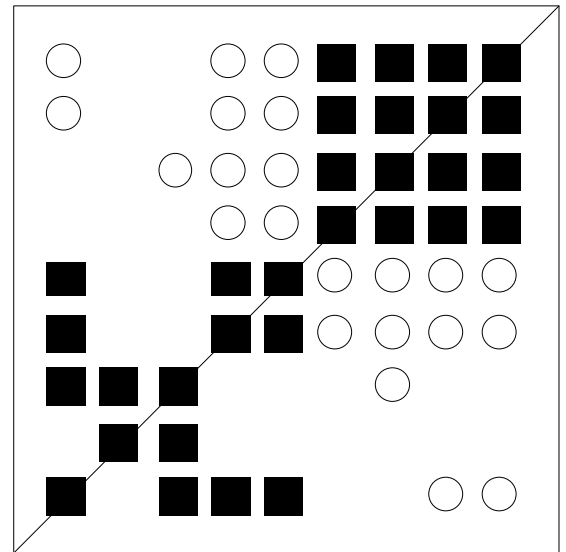
Notes: BDC and MDS reveal two well-separated groups of Carodniidae and outgroup taxa. Carodniidae is likely a holobaramin.

BDC Cluster 1 { *Carodnia inexpectans* sp. nov.
Carodnia feruglioi
Carodnia vieirai
Carodnia cf. feruglioi

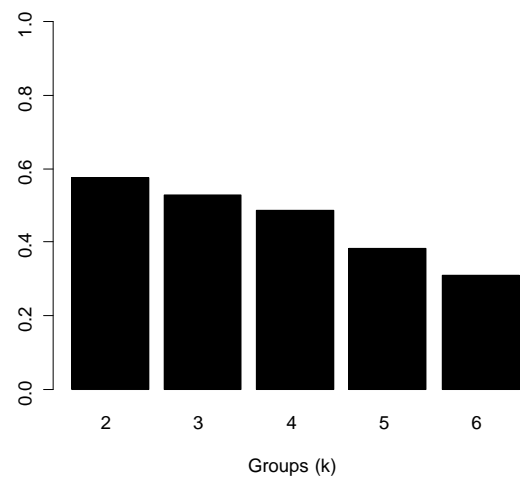
BDC Cluster 2 { *Didolodus multicuspis*
Asmithwoodwardia scotti

BDC Cluster 3 { *Notoetayoa gargantuai*
Etayoa bacatensis

BDC Cluster 2 — *Alcidedorbignya inopinata*



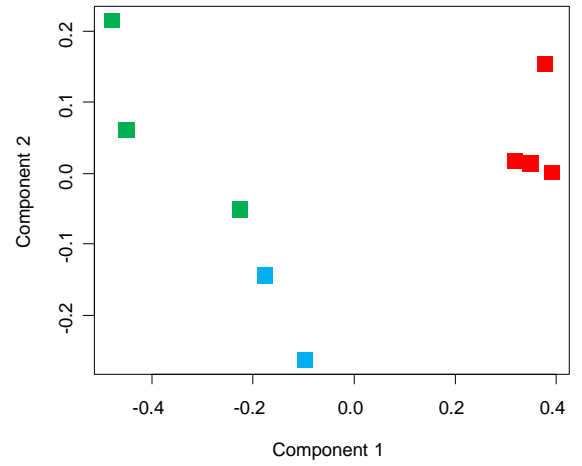
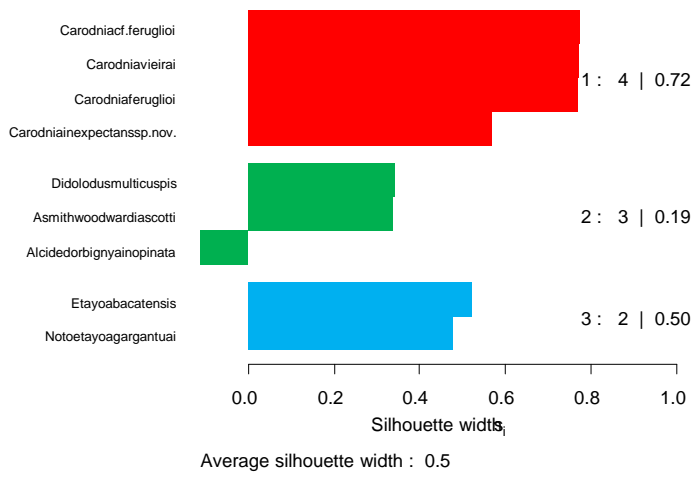
Average Silhouette Widths, Partition Around Medoids



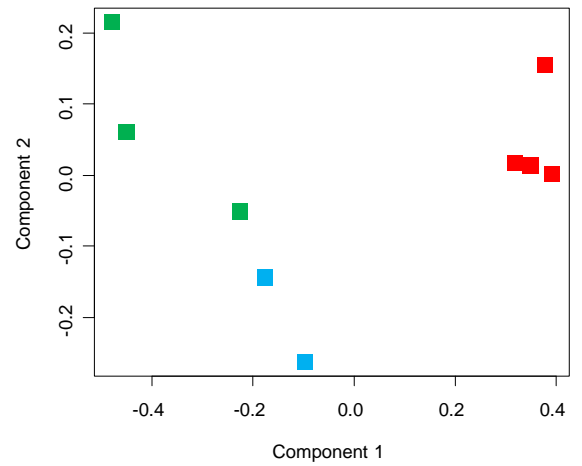
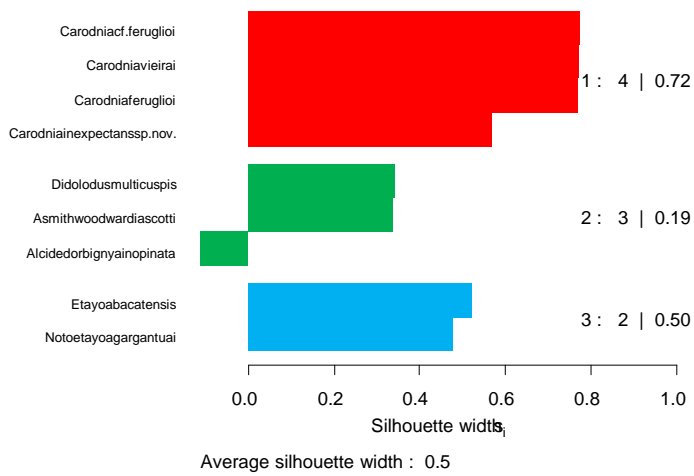
Clade Correspondence: All three BDC clusters contain more than one taxon each. In the phylogeny shown in Figure 4 of Antoine et al. (2014), clusters 1 and 2 are clades, but cluster 3 is paraphyletic with cluster 1.

Silhouette plot, BDC partitions

Pearson Correlation

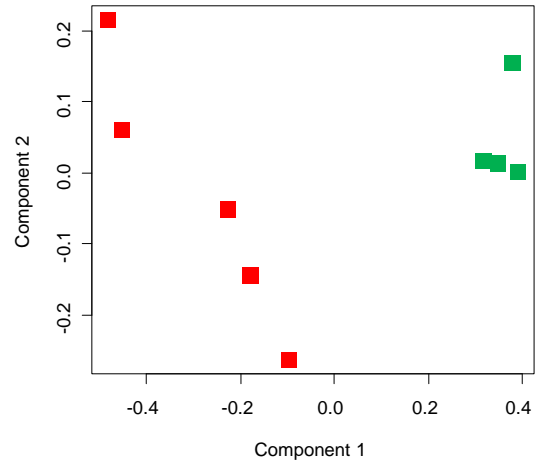
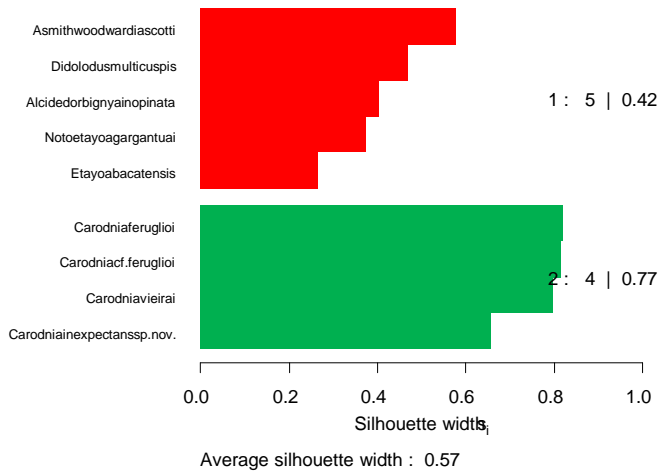


Spearman Correlation

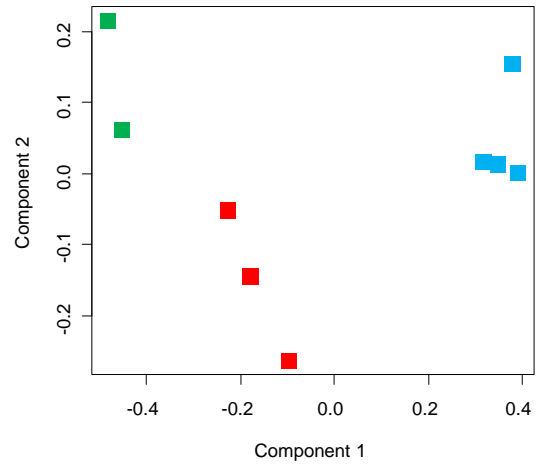
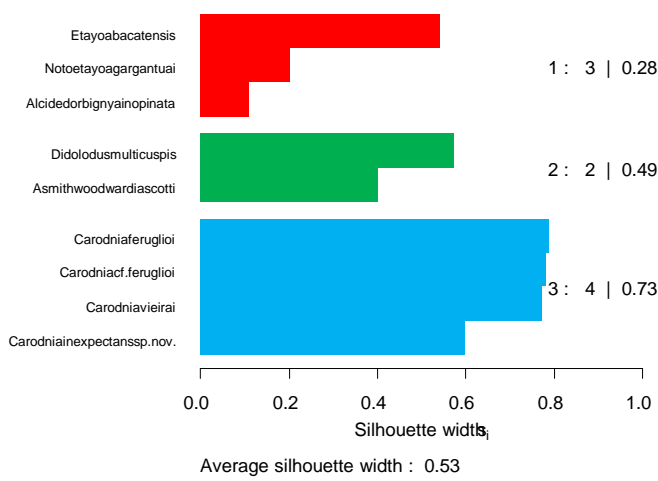


Silhouette plot, Partition Around Medoids

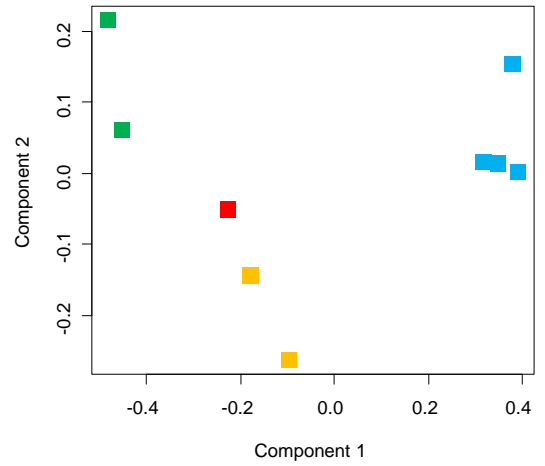
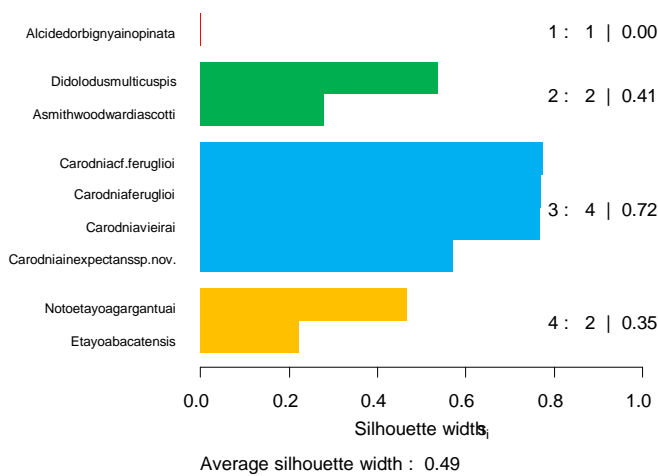
k=2



k=3

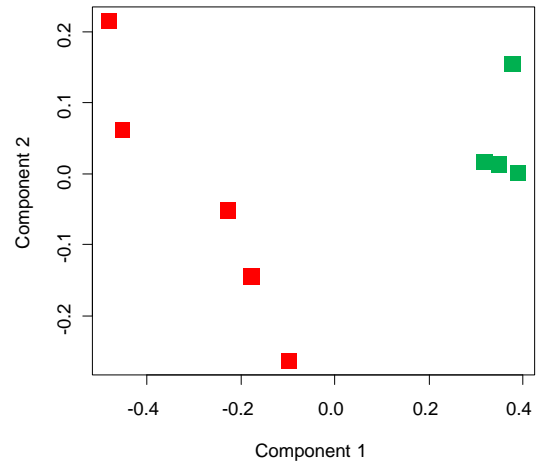
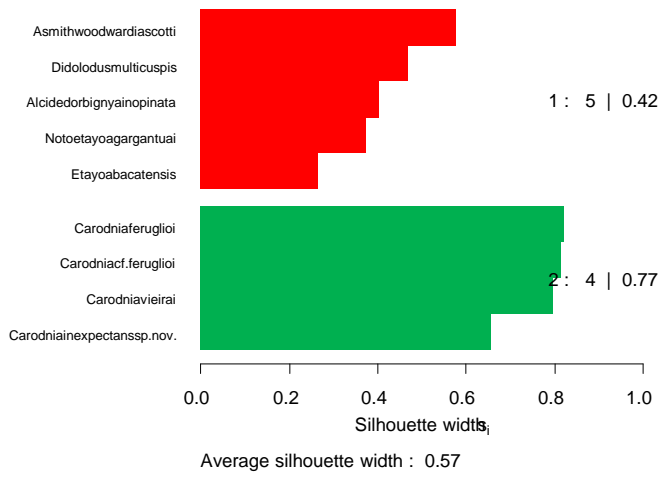


k=4

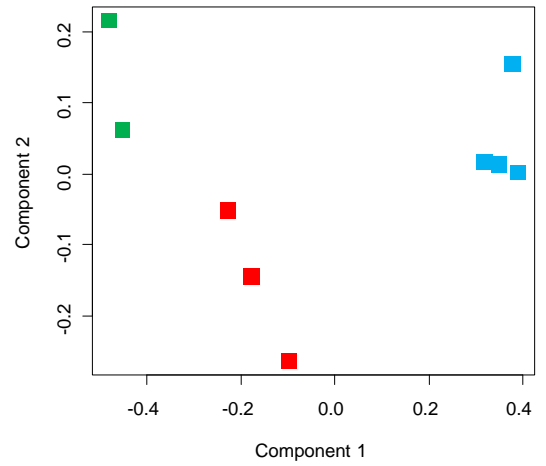
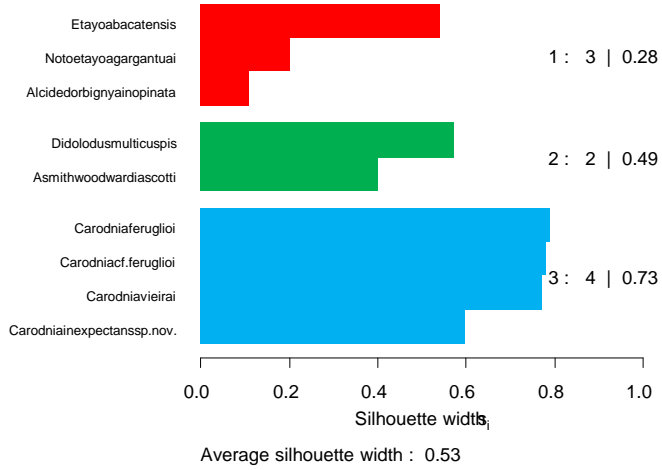


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Palaeotheriidae

Order Perissodactyla

Danilo et al. 2013

Pearson BDC

Negative: 78

Positive: 138

Clusters: 3

Clusterability

Hopkins Statistic: 0.679

Dip test: 0.017

Dip test p-value: 0.789

Spearman BDC

Negative: 61

Positive: 149

Clusters: 2

Spearman BDC adds eleven instances of significant, positive correlation to the Pearson BDC results, the effect of which is the merging of the singleton cluster *Eurohippus parvulus* with the larger of the two remaining clusters. The three-cluster Pearson BDC partition has an average silhouette width of 0.16, with two taxa exhibiting negative silhouette widths. The two-cluster Spearman BDC partition has a substantially higher average silhouette width of 0.35, and no taxa have negative silhouette widths. Though the Spearman BDC results have fewer instances of significant, negative correlation, all 61 occur in intercluster taxon pairs; thus, significant, negative correlation separates these clusters.

Three-cluster medoid partitioning has an average silhouette width of 0.16, but differs substantially from the Pearson BDC clusters (cluster membership difference: 35%). In contrast, the two-cluster medoid partition exactly matches the Spearman BDC clusters.

Three-cluster fuzzy analysis failed. Two-cluster fuzzy analysis yielded a partition with an average silhouette width of 0.27, with two taxa exhibiting negative silhouette widths. The two-cluster fuzzy partition differs from the Spearman BDC clusters by four taxa (cluster membership difference: 15%).

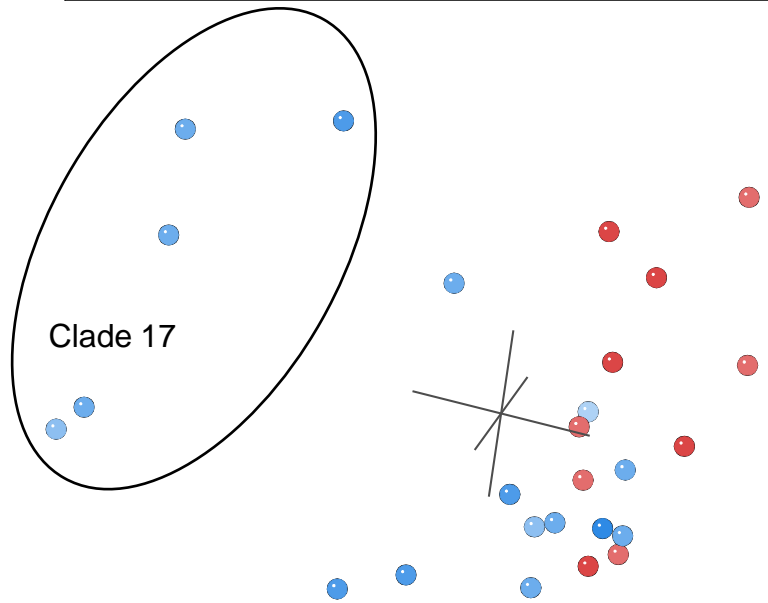
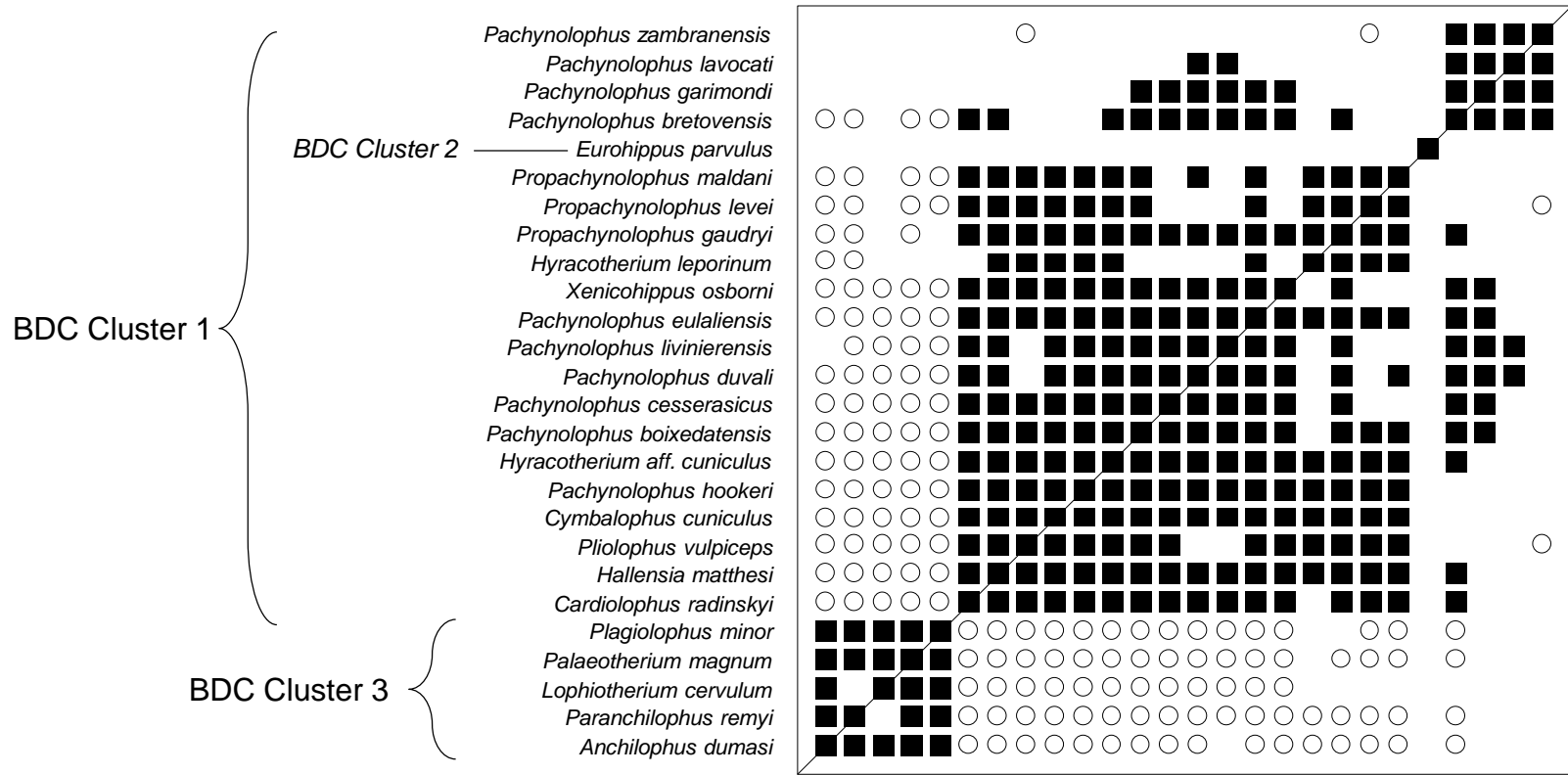
The original analysis concluded that a clade of five taxa from Danilo et al.'s phylogeny was a holobaramin, based on the BDC and MDS results. Here, the presence of that cluster of taxa is affirmed in the Spearman BDC results and the medoid partition. Though the fuzzy analysis does not support the existence of this exact cluster (it adds four additional taxa), the resulting average silhouette width is lower than the two-cluster medoid partition and Spearman BDC clusters (0.27 vs. 0.35). Therefore we may conclude that the original results are confirmed, with a small uncertainty due to the inconsistent fuzzy analysis.

Original conclusion: HB?

Updated conclusion: HB?

Danilo, L., J.A. Remy, M. Vianey-Liaud, B. Marandat, J. Sudre, and F. Lihoreau. 2013. A new Eocene locality in southern France sheds light on the basal radiation of Palaeotheriidae (Mammalia, Perissodactyla, Equoidea). *Journal of Vertebrate Paleontology* 33:195-215.

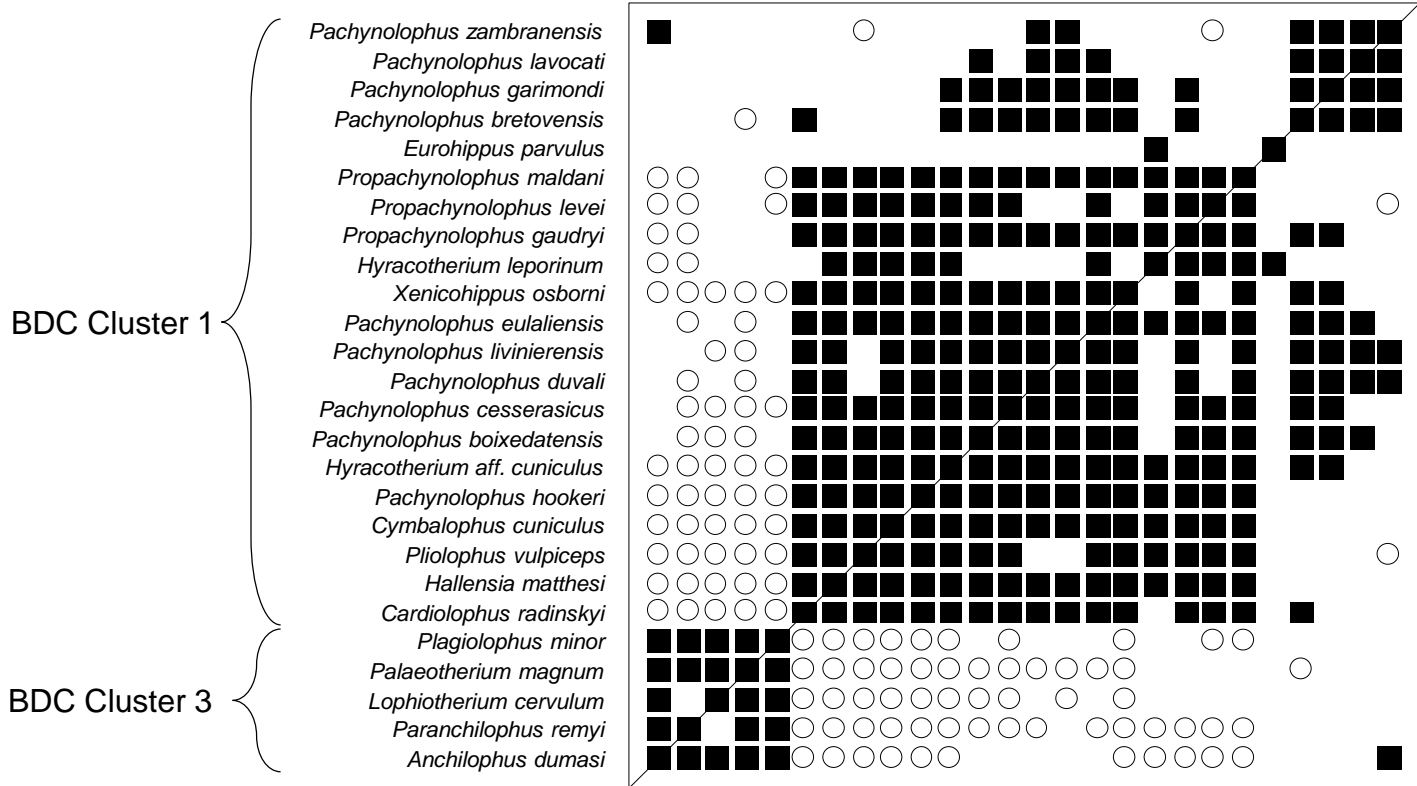
Characters: Craniodental



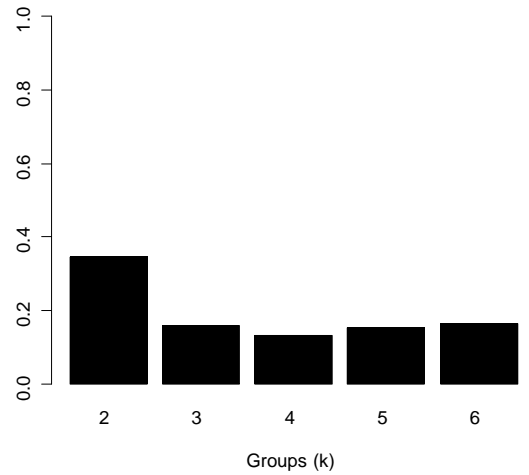
Order Perissodactyla
Family Palaeotheriidae

Published taxa	26
Published characters	72
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	26
Characters used for calculations	57
Median bootstrap value	81
F ₉₀	0.22
Stress of 3D MDS	0.25
k _{min}	8
Conclusion	HB?

Notes: BDC indicates good evidence for discontinuity around a group of five taxa corresponding to clade 17 in Danilo et al.'s (2013) Figure 9. MDS seems to support the separation of this cluster of taxa. Clade 17 includes Palaeotheriinae (*Plagiolophus minor*, *Palaeotherium magnum*) and three additional taxa included here: *Lophiotherium cervulum*, *Paranchilophus remyi*, and *Anchilophus dumasi*. Clade 17 could be a holobaramin.



