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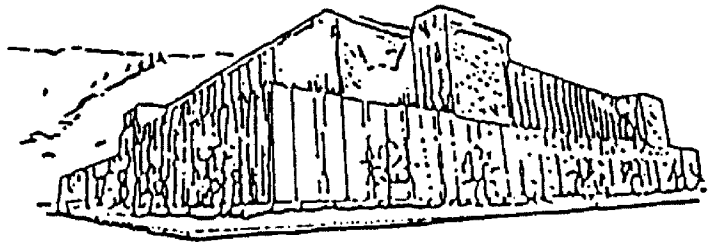*The University of Montana*

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Statistical Character State Recognition in the Phylogeny

of Early Tertiary Archontans Using Parsimony

by

Matthew Alexander Tornow

B.A., Southern Illinois University, Carbondale, Illinois 1993

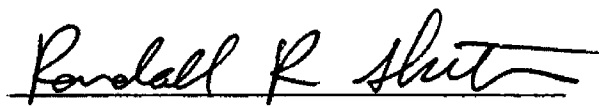presented in partial fulfilment of the requirements

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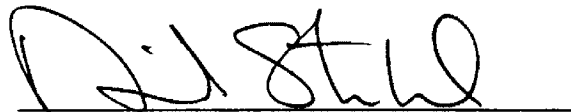1997

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Statistical Character State Recognition in the Phylogeny of Early Tertiary Archontan Evolution Using Parsimony

Director: Randall R. Skelton, Ph.D. *R.S.*

Recent interest in the origins of the order Primates has resulted in increased research into Early Tertiary archontan evolution. Conflicting views regarding the definition of the order primates as well as the familial placement of certain genera may be the direct result of a poor fossil record incapable of producing the anatomical data necessary for informed phylogenetic analyses. Phylogenetic analysis can be informative, despite the lack of fossil evidence, if methods for fashioning informed estimates of missing anatomical features can be developed.

Discriminant function analysis was used to predict missing character states for thirty-one Early Tertiary Archontans. These predicted character states were then used to examine phylogenetic relationships between these taxa and two outgroup taxa using the computer program Phylogenetic Analysis Using Parsimony (P.A.U.P.). Two hypotheses were tested. The first was that the use of data sets with missing character scores replaced with statistically predicted scores would increase the resolution of the resulting cladograms. Second, the use of data sets with missing character scores replaced by statistically predicted scores would not have a negative impact on the accuracy of the cladograms, judged by assessing whether the relationships between well-known taxa were changed by the inclusion of taxa with statistically predicted scores. Additionally, a model was created through which to examine possible error in the taxonomic placement of certain genera.

Though some of the discriminant functions were significantly better than chance at predicting character scores, many were not. It was observed that use of scores predicted by these less reliable discriminant functions introduced homoplasy and inaccuracy into the phylogenetic analysis. Despite this problem, the use of predicted character states resulted in an overall increase in the resolution of the consensus cladogram without significantly compromising the accuracy of the cladogram as judged through the phylogenetic placement of well known taxa.

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Chapter 1
Introduction

Interpreting primate adaptation and evolution is a task that begins with examining the fossil evidence (Fleagle, 1988; 3) from which inferences can be made about morphological and behavioral characteristics (Conroy, 1990; 33). Understanding the origins of the genus *Homo* extends beyond investigating the evolution of the earliest hominids, and includes understanding the early evolution of the order to which we belong. Primates of the Eocene were just as diversified as those of today (Ciochon and Etler, 1994; 38), and as we venture back into the Paleocene, this diversification becomes even greater (Maas, et. al., 1988, 410). It is from this ancient diversity that humans eventually arose (Ciochon and Etler, 1994; 37).

In order to understand the order Primates, we must assess primate origins and evolution through the investigation of primate adaptation, distribution, and the divergence of major primate lineages (Ciochon and Etler, 1994; 37). However, this investigation becomes increasingly difficult as we venture back to the earliest primate ancestors of the late Cretaceous and early Tertiary, where perhaps the best candidate for the ancestor of later primates and other archontans alike (*Purgatorius*) is represented only by dental remains (Szalay, 1979; 41). Despite the scarcity of fossil evidence, the quest for an understanding of our order's origins has become increasingly popular in the past thirty years (Ciochon and Fleagle, 1985; 1).

Aside from the scarce fossil record, other factors add to the difficulty of interpreting primate origins. The discovery of new fossil material is constantly shedding new light on the subject. For example, recent analysis of fossil Plesiadapiformes suggests that these early archontans are not archaic primates at all, but rather archaic Dermoptera (Beard, 1993; 130, see also Kay et. al., 1990 and Beard, 1990), and the discovery of the omomyid *Altiatlasius koulchii* in 1990 not only suggests a much earlier,

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late Paleocene, appearance of the first euprimates, but offers evidence for an African rather than an Asian origin of true primates (Sigé, et. al., 1990; 2). Each new fossil find adds to the complexity of interpreting primate origins and illustrates the confusion which arises from such a diverse fossil record.

Another problem that affects the interpretation of early archontan evolution and the origin of primates is the taxonomic methods commonly used. New finds result in reinterpretations of the taxonomic relationships between extinct and extant archontans (see Beard, 1993), and much of this reinterpretation is influenced by the taxonomic methods used. For example, phenetic (or numerical) taxonomy does an excellent job of grouping taxa according to overall similarity, but fails to give any indication of evolutionary relationship between taxa because it doesn't distinguish between primitive traits (symplesiomorphies) and derived traits (synapomorphies) (Conroy, 1990; 8). Taxonomic relationships should reflect evolutionary relationships (Mayr, 1974; 95), but phenetic taxonomy often fails to offer the refinement necessary to reconstruct taxonomic relationships based on ancestor/descendant relationships. Also, convergence and parallelism can lead to similarities that group unrelated taxa (Poirier, 1993; 21).

Evolutionary systematics uses the observed similarities and differences between taxa and evaluates them according to their presumed phylogeny (Conroy, 1990; 8). Through the investigation of presumed phylogenetic branching and the degree of change between branches, the evolutionary systematist attempts to reconstruct taxonomic relations while taking into account adaptive radiations and climatic change (Mayr, 1974; 95). Problems arise with the subjectivity involved in weighing scores as more or less important in the determination of evolutionary relationships (Conroy, 1990; 8).

Although some consider cladistics to be the same as classical evolutionary taxonomy (see Boucot, 1979), there are some important differences which separate the two. Perhaps the biggest difference involves the extra step of creating a cladogram prior

to the construction of a phylogenetic tree. The cladogram is a generalized tree-like diagram, which represents relationships without attempting to identify actual ancestors (Christoffersen, 1995; 442). Like evolutionary systematics, cladistic taxonomy also possesses a degree of subjectivity in deciding which traits should be used in deciphering evolutionary relationships and thus, taxonomic placement. However, this subjectivity is more defensible in that it is based on the use of synapomorphies rather than symplesiomorphies or autamorphies (unique traits) (Conroy, 1990; 11). Where evolutionary systematists rely more heavily on the degree of evolutionary change between taxa since their last common ancestor to define taxonomic boundaries, cladists classify according to each species' shared derived traits with their last common ancestor (Mayr, 1974; 95). By this comparison it becomes evident that evolutionary systematists rely quite heavily on primitive traits when determining the extent of evolutionary change between sister groups.

Despite its effectiveness in determining the evolutionary relationships of many types of taxa (see Lucas, 1993) including hominids (see Skelton and McHenry, 1992 and Strait et al. ,1997), it has been suggested that cladistic methods may not be appropriate for the phylogenetic analysis of primate origins (MacPhee, 1991; 122). Much of this stems from the fact that little progress has been made in resolving the relationships between living archontans or the origins of primates, and there is still debate over the monophyly of the superorder Archonta (Simmons, 1993; 1). This difficulty in defining the superorder Archonta is evidenced by the inconclusive placement of the fruit eating bats within this superorder (Skelton, 1996; 2).

In addressing the phylogenetic relationships between primates and the archontans of the early Paleocene, this inconclusiveness becomes magnified. This is due primarily to the fact that the earliest specimens assigned to the superorder Archonta are so generalized as to share only superficial dental aspects with any particular archontan

order (Fleagle, 1988; 270). Additionally, the amount of missing data is enormous, not only for the earliest archontans of North America and Europe, but the first true primate, *Altiatlasius koulchii* of the late Paleocene of Morocco and later Primates from the Eocene. This makes it difficult to interpret phylogenetic relationships among the earliest members of our order.

Missing data have many different effects on a computerized cladistic analysis (Simmons, 1993; 22). To begin, including taxa with large amounts of missing data often severely increases the number of most parsimonious trees. To illustrate this problem, Wilkinson (1995; 502) shows how the addition of one taxon with a large amount of missing data to a matrix, consisting of 6 taxa and 9 character states which originally produced a single most parsimonious tree without homoplasy, causes 7 equally parsimonious trees to be produced. This effect is caused by a lack of defining characters for the taxon with missing data, which allows multiple, equally parsimonious placements for it and the other taxa used in the analysis. Incorporating taxonomic units that are not well known may also have deleterious effects on the resolution of the analysis (Simmons, 1993; 22) where "resolution" refers to the number of branches from the nodes of a cladogram, and a fully resolved cladogram would consist only of dichotomous branchings. This effect obscures the relationships between well known taxa particularly when computing consensus trees (Wilkinson, 1995; 501-502).

While the problem of missing data is common in all types of cladistic analyses (Simmons, 1993; 22), the likelihood of having missing data is much greater when the analysis utilizes paleontological as opposed to neontological taxa (Wilkinson, 1995; 501). The fact that our earliest inferred archontan ancestor, *Purgatorius*, preserves only 18 of the 31 character states selected for this study, and some other taxonomic units have even fewer, illustrates this point. There are two conventional methods which are presently used to compensate for missing data.

The first of these methods involves using the underrepresented taxa and accommodating for the missing data through the use of reduced consensus methods. Reduced consensus methods, such as the Adams consensus method, start with the construction of a consensus cladogram based on the taxa that are well represented. This consensus cladogram is then used to hypothesize about the possible placement of those taxa which are underrepresented in the original matrix (Wilkinson, 1995; 504).

Another solution to the problem of poorly represented taxa is to omit those taxa which run the risk of compromising the resolution of the cladogram or significanty compromising the phylogenetic position of well known taxa (referred to as accuracy) within the cladogram. By ommitting those taxa, which through their exclusion would not change the positioning of the well known taxa within the cladogram, problems involving missing character states can be avoided (Wilkinson, 1995; 504). This practice may prove valuable when the majority of the taxa are well represented in the character matrix, but investigating early archontan evolution and the origins of the order Primates involves investigating genera of which the majority are quite poorly represented.

Table 1.1 demonstrates the extent to which the first ten of the thirty-two taxa used in this analysis are underrepresented. With an average of 60% of the 31 character states represented per genus, it is clear that the majority of the Early Tertiary archontan taxonomic groups are not well known anatomically. Omitting those taxa that are not well known would leave so few taxa that the analysis would not be informative. Additionally, there are too many underrepresented taxa to compute a reduced consensus such as the Adam's consensus method.