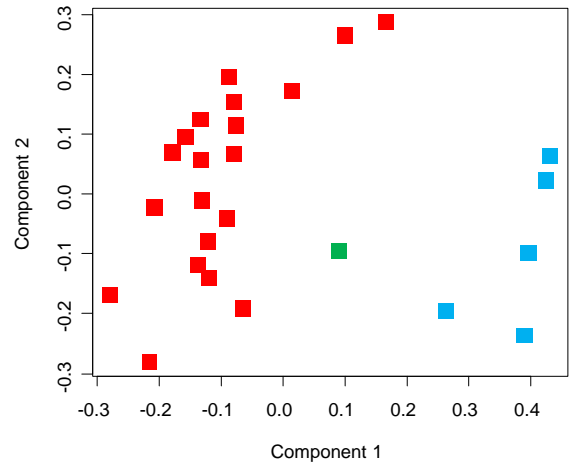
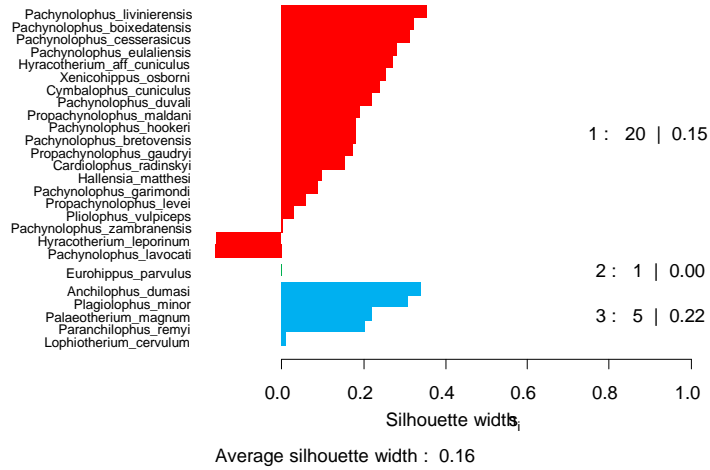
Average Silhouette Widths, Partion Around Medoids



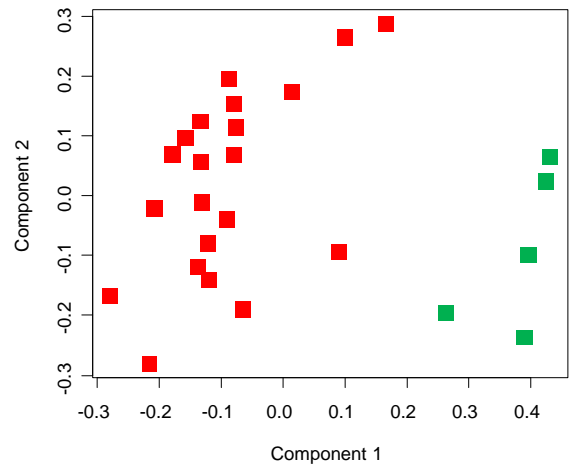
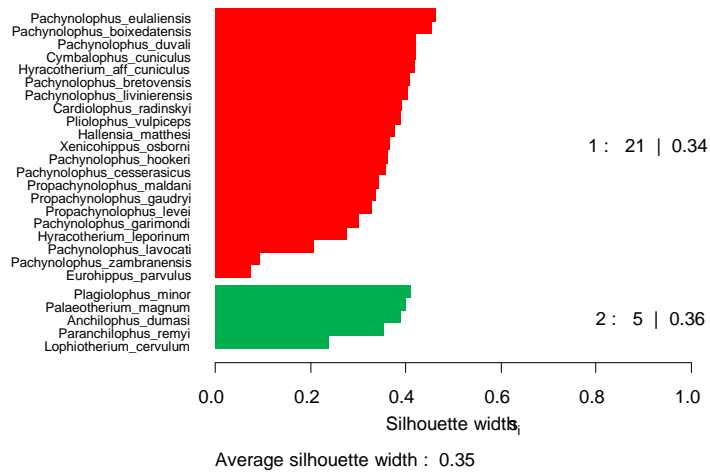
Clade Correspondence: Of the three BDC clusters, cluster 2 is a singleton. In the published phylogeny in Figure 9 of Danilo et al. (2013), only cluster 1 is monophyletic. The singleton is part of a clade with cluster 3.

Silhouette plot, BDC partitions

Pearson Correlation

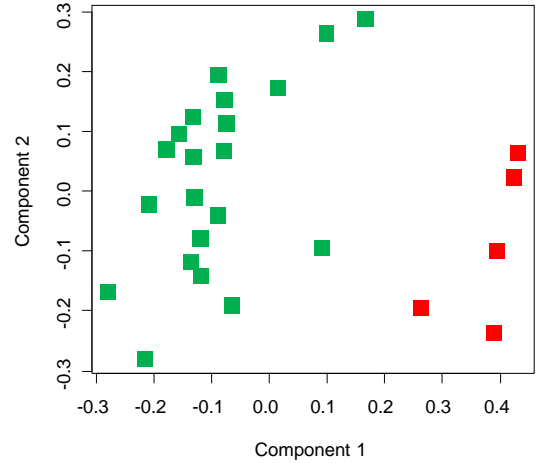
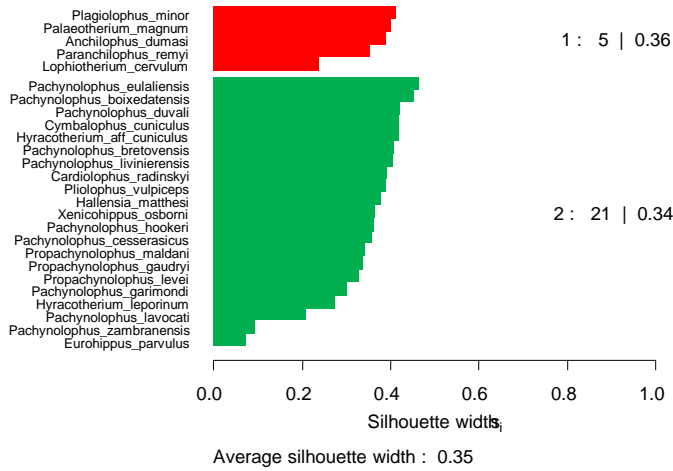


Spearman Correlation

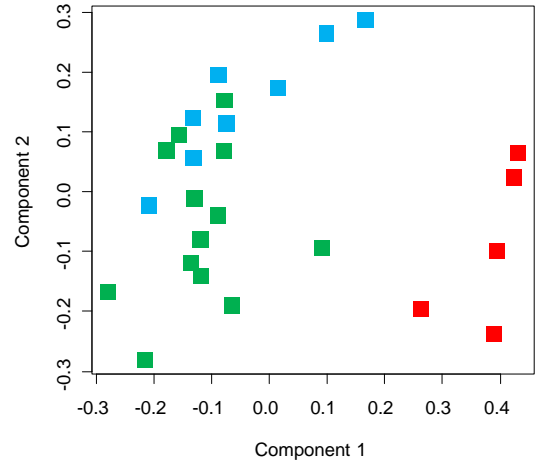
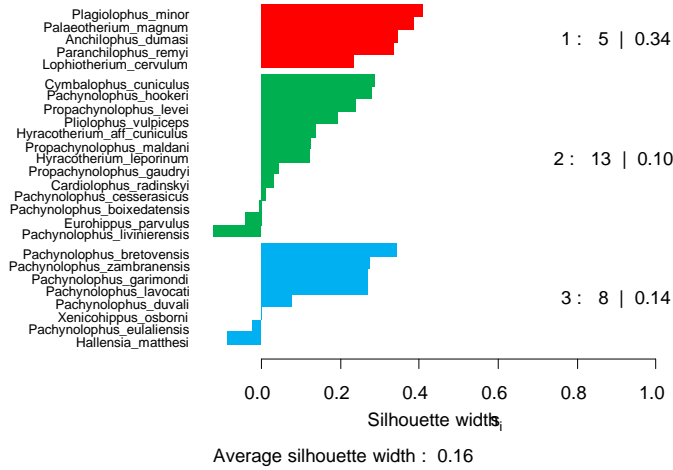


Silhouette plot, Partition Around Medoids

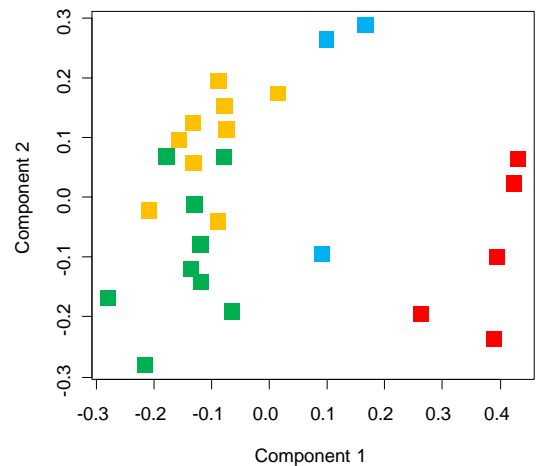
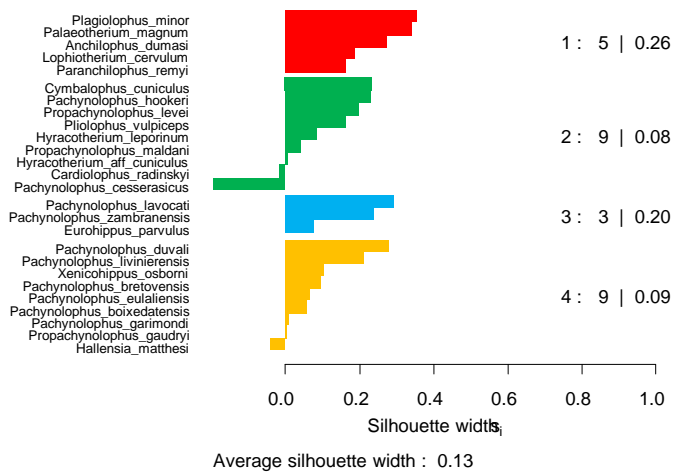
k=2



k=3

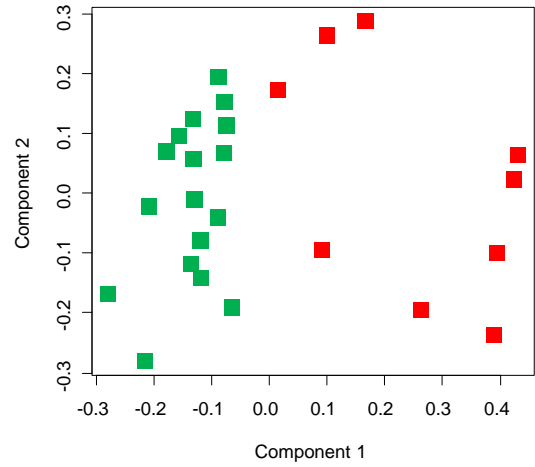
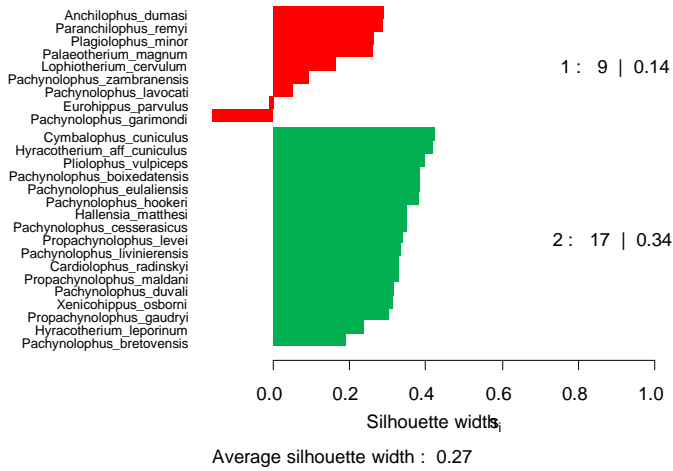


k=4



Silhouette plot, Fuzzy Analysis

k=2



Family Brontotheriidae

Order Perissodactyla

Mihlbachler 2008

Pearson BDC
Negative: 136
Positive: 430
Clusters: 2

Clusterability
Hopkins Statistic: 0.877
Dip test: 0.012
Dip test p-value: 0.739

Spearman BDC
Negative: 122
Positive: 393
Clusters: 2

Spearman BDC reduces the instances of significant, positive correlation from 430 in the Pearson BDC results to 393. As a consequence, the two clusters of taxa recognized in the Pearson BDC results are rearranged into two different clusters. A group of fourteen brontotheriids are separated from the remaining brontotheriids and cluster with the outgroup in the Spearman BDC results. The average silhouette width for the Pearson BDC partition is 0.5, with two taxa exhibiting negative silhouette widths. The average silhouette width for the Spearman BDC partition is only 0.35, also with two taxa exhibiting negative silhouette widths. The cluster membership difference is 35%.

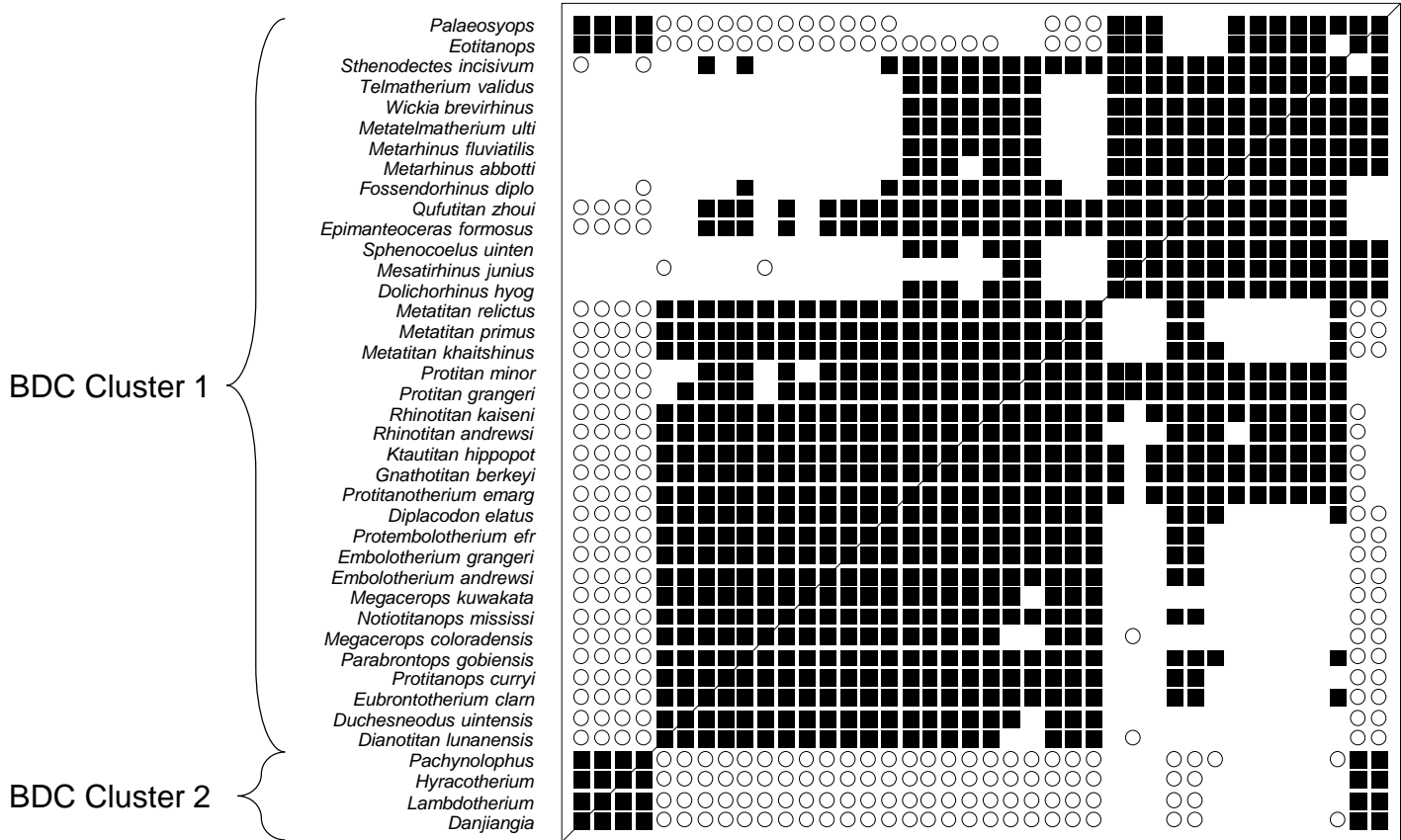
The two-cluster medoid partition has an average silhouette width of 0.48 and differs from the Pearson BDC clusters by two taxa (cluster membership difference: 5%) and from the Spearman BDC clusters by twelve taxa (cluster membership difference: 30%). Three-cluster medoid partition has a substantially lower average silhouette width of 0.3.

Two-cluster fuzzy analysis has an average silhouette width of 0.34 and clusters the taxa in a third way, different from the Spearman BDC, the Pearson BDC, and the two-cluster medoid partition. Compared to the Pearson BDC clusters, the two-cluster fuzzy partition differs by 16 taxa (cluster membership difference: 40%). Compared to the Spearman BDC clusters, the two-cluster fuzzy partition differs by only two taxa (cluster membership difference: 5%).

Only in the original Pearson BDC results are the outgroup and ingroup taxa neatly separated. Here, the Spearman BDC results, fuzzy partition, and medoid partition do not confirm this division nor do they agree with each other. These inconsistencies warrant downgrading the conclusion from tentative holobaramin to inconclusive.

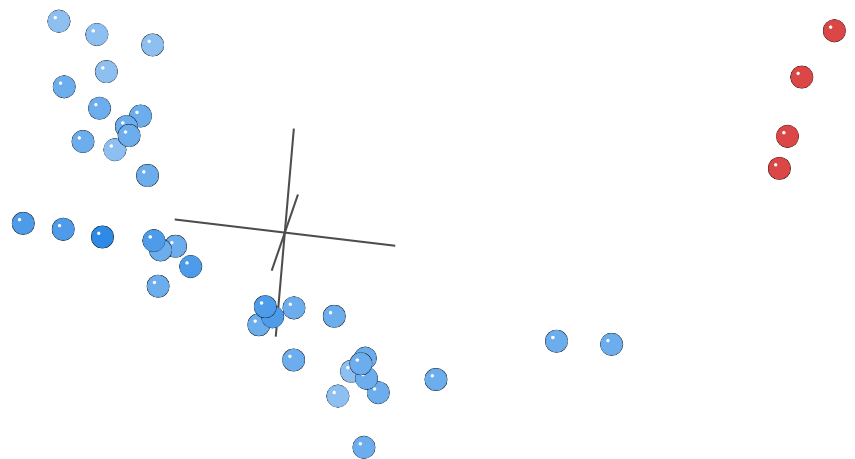
Original conclusion: HB?
Updated conclusion: Inconclusive

Characters: Craniodental



Order Perissodactyla
Family Brontotheriidae

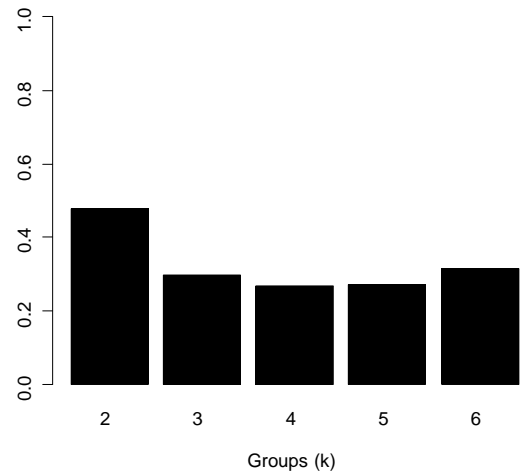
Published taxa	51
Published characters	87
Character relevance	0.75
Taxic relevance	0.5
Taxa used for calculations	40
Characters used for calculations	81
Median bootstrap value	94
F ₉₀	0.53
Stress of 3D MDS	0.17
k _{min}	7
Conclusion	HB?



Notes: In BDC, the Brontotheriidae are well separated from the outgroup, except for two brontotheres, *Paleosyops* and *Eotitanops*, which share significant, positive BDC with all outgroup taxa. The MDS shows an arc of taxa but with a separation between the outgroup and the Brontotheriidae. This suggests that the correlations involving the outgroups, *Paleosyops*, and *Eotitanops* are a result of the linear geometry of the brontothere taxa. Taken together, this suggests that Brontotheriidae is likely a holobaramin.



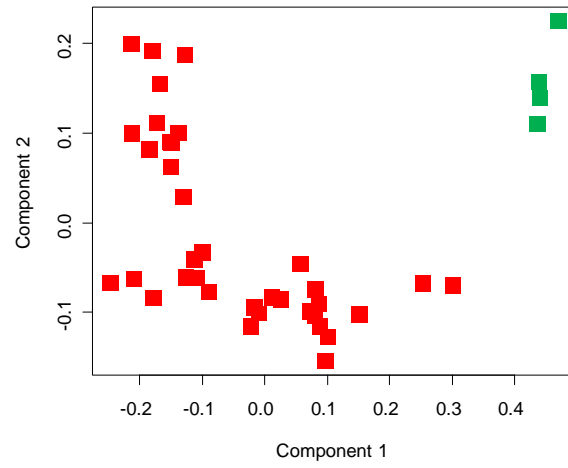
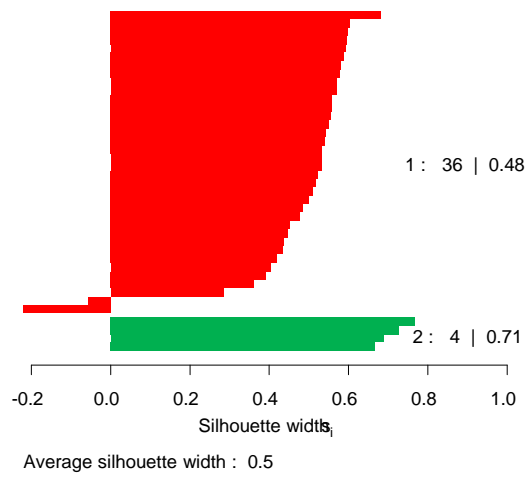
Average Silhouette Widths, Partion Around Medoids



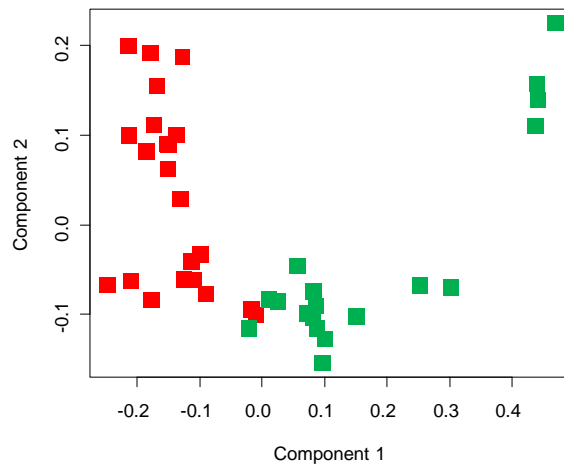
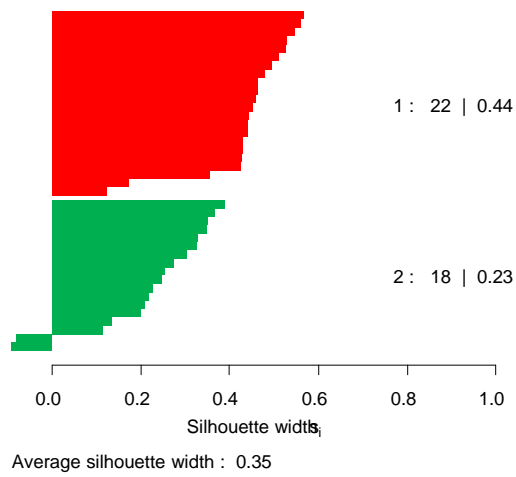
Clade Correspondence: Both BDC clusters contain two or more taxa. Both are monophyletic in the phylogeny shown in Figure 194 of Mhlbachler (2008), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

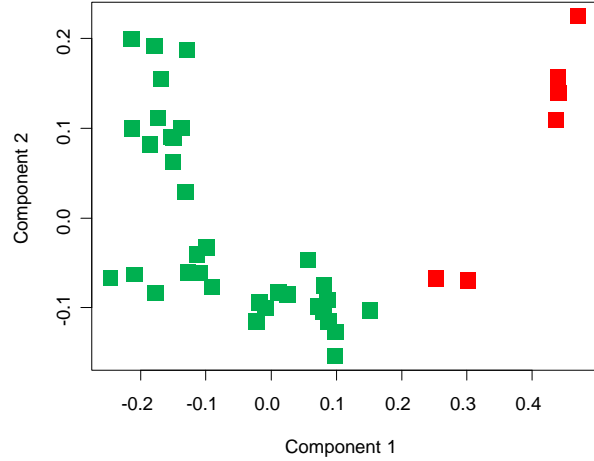
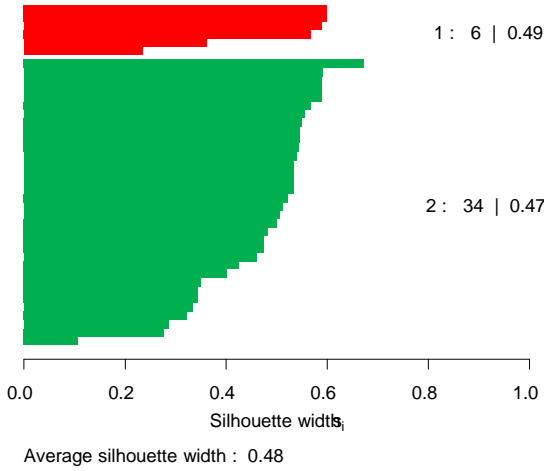


Spearman Correlation

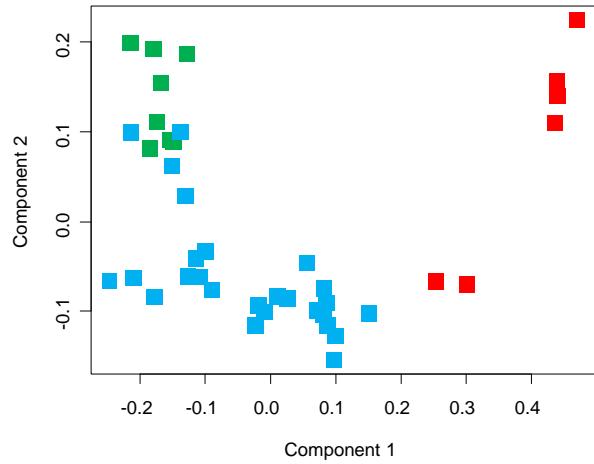
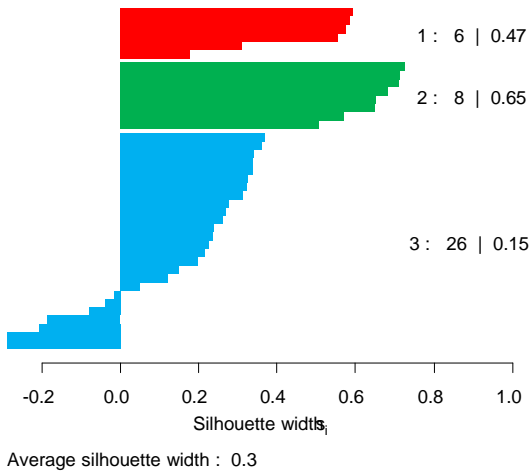


Silhouette plot, Partition Around Medoids

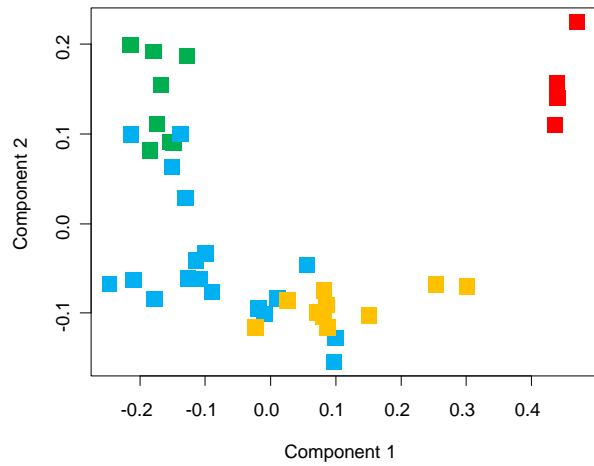
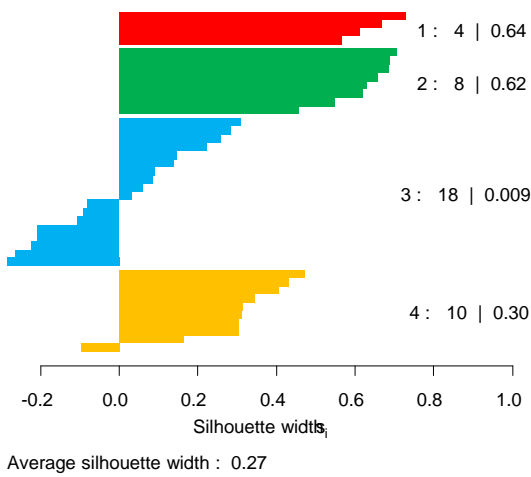
k=2



k=3

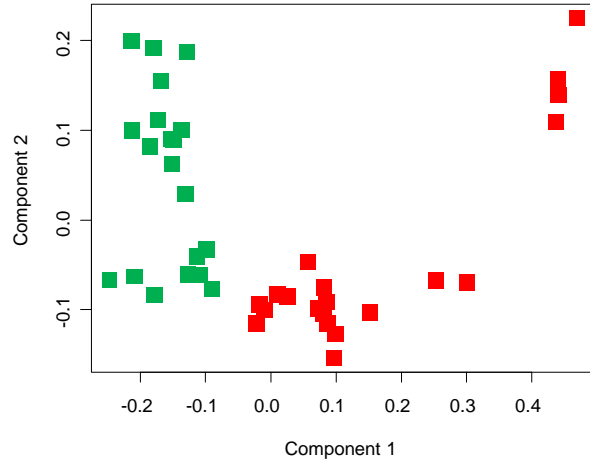
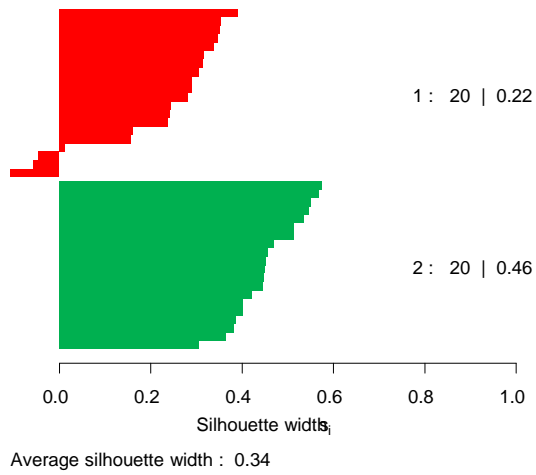


k=4

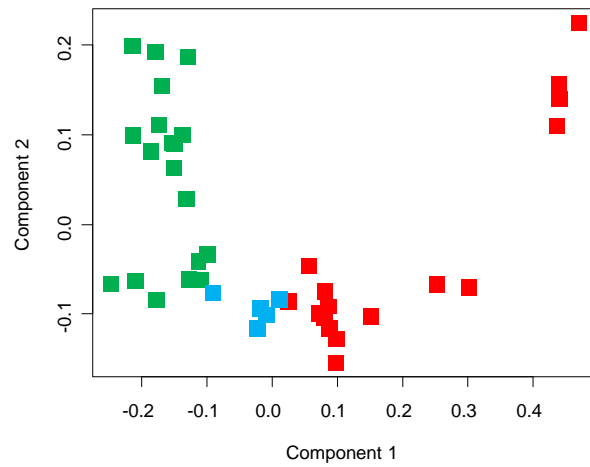
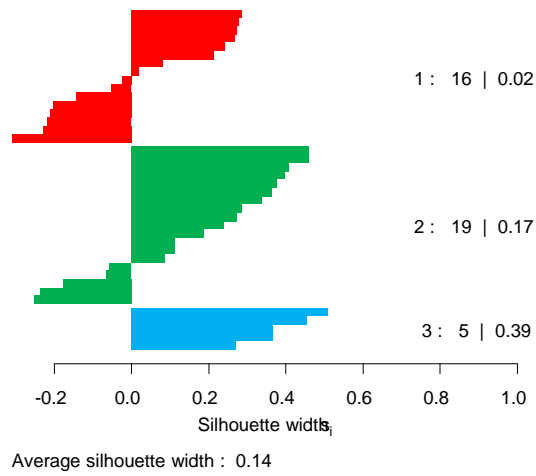


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Chalicotheriidae

Order Perissodactyla

Bai et al. 2010

Pearson BDC

Negative: 34

Positive: 30

Clusters: 5

Clusterability

Hopkins Statistic: 0.706

Dip test: 0.031

Dip test p-value: 0.475

Spearman BDC

Negative: 41

Positive: 52

Clusters: 3

The Spearman BDC results considerably clarify the Pearson BDC results, reducing the number of clusters from five to three. The chalicothere *Lophiaspis* remains a singleton cluster in both Spearman and Pearson BDC results. The average silhouette width for the five-cluster Pearson BDC partition is 0.25, with three taxa exhibiting negative silhouette widths. The average silhouette width for the three-cluster Spearman BDC partition is 0.11, with four taxa exhibiting negative silhouette widths. The cluster membership difference is 29%.

Five-cluster medoid partition has an average silhouette width of 0.33 and differs from the Pearson BDC clusters by five taxa (cluster membership difference: 29%). The three-cluster medoid partition has an average silhouette width of 0.36 and differs from the Spearman BDC clusters by four taxa (cluster membership difference: 24%).

Five-cluster fuzzy analysis failed. Three-cluster fuzzy analysis yielded a partition with an average silhouette width of 0.23. It differs from the Spearman BDC clusters by three taxa (cluster membership difference 18%) and from the three-cluster medoid partition by six taxa (cluster membership difference: 35%).

Despite these inconsistencies, two-cluster medoid partition and fuzzy analysis generate the same clustering with an average silhouette width of 0.33. *Lophiaspis* clusters with the outgroup taxa, resulting in a negative silhouette width. This clustering differs from the Spearman BDC clusters by a single taxon, *Lophiaspis* (cluster membership difference: 6%).

Based on the original results, we concluded that the chalicotheres except for *Lophiaspis* and *Protomoropus* are a tentative holobaramin, since the position of *Lophiaspis* is uncertain. Here, these initial results are partially confirmed with the two-cluster fuzzy analysis and medoid partition, both of which support placing *Lophiaspis* with the outgroups.

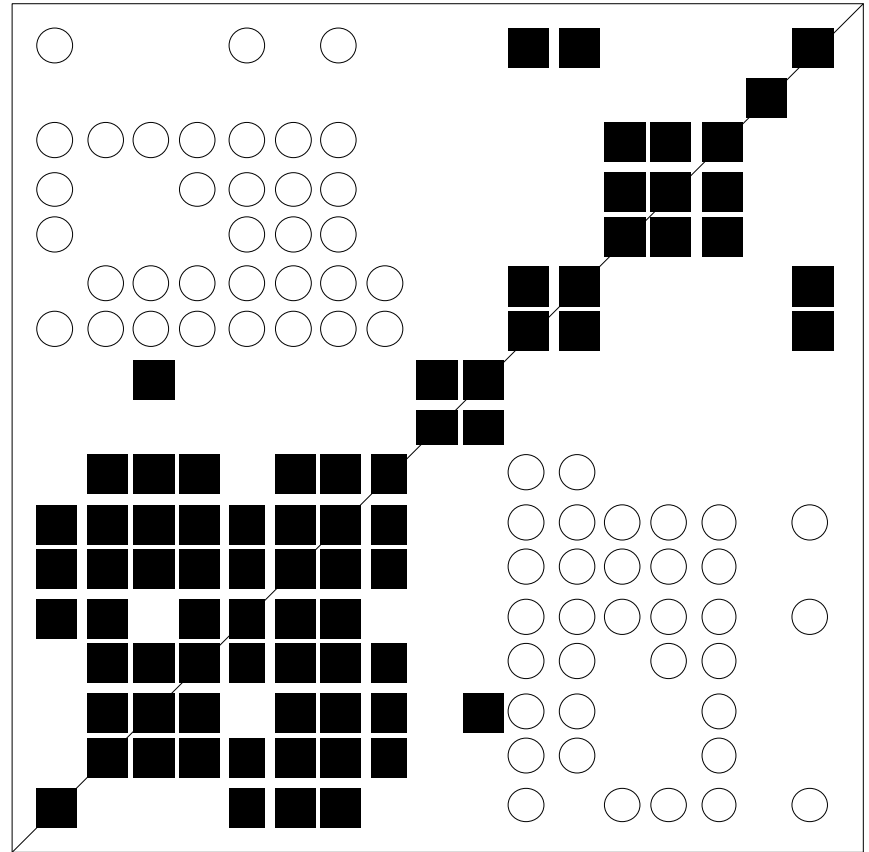
Original conclusion: HB?

Updated conclusion: HB?

Bai, B., Y. Wang, and J. Meng. 2010. New craniodental materials of *Litolophus gobiensis* (Perissodactyla, “Eomoropidae”) from Inner Mongolia, China, and phylogenetic analyses of Eocene chalicotheres. *American Museum Novitates* 3688:1-27.

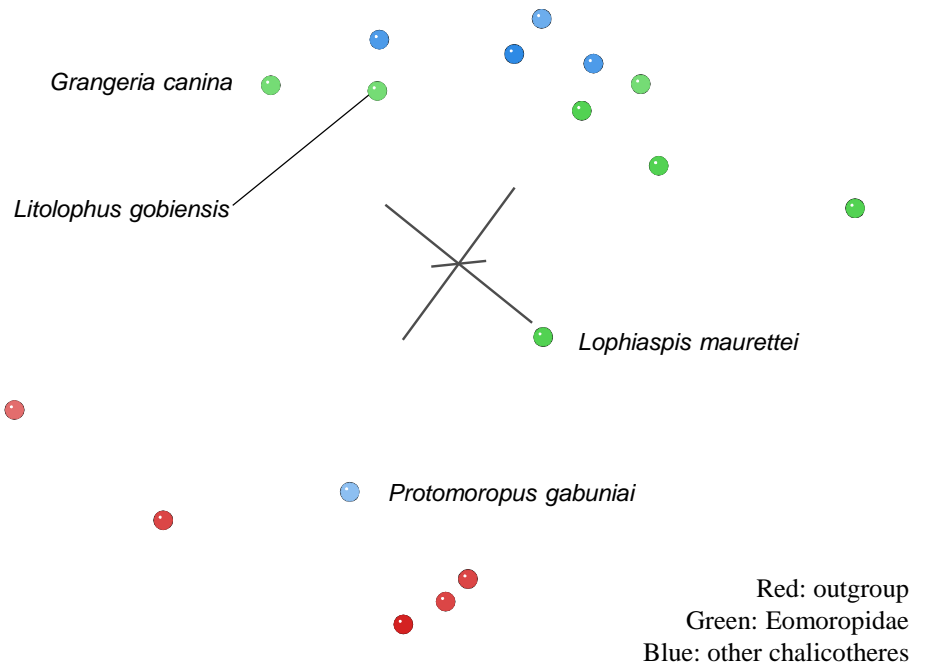
Characters: Craniodental

- BDC Cluster 1 — *Protomoropus gabuniai*
- BDC Cluster 2 — *Lophiaspis maurettei*
- BDC Cluster 3 {
 - Lophiodon remensis*
 - Hyrachyus eximius*
 - Heptodon calciculus*
- BDC Cluster 1 {
 - Homogalax wutuensis*
 - Cardiolphus radinskyi*
- BDC Cluster 4 {
 - Litolophus gobiensis*
 - Grangeria canina*
- BDC Cluster 5 {
 - Eomoropus pawnnyunti*
 - Schizotherium avitum*
 - SDM 84006
 - Moropus elatus*
 - Eomoropus quadridentatus*
 - Grangeria anarsius*
 - Eomoropus amarorum*
 - Ansiodon grande*

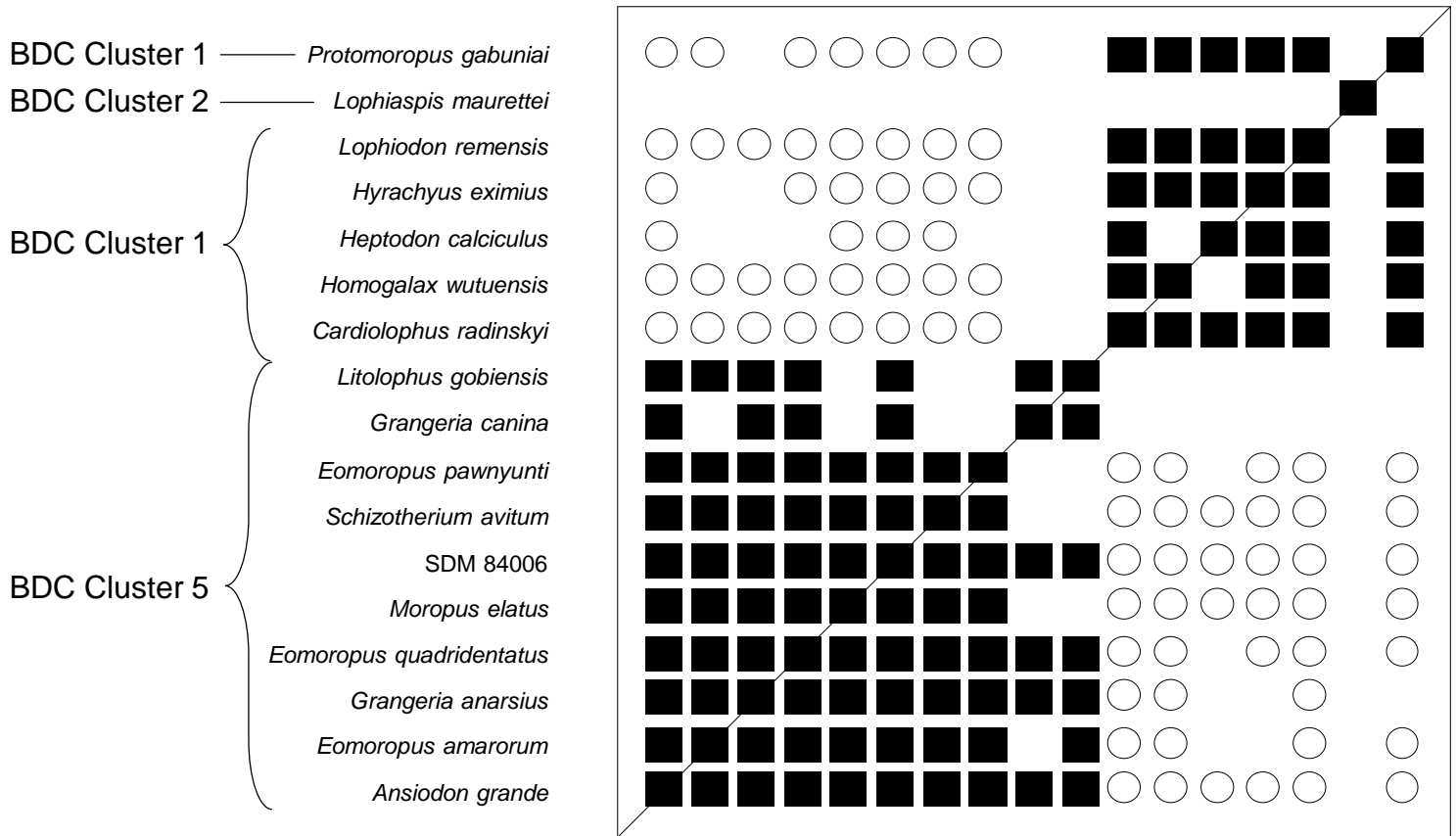


Order Perissodactyla
Family Chalicotheriidae

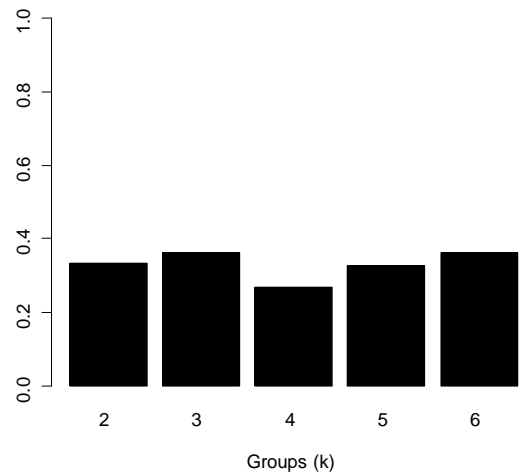
Published taxa	21
Published characters	58
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	17
Characters used for calculations	38
Median bootstrap value	77
F ₉₀	0.16
Stress of 3D MDS	0.2
k _{min}	6
Conclusion	HB?



Notes: The BDC results reveal two groups of taxa, corresponding roughly to the chalicotheres and other taxa. The two groups are well-separated, but the chalicothere *Protomoropus* is part of the outgroup. The chalicothere *Lophiaspis* does not share significant BDC with any other taxa. The MDS results reveal the same groups with *Protomoropus* in the outgroup cluster and *Lophiaspis* in between the two clusters. The chalicotheres (excluding *Protomoropus* and *Lophiaspis*) are likely a holobaramin.



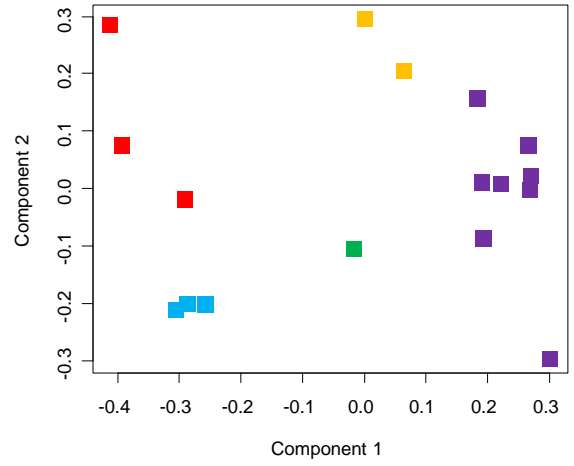
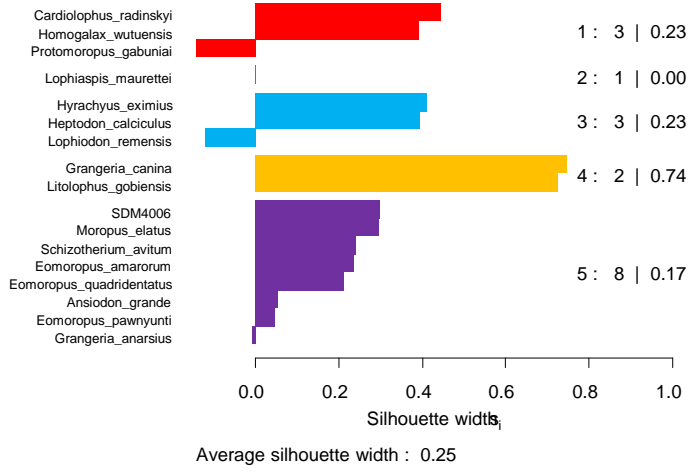
Average Silhouette Widths, Partion Around Medoids



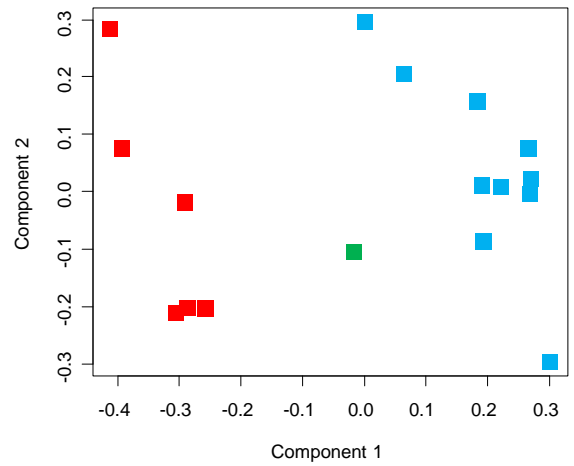
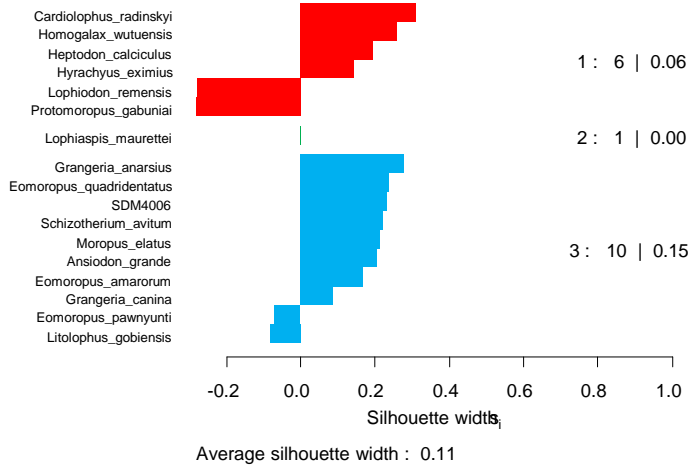
Clade Correspondence: Of the five clusters detected in the BDC results, only cluster 2 is a singleton. All four of the remaining clusters are monophyletic in the majority rule consensus tree in Figure 13 of Bai et al. (2010), if it were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

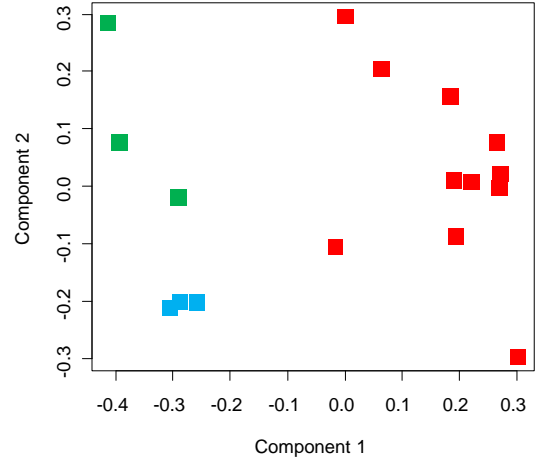
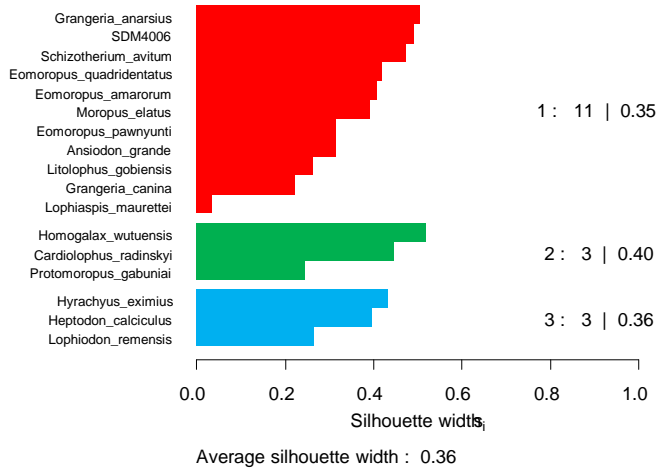


Spearman Correlation

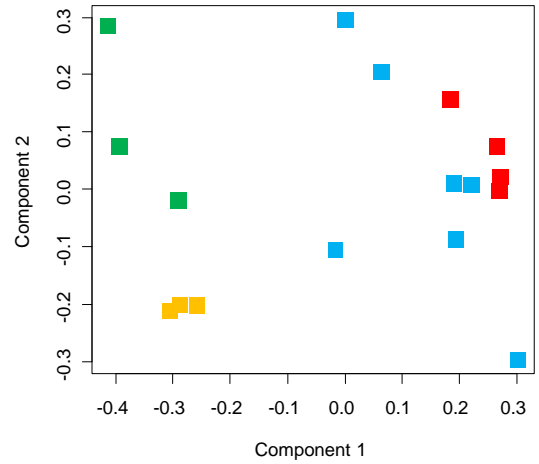
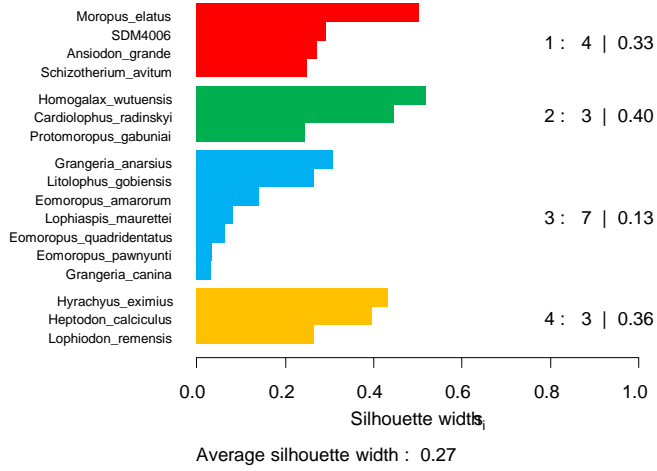


Silhouette plot, Partition Around Medoids

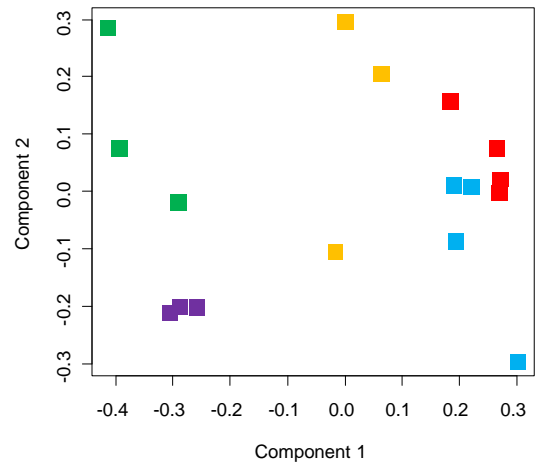
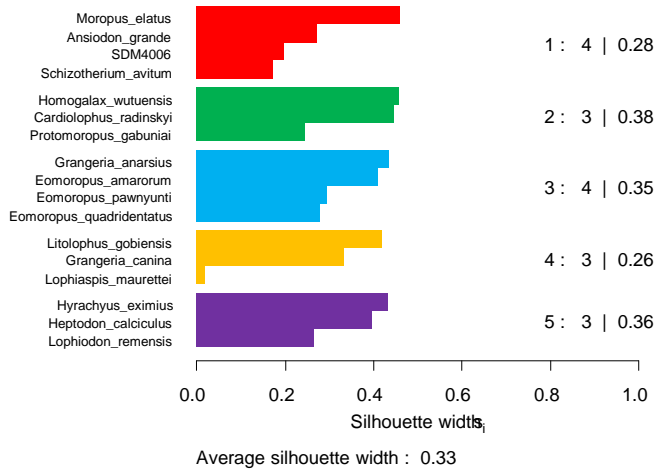
k=3



k=4

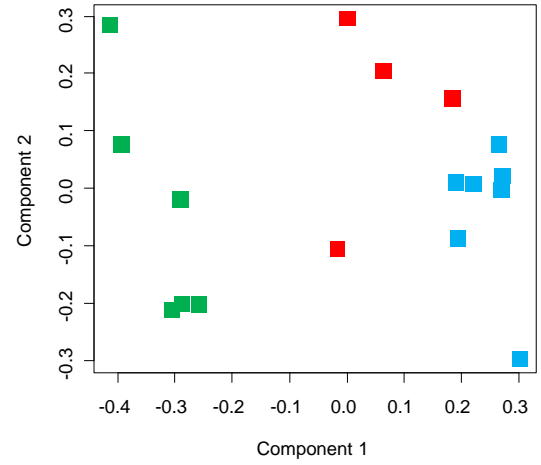
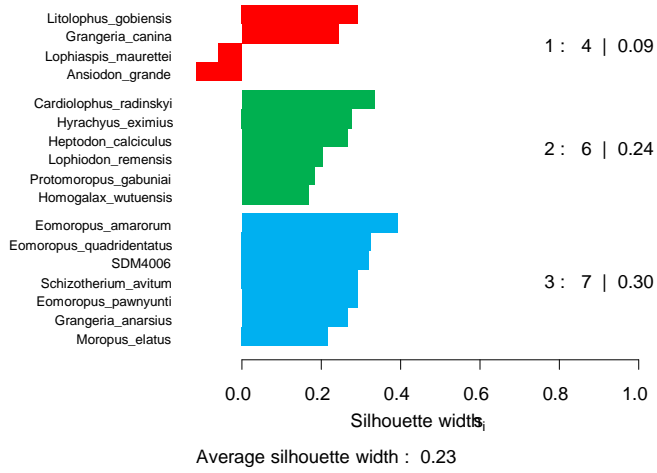


k=5



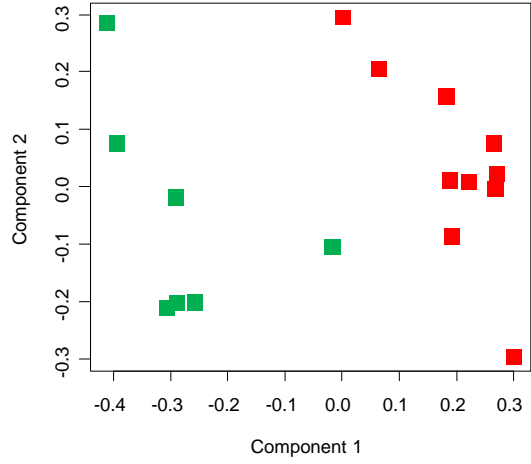
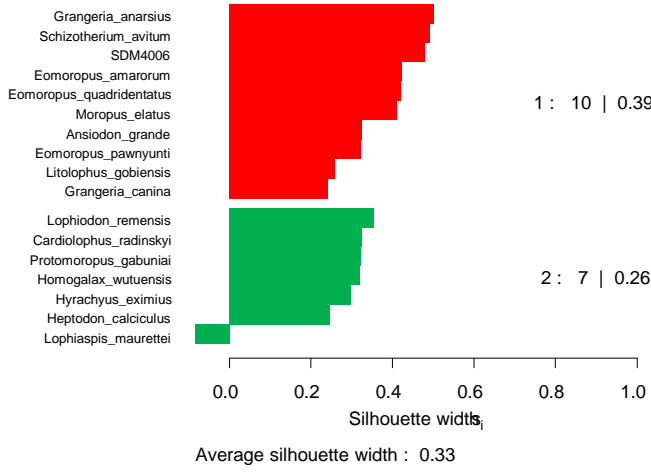
Silhouette plot, Fuzzy Analysis

k=3

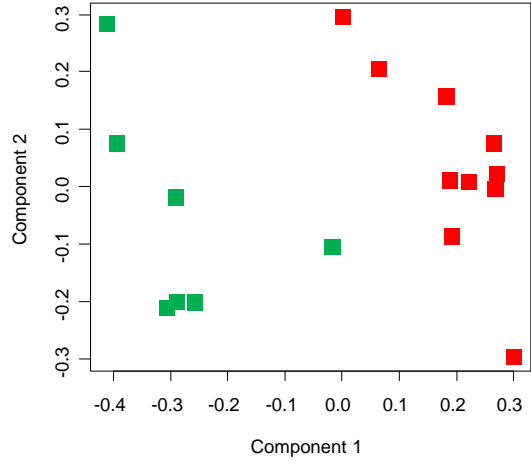
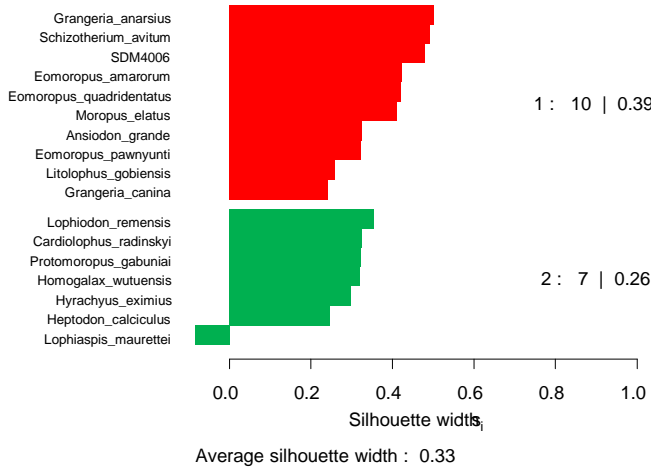


Addendum: Two-cluster partitioning

Medoid Partition



Fuzzy Analysis



Family Rhinocerotidae

Order Perissodactyla

Becker et al. 2013

Pearson BDC

Negative: 47

Positive: 82

Clusters: 5

Clusterability

Hopkins Statistic: 0.648

Dip test: 0.019

Dip test p-value: 0.446

Spearman BDC

Negative: 55

Positive: 132

Clusters: 4

Spearman BDC results considerably expand the instances of significant, positive correlation, which reduces the number of clusters from five in the Pearson BDC results to four. The average silhouette width is 0.2 for the five-cluster Pearson BDC partition and 0.22 for the Spearman BDC partition. The cluster membership difference is 11%.