Table 1.1: Character states for the first ten genera of this analysis.

Pronothodectes	1 1 0 1 1 2 2 2 (23) 1 0 0 0 0 0 0 0 ? ? ? ? ? ? ? ? ? ? ? ? ? ?
Plesiadapis	1 2 0 1 (12) 2 2 1 2 0 2 0 (01) 1 0 1 0 0 0 0 0 ? 0 1 1 0 0 0 ? 0 0
Platychoerops	? 2 (01) ? 2 2 2 1 3 0 0 0 1 1 0 0 0 0 ? ? ? ? ? ? ? ? ? ? ? ? ?
Chiromyoides	1 2 1 1 2 2 2 2 2 2 0 ? 0 1 0 0 0 0 ? ? 1 ? ? ? ? ? ? ? ? ?
Carpodaptes	1 1 0 1 2 1 2 1 0 1 2 0 0 0 0 1 0 0 ? 0 1 ? ? ? ? ? ? ? ? ?
Saxonella	1 2 1 1 2 2 2 1 (02) 0 1 1 0 0 ? 0 0 0 ? ? ? ? ? ? 1 0 ? ? ? ? ?
Purgatorius	0 0 0 0 0 0 1 2 (23) 3 2 0 0 0 0 1 1 0 ? ? ? ? ? ? ? ? ? ? ? ? ?
Palaechthon	1 1 0 1 1 1 1 0 (23) 1 2 0 0 0 0 1 0 0 1 1 1 1 ? 0 ? ? ? ? ? ? ?
Tinimomys	? 2 1 ? 1 2 2 1 3 ? 2 1 0 0 0 1 1 0 ? ? ? ? ? ? ? ? ? ? ? ? ?
Micromomys	? 1 0 ? 2 1 2 1 3 2 ? ? ? 0 0 ? 1 0 ? ? ? ? ? ? ? ? ? ? ? ? ?

Alternatively, a more complete data set could be produced by reducing the number of characters, thus focusing strictly on dental and cranial systems, but this reduction in the number of anatomical systems utilized in the analysis would not offer the most informative analysis. Because incorporating different biological data into a cladistic analysis produces a different result, the more systems incorporated into the analysis the more informative the results will become (Simmons, 1993;). In the case of reconstructing phylogenetic relationships in the early Tertiary, elements of the entire skeleton must be incorporated due to the lack of other types of data such as fetal development or morphology of the nervous system.

Despite the arguments for deleting taxonomic units and limiting the characters to only those which are widely known, others contend that using taxa with multiple missing data is acceptable. Because some suggest that placement of taxa within the cladogram is only affected by those characters with non-missing data (Swofford, 1990; 17), it is argued that large amounts of missing data only affect those taxa for which the data are missing. Therefore, it is proposed that incorporating unknown taxa into the analysis allows for the "parsimonious reconstructions of the values of missing entries" (Wilkinson, 1995; 501). This, in turn, leads to a method for predicting values of missing character scores based on the location of underrepresented taxa within the dendrogram. However, if (as stated previously) the incorporation of large numbers of missing data does, in fact, compromise both the resolution of the consensus cladogram and the

positions of those taxa which are well represented anatomically, then basing

hypothetical character scores on the placement of those less known taxa within the

compromised consensus amounts to basing assumption upon assumption.

In light of the evidence, it becomes clear that investigating the phylogenetic

relationships between the earliest known primates and other contemporary archontans

is only marginally effective using the methods available. Because of this, what one sees

most often is the comparison of those few well known early archontans with extant

archontans and analyses of the relationships between the orders of living archontans

(see Kay, Thorington, and Houde,1990, Adkins and Honeycutt, 1993, Beard, 1993, and

Simmons, 1993). Perhaps primate origins and early archontan evolution cannot be

resolved until the fossil record is more complete.

While the data are certainly not complete enough for a perfectly informed

analysis of Early Tertiary archontan evolution, they do offer the opportunity to

investigate other methods for dealing with the problems which accompany large

amounts of missing data. Because the methods for dealing with missing data are

inappropriate for use with the taxa in question, and, in turn, predicting character scores

according to the results of compromised dendrograms is less than ideal, new methods for

dealing with missing character scores must be investigated if we are to understand the

phylogenetic relationships of the earliest archontans prior to the discovery and

interpretation of multitudes of fossil data. This task could take decades.

I propose that one effective method for handling missing data might be the

statistical prediction of character states prior to the phylogenetic analysis. This could be

done by applying discriminant function analyses to each of the missing character states

in order to predict their respective scores. Discriminant function analysis involves the

prediction of categories based on the combinations of other scored variables (SPSS,

1983; 623). Through the use of this character prediction method, I propose that the

problems of large numbers of "best" trees, lack of resolution in the final cladistic analysis, and inconsistancies associated with using small numbers of traits, might be alleviated.

Statistical prediction of most probable character scores would allow the number of most parsimonious trees to be held to a minimum. This procedure might also help alleviate the problem of uncertainty of placement of those taxa which are not well represented. By limiting the possible range of placements of those taxa which possess large amounts of missing data, the uncertainty that accompanies their placement will be minimized as will the shuffling of well known taxa to accommodate for this uncertainty. Although resolution within the cladogram does not necessarily reflect accuracy, and may lead to the conclusion that relationships have been resolved (Simmons, 1993; 12), in the worst case, the improved resolution should offer some benefits in comparison to the lack of resolution that accompanies large amounts of missing data.

Using discriminant function analysis to estimate missing character states might also allow for the use of more anatomical systems in the phylogenetic analysis. Because this study will focus only on fossil remains, no soft tissue or molecular characters are included. However, by successfully incorporating dental, cranial, and post-cranial remains into this original analysis, avenues will be opened for the incorporation of other anatomical systems in future analyses.

In this study I will explore the use of character state scores predicted by discriminant function analysis. I will compare the results obtained using these predicted scores to the results obtained using the original data set (which includes missing data) to test the following hypotheses.

1. The use of data sets with missing character scores replaced by statistically predicted scores will increase the resolution of the resulting cladograms (i.e. fewer polytomous branchings).

2. The use of data sets with missing character scores replaced by statistically predicted scores will not have an effect on the accuracy of the cladograms. This is judged by assessing whether the relationships between well-known taxa are changed by the inclusion of taxa with statistically predicted scores.

Additionally, through the use of discriminant function analysis for estimating character states, a model will be created by which to compare future fossil finds and the phylogenetic analyses which accompany them. While this prediction technique could be tested first using extant taxa with complete data sets, only a portion of its significance would be realized. The problem to be examined goes further than simply developing techniques for accounting for missing data. The problem involves offering new information to the question of primate origins, the answers to which can be examined through the relationships of well known taxa, the statistically determined character states, and the resolution of the consensus cladogram created through the use of statistically derived scores.

Chapter 2
Materials and Methods

Cladistic analysis involves many steps, including: choosing taxa and outgroups, determining the best anatomical systems and characters to accompany them, weighting characters, and defining character types through the determination of transformation sequences (see Simmons, 1993, Gingerich, 1979, and Hennig, 1966). Additionally, due to the tremendous amount of missing data involved in analyzing fossil archontans, there is also the methodological treatment of the missing data (in this case statistical methods) to consider. Once the preliminary methods are considered, the final cladistic analysis can be executed. This involves further consideration of the cladistic program to use and what options (e.g.. search techniques, consensus methods, and goodness-of-fit statistical considerations) are most beneficial to the problem in question.

TAXA

To begin this analysis, taxa were selected with the intention of accounting for the variety of morphological features represented among archontans of the early Paleocene through the Eocene. Because the focus of this analysis was to delineate the relationships between the earliest known archontan genera of the Paleocene with later primates of the Eocene, taxa choice for the earlier "archaic primates" focused on incorporating the extent of morphological variability among the plesiadapiforms. The true primates of the Paleocene and Eocene were chosen in an attempt to offer the range of variability necessary to decipher plesiadapiform affinity. This involved focusing on

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minor distinctions in morphology for the purpose of identifying possible relations with earlier archontan forms.

Because of the variability among genera within families of plesiadapiforms and primates, and the frequency with which taxa have been reanalyzed and moved between taxonomic units (see Szalay and Delson, 1979, Conroy, 1990, and Rose and Walker, 1985), taxa were recruited at the genus level. This allowed for the incorporation of most of the major variability among the plesiadapiforms, while offering enough information to distinguish between morphologically similar primates. This approach led to the selection of thirty archontan genera from eight families (according to Fleagle's 1988 classification of the order Primates) and one genus of uncertain family. The families represented include Plesiadapidae, Carpolestidae, Saxonellidae, Microsyopidae, Paromomyidae, Picrodontidae, Adapidae (including genera from the subfamilies Notharctinae and Adapinae), and Omomyidae. Because this analysis was executed on taxa at the genus level, these families serve only for the purpose of discussing groups of genera and their similarities and differences.

The family Plesiadapidae is characterized by its extensive specializtions in the anterior dentition, particularly the incisors. This incisor specialization is thought to have evolved independently from those of the family Paromomyidae (Szalay and Delson, 1979: 72). Members of the family Plesiadapidae represented in this research are *Pronothodectes*, *Plesiadapis*, *Platychoerops*, and *Chiromyoides*.

Pronothodectes, the most primitive Plesiadapid, provides a good structural ancestor for comparing the later members of this family. Because *Pronothodectes* has a dental formula of 2-1-3-3 for both the upper and lower dentitions, other genera are easily distinguished through their loss of one or more of the incisors or premolars. *Plesiadapis* is characterized by its loss of I_2, the upper canine in some species, (Szalay and Delson, 1979: 75), and the loss of P_2 in all species except *P. gidleyi* (Simpson, 1935:

3). *Platychoerops* differs from *Plesiadapis* in having a two (as opposed to a three) cusped

incisor, more molarized premolars, crenulated enamel on the upper molars, and strong

mesostyles on the upper molars (Szalay and Delson, 1979; 89). *Chiromyoides* is

characterized by a much deeper jaw, and larger upper and lower incisors when compared

with other genera from the family Plesiadapidae.

Of the three genera belonging to the family Carpolestidae, only one, *Carpodaptes*,

is included in this study. As is characteristic of all members of the family Carpolestidae,

Carpodaptes sp. posseses a highly derived condition called plagiaulacoidy in which P_4 is

enlarged and compressed bucco-lingually to form a blade which runs mesio-distally and

continues through an elongated M_1 trigonid (Binkevicius, 1986; 157). The dental

formula for *Carpodaptes* is (upper) 2-1-3-3 and (lower) 2-1-2-3 (Szalay and Delson, 1979;

98).

Saxonella is the only genus of the family Saxonellidae (Fleagle, 1988; 471). It is

similar to *Carpodaptes* in possessing the plagiaulacoid condition, the occurrence of this

condition in the third rather than the fourth premolar indicates that this trait is

convergent between the two genera (Fox, 1984; 893). *Saxonella* has an upper dental

formula of 2-1-3-3 and a lower dental formula of 1-0-2-3 (Szalay and Delson, 1979; 91).

Of the fifteen genera assigned to the family Microsyopidae (Fleagle, 1988; 471),

this analysis uses five. Microsyopidae represents the most primitive of those taxa often

assigned to the archaic forms of the order Primates. This can be seen primarily in the

morphology of the cheek teeth (Rose and Fleagle, 1981; 111) where the genus

Palaechthon approaches the early Paleocene *Purgatorius* in dental morphology (Kay and

Cartmill, 1977; 19). With a dental formula of 2-1-3-4 for the upper and lower dentitions,

Palaechthon is thought to be too derived to have been ancestral to the Eocene

prosimians which retain P1 (Kay and Cartmill, 1974; 37). The other Microsyopids

analyzed in this research are *Tinimomys* and *Micromomys*, which are characterized by

their enlarged P4 (the dental formulae for these genera is uncertain), *Navajovius*, which possesses a primitive dental morphology and a dental formula of 2-1-2-3 (both upper and lower)(Szalay and Delson, 1979; 61-65), and *Microsyops*, which has lost an incisor on the upper and lower dentitions as well as the upper canine (Szalay, 1969; 265, 271, and 301).

Two genera from the family Paromomyidae are used in this research. Both *Ignacius* and *Phenacolemur*, while once thought to be close relatives of primates, show morphological features which suggest a closer relationship with *Cynocephalus* (the extant genus of the order Dermoptera) (Kay and Thorington, 1990; 342). Both genera have an upper dental formula of 2-1-3-3. The lower dental formulae are 2-1-2-3 for *Ignacius*, and 1-0-1-3 for *Phenacolemur*.

Both genera of the family Picrodontidae, *Picrodus* and *Zanycteris*, are used in this analysis primarily due to their highly derived dental morphologies, particularly in the molar region where the trigonids are reduced, the talonid is enlarged, and the hypoconulid is lost. The upper molars show reduced cusp heights and lack conules. The dental formula of *Picrodus* is 2-1-3-3 and 2-1-2-3 for the upper and lower dentitions respectively. The upper dental formula for *Zanycteris* is the same as that of *Picrodus*. The lower is unknown, but thought to be the same as well (Szalay and Delson, 1979; 68-72).

The family Adapidae is subdivided into three subfamilies: Notharctinae, Adapinae, and Sivaladapinae (Fleagle, 1988; 472). Of these three subfamilies, two (Notharctinae and Adapinae) are represented in this analysis. Notharctinae is the more primitive of the subfamilies of Adapidae while genera of the Subfamily Adapinae show both primitive and derived features. It is questionable whether the earliest notharctine primates were ancestral to the adapines, though it has been suggested that this is the case (Szalay and Delson, 1979; 108). Four Genera of Notharctinae (*Cantius, Copelemur,*

Notharctus, and *Smilodectes*) and seven genera of Adapinae (*Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis,* and *Caenopithecus*) are included in this analysis.

Of the Notharctinae, *Cantius* is the most primitive. Originally assigned to the genus *Pelycodus* (Rose and Walker, 1985: 74), *Cantius* is characterized by its robust hypocone, mesostyle, and protocone fold, which originates from the protocone's distal slope. *Cantius* is distinguished from *Notharctus* by its lack of symphyseal fusion (Szalay and Delson, 1979: 108-109). Recent post-cranial discoveries of *Cantius* and *Copelemur* (another genus originally assigned to the genus *Pelycodus*) have fertilized hypotheses of phylogenetic relation between adapids and lemuriforms (Gebo, Dagasto, and Rose, 1991: 51). The dental formula for both genera is 2-1-4-4/2-1-4-4.

Notharctus shows derivations from its ancestor *Cantius* in possessing a fused mandible and a more developed cuspate hypocone and mesostyle. *Smilodectes* shows differences from *Notharctus* in possessing smaller canines, an unfused mandible, smaller body size, and minor differences in cranial anatomy. Postcranially, *Smilodectes* and *Notharctus* appear to be quite similar. The dental formula for both species is the same as that of *Cantius* and *Copelemur* (Szalay and Delson, 1979: 110-116).

The Adapinae, not as well known as the Notharctinae, are characterized by their possession of both primitive and derived characteristics. Of the Adapinae used in this research, *Mahgarita* and *Caenopithecus* have lost their upper and lower first premolars. The other members of this subfamily retain a greatly reduced P1. While genera of Adapinae possess the distinct hypocone found in notharctid primates, it is not as bulbous, nor does it have the distinctive connection to the protocone so evident in *Notharctus* and *Smilodectes* (See Szalay and Delson, 1979).

The discovery of the late Paleocene omomyid *Altiatlasius* in 1990 necessitates the incorporation of genera from the family omomyidae. *Altiatlasius,* discovered in Morocco

(Sigé, et.al., 1990; 1) predates the both the notharctine primates and other genera of omomyidae,all of which appear during the early Eocene (Szalay and Delson, 1979; 108 and 209). Additionally, resemblances between *Altiatlasius*, certain genera of Microsyopidae such as *Tinimoms* and *Micromomys*, and some omomyids from the Early Eocene of North America (Sigé, et.al., 1990; 1) suggest some degree of affinity between these late Paleocene to early Eocene microsyopids and the omomyids. Therefore, in addition to *Altiatlasius*, early Eocene *Altanius*, from Mongolia, and the North American early to middle Eocene omomyid *Omomys* are included in this analysis. The early Eocene genus *Tetonius* was also included due to its existence in both North America and Mongolia (Szalay and Delson, 1979; 223-231) and because of the existence of cranial remains by which to represent the family Omomyidae.

Purgatorius, of uncertain family affinity, is the final genus studied in this examination. Known by two species, *P. ceratops* from the latest Cretaceous and *P. unio* from the earliest Paleocene, *Purgatorius* represents the best possibility of a common ancestor to all later primates and archontans (Fleagle, 1988; 270-271). With a primitive dental morphology, which reflects the initial selective pressures which shaped primate tooth structure, *Purgarorius* is the most primitive of the archontans investigated. *Purgatorius* retains three incisors making its dental formula 3-1-4-3 for both the upper and lower dentaries (Szalay and Delson, 1979; 41-43).

OUTGROUPS

In addition to the thirty-one genera used in this study, two outgroups were included. The use of outgroups in archontan phylogenetic analysis is important for the purpose of polarizing the character states, i.e. determine which condition is most primitive, but can be difficult due to the uncertainty involved with using early eutherian mammals (Simmons, 1993; 12) such as *Purgatorius*. Based on the theory that the

earliest fossil conditions for a particular character are the most primitive (See Tattersall

and Eldridge, 1977), characters were polarized by creating a hypothetical ancestor

(ANCESTRAL) consisting of the primitive primate conditions suggested by Szalay and

Delson (1979).

Because the focus of this research is to better understand the origins of the order

Primates and their relation to archontans of the Paleocene, the other outgroup was

chosen from extant non-primate members of the superorder Archonta. This outgroup

represents an extant archontan. *Pteropus* (a genus of extant fruit bat) was included in

this analysis because of its derived molar morphology. The fact that most of the genera

included in the ingroup are known only by dental remains, necessitated a derived

condition from which skeletal morphology could be predicted. *Pteropus* offers a possible

link between derived dental morphology and derived postcrania; a link that the

prediction stage of this analysis relies upon to a great degree.

CHARACTERS

Choosing morphological systems and character states to represent them becomes

complicated for the primary reason that different anatomical systems yield different

results in archontan phylogeny (Simmons, 1993; 15). This analysis, because it deals

with fossil archontans, is limited to dental, cranial, and post-cranial characters.

However, the fact that the majority of available data is dental, creates further problems

with identifying phylogenetic relationships. This problem can be seen among the genera

of Paromomyidae where the dentition resembles that of primates, but cranial and post-

cranial elements resemble dermopterans (see Beard, 1990, and Kay and Thorington,

1990).

For this analysis, thirty-one character states were chosen based on dental,

cranial, and post-cranial elements. The eighteen dental and mandibular traits were

chosen due to their high frequency of presence among the thirty-one fossil taxa. Six cranial traits were chosen, which account for variation in the auditory region, brain size, construction of the orbits, and morphological aspects of the snout and palate. The remaining seven characters were chosen to analyze post-cranial aspects of locomotion and mobility of the fore and hind limbs.

Characters were defined as either ordered or unordered. Ordered characters were those which must change states by passing through the character state adjacent to it. For example, in order for a character state "1" to change to a character state "3" it must first pass through state "2", otherwise, a state is skipped causing homoplasy. Unordered characters may skip states without causing homoplasy.

Character one, an ordered trait, defines the number of upper incisors present for each genus. It includes four states, thus four transformations, beginning with the primitive state (scored as "0"). The primitive state of three upper incisors is based on the inferred primitive primate condition discussed in Szalay and Delson (1979; 41). Each subsequent transformation marks the loss of an upper incisor so that a score of "1" indicates the presence of two upper incisors, "2" indicates one upper incisor, and "3" indicates the loss of all upper incisors. Character two, the number of lower incisors, follows the same transformations using the same character scores.

Character three is also an ordered character. It defines the number of lower canines present beginning with the primitive condition (score "0"), one canine. The single transformation from "0" to "1" indicates the loss of the lower canine. This character is also based on the primitive and derived primate conditions for lower canines as discussed by Szalay and Delson (1979).

Characters four and five indicate the number of upper and lower premolars respectively. Beginning with the ANCESTRAL state "0", indicating the presence of four premolars (Fleagle, 1988; 270-271), and continuing through subsequent states 1-4, the

number of premolars is accounted for through each transformation three, two , one and none. Characters four and five are ordered.

The large canine present in *Purgatorius* is thought to be the primitive primate condition (Szalay and Delson, 1979; 41), and character six "canine size" is an ordered trait marking the transformations through which the canine becomes reduced or even absent. For the purpose of this research, the character states are defined as follows:

1. "0" Large- the canine extends beyond the opposing dentary.
2. "1" Medium- the canine overlaps the opposing dentary but does not extend beyond it.
3. "2" small- The canine is reduced to the point where it does not overlap the opposing dentary.
4. "3" absent- One canine (either top or bottom) has been lost.

Character seven, mesial incisor size, is an ordered character, but shares two equally derived states beyond the primitive state. In this case, the primitive trait is scored as "1" defining the condition as nominal indicating that the mesial incisors meet but do not overlap when the top and bottom dentaries occlude. From this point, there are two transformation possibilities, both of which are equally derived. The score "0" indicates a reduction in mesial incisor size from the primitive (nominal) condition. A score of "2" indicates that the mesial incisors are enlarged. Enlarged is defined as overlapping the opposing teeth such as is the case with rodents. This character is defined so that each score indicates a transformation so that in order to go from a "0" to a "2", the taxon must go through state "1".

Character eight, molar series size, is another ordered trait with the primitive condition, all molars the same size, scored as "1". Again, from this point, there are two transformations each of which is equally derived. The score "0" indicates that the rear molar is smaller, and a score of "2" indicates that the rear molar is larger. As is the case with character seven, because the characters are ordered, the condition must pass through stage "1" to go from "0" to "2" or vice-versa.