The five-cluster medoid partition has an average silhouette width of 0.17 and differs from the Pearson BDC clusters by 25%. The four-cluster medoid partition has an average silhouette width of 0.12 and differs substantially from the Spearman BDC clusters.

Fuzzy analysis failed for these distances and cluster counts.

The results reveal a substantial lack of consistency and confirm the uncertainty of the original analysis.

Original conclusion: Inconclusive

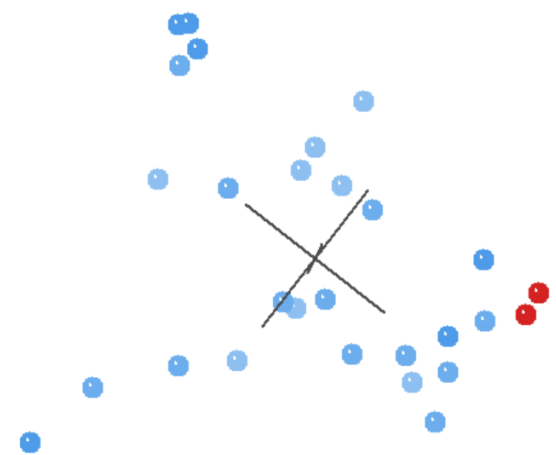
Updated conclusion: Inconclusive

Characters: Craniodental and postcranial



Order Perissodactyla
Family Rhinocerotidae

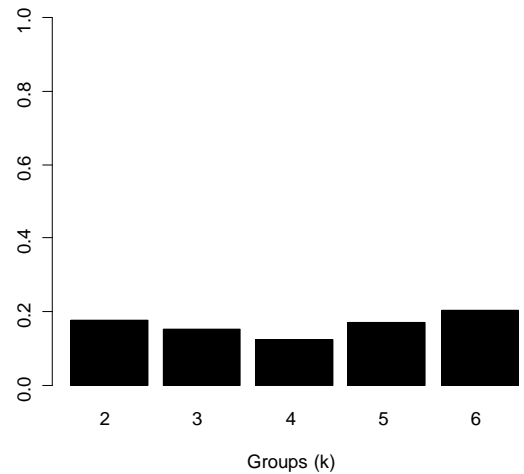
Published taxa	30
Published characters	214
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	28
Characters used for calculations	161
Median bootstrap value	89
F ₉₀	0.45
Stress of 3D MDS	0.34
k _{min}	15
Conclusion	Inc



Notes: No evidence of discontinuity.



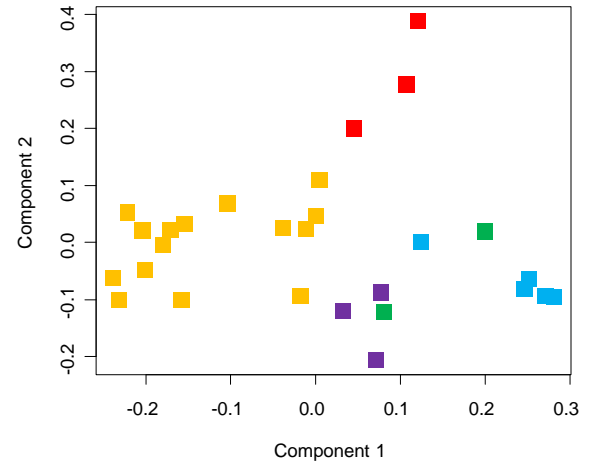
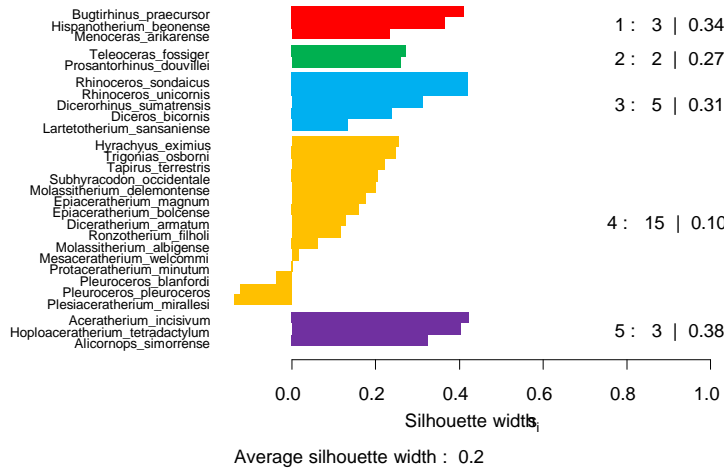
Average Silhouette Widths, Partion Around Medoids



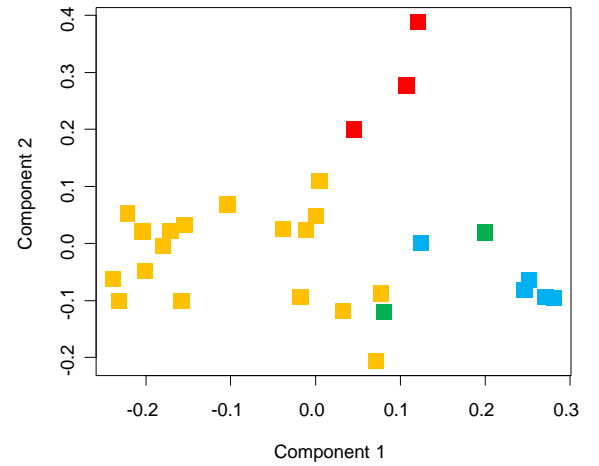
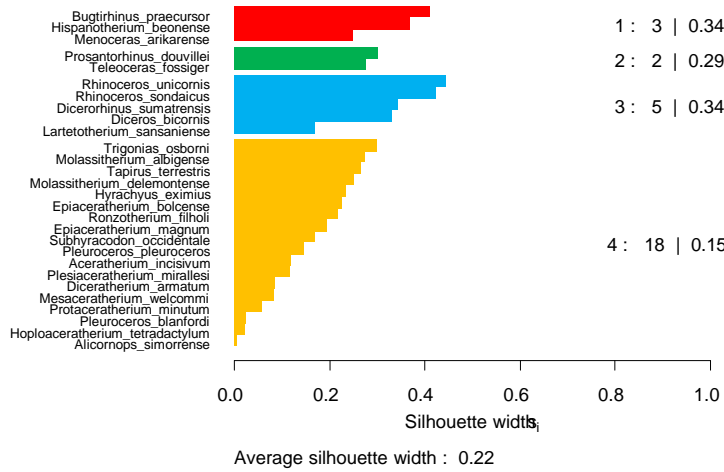
Clade Correspondence: All five BDC clusters contain two or more taxa. Clusters 1, 2, 3, and 5 are monophyletic in the phylogeny shown in Figure 6 of Becker et al. (2013).

Silhouette plot, BDC partitions

Pearson Correlation

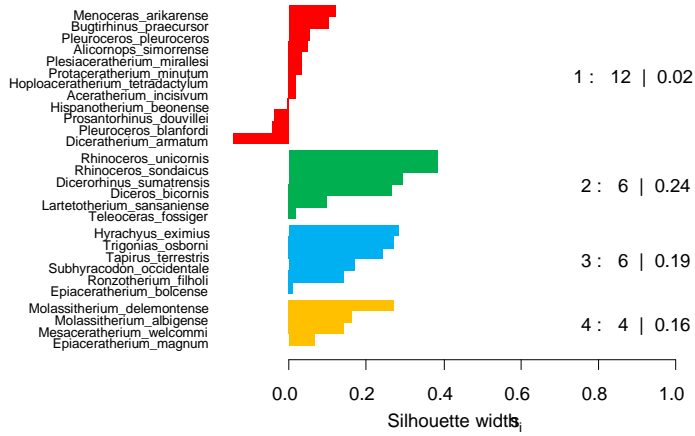


Spearman Correlation

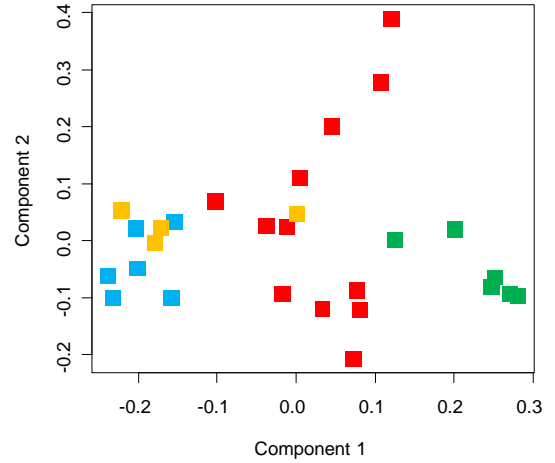


Silhouette plot, Partition Around Medoids

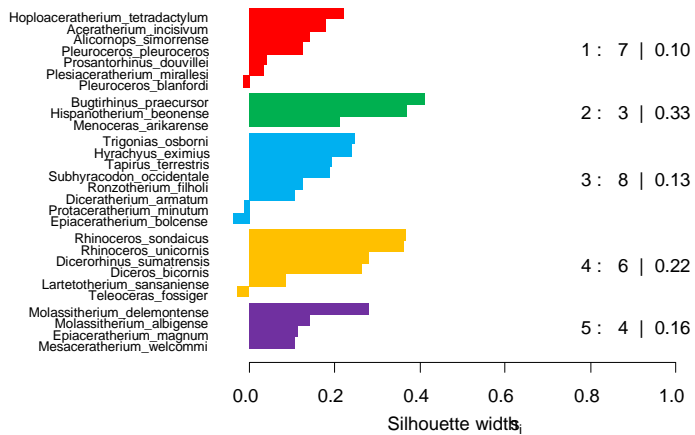
k=4



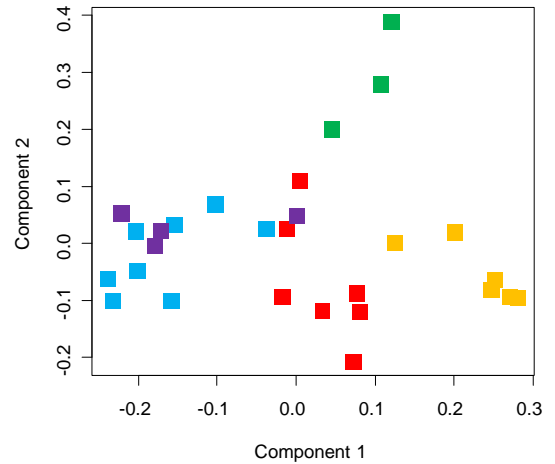
Average silhouette width : 0.12



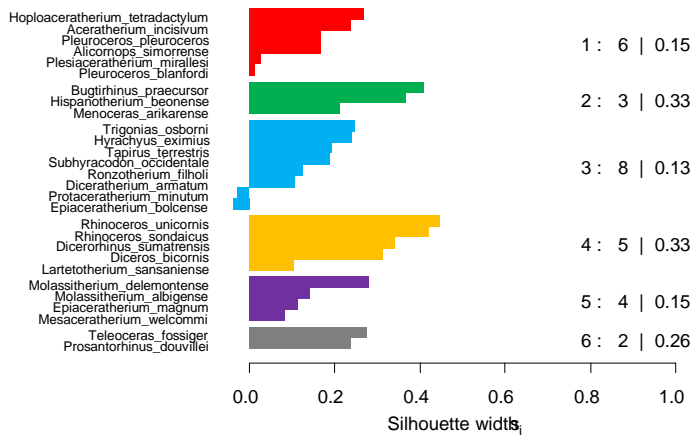
k=5



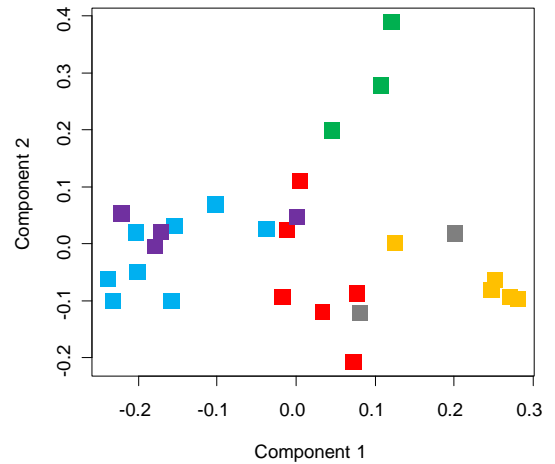
Average silhouette width : 0.17



k=6



Average silhouette width : 0.2



Family Lophodontidae

Order Perissodactyla

Robinet et al. 2015

Pearson BDC

Negative: 42

Positive: 37

Clusters: 2

Clusterability

Hopkins Statistic: 0.653

Dip test: 0.039

Dip test p-value: 0.215

Spearman BDC

Negative: 59

Positive: 57

Clusters: 2

The additional instances of significant positive and negative correlation in the Spearman BDC results nearly fill all possible taxon pairs (116 out of 120 possible taxon pairs exhibit either significant, negative or significant, positive correlation). The result is two very clearly defined groups of taxa that correspond exactly to the clusters evident in the Pearson BDC results. The average silhouette width for this partition is 0.35.

Two-cluster medoid partition and fuzzy analysis agree exactly with the BDC clusters.

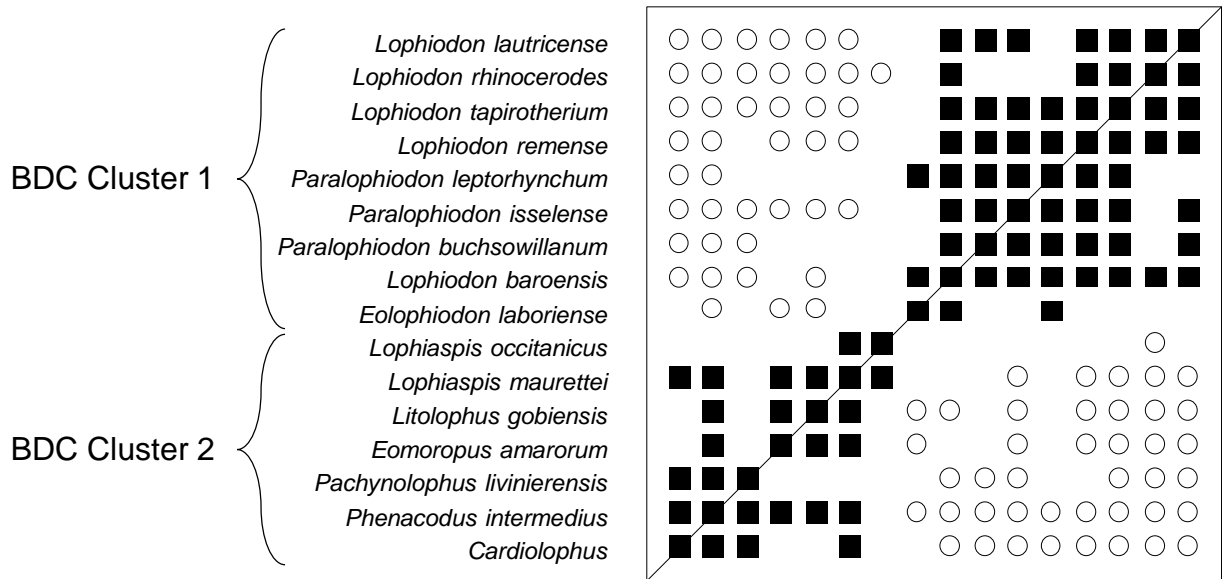
The original conclusion is confirmed.

Original conclusion: HB

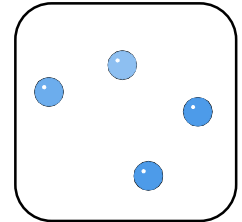
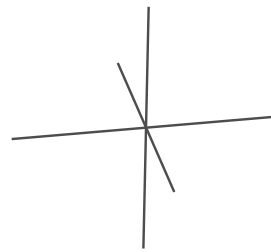
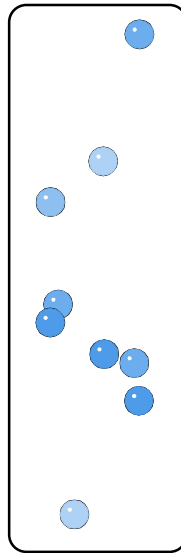
Updated conclusion: HB

Robinet, C., J.A. Remy, J.A., Y. Laurent, L. Danilo, and F. Lihoreau. 2015. A new genus of Lophiodontidae (Perissodactyla, Mammalia) from the early Eocene of La Borie (Southern France) and the origin of the genus *Lophiodon* Cuvier, 1822. *Geobios* 48:25-38.

Characters: Craniodental



Lophiodontinae

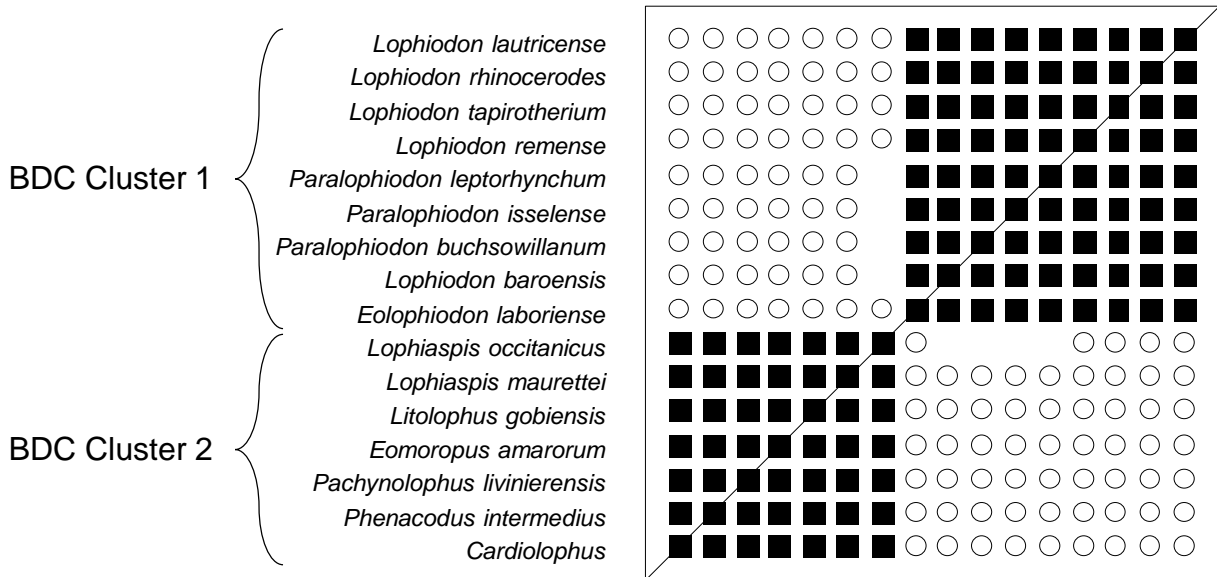


Lophiaspis,
Eomoropus,
Litolophus

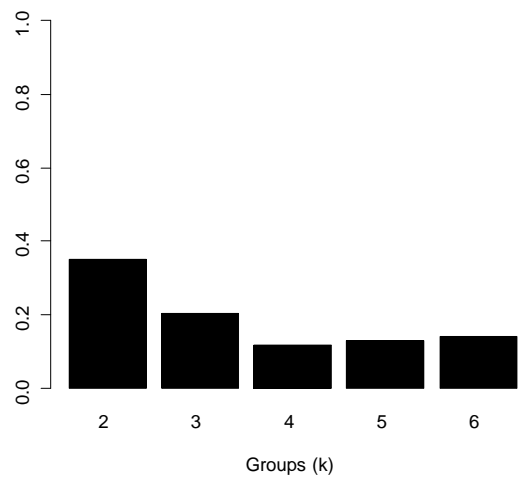
Order Perissodactyla
Family Lophiodontidae

Published taxa	18
Published characters	149
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	16
Characters used for calculations	118
Median bootstrap value	77
F ₉₀	0.28
Stress of 3D MDS	0.24
k _{min}	10
Conclusion	HB

Notes: BDC and MDS both support two distinct groups, one consisting of subfamily Lophiodontinae (*Lophiodon*, *Paralophiodon*, and *Eolophiodon*), and the other containing all other taxa. Lophiodontinae is likely a holobaramin.



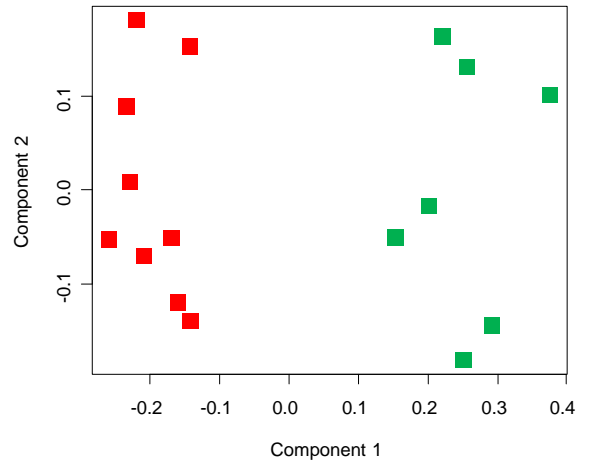
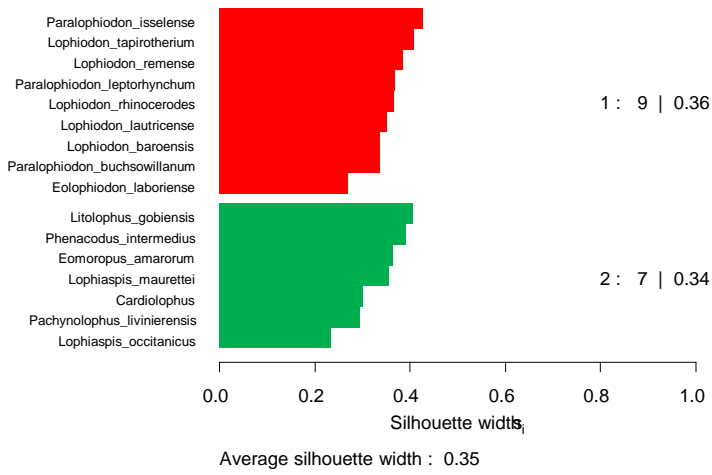
Average Silhouette Widths, Partion Around Medoids



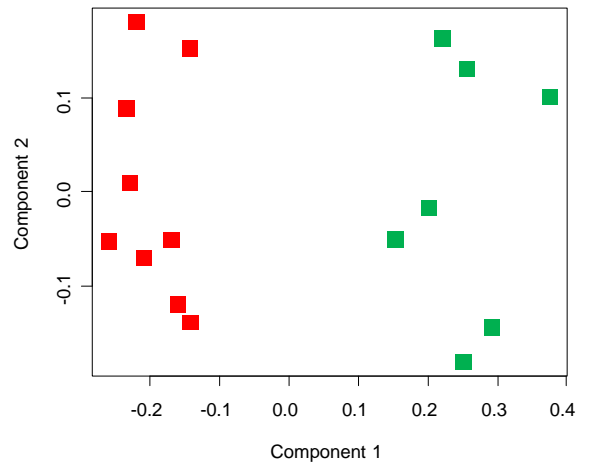
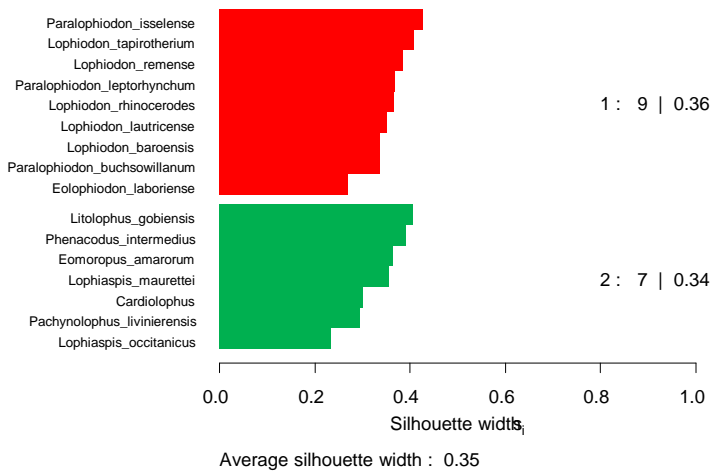
Clade Correspondence: Two large BDC clusters both contain more than two taxa each. The published phylogeny in Figure 6 of Robinet et al. (2014) shows both clusters as monophyletic if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

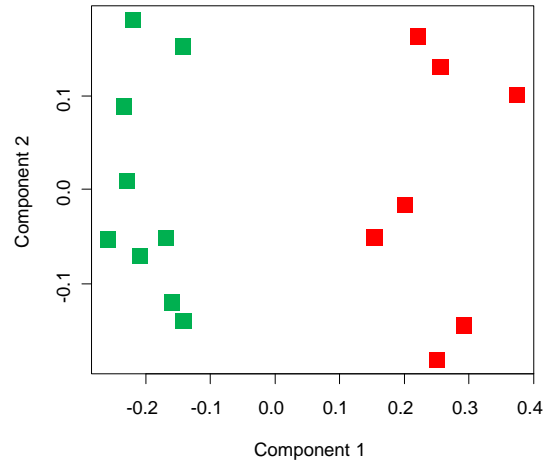
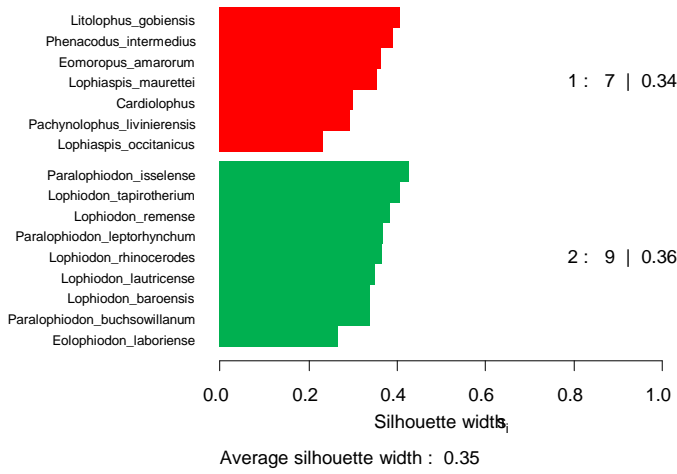


Spearman Correlation

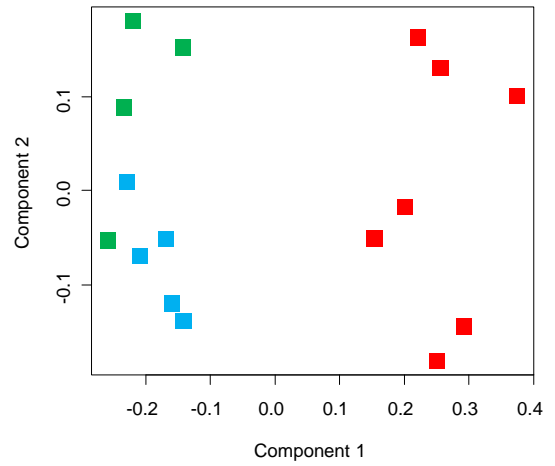
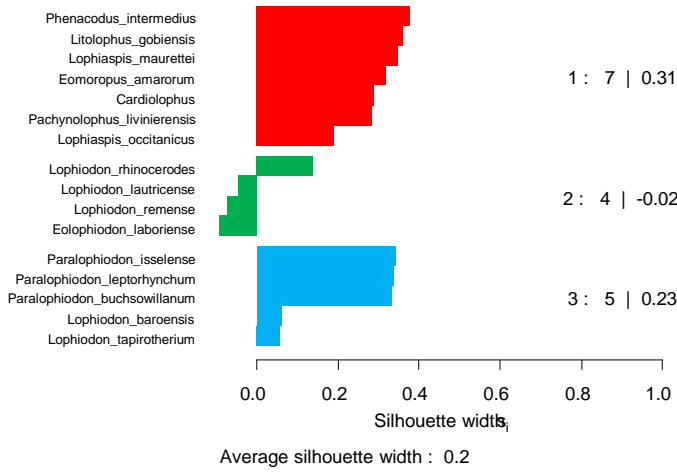


Silhouette plot, Partition Around Medoids

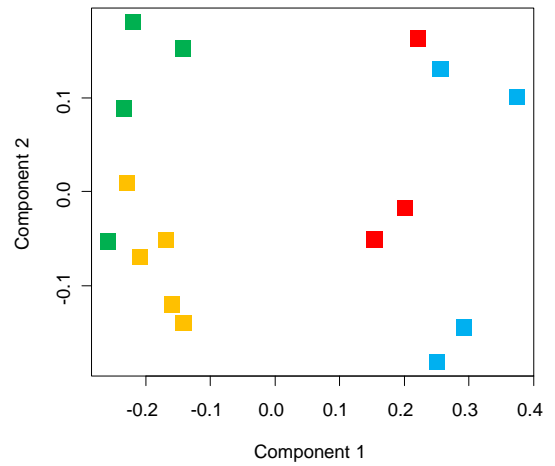
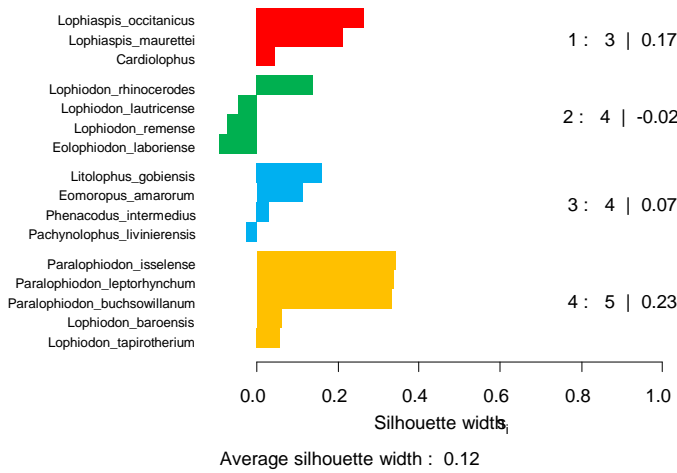
k=2



k=3

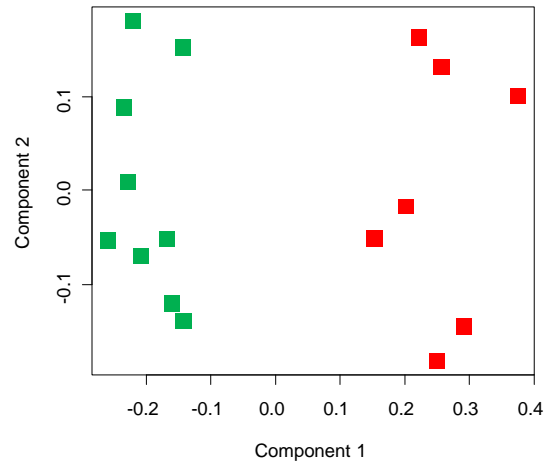
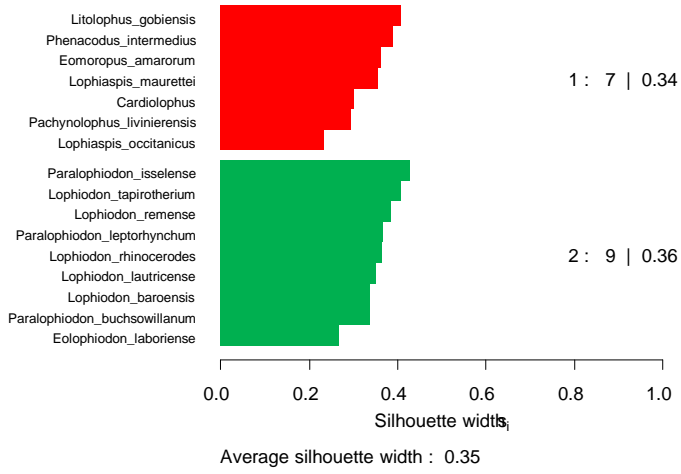


k=4



Silhouette plot, Fuzzy Analysis

k=2



Infraorder Sirenia

Order Uranotheria

Sorbi 2008

Pearson BDC

Negative: 57

Positive: 249

Clusters: 2

Clusterability

Hopkins Statistic: 0.854

Dip test: 0.014

Dip test p-value: 0.884

Spearman BDC

Negative: 36

Positive: 228

Clusters: 2

The Spearman BDC partitions the taxa into the same two clusters as the Pearson BDC. The average silhouette width for the BDC partition is 0.5.

The two-cluster medoid partition agrees exactly with the BDC partition. The three-cluster medoid partition has a substantially lower average silhouette width of 0.36.

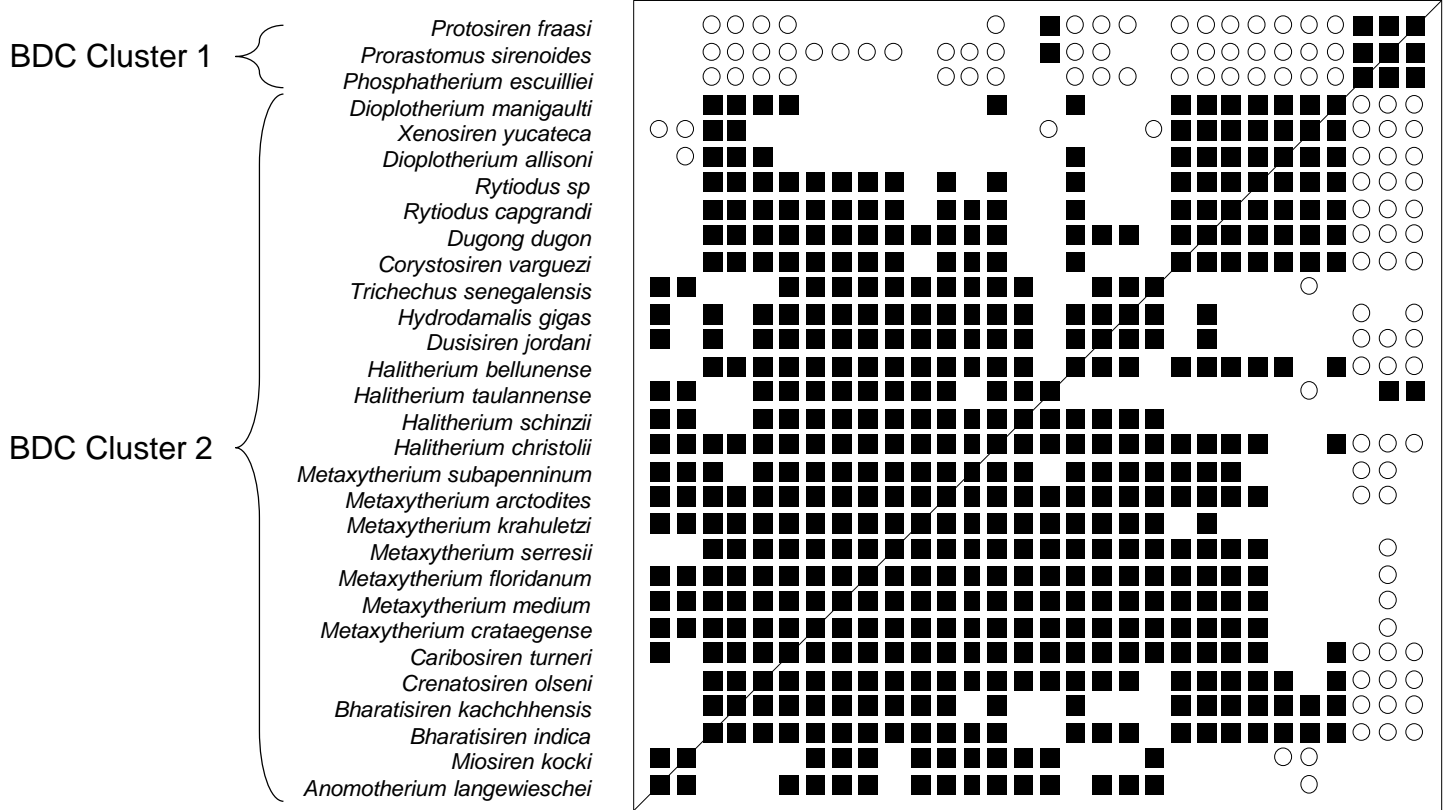
Two-cluster fuzzy analysis yielded a different partition with a much lower average silhouette width of 0.24.

These results confirm the original results. Given the much lower average silhouette width of the fuzzy analysis, we may reasonably discount its results.

Original conclusion: HB

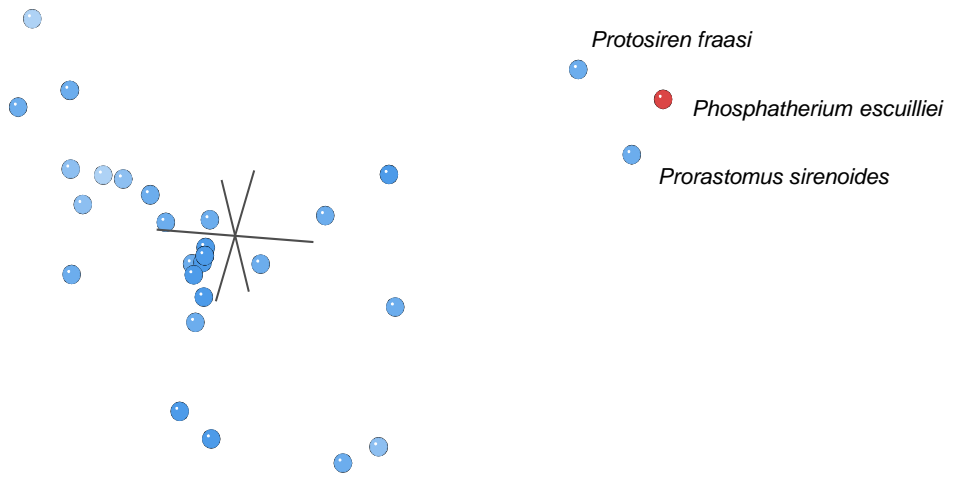
Updated conclusion: HB

Characters: Craniodental



Order Uranotheria
Infraorder Sirenia

Published taxa	32
Published characters	57
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	30
Characters used for calculations	50
Median bootstrap value	78
F ₉₀	0.33
Stress of 3D MDS	0.16
k _{min}	5
Conclusion	HB



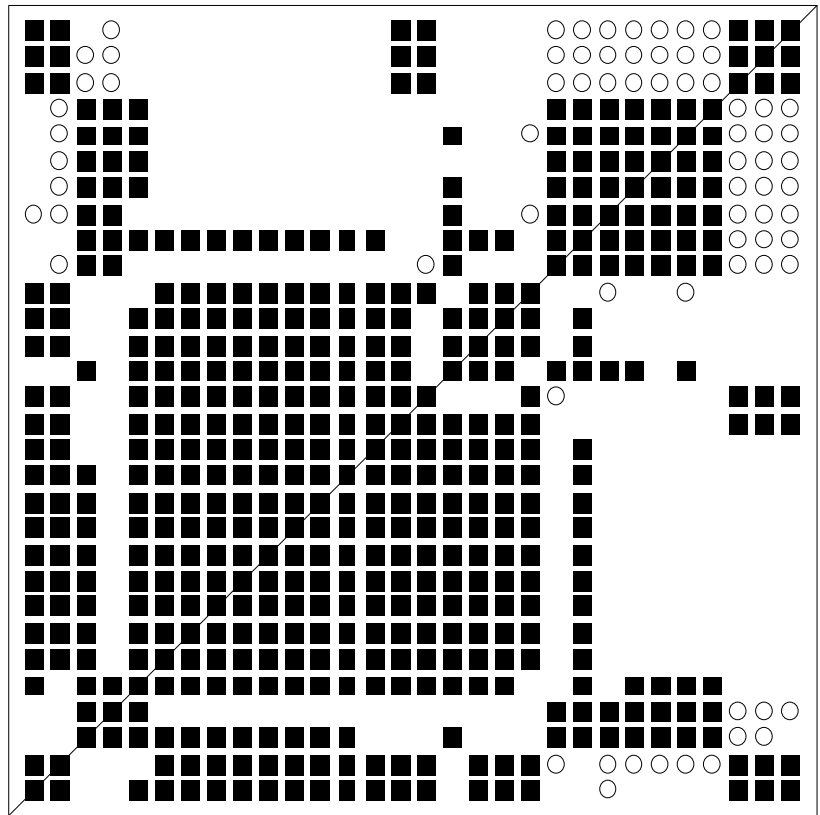
Notes: BDC and MDS both support two groups: 1. The outgroup *Phosphatherium escuilliei* together with the sirenians *Protosiren fraasi* and *Prorastomus sirenoides*. 2. The rest of the Sirenia. There is significant, positive BDC with low bootstrap values only between *Halitherium taulannense* and the two sirenians that cluster with the outgroup, but in the MDS results, *Halitherium taulannense* is part of the sirenian cluster and separate from the three taxa in the outgroup cluster. We may infer that Sirenia *sensu stricto* (excluding *Protosiren* and *Prorastomus*) is a holobaramin.

BDC Cluster 1

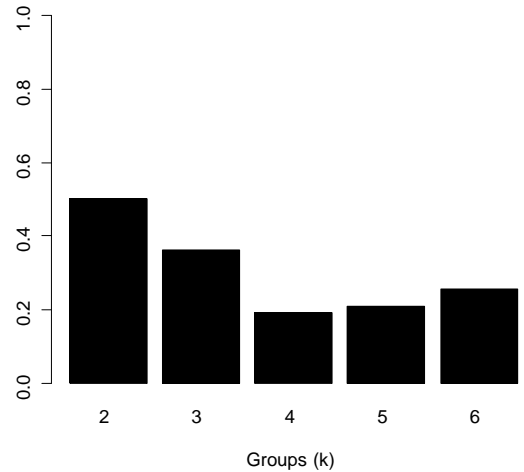
- Protosiren fraasi*
- Prorastomus sirenooides*
- Phosphatherium escuilliei*
- Dioplotherium manigaulti*
- Xenosiren yucateca*
- Dioplotherium allisoni*
- Rytiodus sp*
- Rytiodus capgrandi*
- Dugong dugon*
- Corystosiren varguezii*

BDC Cluster 2

- Trichechus senegalensis*
- Hydrodamalis gigas*
- Dusisiren jordani*
- Halitherium bellunense*
- Halitherium taulannense*
- Halitherium schinzii*
- Halitherium christolii*
- Metaxytherium subapenninum*
- Metaxytherium arctodites*
- Metaxytherium krahuletzii*
- Metaxytherium serresii*
- Metaxytherium floridanum*
- Metaxytherium medium*
- Metaxytherium crataegense*
- Caribosiren turneri*
- Crenatosiren olseni*
- Bharatisiren kachchensis*
- Bharatisiren indica*
- Miosiren kocki*
- Anomotherium langewieschei*



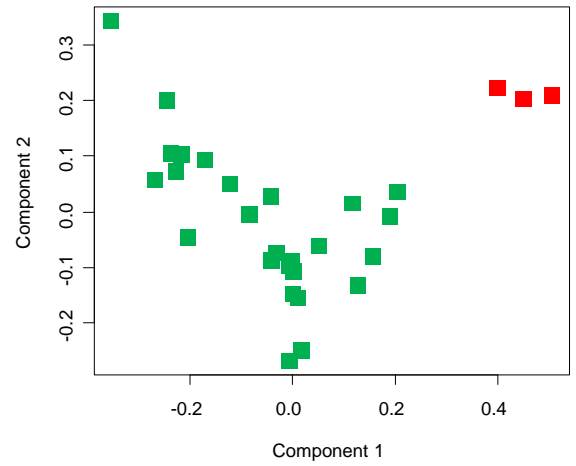
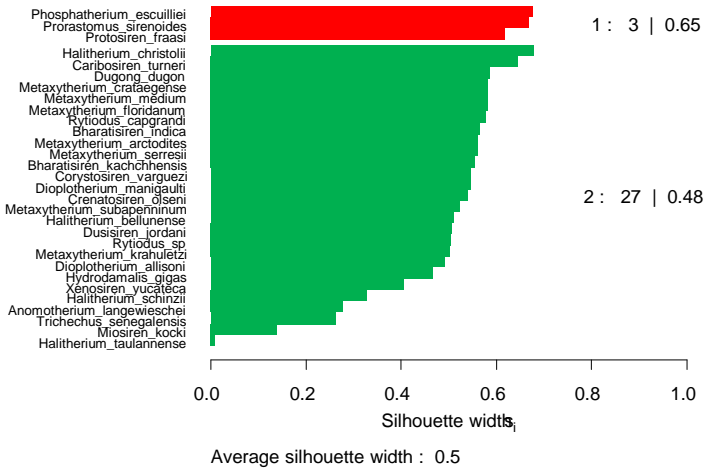
Average Silhouette Widths, Partion Around Medoids



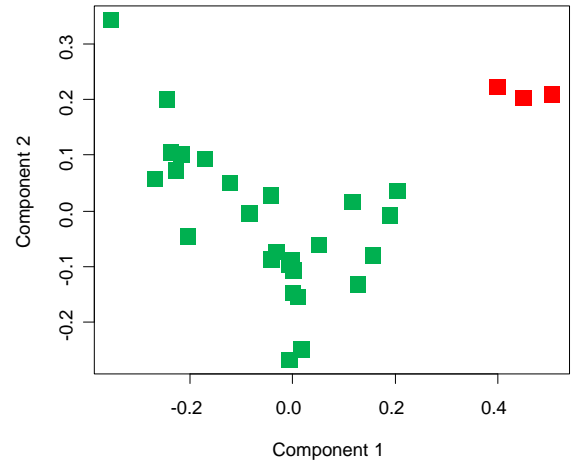
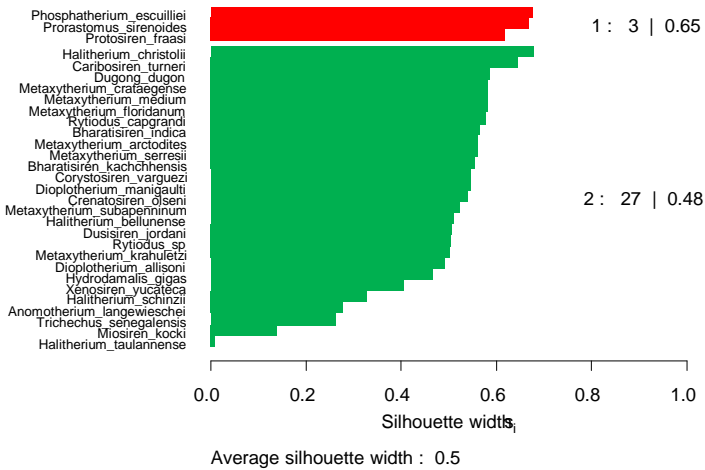
Clade Correspondence: Both BDC clusters contain three or more taxa. Both are monophyletic in the phylogeny shown on p. 181 of Sorbi (2008).

Silhouette plot, BDC partitions

Pearson Correlation

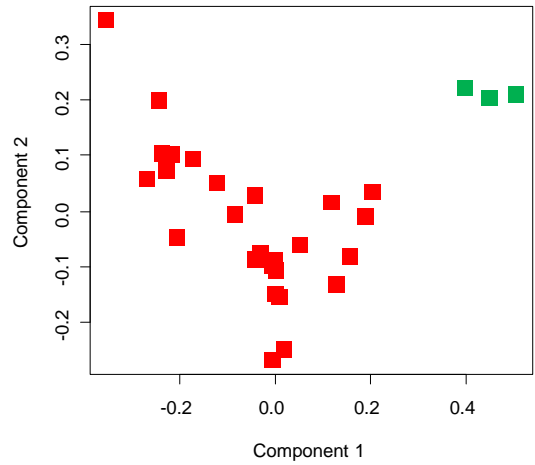
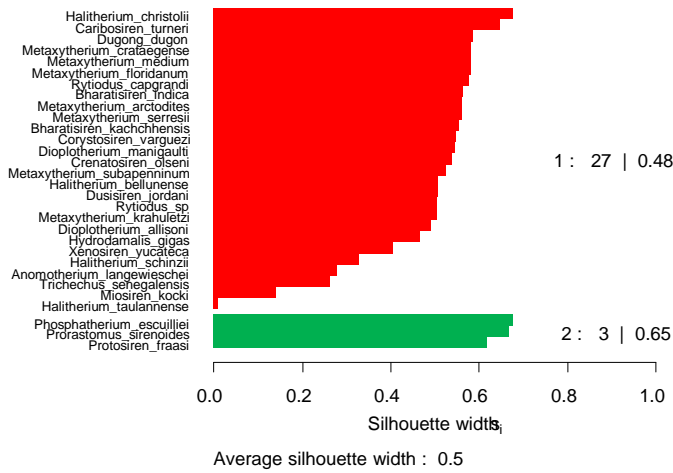


Spearman Correlation

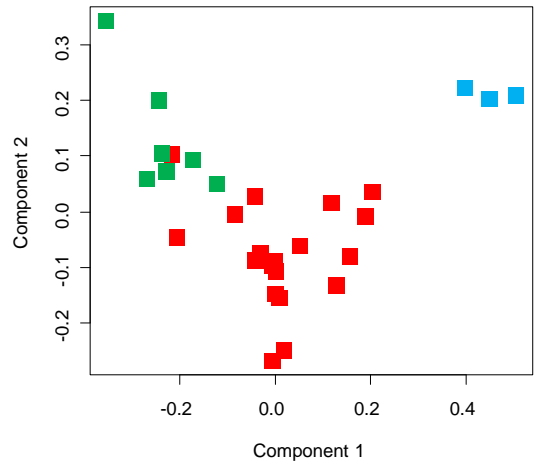
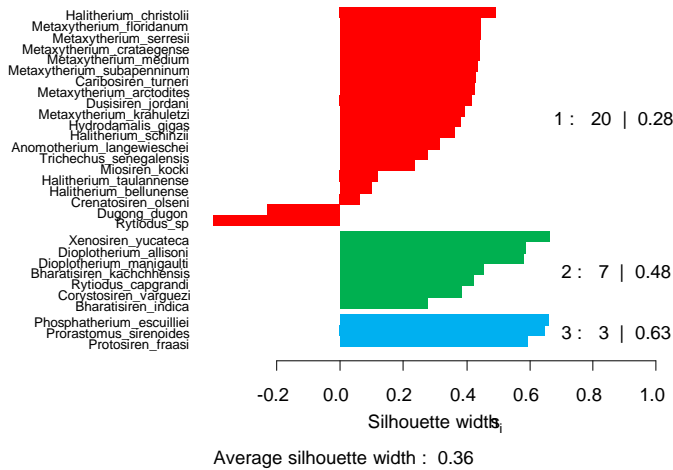


Silhouette plot, Partition Around Medoids

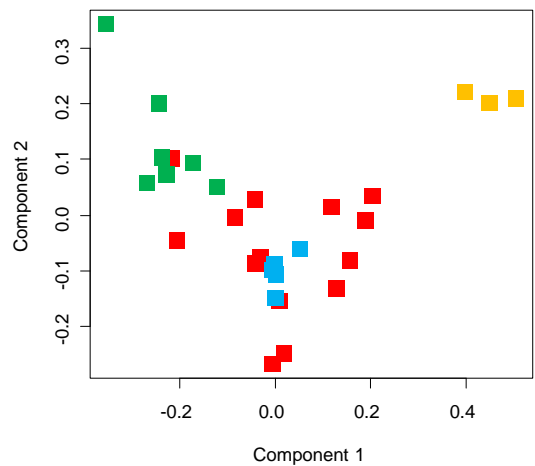
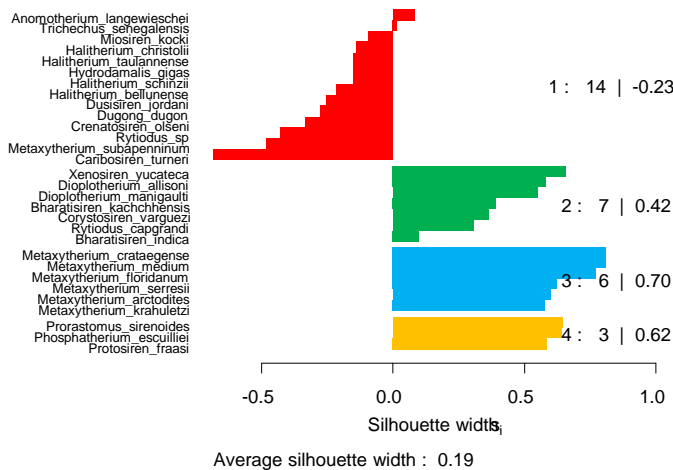
k=2



k=3

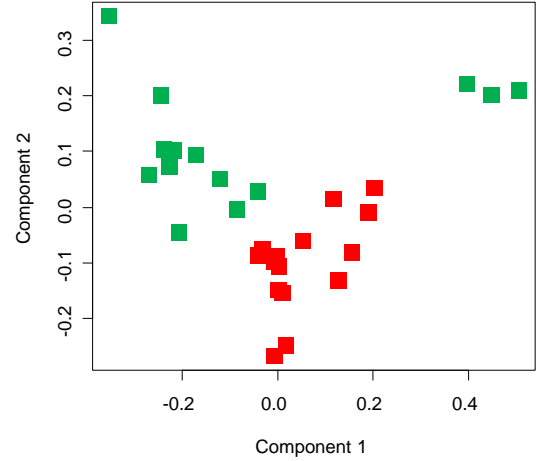
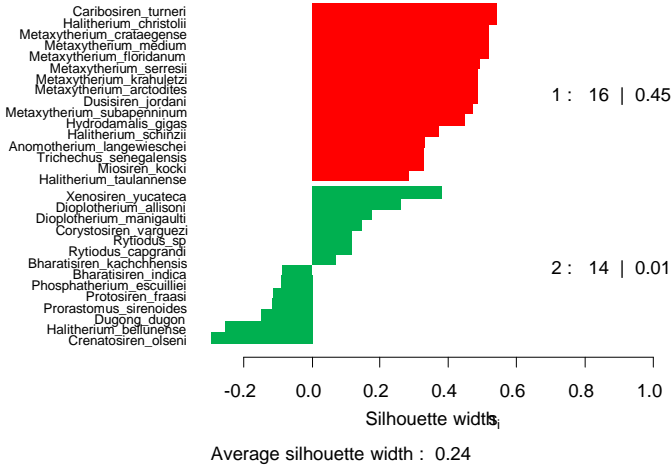


k=4

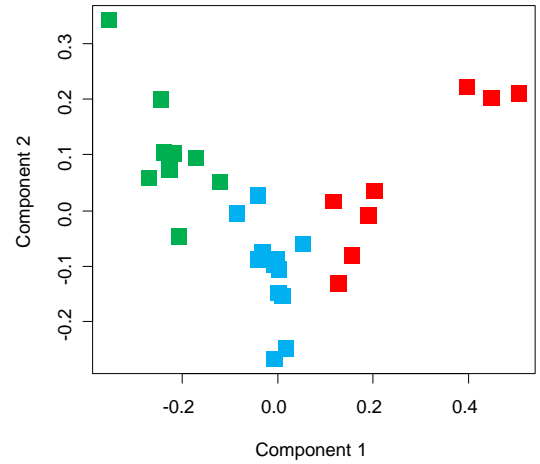
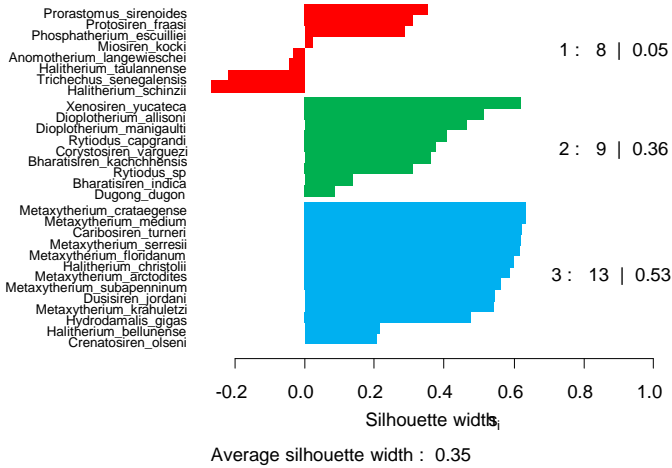


Silhouette plot, Fuzzy Analysis

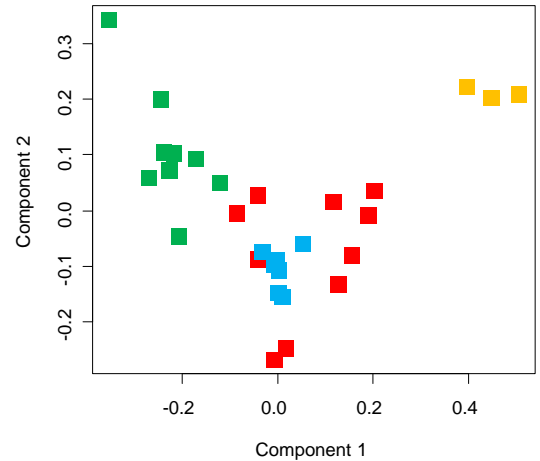
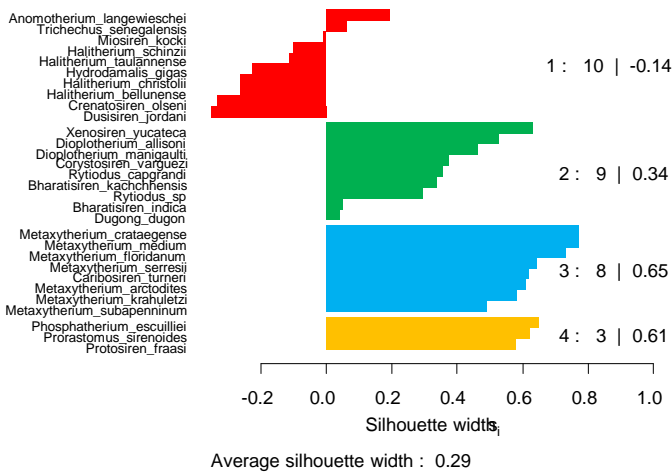
k=2



k=3



k=4



Family Desmostylidae

Order Uranotheria

Beatty 2009

Pearson BDC

Negative: 10

Positive: 7

Clusters: 3

Clusterability

Hopkins Statistic: 0.753

Dip test: 0.045

Dip test p-value: 0.862

Spearman BDC

Negative: 9

Positive: 8

Clusters: 3

The Spearman BDC results partition the taxa in the exact same clusters as the Pearson BDC. The average silhouette width of this partition is 0.5.

The three-cluster medoid partition and fuzzy analysis agree with the BDC partition exactly.