Character nine is an unordered character which involves five states defining premolar form. The primitive state is scored as "2" and denotes an unspecialized premolar. A score of "0" indicates the occurrence of plagiaulacoidy. A sharp premolar, indicated by "1", is defined by high pointed cusps or caniform premolars as opposed to lower cusped premolars used for the purpose of grinding. Semi-molarform, indicated by "3", indicates that the premolar shows an increase in the number of cusps from two to three. On an upper premolar, this is evidenced by the presence of the paracone, metacone, and protocone, and the lower premolar will have an identifiable metaconid. Molarized premolars ("4") exhibit little discernible difference from molars on the occlusial surface. Upper premolars will possess a paracone, metacone, protocone, and hypocone. Additionally, the presence of conules may exist. The lower molarized premolar has a discernible trigonid and talonid basin.

Character ten is an ordered trait which scores the varying degrees of diastema presence. A score of "0" (the score used for ANCESTOR) indicates the existence of a large diastema. A "1" indicates the presence of a diastema. The score of "2" indicates the presence of a reduced diastema, and a "3" indicates the absence of a diastema.

Character eleven, hypocone presence, is an ordered trait based on Szalay and Delson's (1979) scheme for the evolution of molar structure. The primitive primate condition (scored as "0") is the existence of a pseudohypocone caused by the post-hypocone crista and/or the protocone fold (Szalay and Delson, 1979; 20). Scores 1-3 indicate different levels of development from absent to present to robust respectively. The robust condition is subjective, but consists of a hypocone that approaches the protocone in size forming a connection between the hypocone and protocone.

The twelfth character indicates the presence ("0") or absence ("1") of a protocone fold. The protocone fold is a crease in the enamel that runs disto-lingually from the protocone (Szalay and Delson, 1979; 20). In some instances, the protocone fold may

create the illusion of another cusp on the distal edge of the fold. for the purposes of this research. this effect is termed pseudohypocone.

Character thirteen, mesostyle presence, is an ordered trait based on the presence or absence of a mesostyle on M^1. Based on the primitive primate condition, in which M^1 lacks a mesostyle. the Ancestral outgroup scores a "0", absent. A score of "1" indicates the presence of a mesostyle.

There are three scores for the fourteenth character based on lower molar shape. The primitive condition of this ordered character is "two level," which is defined by a distinctive separation of occlusial surfaces caused by the elevation of the trigonid and denoted by "0". A "1" indicates a square shaped molar with relatively level trigonid and talonid. The waisted molar shape (scored with a "2") produces an hourglass shape when viewing the occlusial surface from above.

Character fifteen defines the presence of the paraconid. In the primitive condition, the paraconid is retained (Szalay and Delson, 1979; 20). This is scored as a "0". A reduced paraconid (scored as "1") is still present. but only remnants remain, and it no longer exists as a distinct cusp. The most derived condition for this character is the loss of the paraconid, which is scored as a "2".

Character sixteen, hypocone/protocone connection, was developed for the purpose of discerning between the two subfamilies of Adapidae. Notharctinae and Adapinae. An ordered trait, hypocone/protocone connection is divided into three scores. A score of "0"' indicates the absence of a connection. Scores of "1" and "2" indicate the presence of the connection and a prominent connection respectively.

Characters seventeen and eighteen both concern morphological aspects of the mandible. Character seventeen, jaw depth, is an ordered character with two states, deep ("0") and shallow ("1"). In this analysis, a jaw is considered to be deep if the depth of the jaw below M_2 is greater than the length of M_1-M_2. Character eighteen is another

ordered character used to discern between the primitive unfused jaw and the derived fused jaw. These states are scored "0" and "1" respectively.

Character nineteen measures the degree of post orbital constriction by measuring the distance from the sagital suture (where it meets the coronal suture) to the edge of the zygomatic arch. This number is then divided into the measurement from the same point on the sagital suture to the edge of the cranial vault to give a ratio of cranium to possible space. There are four scores, "0"- .30 or less, "1"- .31-.40, "2"- .41-.50, and "3"- .51 and above. This is an ordered character.

Post-orbital closure is described by four ordered states for character twenty. The absence of any kind of post orbital process is considered primitive and scored as "0". The remaining three states are Partial ("1"), which indicates the presence of a post-orbital process which does not form a complete bony ring, ring ("2"), which indicates the presence of a process that forms a complete bony ring around the orbit, and complete ("3"), which indicates a ring with complete closure behind the orbit as well.

Character twenty-one measures the snout length compared to brain case length. The snout length is measured from the anterior edge of the orbits to the most anterior portion of the face, and the brain case is measured from the anterior edge of the brain case to its posterior margin. An ordered character, snout length is scored "0"- snout longer, "1" same size, "2" snout shorter. Zero is primitive.

Character twenty-two, center of bulla ossification, is an ordered character geared towards differentiating between bones from which the auditory bulla ossifies. While no ossified bulla (scored as "0") is the most primitive, there is no certainty as to whether one form of bulla ossification is more derived than another. Entotympanic ossification is scored as a "1", petrosal (from the petrous portion of the temporal) is scored "2", and ectotympanic is scored as a "3".

Character twenty-three scores taxa according to the location of the posterior margin of the palate. A score of "0" indicates that the posterior margin of the palate (formed by the palatines) extends posterior to the third molars. If the palate extends between the third molars, a "1" is scored. If the posterior margin of the palate ends anterior to the third molars, a "2" is scored. This is an ordered character.

Character twenty-four compares the extent to which the palatine contributes to the palate by comparing it with the premaxilla. If the palatine contributes more to the palate than does the premaxilla, a "0" is scored. If it contributes less, a "1" is scored. This is an ordered trait.

Character twenty-five scores the shape of the capitulum into the primitive spindle shape ("0") and the more derived round shape ("1"). The spindle shaped capitulum appears as a continuation of the trochlea such that the entire distal humerus looks like a spool or spindle. The round capitulum is more bulbous and clearly distinct when compared to the trochlea. This is an ordered trait.

The twenty-sixth character scores each taxon according to the presence or absence of a trochlear shelf. A trochlear shelf is a ridge of bone that produces a distinct separation between the trochlea and the capitulum. This character is ordered with "0" representing the absence of a trochlear shelf and "1" indicating its presence.

Character twenty-seven describes the radius head shape for the taxon. An ordered character, it is represented by two scores. When viewing the articular surface of the head of the radius, the primitive shape is ovoid and is scored as "0", while the derived condition (scored as "1") is round.

Character twenty-eight divides the presence of nails into three ordered scores. The primitive score "0" denotes the absence of nails. While scores "1" and "2" indicate the presence of nails and a grooming claw and nails on all digits respectively. This character applies to both the hind limb and fore limb.

Character twenty-nine examines the length of the intermediate phalanx (of the hand) in comparison to the proximal phalanx. Because members of the order Dermoptera posses the derived trait of an elongated intermediate phalanx (Shipman, 1990: 56), this character proves beneficial when determining the Primate/Dermoptera boundary. the primitive score "0" indicates that the intermediate phalanx is shorter than the proximal. and the derived state "1" indicates that the intermediate phalanx is longer.

The thirtieth character scores the shape of the patellar grove. An ordered character. the patellar grove is divided into "0", short and wide, and "1", long and narrow. A short and wide patellar groove is distinguished by the groove not extending dorsally past the condyles and retaining its width throughout its length. On the contrary. the long and narrow patellar groove extends past the proximal ends of the femoral condyles. Additionally, the groove itself narrows as it extends dorsally forming an apex at is most dorsal point.

The final character scores the shape of the astragalar tibial trochlea. If it is broad and short (making the dorsal/articular surface of the astragalus appear square), a "0" is scored. If the tibial trochlea of the astragalus is long and narrow (causing a rectangular appearance) the taxon receives a "1". This character is ordered.

SCORING

Because of the inaccessability of fossil specimines and casts, the majority of character scoring was done according to the description and figures of each taxa as presented in Szalay and Delson (1979). Additionally, other resources were used for each genera where available and are listed in the appendix. Fossil notharctid (*Notharctus* and *Smilodectes*) mandibles, teeth, and cranial elements were examined for some information, but prior to proper preparation. Outgroup data were gathered through

journal articles (listed in appendix) and specimens located at the University of Montana

Bird and Mammal Museum.

STATISTICAL METHODS

Statistical character prediction was performed using SPSS-X on the University of

Montana's DEC-VAX computer. Unknown character scores were predicted one

character at a time for each taxon. Because preliminary analyses indicated that the

number of characters used in the analysis was of less importance than the number of

taxa included, data matrices were constructed using a five step method aimed at

utilizing the greatest number of taxa for which the character in question was present.

To begin statistical analysis, a data matrix was constructed for each character to

be predicted. The first step was to exclude all taxa that did not possess the character in

question. These were the taxa for which the character would be statistically determined.

The second step in matrix construction involved removing all characters that

were missing from over 1/2 of the taxa that possessed a known score for the character

to be predicted. For example, if character "Y" was the character to be predicted by twenty

genera and eleven of those genera were missing character "X," character "X" would be

removed form the analysis. This step greatly narrowed the number of predicting

variables, but helped retain a large number of genera through which to analyze those

taxa missing the character in question.

Step three was developed in order to ensure that all states possible for the

character in question remained in the analysis. This was accomplished by removing all

missing characters for any taxon in the prediction matrix that had a score for the

character in question not represented by another taxon. This step also applied to

character states that occurred for more than one genus if each of those genera had

missing scores for multiple characters. In this case, characters were deleted for the genus possessing the smallest amount of missing data.

Step four was developed to further retain taxa at the expense of keeping fewer characters. This step involved deleting any characters that, through their removal, would create a complete set of character states for one or more genera. Beginning with the removal of any characters that were the only missing character for a taxon, more characters were removed if the removal of character "X" left only one character "Y" as missing for one or more genera. For example, if one genus was missing character "X" and another was missing "X" and "Y," the removal of "X" allowed for the deletion of "Y" due to the fact that "Y" was the only remaining missing variable for the second genus. This process continued until all characters with missing states were deleted, or the removal of any one character would not allow a taxon to be without missing scores. Those taxa with more than one missing character state after step four were deleted in step five.

Despite the effectiveness of narrowing characters and taxa used to create each prediction matrix, some prediction matrices were developed using exceptions to the five step process. In order to maintain the highest possible number of predicting taxa for those characters present in few taxa (e.g.. character 32 "astragalar tibial trochlea"), all characters that were missing for any of the genera used as predictors were deleted from the matrix if ten or fewer genera possessed a score for the character to be predicted. In most cases, few traits were deleted, because those taxa possessing a score for one of the "highly unknown" characters possessed a score for most other characters as well. Because some genera possessed more than one character state for one or more of the characters used in this analysis, the more derived (that furthest from the primitive condition) of those conditions possessed was used in the prediction matrix.

Thirty-two data matrices were constructed according to the criteria discussed above, and were used to predict missing character states for taxa with missing data. Because some genera had missing states for some of the scores used in the prediction matrix, each genus was analyzed individually using those characters used in the prediction matrix that were also present for the genus being analyzed. In some instances, taxa being analyzed were missing scores for the same characters. In these cases, these taxa were analyzed together. Each finalized prediction matrix consisted of one missing character (that to be predicted) and those taxa and characters to be used in its prediction.