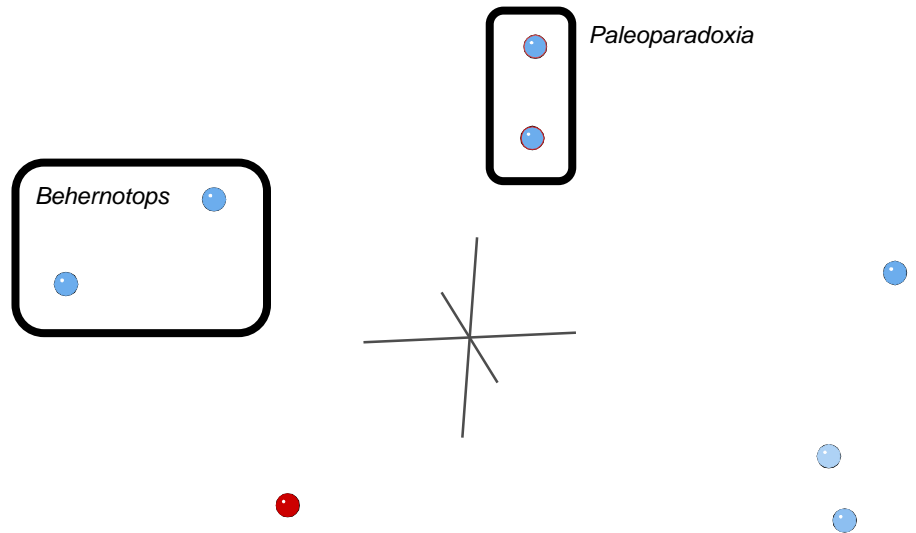
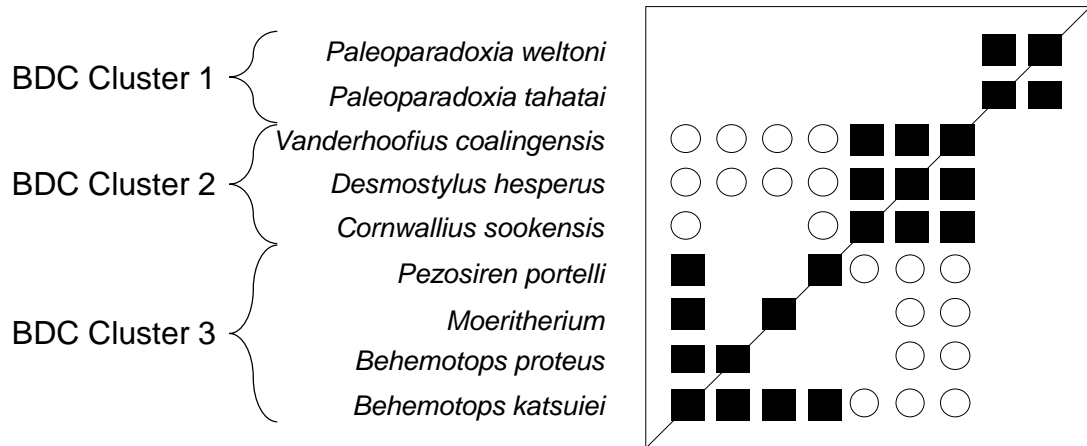
These results confirm the original findings and conclusion.

Original conclusion: HB?

Updated conclusion: HB?

Beatty, B.L. 2009. New material of *Cornwallius sookensis* (Mammalia: Desmostylia) from the Yaquina Formation of Oregon. *Journal of Vertebrate Paleontology* 29:894-909.

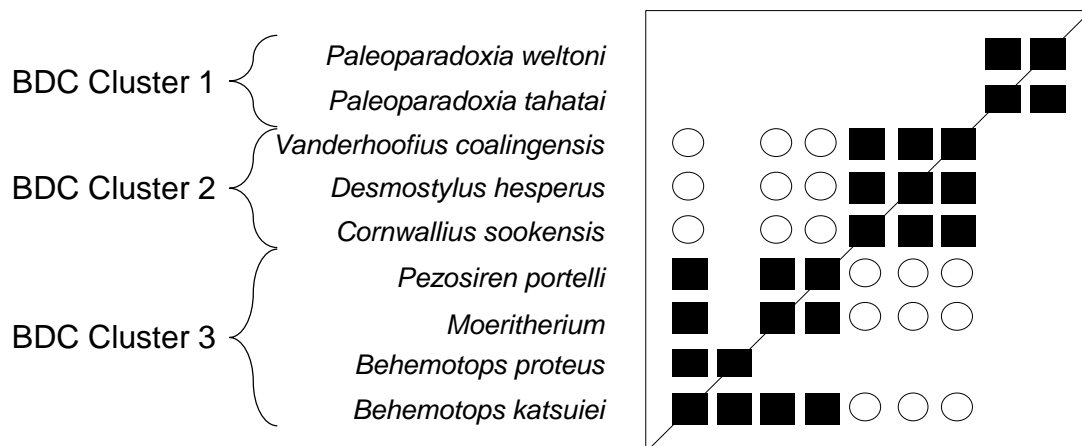
Characters: Craniodental



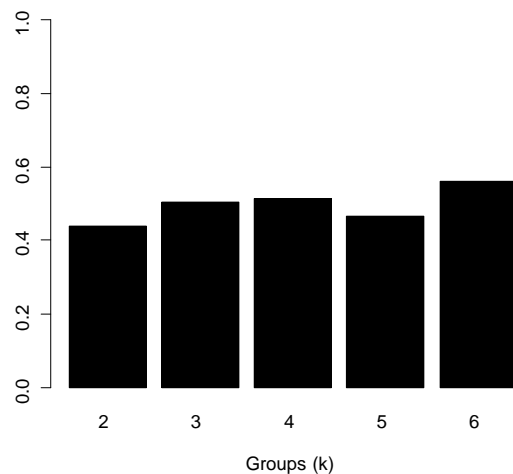
Order Uranotheria
Family Desmostylidae

Published taxa	10
Published characters	37
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	9
Characters used for calculations	25
Median bootstrap value	83.5
F ₉₀	0.28
Stress of 3D MDS	0.1
k _{min}	3
Conclusion	HB?

Notes: BDC results reveal three clusters: 1. the *Palaeoparadoxia* species, 2. the desmostylids *Vanderhoofius*, *Desmostylus*, and *Cornwallius*, and 3. the remaining taxa. There is significant, negative BDC between the restricted desmostylid group and the outgroup taxa. Bootstrap values for all BDC are poor. The MDS results reveal four clusters, separating the *Behemotops* species from the remaining outgroup taxa. We may provisionally accept the restricted Desmostylidae *sensu stricto* (*Vanderhoofius*, *Desmostylus*, and *Cornwallius*) as a holobaramin.



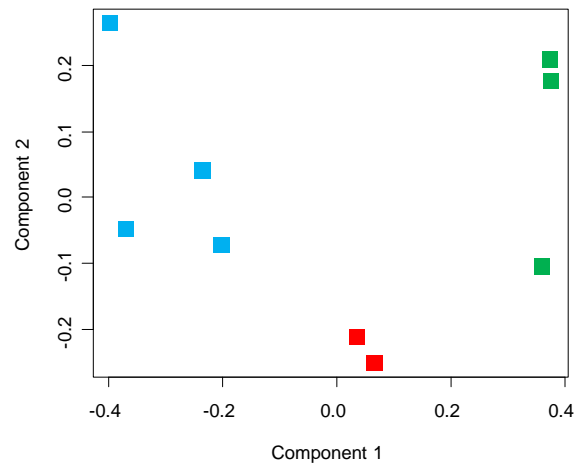
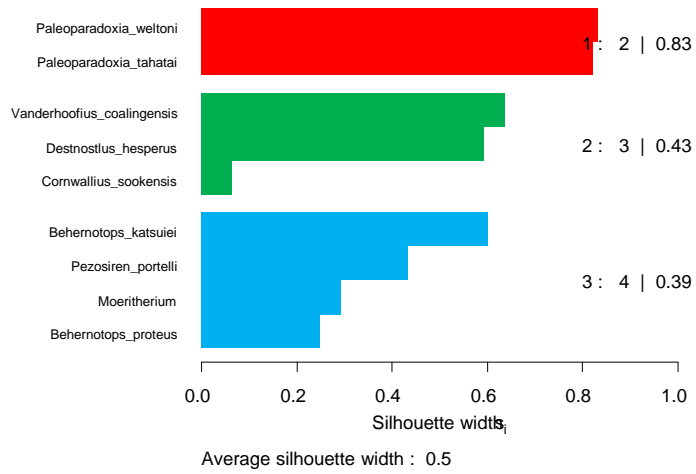
Average Silhouette Widths, Partion Around Medoids



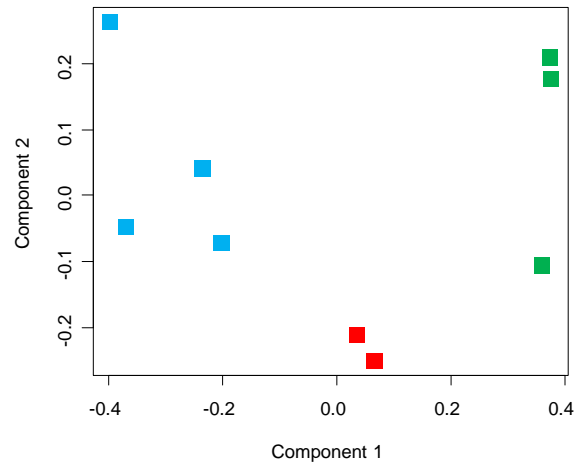
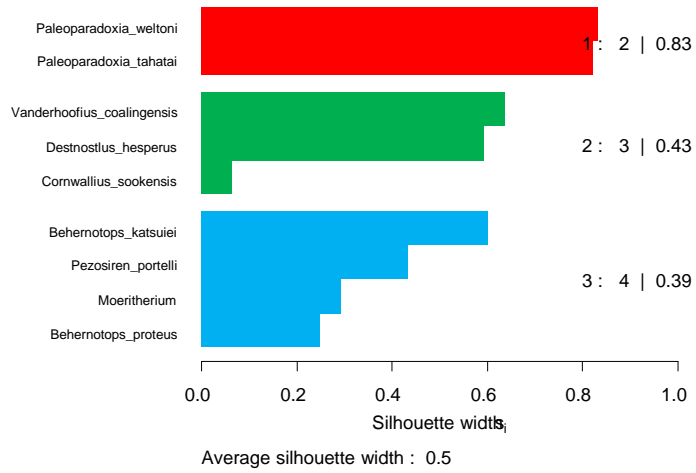
Clade Correspondence: All three BDC clusters contain two or more taxa. All three are monophyletic in the published phylogeny (Beatty 2009, Figure 11), if the tree were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

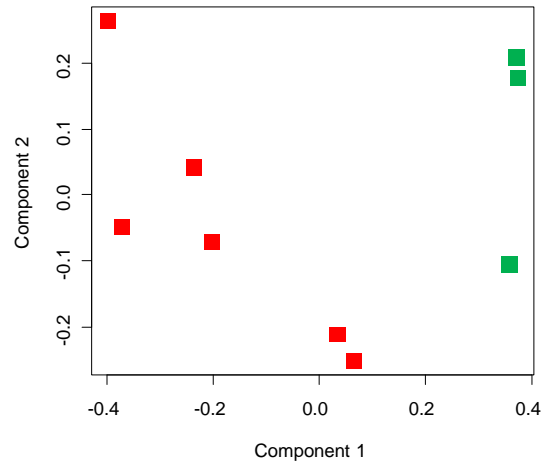
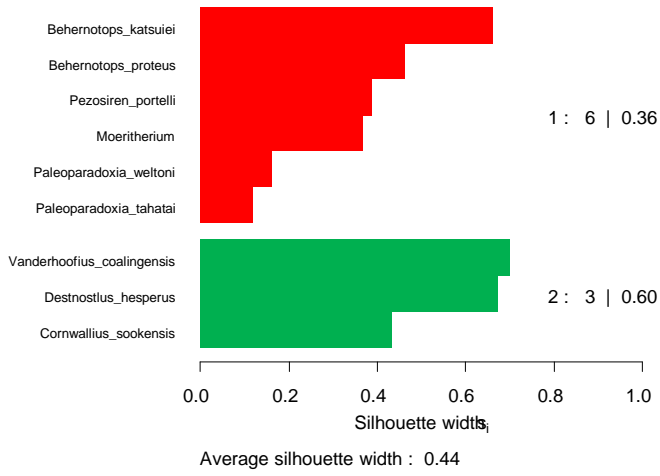


Spearman Correlation

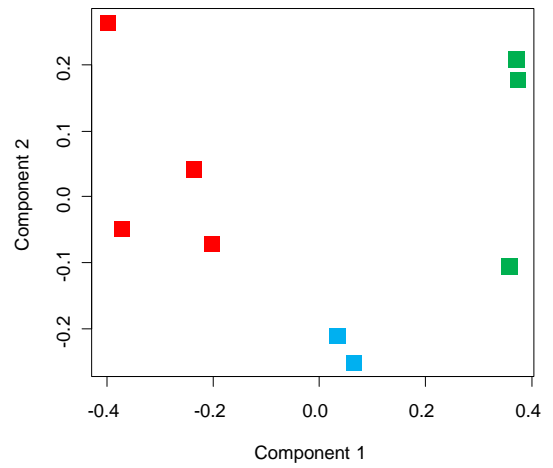
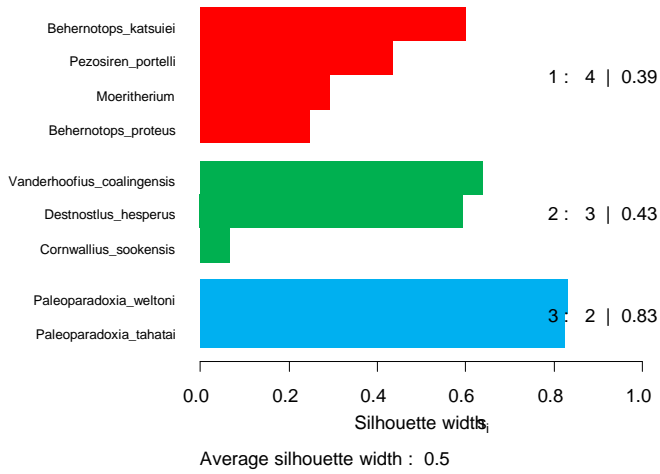


Silhouette plot, Partition Around Medoids

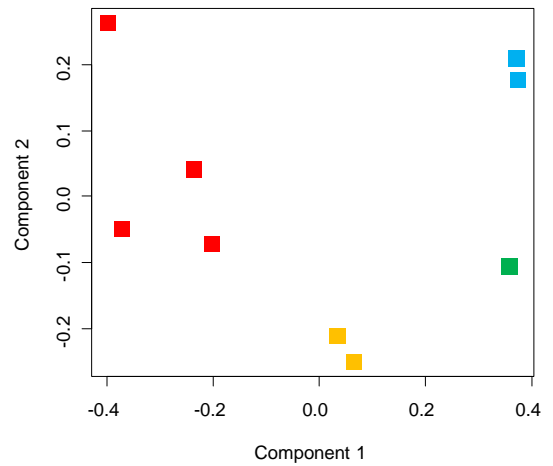
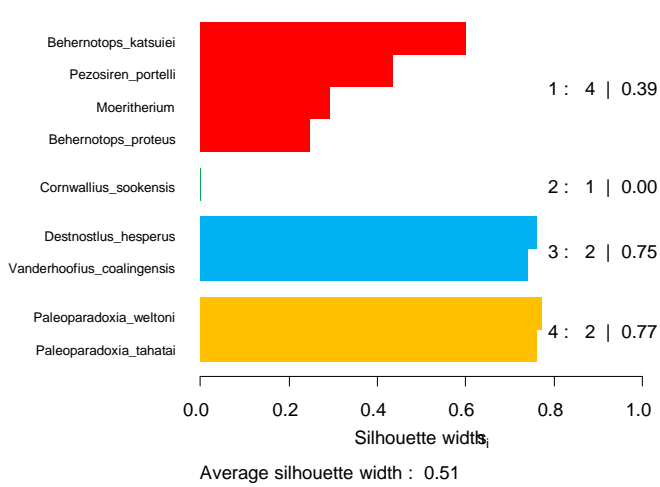
k=2



k=3

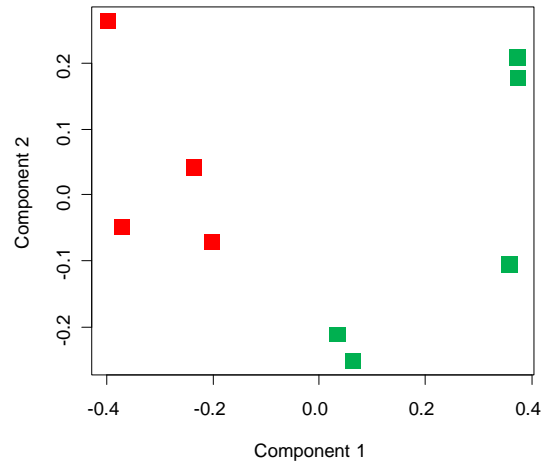
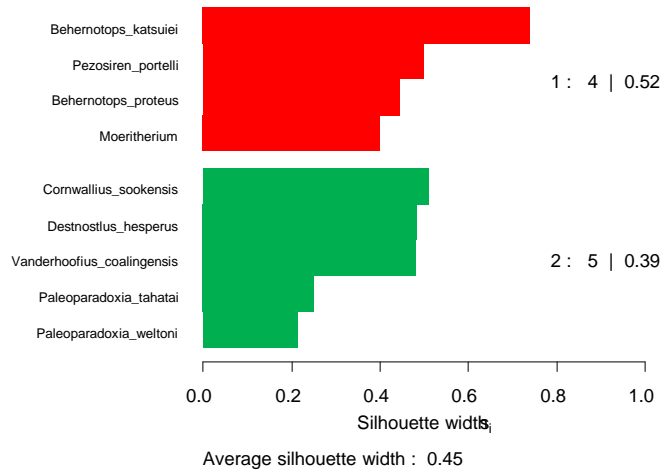


k=4

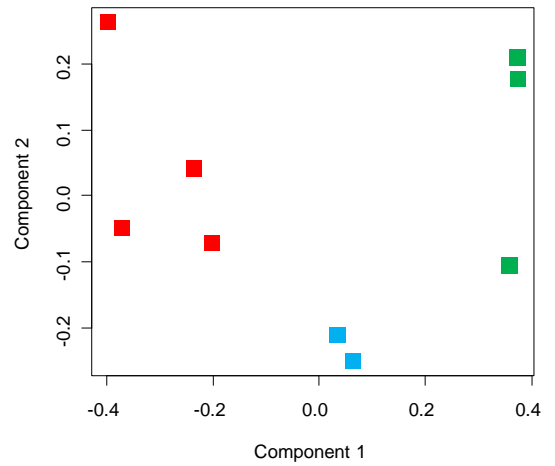
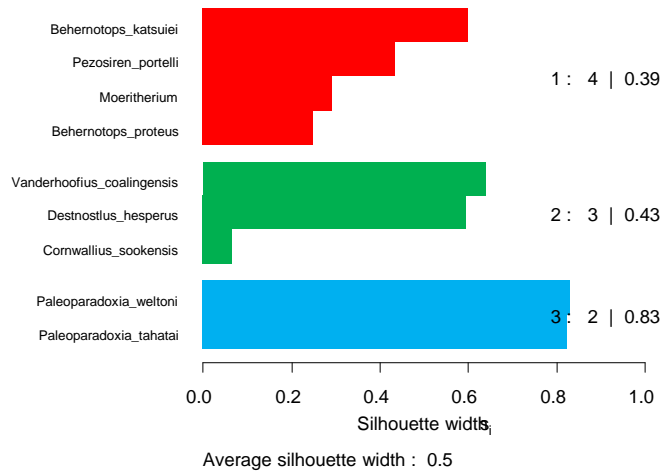


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Procaviidae

Order Hyracoidea

Seiffert et al. 2012

Pearson BDC

Negative: 49

Positive: 106

Clusters: 2

Spearman BDC

Negative: 46

Positive: 109

Clusters: 2

Clusterability

Hopkins Statistic: 0.774

Dip test: 0.041

Dip test p-value: 0.013

The Spearman BDC results partition the taxa in the same two clusters as the Pearson BDC results. The average silhouette width for this partition is 0.42.

The two-cluster medoid partition also clustered the taxa in the same way. The two-cluster fuzzy analysis had an average silhouette width of 0.39, with one taxon *Procavia capensis* exhibiting a silhouette width of -0.215. The two-cluster fuzzy partition differs only by this taxon with a cluster membership difference of 5%.

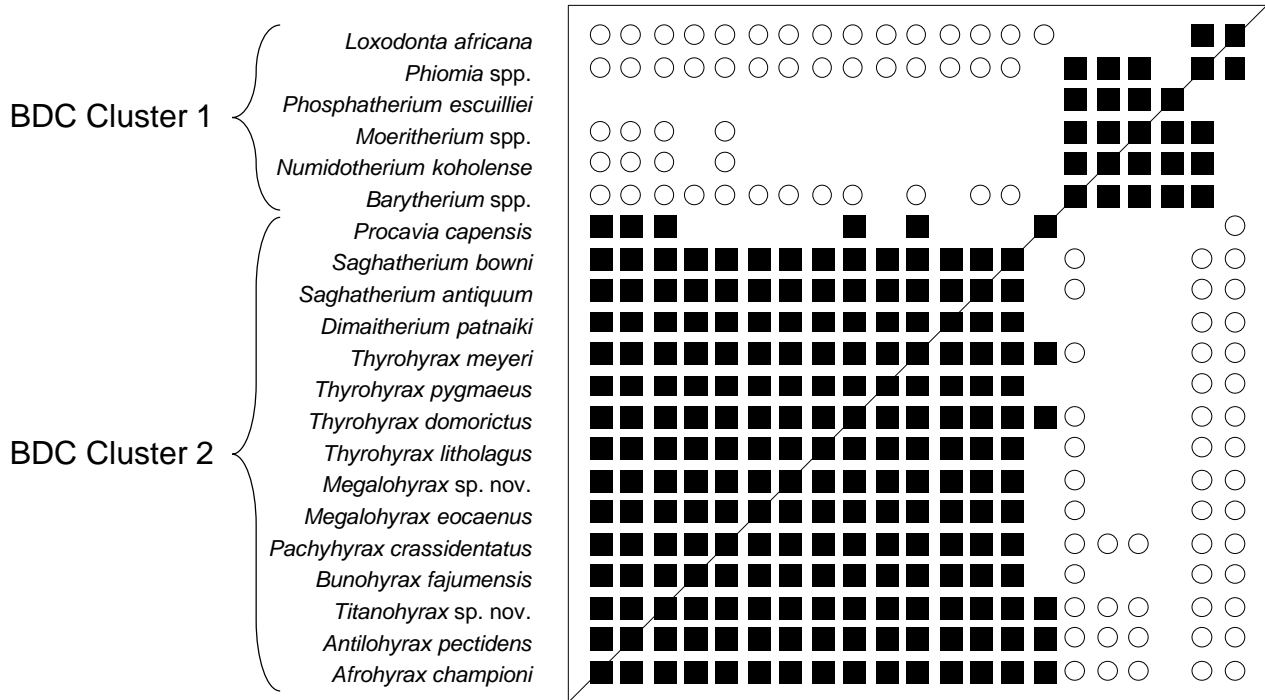
These results largely confirm the original analysis. The fuzzy partition is of lower quality than the BDC partition, as illustrated by the slightly lower average silhouette width and the negative silhouette width for *Procavia capensis*.

Original conclusion: HB

Updated conclusion: HB

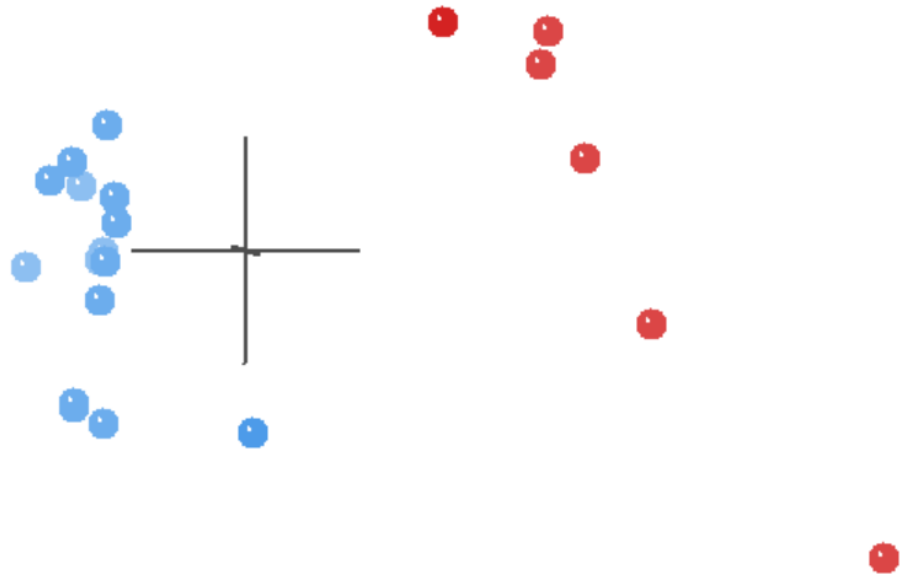
Seiffert, E.R., S. Nasir, A. Al-Harthy, J.R. Groenke, B.P. Kraatz, N.J. Stevens, and A.R. Al-Sayigh. 2012. Diversity in the later Paleogene proboscidean radiation: a small barytheriid from the Oligocene of Dhofar Governorate, Sultanate of Oman. *Naturwissenschaften* 99:133-141.

Characters: Craniodental, postcranial, soft tissue

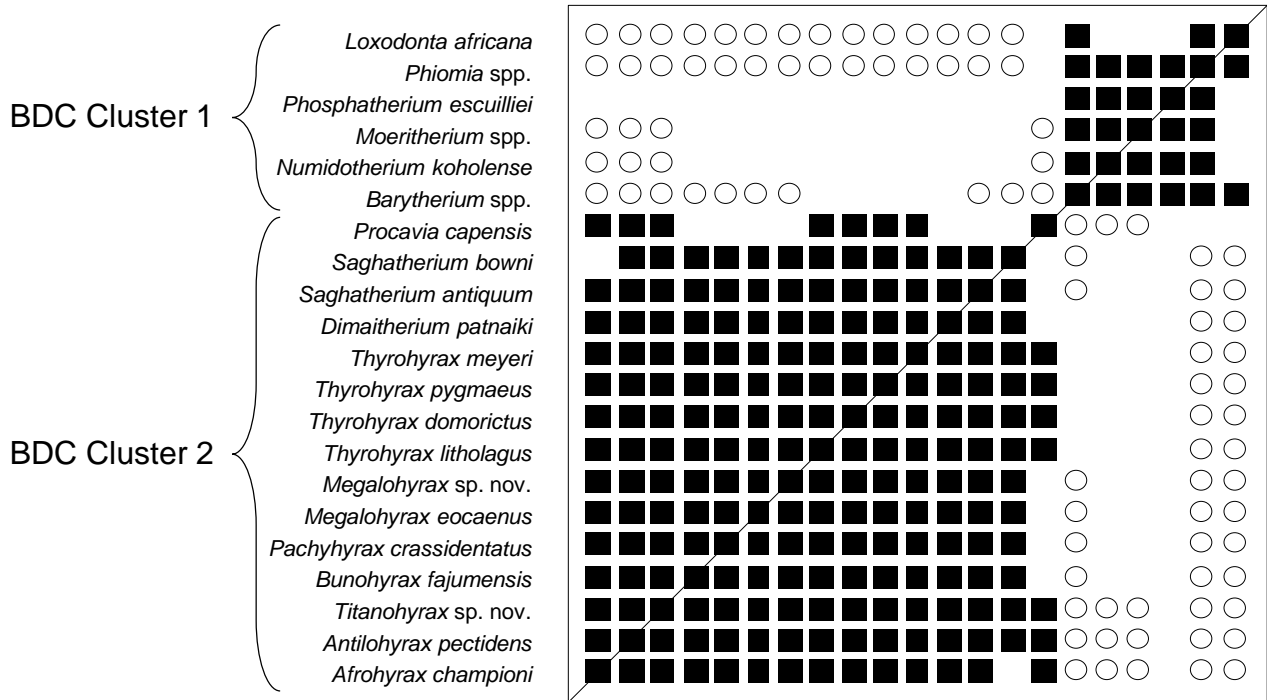


Order Hyracoidea
Family Procaviidae

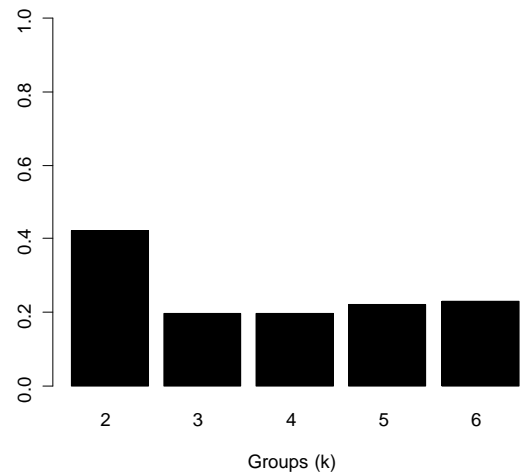
Published taxa	63
Published characters	422
Character relevance	0.75
Taxic relevance	0.4
Taxa used for calculations	21
Characters used for calculations	208
Median bootstrap value	100
F ₉₀	0.75
Stress of 3D MDS	0.25
k _{min}	15
Conclusion	HB



Notes: Procaviidae is well separated from the outgroup taxa in BDC and MDS results. Procaviidae is likely a holobaramin.