Because the prediction process involved delineating between groups rather than measured data, missing scores were predicted using the SPSS-X "DISCRIMINANT" program. The "DIRECT" method was used, which entered all discriminating variables concurrently. This insured that only those variables which failed tolerance (set at 0.001) would be excluded from the analysis. Scores were plotted, and discriminant function results were listed with their probability and accuracy.

PHYLOGENETIC METHODS

Once taxa and outgroups were chosen and characters were developed and assigned according to the specifications previously stated, two cladistic analyses were executed. The first of these was a preliminary analysis consisting of the original data matrix without any of the predicted scores. The second was run in the same manner and included the predicted scores for missing character states. The results of these analyses were compared.

Both analyses were run using the program Phylogenetic Analysis Using Parsimony (P.A.U.P.) for Apple™ computers. Missing character states were labeled as "?", and two states within "( )" denoted polymorphism. In order to account for the

uncertainty of "underrepresented" characters and to help prevent altering the taxonomic placement of well known taxa in the preliminary analysis, the characters were weighted according to the percentage of missing data. For example, a character that was missing in twenty-five percent of the taxa would score seventy-five; the weight reflecting the percentage of taxa for which there was a known score.

Each data file was executed following the previously mentioned definitions of character types and weights. Following a file's execution, the genera ANCESTRAL and *Pteropus* were defined as outgroup taxa. The assumption set "MIXED" was chosen, which defined the ancestral character states as those possessed by the taxon ANCESTRAL.

Once the data file was executed and the assumptions were entered, tree searching was performed using Heuristic search methods. The reference taxon was again defined as ANCESTRAL. Stepwise addition was used holding one tree at each step. Branch swapping was performed, zero length branches were collapsed, and the trees were rooted. Any taxon with multiple states for a character were interpreted as polymorphic.

Once the search was executed and trees were found, the strict consensus cladogram was formulated using all trees saved during the tree search. The consensus trees for both the preliminary and final analyses were then analyzed for statistical information including tree length, , consistency, homoplasy, and retention indices, and node descriptions. The trees were then compared against each other to determine the affects that statistical character state determination had on the consensus cladogram.

CHAPTER 3
RESULTS OF ANALYSES

RESULTS OF CHARACTER STATE PREDICTION

Following are the results of the statistical analyses. Results are presented for each character and are subdivided into individual analyses. These analyses represent the characters used as discriminating variables to predict scores for one or more genera. For each analysis, four tables are presented. The first table lists the genera for which the character state was predicted, the predicted character state (this refers to the numerical state entered in the cladistic analysis), the probability that the taxon belonged to the assigned group given its discriminant function score, and the accuracy of the discriminant function correctly classifying the chracter states of those taxa used for predicting the unknown groups. The second table lists the characters used as predicting variables for that analysis. In the third table, each function is assessed according to the eigen value (a relative score corresponding to the percent of variance explained by the function), the percent of variance that the function accounts for, and the correlation between the function and the variable being predicted. The fourth table lists after function statistics, which are used to assess the statistical significance of the function (i.e. whether its predictive ability is actually greater than chance alone). Therefore, the scores referring to "after function 0" reflect the discriminating power of the predicting variables prior to the execution of the first function. The eigenvalue represents an inverse of the discriminating power of the discriminating variables. This score is converted to a chi square statistic which tests for the significance of the functtions' discriminating power using those variables. The significance is that of the chi square given the degrees of freedom listed in table four.

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CHARACTER 1
"NUMBER OF UPPER INCISORS"

Scores for character one "number of upper incisors" were predicted using the genera ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus., Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and Pteropus.* The characters used to create this prediction matrix were two, three, four, five, six, seven, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen. For character one, states were scored for five genera using four analyses. The results are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	100.00%	100.00%
Tinimomys	1	99.43%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.3233	70.17	0.8361
2	0.9876	29.83	0.7049

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1514	33.982	22	0.0493
1	0.5031	12.365	10	0.2614

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	1	99.70%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.9864	74.69	0.8156
2	0.6731	25.31	0.6343

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.2001	31.370	16	0.021
1	0.5977	10.036	7	0.1865

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	94.89%	88.46%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.5354	69.27	0.5905
2	0.2376	30.73	0.4381

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.5263	13.801	8	0.0871
1	0.8080	4.583	3	0.2050

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	95.26%	84.62%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.0800	75.25	0.7206
2	0.3552	24.75	0.5119

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.3548	20.726	14	0.1089
1	0.7379	6.078	6	0.4145

CHARACTER 2
"NUMBER OF LOWER INCISORS"

Scores for character two "number of lower incisors" were predicted using the taxa ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius,* and *Pteropus.* Included in the matrix were the characters three, four, five, six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen. Two analyses were executed to determine scores for two taxa. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	91.10%	84.62%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.6884	71.48	0.6385
2	0.2747	28.52	0.4642

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.4646	16.479	8	0.0360
1	0.7845	5.218	3	0.1565

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	93.19%	80.77%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.2976	72.48%	0.7515
2	0.4927	27.52	0.5745

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2916	24.649	14	0.0382
1	0.6699	8.012	6	0.2373

CHARACTER 3
"NUMBER OF LOWER CANINES"

Missing values for character three "number of lower canines" were determined using the genera ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius,* and *Pteropus.* The Predicting variables were two, four, five, six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen. Scores for two genera were derived using two separate analyses, and the results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	57.11%	73.08%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4132	100.00	0.5407

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.7076	7.609	4	0.1070

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	96.23%	96.15%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.3211	100.00	0.7544

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.4308	17.262	7	0.0158

CHARACTER 4
"NUMBER OF UPPER PREMOLARS"

The prediction matrix for character four "number of upper premolars" consisted of the genera ANCESTRAL, *Pronothodectes*, *Plesiadapis*, *Chiromyoides*, *Carpodaptes*, *Saxonella*, *Purgatorius*, *Palaechthon*, *Navajovius*, *Microsyops*, *Ignacius*, *Phenacolemur*, *Picrodus*, *Cantius*, *Notharctus*, *Smilodectes*, *Mahgarita*, *Europolemur*, *Pronycticebus*, *Microadapis*, *Leptadapis*, *Adapis*, *Caenopithecus*, *Omomys*, and *Pteropus*. Characters two, three, five, six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen were the available variables by which to discriminate the missing scores for character four. Four analyses were executed to determine character states for five genera. The results of these analyses follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	99.62%	96.15%
Tinimomys	0	83.74%	96.15%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.8754	91.34	0.9344
2	0.6520	8.66	0.6282

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0769	46.183	22	0.0019
1	0.6053	9.036	10	0.5287

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	2	84.74%	92.31%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.4388	94.22	0.9304
2	0.3953	5.78	0.5322

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0963	45.626	16	0.0001
1	o.7167	6.495	7	0.4833

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	1	71.71%	61.54%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4324	76.33	0.5494
2	0.1341	23.67	0.3439

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.6156	10.432	8	0.2360
1	0.8808	2.706	3	0.4393

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	2	85.67%	69.23%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.7361	76.78	0.6511
2	0.2226	23.22	0.4267

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.4711	15.052	14	0.3746
1	0.8179	4.019	6	0.6741

CHARACTER 5
"NUMBER OF LOWER PREMOLARS"

Character five "number of lower premolars" was determined using the genera

ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella,*

Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus,

Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis,

Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* The prediction

matrix consisted of characters two, three, four, six, eight, nine, eleven, thirteen,

fourteen, sixteen, and seventeen. Character states for character five were determined for

two genera using two analyses. Results of these analyses follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	2	44.21%	57.69%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.6701	77.68	0.6334
2	0.1630	18.90	0.3744
3	0.0296	3.43	0.1695

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.5001	14.553	12	0.2668
1	0.8352	3.783	6	0.7060
2	0.9713	0.612	2	0.7364

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	46.42%	65.38%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.1477	71.29	0.7310
2	0.3256	20.22	0.4956
3	0.1366	8.49	0.3467

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3090	22.899	21	0.3494
1	0.6637	7.993	12	0.7856
2	0.8798	2.498	5	0.7769

CHARACTER 6
"CANINE SIZE"

States for character six "canine size" were determined using the genera

ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella,*

Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus,

Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis,

Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* The variables used

in constructing the matrix of predicting genera were one, two, three, four, five, eight,

nine, eleven, thirteen, fourteen, sixteen, and seventeen. Scores for three genera were

determined using three different analyses. Results of these analyses follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	48.92%	73.08%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.0676	87.12	0.8210
2	0.3057	12.88	0.4839

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2497	27.058	16	0.0408

1	0.7659	5.201	7	0.6354

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	2	65.98%	57.69%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4272	87.89	0.5471
2	0.0589	12.11	0.2358

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.6617	8.878	8	0.3527
1	0.9444	1.230	3	0.7458

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	48.73%%	65.38%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.6558	88.74	0.6293
2	0.0832	11.26	0.2771

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.5575	11.684	14	0.6316
1	0.9232	1.598	6	0.9527

CHARACTER 7
"MESIAL INCISOR SIZE"

All discriminant functions used to determine missing values for character seven "mesial incisor size" were based on scores for ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita,*

Europolemur, Pronycticebus, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and

Pteropus. The characters used in the prediction matrix include one, two, three, four, five,

six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen. Missing character

states for character seven were predicted for four genera using four analyses; the results

of which follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	94.42%	84.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.8423	91.50	0.9104
2	0.4501	8.50	0.5571

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.1180	39.529	16	0.0009
1	0.6896	6.875	7	0.4420

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	1	73.10%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	14.7270	88.67	0.9677
2	1.8814	11.33	0.8080

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0221	61.018	26	0.0001
1	0.3471	16.932	12	0.1522

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	2	50.06	52.00%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.5260	71.25	0.5871
2	0.2122	28.75	0.4184

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.5406	12.610	8	0.1260
1	0.8249	3.945	3	0.2674

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	2	62.23%	72.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.3641	80.31	0.7596
2	0.3344	19.69	0.5006

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3170	21.829	14	0.0822
1	0.7494	5.482	6	0.4837

CHARACTER 8
"MOLAR SERIES SIZE"

Scores for character eight "molar series size" were based on characters one, two, three, four, five, six, nine, eleven, thirteen, fourteen, sixteen , and seventeen of the genera ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius,* and *Pteropus.* A score for one genus was determined using one analysis. The results of this analysis follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	68.23%	84.62%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.7427	53.23	0.6528
2	0.6526	46.77	0.6284

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	o.3472	20.627	16	0.1933
1	0.6051	9.796	7	0.2004

CHARACTER 10
"DIASTEMA"

Because no states were missing for character nine "premolar form," no analyses

were run. Scores for character ten "diastema" were determined using the genera

ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella,*

Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus,

Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis,

matrix included one, two, three, four, five, eight nine, eleven, thirteen, fourteen, sixteen,

and seventeen. Scores for six genera were designated through the execution of five

different analyses. Results of the five analyses are presented below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	1	51.97%	79.17%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	5.6221	77.63	0.9214
2	1.3821	19.08	0.7617
3	0.2383	3.29	0.4387

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0512	46.068	33	0.0649
1	0.3390	16.767	20	0.6681
2	0.8076	3.313	9	0.9506

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Cantius	0	81.45%	95.83%
caenopithecus	1	55.42%	95.83%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	9.3513	78.13	0.9505
2	1.7775	14.85	0.8000
3	0.8406	7.02	0.6758

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0189	57.547	39	0.0281
1	0.1956	23.659	24	0.4812
2	0.5433	8.846	11	0.6361

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	51.94%	66.67%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.5636	72.23	0.7810
2	0.4450	20.55	0.5549
3	0.1562	7.22	0.3676

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2335	24.729	24	0.4206
1	0.5985	8.725	14	0.8482
2	0.8649	2.468	6	0.8720

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	1	54.42%	70.83%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.2831	92.57	0.8339
2	0.1767	7.16	0.3875
3	0.0067	0.27	0.0816

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2471	25.805	12	0.0114
1	0.8442	3.218	6	0.7811
2	0.9933	0.127	2	0.9386

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	37.25%	83.33%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.1190	81.98	0.8702
2	0.6284	16.51	0.6212
3	0.0575	1.51	0.2331

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1410	34.283	21	0.0338
1	0.5808	9.510	12	0.6589
2	0.9457	0.978	5	0.9644

CHARACTER 11
"HYPOCONE PRESENCE"

Scores for character eleven '"hypocone presence" were calculated using the

genera ANCESTRAL, *Pronothodectes*, *Plesiadapis*, *Chiromyoides*, *Carpodaptes*, *Saxonella*,

Purgatorius, *Palaechthon*, *Navajovius*, *Microsyops*, *Ignacius*, *Phenacolemur*, *Picrodus*,

Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* The characters represented in the original matrix included one, two, three, four, five, six, eight, nine, thirteen, fourteen, sixteen, and seventeen. Scores were determined for two genera using two analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	2	90.00%	92.31%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	5.8769	82.93	0.9244
2	0.8840	12.47	0.6850
3	0.3259	4.60	0.4958

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0582	54.029	24	0.0004
1	0.4003	17.394	14	0.2358
2	0.7542	5.360	6	0.4986

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	86.00%	88.46%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.5231	93.41	0.9050
2	0.2560	5.29	0.4515
3	0.0633	1.31	0.2439

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1356	41.963	12	0.0000
1	0.7488	6.075	6	0.4148
2	0.9405	1.288	2	0.5251

CHARACTER 12
"PROTOCONE FOLD"

Missing scores for character twelve "protocone fold" were predicted using the genera ANCESTRAL, *Pronothodectes, Plesiadapis, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Caenopithecus, Omomys, Tetonius,* and *Pteropus.* The characters used in constructing the prediction matrix included one, two, three, four, five, six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen. Scores were predicted for six genera using four analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Chiromyoides	1	100.00%	100.00%
Leptadapis	1	100.00%	100.00%
Adapis	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	14.0420	100.00	0.9662

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0665	39.307	13	0.0002

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	1	76.24%	86.96%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.6063	100.00	0.7851

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.3837	16.285	8	0.0385

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	72.43	86.96

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.4451	100.00	0.7688

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.4090	15.200	8	0.0554

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	83.94	73.91

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.1816	100.00	0.3921

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.8463	3.171	4	0.5296

CHARACTER 13
"MESOSTYLE"

Character thirteen "mesostyle" was determined using the genera ANCESTRAL,

Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius,

Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius,

Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis,

Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* The characters entered for

these genera were one, two, three, four, five, six, eight, nine, eleven, fourteen, sixteen,

and seventeen. Scores for three genera were designated using three analyses. The
results appear below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	0	99.14%	96.15%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.1302	100.00	0.8249

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3195	22.822	8	0.0036

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	92.43%	92.31%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.1257	100.00	0.8257

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3199	22.793	8	0.0036

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	96.67%	80.77%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.8372	100.00	0.6750

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.5443	13.831	4	0.0096

CHARACTER 14
"LOWER MOLAR SHAPE"

Scores for character fourteen "lower molar shape" were based on characters one,

two, three, four, five, six, eight, nine, eleven, thirteen, sixteen, and seventeen of the

genera ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella,*

Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus,

Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis,

Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* Only one analysis

was run to designate a score for one taxon. Results of this analysis follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Zanycteris	0	90.66%	96.15%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.5629	100.00%	0.8837

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2192	28.082	11	0.0031

CHARACTER 15
"PARACONID PRESENCE"

The matrix for character fifteen "paraconid presence" consisted of the genera

ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Purgatorius,*

Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius,

Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis,

Adapis, Caenopithecus, Omomys, Tetonius, and *Pteropus.* Characters one, two, three,

four, five, six, eight, nine, eleven, thirteen, fourteen, sixteen, and seventeen were entered

as the original variables by which to predict the missing values for character fifteen.

Scores were assessed for two genera using two different analyses. The results of the analyses are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Saxonella	1	70.80%	92.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.1102	65.97	0.8237
2	1.0885	34.03	0.7219

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1540	29.938	26	0.2702
1	0.4788	11.783	12	0.4633

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Zanycteris	0	76.52%	88.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.2804	54.34	0.7943
2	1.0761	45.66	0.7199

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2112	26.433	22	0.2336
1	0.4817	12.418	10	0.2580

CHARACTER 16
"HYPOCONE PROTOCONE CONNECTION"

Character sixteen "hypocone/protocone connection" was predicted using the genera ANCESTRAL, *Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius,* and *Pteropus.* The characters used in developing the matrix include one, two, three, four, five, six, eight, nine, eleven, thirteen, fourteen, and seventeen. Scores for three genera were predicted in three analyses, and the results appear below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	0	90.37%	69.23%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.6641	56.02	0.6317
2	0.5215	43.98	0.5854

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3950	18.114	16	0.3172
1	0.6573	8.184	7	0.3167

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	70.29%	60.23%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4603	64.15	0.5614
2	0.2572	35.85	0.4523

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.5447	11.847	16	0.7544
1	0.7954	4.464	7	0.7251

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	1	59.02%	53.85%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4040	70.22	0.5364
2	0.1713	29.78	0.3824

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.6081	10.695	8	0.2196
1	0.8538	3.399	3	0.3340

CHARACTER 17
"JAW DEPTH"

Missing states for character seventeen "jaw depth" were designated using a matrix consisting of the genera ANCESTRAL, Pronothodectes, Plesiadapis, Chiromyoides, Carpodaptes, Saxonella, Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus, Cantius, Notharctus, Smilodectes, Mahgarita, Europolemur, Pronycticebus, Microadapis, Leptadapis, Adapis, Caenopithecus, Omomys, Tetonius, and Pteropus. The characters included in the original prediction matrix were one, two, three, four, five, six, eight, nine, eleven, thirteen, fourteen, and sixteen. Two genera were missing scores for character seventeen, and these scores were designated through the execution of two separate analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Zanycteris	0	99.94%	96.15%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.1575	100.00	0.8715

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2405	26.361	11	0.0057

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	84.87%	96.15%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.5097	100.00	0.8456

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2849	25.111	8	0.0015

CHARACTER 18
"JAW SYMPHASIS"

The genera ANCESTRAL, *Plesiadapis, Chiromyoides, Carpodaptes, Saxonella,*

Purgatorius, Palaechthon, Navajovius, Microsyops, Ignacius, Phenacolemur, Picrodus,

Cantius, Notharctus, Smilodectes, Mahgarita, Microadapis, Leptadapis, Adapis,

Caenopithecus, Omomys, Tetonius, and *Pteropus* were used to assess the missing values

for character eighteen "jaw symphasis." The original character matrix consisted of

characters one, two, three, four, five, six, eight, nine, eleven, thirteen, fourteen, sixteen,

and seventeen. Scores for six genera were predicted using four analyses. The results to

these analyses are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	99.96%	86.96%
Europolemur	1	99.46%	86.96%
Pronycticebus	1	99.09%	86.96%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.687	100.00	0.7916

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3733	14.287	13	0.3539

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Zanycteris	0	86.27%	91.30%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 11, 13, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.6589	100.00	0.7899

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3761	15.158	11	0.1754

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	88.69%	82.61%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.3705	100.00	0.5200

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.7296	5.989	4	0.2000

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	62.94%	86.96%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.5427	100.00	0.5931

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.6482	7.587	7	0.3704

CHARACTER 19
"POST-ORBITAL CONSTRICTION"

Character nineteen was assessed using the genera ANCESTRAL, *Plesiadapis*,
Palaechthon, *Microsyops*, *Ignacius*, *Notharctus*, *Smilodectes*, *Pronycticebus*, *Leptadapis*,
Adapis, *Tetonius*, and *Pteropus*. The characters entered as the original predicting
variables were one, two, three, four, five, six, seven, eight, nine, ten, eleven, thirteen,
fourteen, fifteen, sixteen, seventeen, twenty, and twenty-one. Scores for twenty-two
genera were determined using eight analyses. The results appear below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	99.49%	83.33%
Carpodaptes	3	100.00%	83.33%
Purgatorius	0	84.48%	83.33%
Phenacolemur	0	100.00%	83.33%
Picrodus	3	100.00%	83.33%
Mahgarita	1	96.43%	83.33%
Europolemur	2	99.90%	83.33%
Omomys	1	99.74%	83.33%
Chiromyoides	0	99.99%	83.33%
Saxonella	0	99.98%	83.33%
Navajovius	1	99.74%	83.33%
Cantius	3	99.90%	83.33%
Caenopithecus	0	99.35%	83.33%
Zanycteris	1	99.04%	83.33%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	12.9282	89.65	0.9634
2	1.0949	7.59	0.7230
3	0.3970	2.75	0.5331

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0245	18.539	24	0.7761
1	0.3417	5.369	14	0.9800
2	0.7158	1.672	6	0.9473

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	2	86.46%	91.67

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	5.1535	76.35	0.9151
2	1.2925	19.15	0.7509
3	0.3040	4.50	0.4828

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0544	14.560	24	0.9330
1	0.3345	5.475	14	0.9780
2	0.7669	1.327	6	0.9701

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	100.00%	100.00%
Micromomys	2	96.84%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	125.0359	98.97	0.9960
2	0.8575	0.68	0.6794
3	0.4469	0.35	0.5555

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0030	29.126	24	0.2154
1	0.3721	4.943	14	0.9866
2	0.6911	1.847	6	0.9332

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	0	100.00%	83.33%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	8.0882	84.50	0.9434
2	1.0859	11.35	0.7215
3	0.3977	4.15	0.5334

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0377	16.385	24	0.8737
1	0.3430	5.350	14	0.9803
2	0.7155	1.674	6	0.9471

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	100.00%	83.33%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14, 20

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	176.5123	97.97	0.9972
2	3.2139	0.24	0.5530
3	0.4405	0.24	0.5530