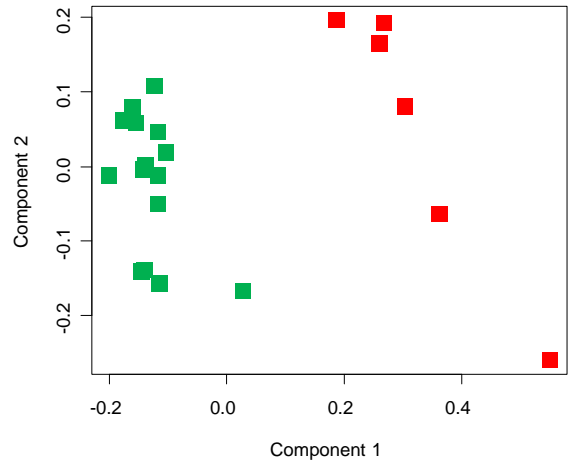
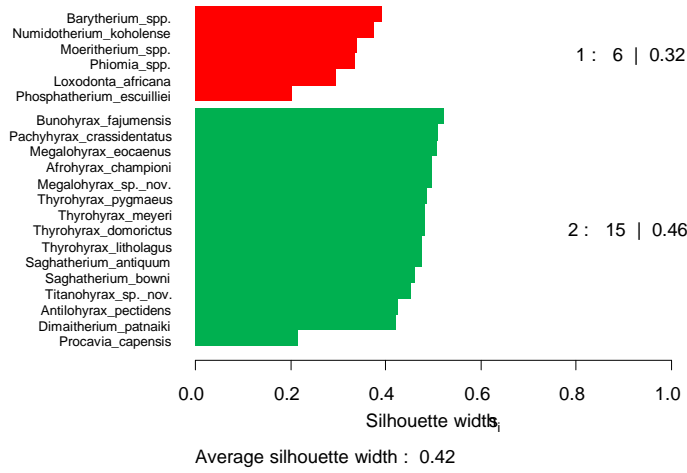
Average Silhouette Widths, Partion Around Medoids



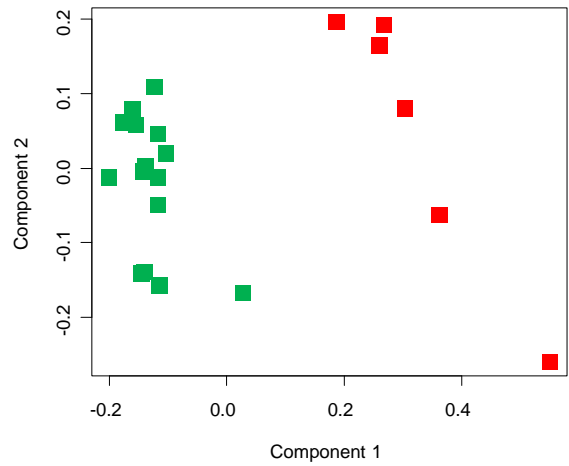
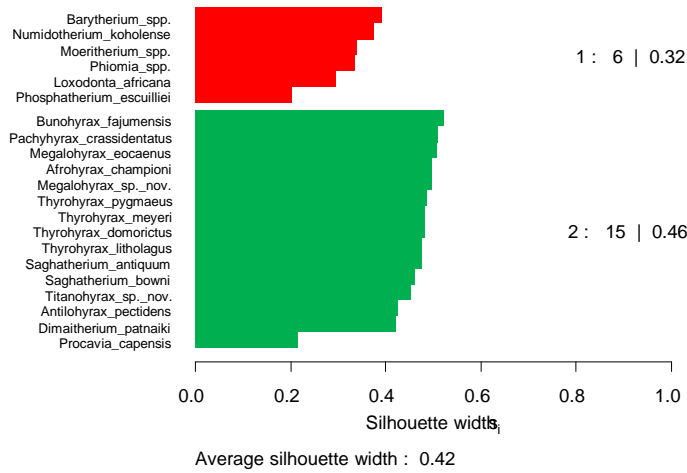
Clade Correspondence: The two large BDC clusters both contain more than two taxa. Both are monophyletic in the tree shown in Figure 4 of Seiffert et al. (2012) if it were drawn unrooted.

Silhouette plot, BDC partitions

Pearson Correlation

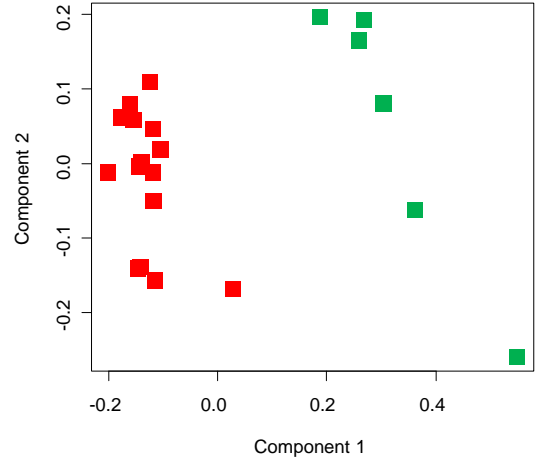
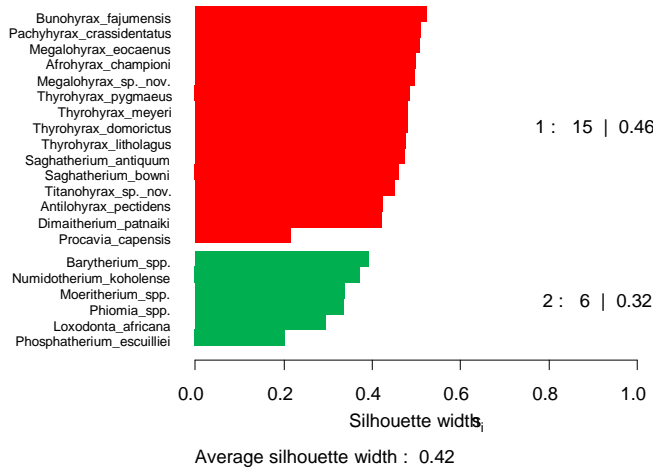


Spearman Correlation

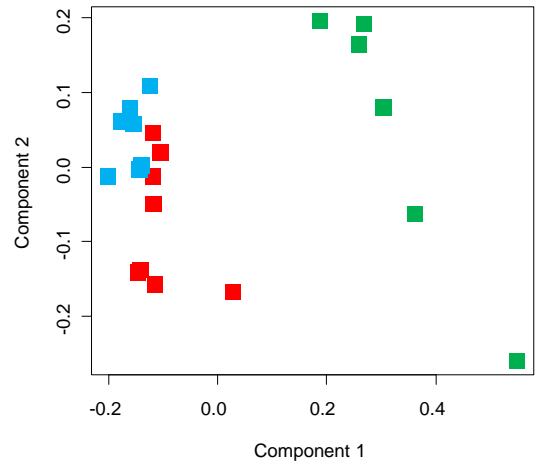
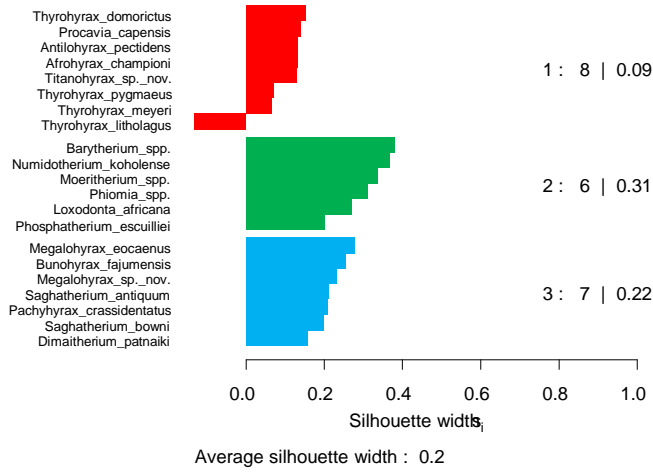


Silhouette plot, Partition Around Medoids

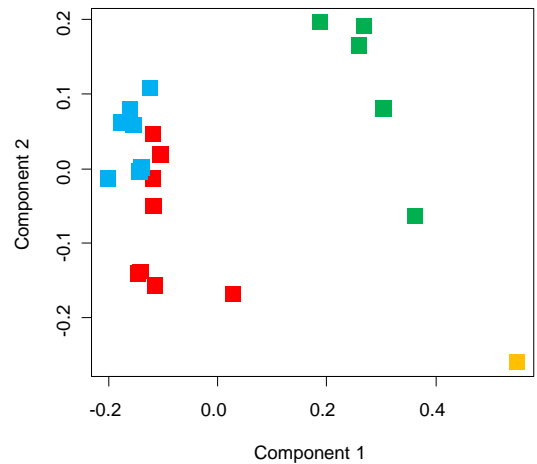
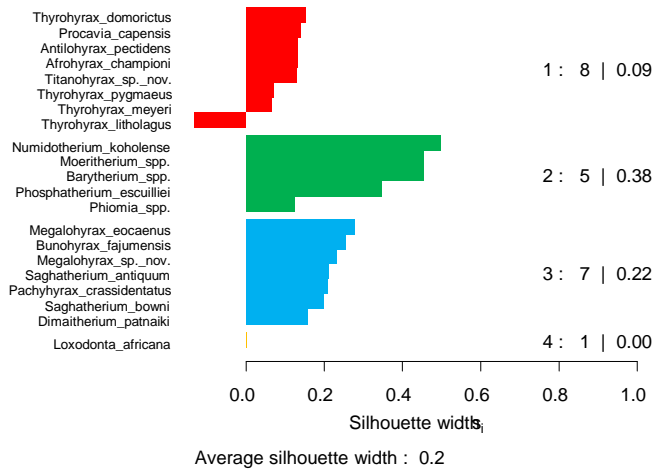
k=2



k=3

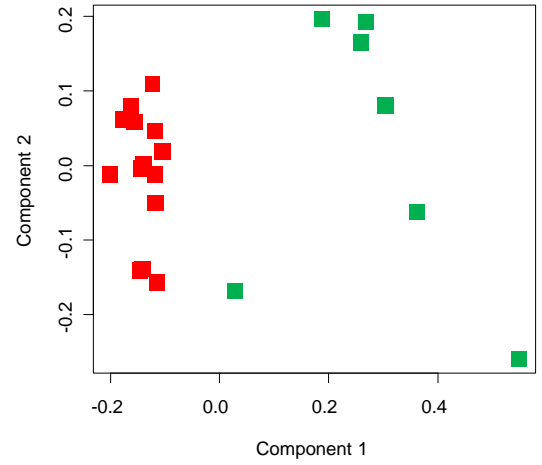
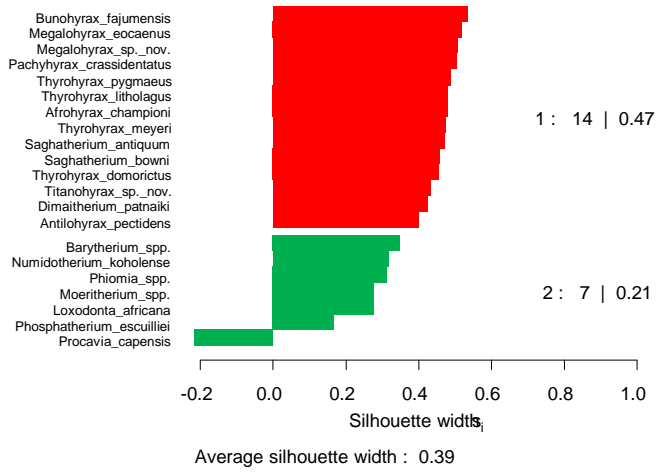


k=4

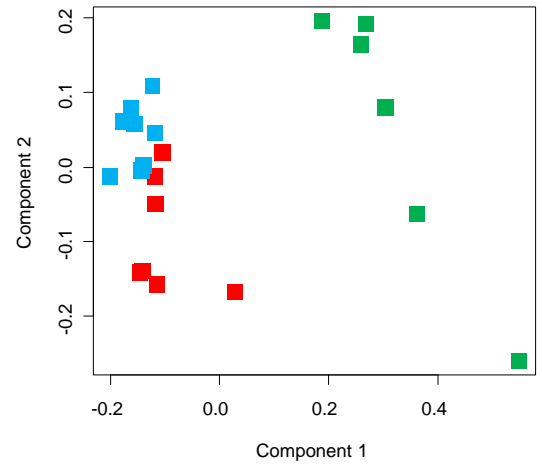
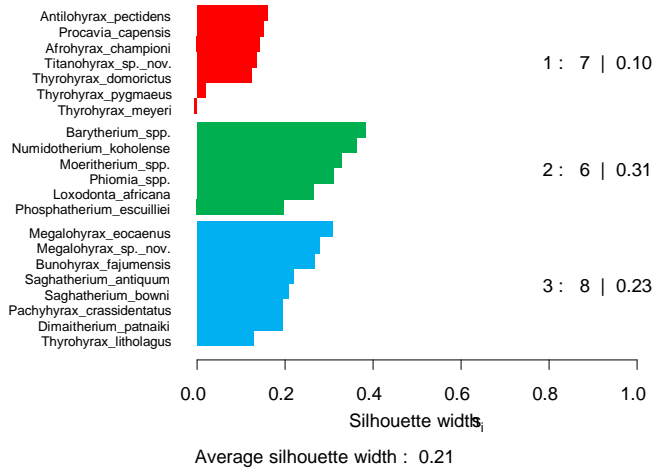


Silhouette plot, Fuzzy Analysis

k=2



k=3



Family Gompotheriidae

Order Proboscidea

Cozzuol et al. 2012

Pearson BDC

Negative: 13

Positive: 68

Clusters: 2

Clusterability

Hopkins Statistic: 0.767

Dip test: 0.04

Dip test p-value: 0.366

Spearman BDC

Negative: 3

Positive: 23

Clusters: 4

The Pearson BDC results are another textbook example of a holobaramin, with nearly every ingroup taxon pair exhibiting significant, positive correlation and every taxon pair with an outgroup taxon exhibiting significant, negative correlation. The Spearman BDC reduces the instances of significant, positive correlation from 68 to 23 and the instances of significant, negative correlation from 13 to three. This results in a proliferation of clusters from two to four, with a cluster membership difference of 43%. The average silhouette width is 0.68 for the Pearson BDC partition and 0.42 for the Spearman BDC partition. Hence the Pearson BDC partition appears to be much better.

The two-cluster medoid partition agrees precisely with the Pearson BDC clusters. The four-cluster medoid partition has an average silhouette width of 0.37 and differs from the Spearman BDC clusters by two taxa (cluster membership difference: 14%). The average silhouette width of the three-cluster medoid partition is 0.34, which is also lower than the two-cluster medoid partition.

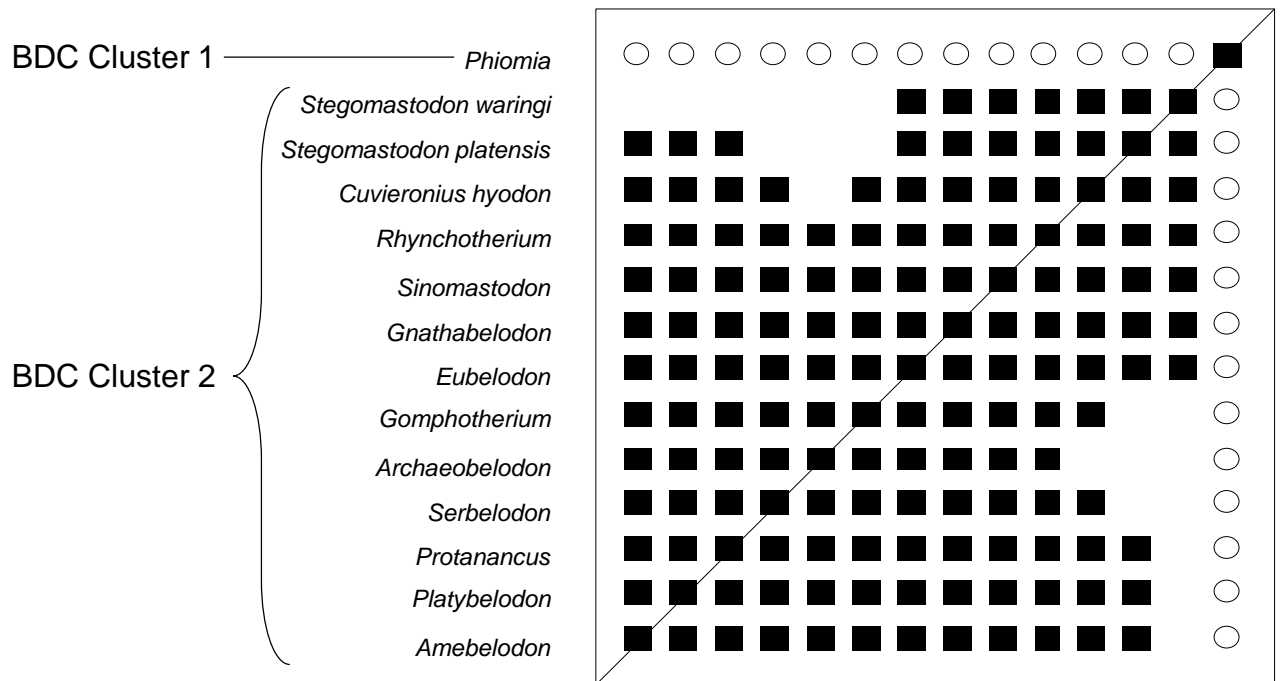
Fuzzy analysis at $k=2$ produces a partition with an average silhouette width of 0.32 that differs from the Pearson BDC clustering by six taxa (cluster membership difference: 43%). The four-cluster fuzzy partition has an average silhouette width of 0.43 and differs from both the Spearman BDC clusters and the four-cluster medoid partition. All of the fuzzy partitions have substantially lower average silhouette widths than the Pearson BDC clusters.

Despite the disagreement with the Spearman BDC clusters and the fuzzy analysis, the original Pearson BDC results are strongly confirmed by the medoid partition and the extreme difference between the average silhouette width of the Pearson BDC clusters and any alternative clustering discovered here. Gompotheriidae is a holobaramin.

Original conclusion: HB

Updated conclusion: HB

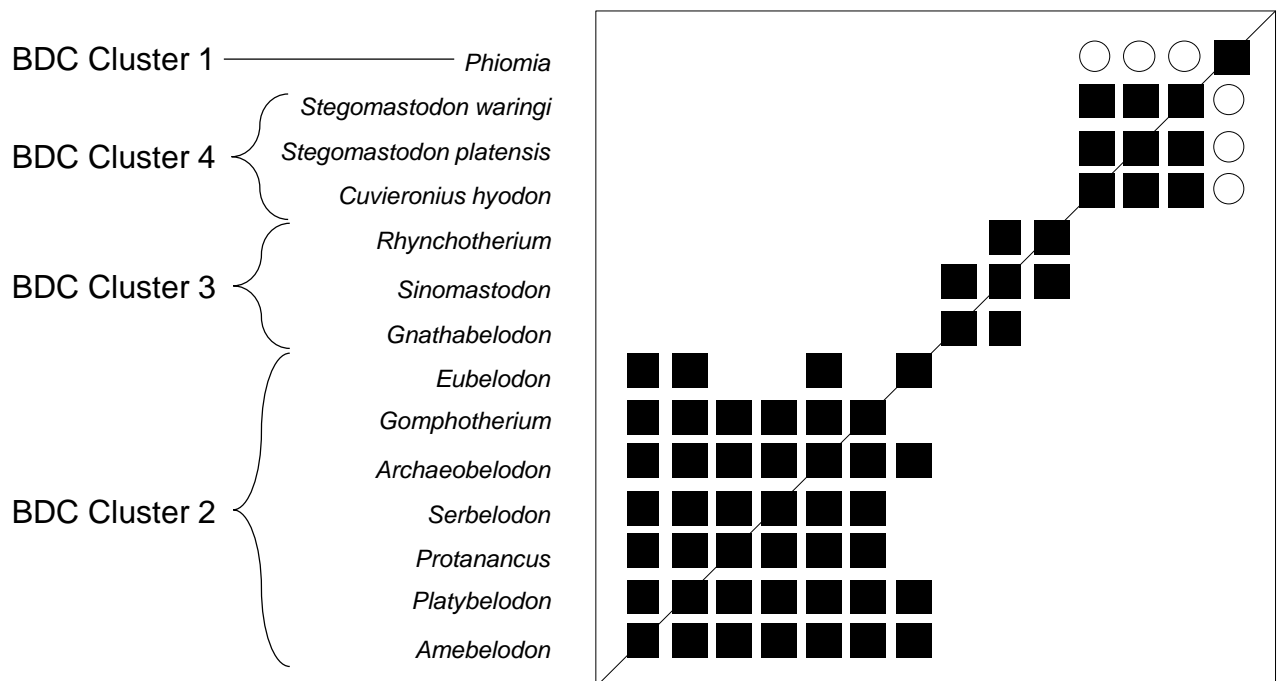
Characters: Craniodental and postcranial



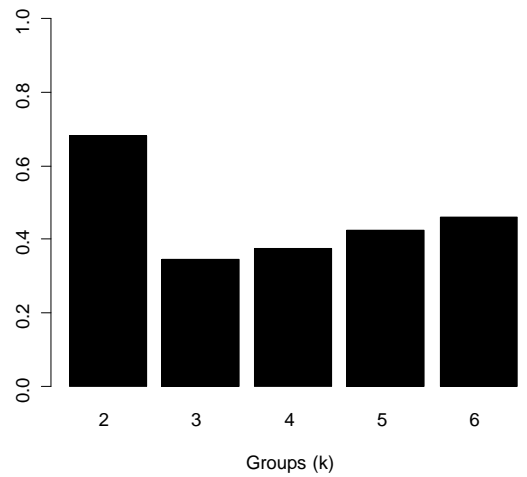
Order Proboscidea
 Family Gomphotheriidae

Published taxa	14
Published characters	43
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	14
Characters used for calculations	34
Median bootstrap value	85
F ₉₀	0.33
Stress of 3D MDS	0.11
k _{min}	5
Conclusion	HB?

Notes: Gomphotheriidae is well separated from the outgroup taxa in BDC and MDS results.
 Gomphotheriidae is likely a holobaramin; although, the outgroup may not be suitable for these taxa.



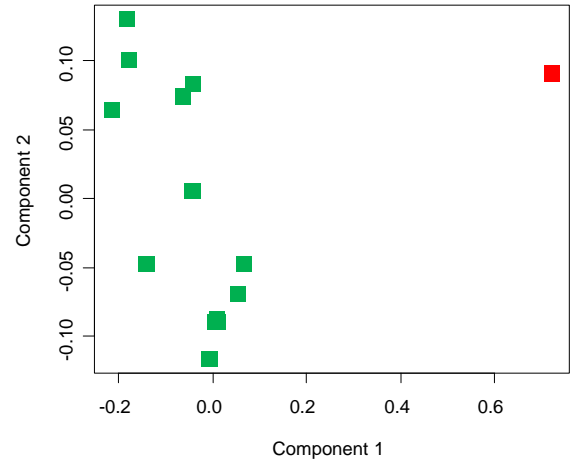
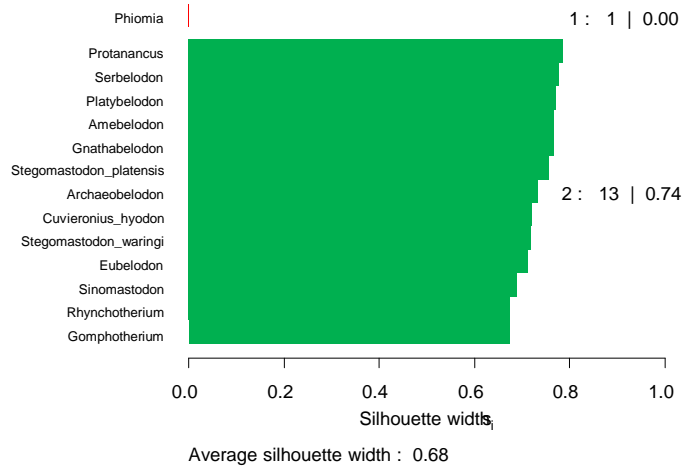
Average Silhouette Widths, Partion Around Medoids



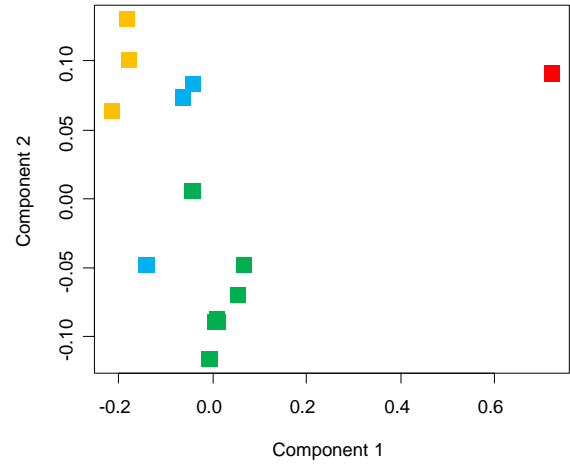
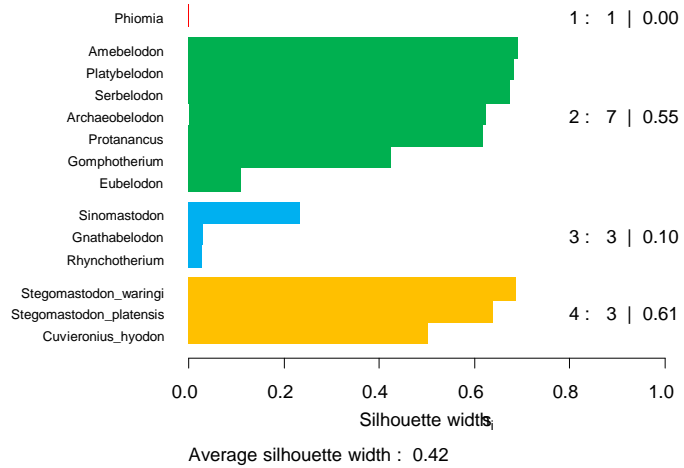
Clade Correspondence: There is one large BDC cluster and one singleton. By definition, the large cluster must be monophyletic in an unrooted tree.

Silhouette plot, BDC partitions

Pearson Correlation

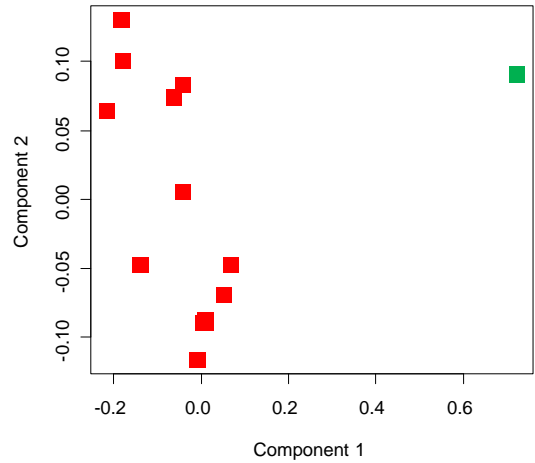
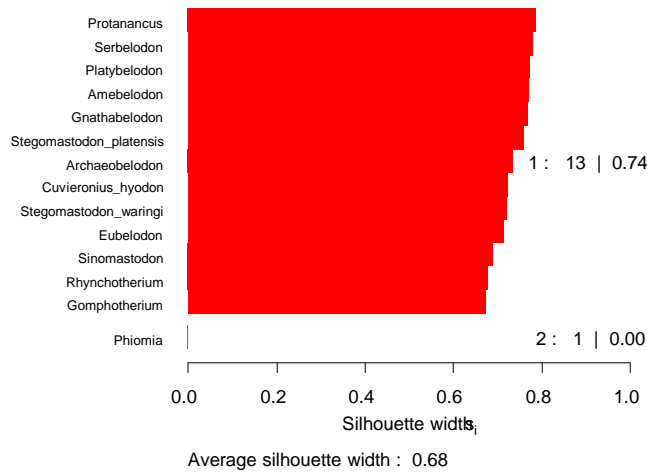


Spearman Correlation

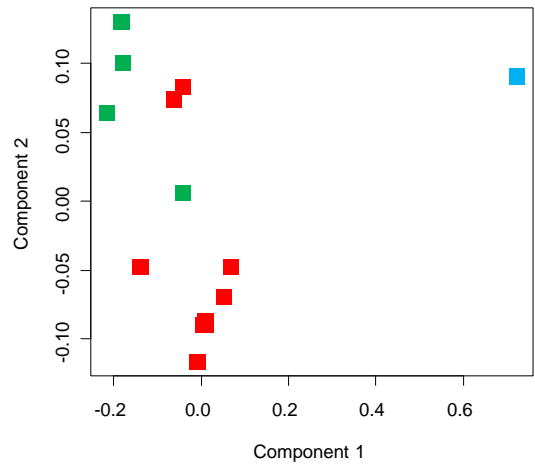
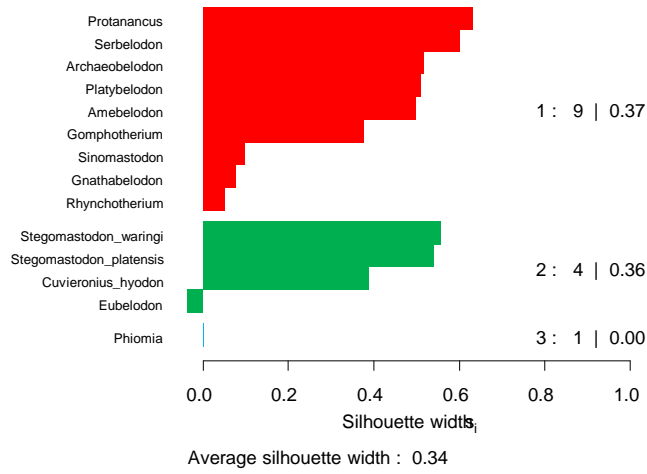


Silhouette plot, Partition Around Medoids

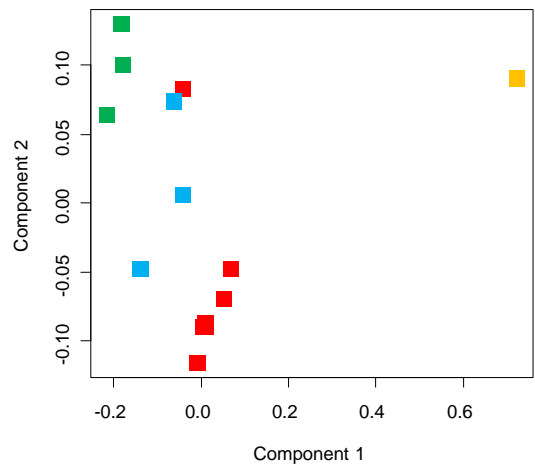
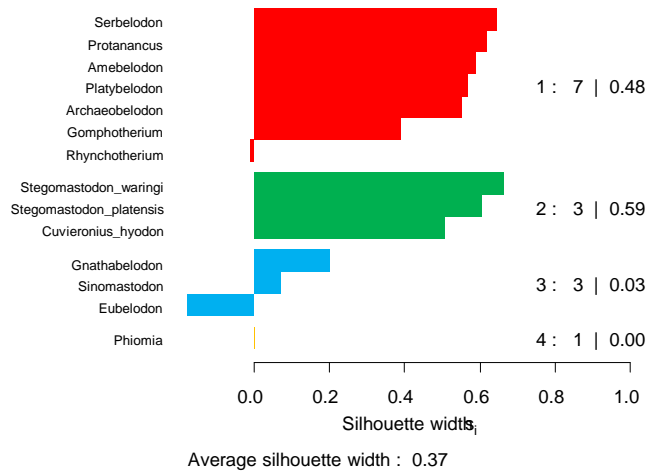
k=2



k=3

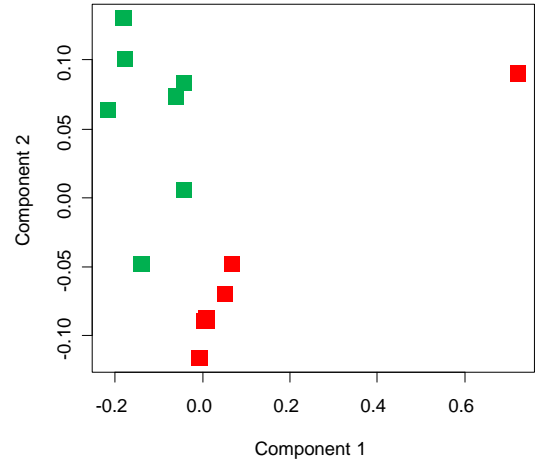
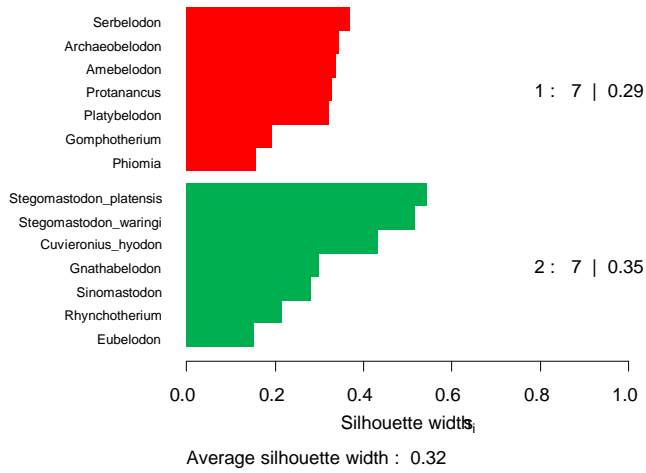


k=4

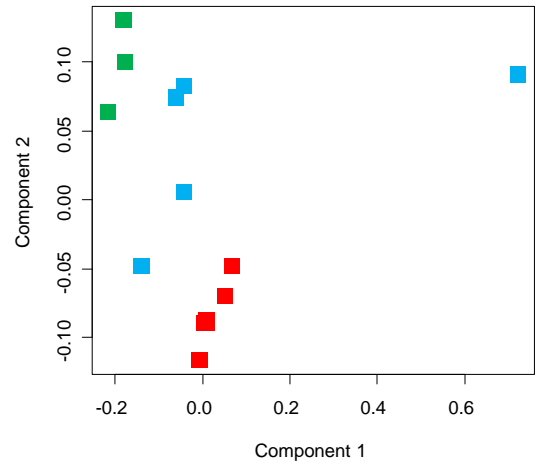
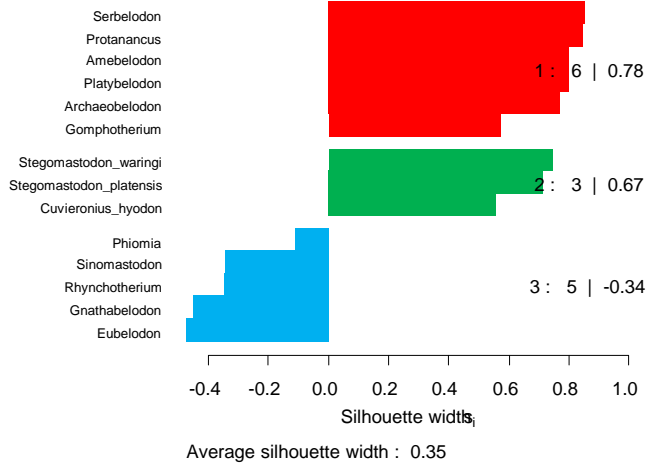


Silhouette plot, Fuzzy Analysis

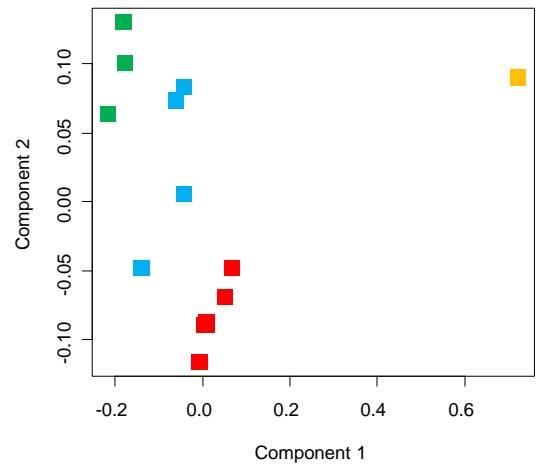
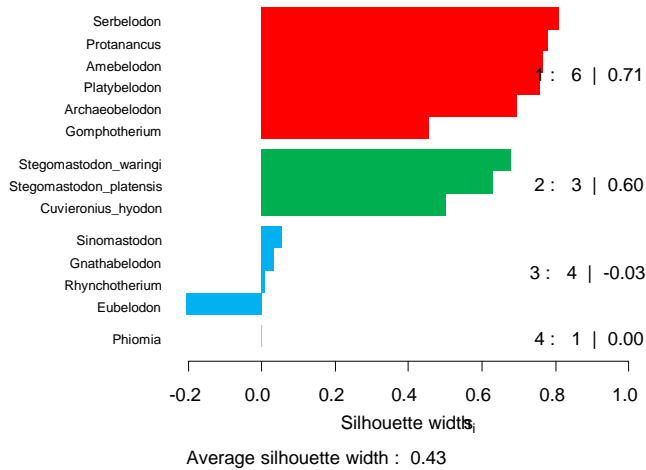
k=2



k=3



k=4



Family Elephantidae

Order Proboscidea

Ferretti and Debruyne 2010

Pearson BDC

Negative: 51

Positive: 39

Clusters: 3

Spearman BDC

Negative: 48

Positive: 57

Clusters: 2

Clusterability

Hopkins Statistic: 0.879

Dip test: 0.088

Dip test p-value: 2.20E-16

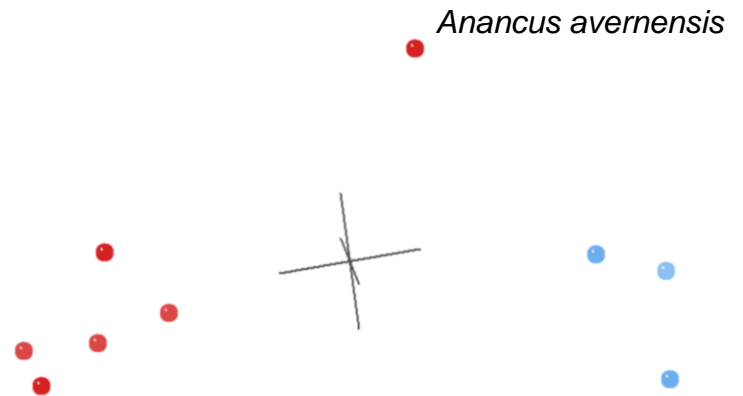
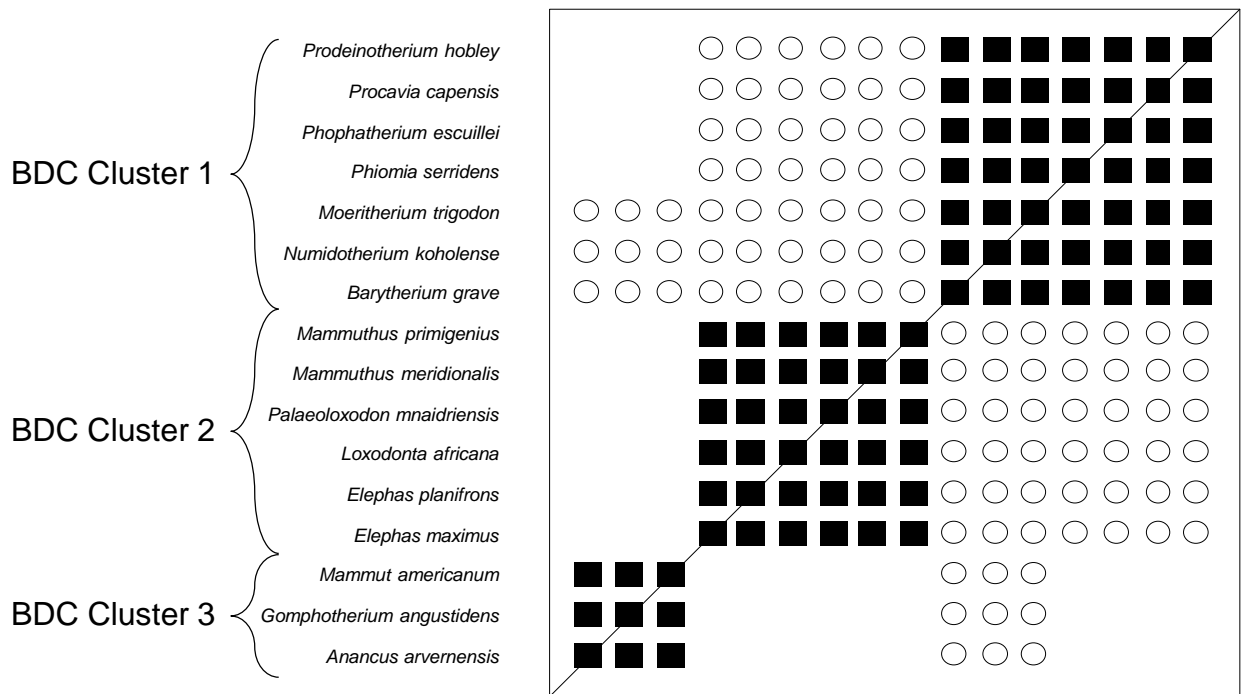
Spearman BDC results decisively reduce the number of clusters from three to two. The three-cluster Pearson BDC partition has an average silhouette width of 0.81, but the two-cluster Spearman BDC partition has an average silhouette width of 0.69. The partitions differ by three taxa, with a cluster membership difference of 19%.

Three-cluster medoid partitioning agrees exactly with the Pearson BDC clusters, and the two-cluster medoid partition is the same as the Spearman BDC clustering. Likewise, with the fuzzy analysis, which agrees with the Pearson BDC clusters at $k=3$ and with the Spearman BDC clusters at $k=2$.

Should these taxa be partitioned into two or three clusters? Since all the methods agree, the only difference is the average silhouette width, which supports the three-cluster partition over the two-cluster partition (0.81 vs. 0.69). Therefore, the original Pearson BDC results are confirmed.

Original conclusion: HB?

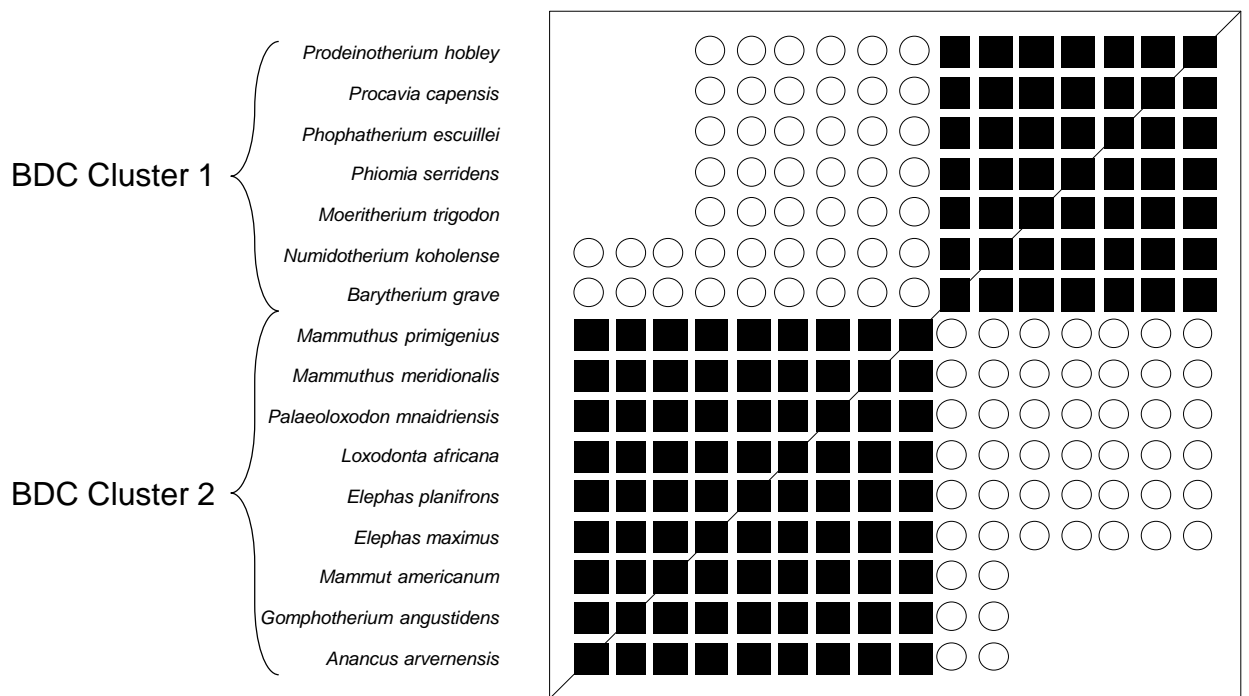
Updated conclusion: HB



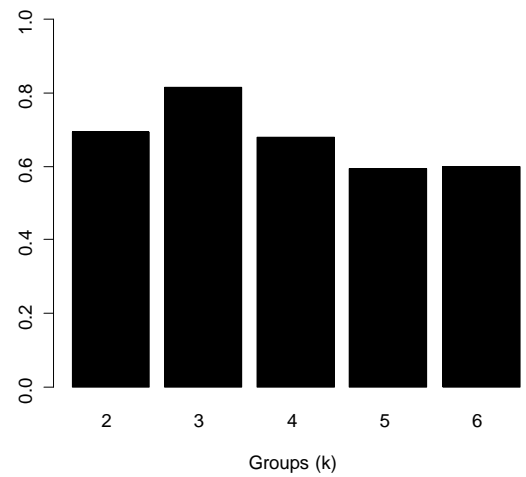
Order Proboscidea
Family Elephantidae

Published taxa	16
Published characters	10
Character relevance	0.75
Taxic relevance	0
Taxa used for calculations	16
Characters used for calculations	10
Median bootstrap value	97
F ₉₀	0.61
Stress of 3D MDS	0.03
k _{min}	3
Conclusion	HB?

Notes: BDC and MDS reveal Elephantidae clearly separated from the outgroup taxa. Elephantidae is likely a holobaramin. The ten characters are not remotely holistic, so the elephantid holobaramin should be considered extremely provisional.



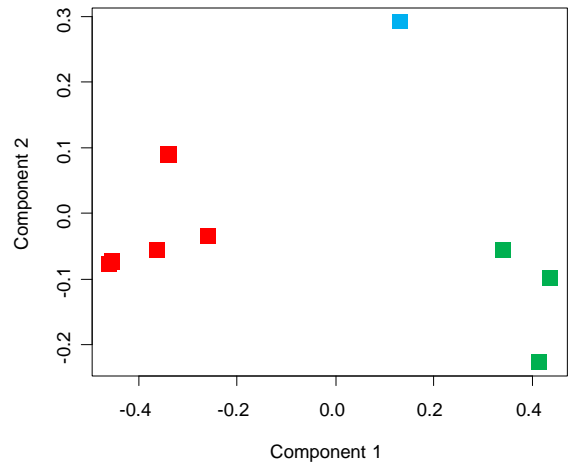
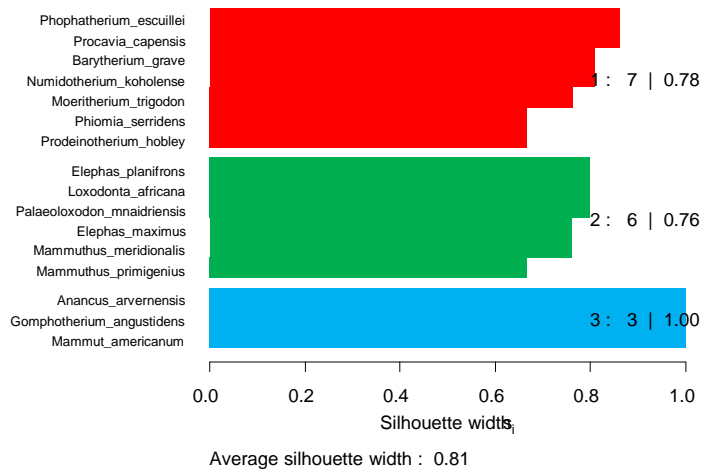
Average Silhouette Widths, Partion Around Medoids



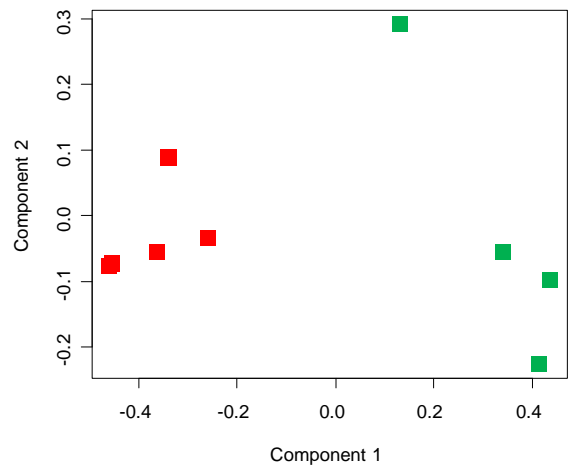
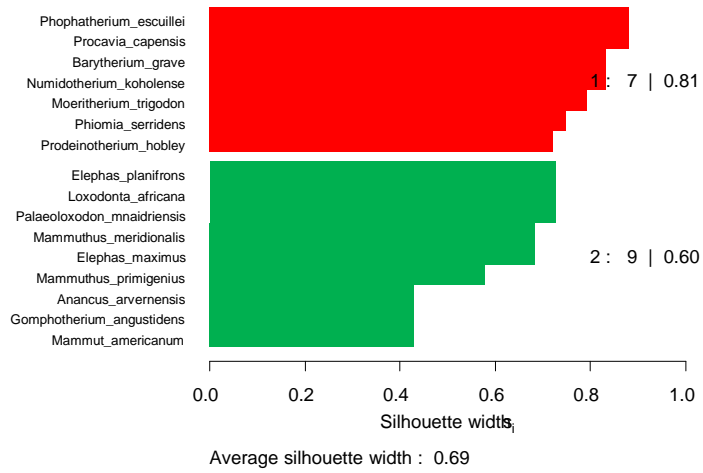
Clade Correspondence: All three BDC clusters contain three or more taxa. In the published phylogenetic tree (Ferretti and Debruyne 2011, Figure 10), clusters 1 and 2 are monophyletic and cluster 3 is paraphyletic.

Silhouette plot, BDC partitions

Pearson Correlation

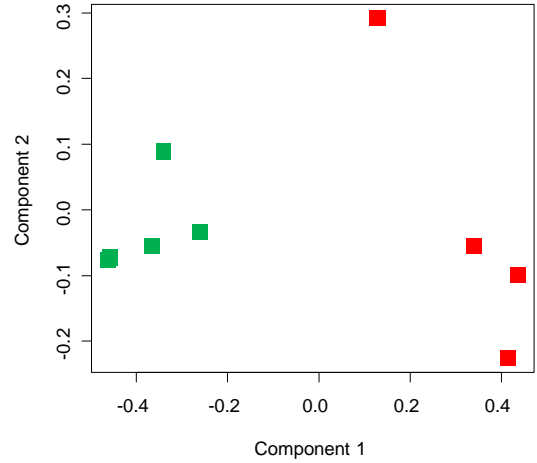
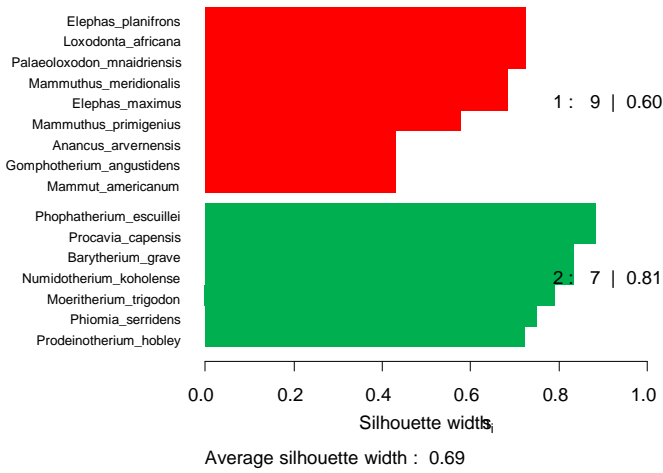


Spearman Correlation

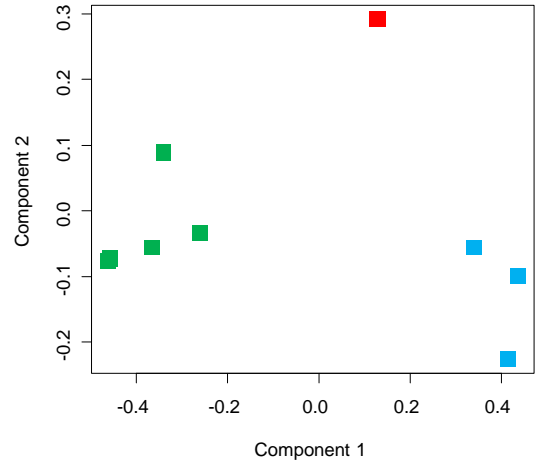
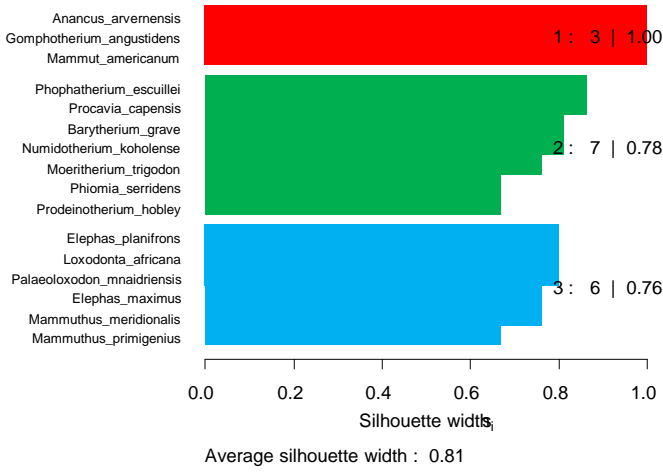


Silhouette plot, Partition Around Medoids

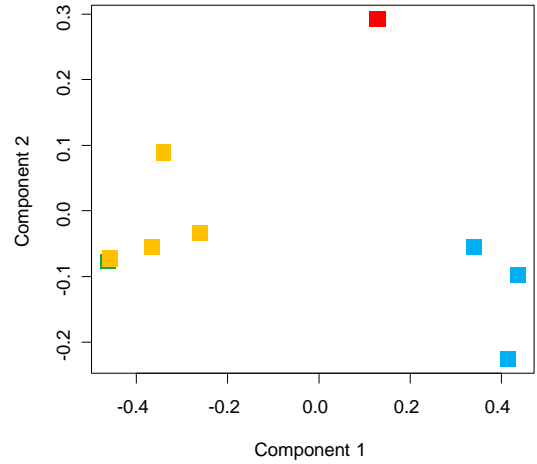
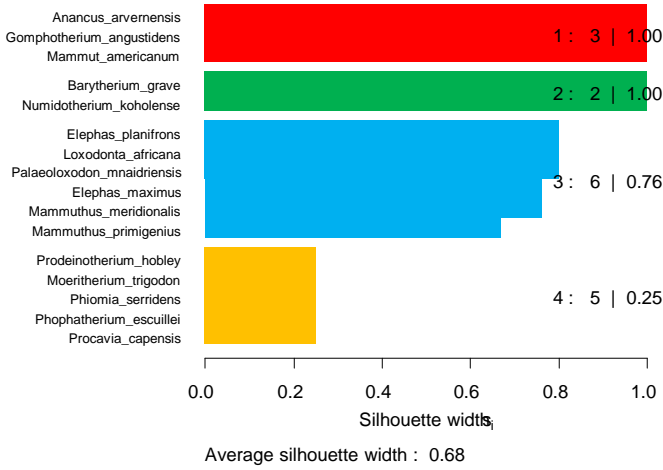
k=2



k=3

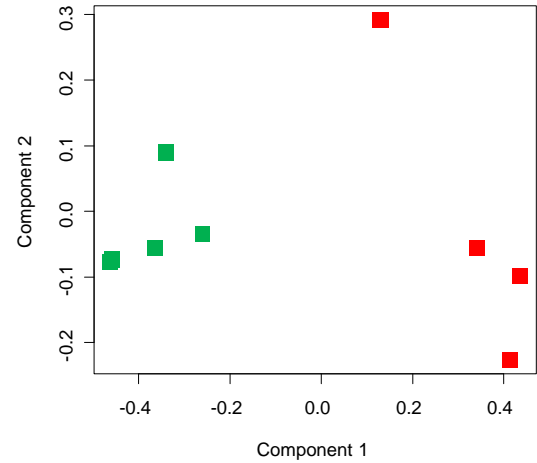
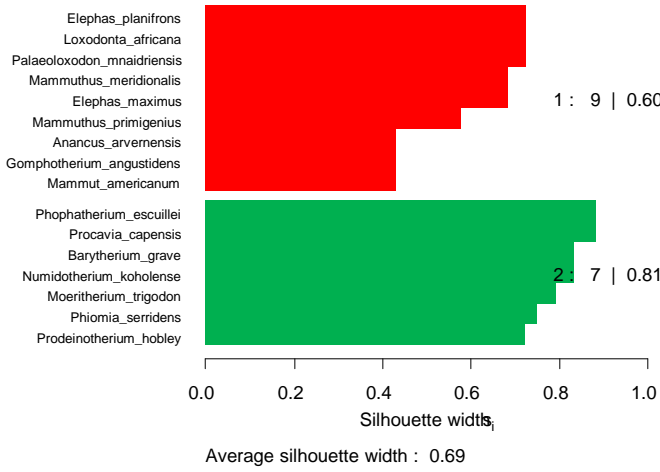


k=4

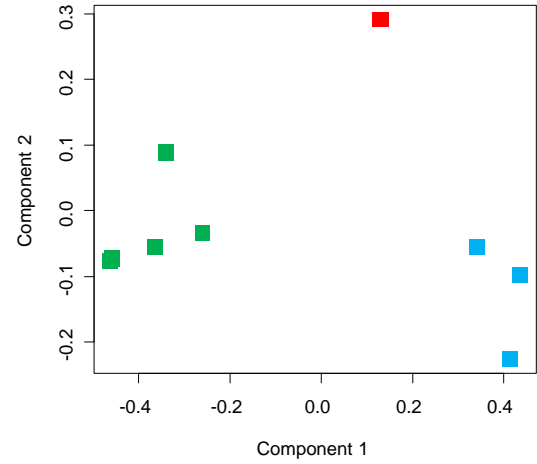
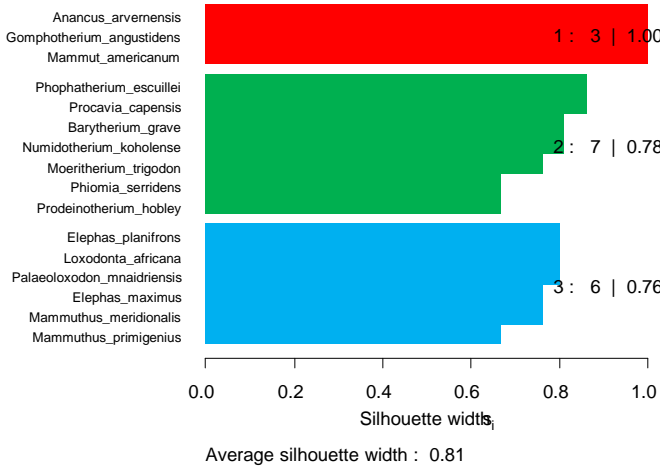


Silhouette plot, Fuzzy Analysis

k=2



k=3



k=4