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0009	34.912	24	0.0697
1	0.1647	9.017	14	0.8300
2	0.6942	1.825	6	0.9351

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	100.00%	83.33%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	9.4913	87.84	0.9511
2	1.0033	9.29	97.13
3	0.3106	2.87	0.4868

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0363	21.553	15	0.1201
1	0.3809	6.274	8	0.6165
2	0.7630	1.758	3	0.6241

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	2	84.55%	75.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 15, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	305.3755	99.62	0.9984
2	0.8378	0.27	0.6752
3	0.3326	0.11	0.4996

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0013	36.413	21	0.0196
1	0.4083	4.926	12	0.9604
2	0.7504	1.579	5	0.9038

CHARACTER 20
"POST-ORBITAL CLOSURE"

Missing scores for character twenty "post-orbital closure" were predicted using

the genera ANCESTRAL, *Plesiadapis, Carpodaptes, Palaechthon, Navajovius, Microsyops,*

Ignacius, Phenacolemur, Notharctus, Smilodectes, Mahgarita, Pronycticebus, Leptadapis,

Adapis, Tetonius, and *Pteropus.* The characters used to create this matrix were one, two,

three, four, five, six, seven, eight, nine, ten, eleven, thirteen, fourteen, fifteen, and

seventeen. Ten analyses were performed, predicting character states for seventeen genera. The results of these analyses appear below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	100.00%	100.00%
Chiromyoides	1	100.00%	100.00%
Purgatorius	1	99.98%	100.00%
Picrodus	2	100.00%	100.00%
Europolemur	1	99.99%	100.00%
Omomys	0	100.00%	100.00%
Saxonella	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	236.272	89.48	0.9979
2	27.7915	10.52	98.25

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0001	61.805	26	0.0001
1	0.0347	23.521	12	0.0236

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 11, 13, 14, 15, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	61.3291	93.21	0.9919
2	4.4672	6.79	0.9039

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0029	40.818	26	0.0324
1	0.1829	11.891	12	0.4544

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	1	100.00%	93.75%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 11, 13, 14, 15, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.1757	59.52	0.9277
2	4.2000	40.48	0.8987
3	0.3326	0.11	0.4996

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0268	27.145	24	0.2977
1	0.1923	12.365	11	0.3368

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	21.5663	72.34	0.9776
2	8.2458	27.66	0.9444

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0048	42.725	22	0.0051
1	0.1082	17.793	10	0.0586

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Zanycteris	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	236.2282	96.86	99.79
2	7.6540	3.14	0.9405

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0005	57.203	24	0.0002
1	0.1156	16.185	11	0.1344

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Cantius	1	100.00%	100.00%
Caenopithecus	1	73.74%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 13, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	32.0407	65.51	98.48
2	16.8720	34.49	0.9716

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0017	47.857	24	0.0026
1	0.0560	21.624	11	0.0275

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	74.31%	81.25%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.5419	69.78	0.9053
2	1.9672	30.22	0.8142

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0608	25.200	18	0.1195
1	0.3370	9.789	8	0.2802

Analysis #8

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 13, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	236.5292	97.83	0.9979
2	5.2586	2.17	0.9166

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0007	51.130	26	0.0023

1	0.1598	12.838	12	0.3809

Analysis #9

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	97.62%	81.25%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.4859	97.11	0.9308
2	0.1930	2.89	0.4022

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1120	24.084	10	0.0074
1	0.8382	1.941	4	0.7466

Analysis #10

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	2	90.89%	87.50%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 15, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	7.8638	91.42	0.9419
2	0.7384	8.58	0.6517

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0649	25.982	16	0.0543
1	0.5752	5.253	7	0.6291

CHARACTER 21
"SNOUT LENGTH"

The prediction matrix for character twenty-one "snout length" consisted of characters one, two, three, four, five, six, seven, eight, nine, ten, eleven, thirteen, fourteen, fifteen, sixteen, and seventeen of the genera ANCESTRAL, *Plesiadapis, Chiromyoides, Carpodaptes, Palaechthon, Microsyops, Ignacius, Notharctus, Smilodectes,*

Pronycticebus, Leptadapis, Adapis, Tetonius, and *Pteropus.* Implementing nine analyses,

nineteen taxa were analyzed. The results of these analyses are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	100.00%	100.00%
Purgatorius	0	92.30%	100.00%
Navajovius	0	100.00%	100.00%
Phenacolemur	2	100.00%	100.00%
Picrodus	2	79.47%	100.00%
Mahgarita	1	100.00%	100.00%
Europolemur	2	100.00%	100.00%
Omomys	1	100.00%	100.00%
Saxonella	1	99.98%	100.00%
Zanycteris	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	56.7578	95.14	0.9913
2	2.8967	4.86	0.8622

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0044	35.207	20	0.0190
1	0.2666	8.841	9	0.4521

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 11, 13, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	9.3080	75.72%	0.9503
2	2.9846	24.28	0.8655

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0243	22.292	22	0.4426
1	0.2510	8.295	10	0.6001

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 11, 13, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	7.7897	56.78	0.9414
2	5.9293	43.22	0.9250

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0164	24.656	22	0.3138
1	0.1443	11.615	10	0.3117

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	36.1754	93.72	0.9865
2	2.4234	6.28	0.8414

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0079	31.501	20	0.0489
1	0.2921	7.999	9	0.5342

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Cantius	2	78.92%	100.00%
Caenopithecus	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 13

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	8.4759	58.77	0.9458
2	5.9469	41.23	0.9252

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0152	25.122	22	0.2913

1	0.1439	11.630	10	0.3106

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	98.32%	92.86%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.2560	69.20	0.8748
2	1.4494	30.80	0.7692

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0959	16.409	18	0.5640
1	0.4083	6.271	8	0.6169

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 13

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	8.2363	63.08	0.9443
2	4.8199	36.92	0.9100

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0186	23.907	22	0.3521
1	0.1718	10.568	10	0.3922

Analysis #8

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	83.81%	78.57%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.7697	97.06	0.8890

2	0.1140	2.94	0.3200

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1882	15.032	10	0.1309
1	0.8976	0.972	4	0.9140

Analysis #9

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	2	100.00%	92.86%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 15, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	29.4483	97.46	0.9834
2	0.7690	2.54	0.6593

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0186	29.898	16	0.0185

CHARACTER 22
"CENTER OF BULLA OSSIFICATION

Discriminant functions to predict states for character twenty-two "center of bulla ossification" were based on the scores of characters one, two, three, four, five, six, seven, eight, nine, ten, eleven, thirteen, fourteen, fifteen, sixteen, seventeen, and twenty of the genera ANCESTRAL, *Palaechthon, Microsyops, Ignacius, Phenacolemur, Mahgarita, Pronycticebus, Leptadapis, Adapis,* and *Pteropus*. Character states for twenty-three taxa were described using seven analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	100.00%	100.00%
Chiromyoides	2	100.00%	100.00%
Purgatorius	2	100.00%	100.00%

Picrodus	1	100.00%	100.00%
Europolemur	0	93.25%	100.00%
Omomys	1	100.00%	100.00%
Plesiadapis	2	100.00%	100.00%
Carpodaptes	1	100.00%	100.00%
Navajovius	1	100.00%	100.00%
Notharctus	0	93.25%	100.00%
Smilodectes	1	96.39%	100.00%
Tetonius	2	100.00%	100.00%
Saxonella	2	100.00%	100.00%
Zanycteris	1	100.00%	100.00%
Microadapis	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	53.9975	84.61	0.9909
2	9.8247	15.39	0.9527

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0017	25.556	14	0.0295
1	0.0924	9.527	6	0.1460

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	100.00%	100.00%
Micromomys	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	26.4505	64.27	0.9816
2	14.7050	35.73	0.9676

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0023	24.265	14	0.0426
1	0.0637	11.016	6	0.0879

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	21.1220	76.65	0.9771
2	6.4335	23.35	0.9303

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0061	20.410	14	0.1177
1	0.1345	8.024	6	0.2364

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Cantius	1	96.39%	100.00%
Caenopithecus	2	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	14.2000	55.86	0.9665
2	11.2222	44.14	0.9582

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0054	20.898	14	0.1043
1	0.0818	10.013	6	0.1241

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	2	99.28%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	14.1988	71.28	0.9665
2	5.7220	28.72	0.9226

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0098	20.820	12	0.0531
1	0.1488	8.574	5	0.1273

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	93.85%	90.00%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.8906	89.15	0.9112
2	0.5954	10.85	0.6109

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1064	12.323	8	0.1374
1	0.6268	2.569	3	0.4629

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 14, 15, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	28.9624	74.72	0.9832
2	9.7987	25.28	0.9526

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0031	26.001	12	0.0107
1	0.0926	10.707	5	0.0575

CHARACTER 23
"POSTERIOR MARGIN OF PALATE"

Predicted states for character twenty four were based on the genera ANCESTRAL,

Plesiadapis, Microsyops, Ignacius, Notharctus, Smilodectes, Pronycticebus, Leptadapis,

Adapis, Tetonius, and *Pteropus.* The character matrix consisted of characters one

through eleven, thirteen through seventeen, and nineteen through twenty one. Scores

were derived for twenty-one genera by executing seven analyses.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	100.00%	100.00%
Purgatorius	0	100.00%	100.00%
Picrodus	1	100.00%	100.00%
Europolemur	0	100.00%	100.00%
Omomys	1	100.00%	100.00%
Chiromyoides	0	100.00%	100.00%
Carpodaptes	0	100.00%	100.00%
Saxonella	0	100.00%	100.00%
Palaechthon	1	100.00%	100.00%
Navajovius	1	100.00%	100.00%
Phenacolemur	0	100.00%	100.00%
Mahgarita	0	100.00%	100.00%
Cantius	0	100.00%	100.00%
Caenopithecus	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 7, 8, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	7.7273	100.00	0.9410

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1146	9.749	9	0.3712

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	11.8001	100.00	0.9601

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0781	11.473	9	0.2447

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 11, 13

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	7.7273	100.00	0.9410

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1146	9.749	9	0.3712

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Micromomys	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	5.6801	100.00	0.9221

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1497	8.546	9	0.4802

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	99.98%	90.91%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.3636	100.00	0.8780

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.2292	7.367	8	0.4977

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 5, 6, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.9079	100.00	0.8923

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2038	7.159	9	0.6206

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	100.00%	90.91%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
I	2.9007	100.00	0.8623

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2564	8.848	5	0.1153

Analysis #8

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	71.86%	90.91%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 15, 16, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.3636	100.00	0.8780

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2292	7.367	8	0.4977

CHARACTER 24
"PALATINE CONTRIBUTION TO PALATE"

Predictions on missing scores for character twenty-five "palatine contribution to palate" were based on the genera ANCESTRAL, *Plesiadapis, Palaechthon, Microsyops, Ignacius, Notharctus, Pronycticebus, Leptadapis, Adapis,* and *Pteropus.* The characters used to determine the missing character states were derived from the characters one through eleven, thirteen through seventeen, and nineteen through twenty-one. Scores

for twenty-two taxa were derived through the execution of seven analyses. The results

follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	100.00%	100.00%
Purgatorius	0	100.00%	100.00%
Picrodus	1	100.00%	100.00%
Europolemur	0	100.00%	100.00%
Omomys	1	100.00%	100.00%
Chiromyoides	0	100.00%	100.00%
Carpodaptes	0	100.00%	100.00%
Saxonella	0	99.12%	100.00%
Navajovius	1	81.76%	100.00%
Phenacolemur	1	100.00%	100.00%
Mahgarita	0	100.00%	100.00%
Cantius	0	100.00%	100.00%
Caenopithecus	0	95.00%	100.00%
Smilodectes	0	100.00%	100.00%
Tetonius	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 7, 8, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	12.1556	100.00	0.9612

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0760	10.307	8	0.2441

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	100.00%	100.00%
Micromomys	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	149.2222	100.00	0.9976

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0067	20.048	8	0.0102

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Tinimomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 8, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	27.4889	100.00	0.9823

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0351	13.398	8	0.0989

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	408.6000	100.00	0.9988

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0024	27.068	7	0.0003

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 8, 9, 10

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	117.7556	100.00	0.9958

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0084	19.108	8	0.0143

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	62.56%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.7871	100.00	0.9095

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1728	9.656	5	0.0856

Analysis #7

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	96.35%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 13, 14, 15, 16

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.2413	100.00	0.8996

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1908	7.455	7	0.3831

CHARACTER 25
"CAPITULUM"

This character was predicted using characters one through fourteen, and sixteen through eighteen of the taxa ANCESTRAL, Plesiadapis, Saxonella, Phenacolemur, Notharctus, Smilodectes, and Pteropus. Character states for twenty-six genera were designated using five analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	99.99%	100.00%
Europolemur	0	100.00%	100.00%
Pronycticebus	0	100.00%	100.00%
Chiromyoides	1	100.00%	100.00%
Leptadapis	0	100.00%	100.00%
Adapis	0	100.00%	100.00%
Carpodaptes	1	81.13%	100.00%
Purgatorius	0	100.00%	100.00%
Palaechthon	0	99.98%	100.00%

Navajovius	0	97.19%	100.00%
Microsyops	1	99.84%	100.00%
Ignacius	1	100.00%	100.00%
Picrodus	1	81.13%	100.00%
Mahgarita	0	100.00%	100.00%
Omomys	1	99.99%	100.00%
Tetonius	1	81.13%	100.00%
Cantius	0	100.00%	100.00%
Caenopithecus	0	99.98%	100.00%
Zanycteris	0	99.98%	100.00%
Microadapis	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 5, 6

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	15.2857	100.00	0.9688

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0614	6.976	5	0.2225

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	100.00%	100.00%
Tinimomys	1	100.00%	100.00%
Micromomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	95.0000	100.00	0.9948

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0104	11.411	5	0.0438

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 5, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.7143	100.00	0.9329

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1296	7.455	5	0.4029

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	23.0000	100.00	0.9789

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0417	9.534	4	0.0491

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	98.91%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 12

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.8036	100.00	0.8585

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2629	4.008	4	0.4049

CHARACTER 26
""TROCHLEAR SHELF PRESENCE"

Statistical character state assignments for character twenty-six "trochlear shelf presence" were based on characters one through fourteen, sixteen through eighteen, and twenty-six of the genera ANCESTRAL, *Plesiadapis, Saxonella, Phenacolemur,*

Notharctus, Smilodectes, and *Pteropus*. Scores were derived for twenty-seven taxa

implementing five analyses. The results are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	100.00%	100.00%
Europolemur	1	100.00%	100.00%
Pronycticebus	1	100.00%	100.00%
Chiromyoides	0	100.00%	100.00%
Leptadapis	1	100.00%	100.00%
Adapis	1	99.91%	100.00%
Carpodaptes	1	95.26%	100.00%
Purgatorius	0	100.00%	100.00%
Palaechthon	1	95.26%	100.00%
Navajovius	0	73.11%	100.00%
Microsyops	1	100.00%	100.00%
Ignacius	0	100.00%	100.00%
Picrodus	1	95.26%	100.00%
Mahgarita	1	100.00%	100.00%
Omomys	0	100.00%	100.00%
Tetonius	1	95.26%	100.00%
Phenacolemur	0	100.00%	100.00%
Zanycteris	1	95.26%	100.00%
Cantius	1	99.91%	100.00%
Caenopithecus	1	95.26%	100.00%
Microadapis	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 6

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	10.2500	100.00	0.9545

AFTER FCTN.	WILKS Λ	χ^2	df	SIGNIFICANCE
0	0.0889	4.841	4	0.3040

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	98.20%	83.33%
Tinimomys	0	88.08%	83.33%
Micromomys	0	98.20%	83.33%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.0000	100.00	0.8165

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3333	2.197	4	0.6995

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	99.91%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.7500	100.00	0.8563

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2667	2.644	4	0.6191

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	73.11%	83.33%

CHARACTERS USED IN ANALYSIS	9, 14, 17

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.2500	100.00	0.7454

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.4444	2.027	3	0.5668

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	9, 11, 12

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	3.5000	100.00	0.8819

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2222	3.760	3	0.2886

CHARACTER 27
"RADIUS HEAD SHAPE"

The matrix used to determine the missing scores for character twenty-seven

"radius head shape" contained the genera ANCESTRAL, *Plesiadapis, Navajovius,*

Phenacolemur, Cantius, Notharctus, Smilodectes, and *Pteropus.* The characters used for

the analyses came from characters one through nine, eleven through fourteen, and

sixteen through eighteen. Six different analyses were run to predict scores for twenty-

five genera. The results of these analyses are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	93.09%	87.50%
Europolemur	1	99.63%	87.50%
Pronycticebus	1	100.00%	87.50%
Chiromyoides	1	99.63%	87.50%
Carpodaptes	1	99.98%	87.50%
Purgatorius	0	99.83%	87.50%
Palaechthon	1	93.09%	87.50%
Microsyops	1	100.00%	87.50%
Ignacius	1	100.00%	87.50%
Picrodus	1	99.98%	87.50%
Mahgarita	1	99.98%	87.50%
Caenopithecus	0	99.83%	87.50%
Omomys	1	93.09%	87.50%
Tetonius	1	99.98%	87.50%
Saxonella	1	99.63%	87.50%
Zanycteris	1	99.98%	87.50%
Leptadapis	1	100.00%	87.50%
Adapis	1	99.63%	87.50%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 7

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.7500	100.00	0.8563

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2667	3.965	6	0.6814

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	99.00%	87.50%
Tinimomys	0	98.79%	87.50%
Micromomys	1	99.63%	87.50%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.7500	100.00	0.8563

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2667	3.965	6	0.6814

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	99.63%	87.50%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 9, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.7500	100.00	0.8563

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2667	3.965	6	0.6814

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Microadapis	1	99.98%	87.50%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6, 9

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.7500	100.00	0.8563

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2667	3.965	6	0.6814

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	68.88%	75.00%

CHARACTERS USED IN ANALYSIS	9, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.4309	100.00	0.5488

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.6989	1.612	3	0.6566

Analysis #6

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	9, 11, 12, 13

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.5000	100.00	0.9309

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1333	8.060	4	0.0894

TRAIT 28
"NAILS"

Scores for trait twenty-eight were determined according to the genera

ANCESTRAL, Plesiadapis, Ignacius, Phenacolemur, Notharctus, Smilodectes, and Pteropus.

The original data matrix consisted of characters one through fourteen, sixteen through

eighteen, twenty, and twenty-three. five analyses were executed to determine scores for

twenty-six genera. the results of these analyses follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	100.00%	100.00%
Europolemur	1	100.00%	100.00%
Chiromyoides	0	100.00%	100.00%
Carpodaptes	0	100.00%	100.00%
Palaechthon	0	100.00%	100.00%
Navajovius	0	100.00%	100.00%
Microsyops	1	100.00%	100.00%
Saxonella	0	100.00%	100.00%
Purgatorius	0	100.00%	100.00%
Picrodus	0	100.00%	100.00%
Omomys	0	100.00%	100.00%
Zanycteris	0	100.00	100.00
Cantius	1	100.00%	100.00%
Mahgarita	1	99.68%	100.00%
Tetonius	0	100.00%	100.00%
Pronycticebus	1	100.00%	100.00%
Microadapis	1	100.00%	100.00%
Leptadapis	1	100.00%	100.00%
Adapis	1	100.00%	100.00%
Caenopithecus	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 6

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	53.2857	100.00	0.9907

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0184	9.986	5	0.0756

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	100.00%	100.00%
Tinimomys	1	67.92%	100.00%
Micromomys	0	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 7

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	79.0000	100.00	0.9937

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0125	10.955	5	0.0523

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 3, 4, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	24.7143	100.00	0.9309

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.0389	8.118	5	0.1499

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	99.78%	85.71%

CHARACTERS USED IN ANALYSIS	8, 9, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	0.7857	100.00	0.6633

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.5600	2.029	3	0.56633

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	62.25%	100.00%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.1429	100.00	0.7303

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.4667	2.286	4	0.6832

CHARACTER 29
"INTERMEDIATE PHALANX LENGTH (COMPARED TO PROXIMAL)"

To determine missing character states for character twenty-nine "intermediate

phalanx length" the genera ANCESTRAL, *Plesiadapis, Ignacius, Phenacolemur,*

Notharctus, Smilodectes, and *Pteropus* were used. The variables used to discriminate

these scores came from the original matrix which consisted of characters one through

fourteen, sixteen through eighteen, twenty, twenty-three, and twenty-nine. Scores were

determined for twenty six taxa using four separate analyses. The results are listed

below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	1	100.00%	100.00%
Europolemur	0	100.00%	100.00%
Plesiadapis	1	100.00%	100.00%
Chiromyoides	1	100.00%	100.00%
Carpodaptes	0	92.41%	100.00%
Palaechthon	0	92.41%	100.00%
Navajovius	1	81.76%	100.00%
Microsyops	1	81.76%	100.00%
Saxonella	1	100.00%	100.00%
Purgatorius	0	100.00%	100.00%
Picrodus	0	92.41%	100.00%
Omomys	1	100.00%	100.00%
Zanycteris	0	92.41%	100.00%
Cantius	0	99.85%	100.00%
Mahgarita	0	100.00%	100.00%
Tetonius	0	92.41%	100.00%
Pronycticebus	0	100.00%	100.00%
Microadapis	0	100.00%	100.00%
Leptadapis	0	100.00%	100.00%
Adapis	0	99.85%	100.00%
Caenopithecus	1	81.76%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 4, 6

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	9.0000	100.00	0.9487

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1000	4.605	4	0.3303

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	1	100.00%	100.00%
Tinimomys	1	100.00%	100.00%
Micromomys	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	2, 5, 6, 7

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	39.0000	100.00	0.9874

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.0250	7.378	4	0.1172

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	0	99.85%	100.00%

CHARACTERS USED IN ANALYSIS	1, 2, 4, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.3333	100.00	0.8367

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.3000	2.408	4	0.6612

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	99.98%	83.33%
Altiatlasius	1	97.07%	83.33%

CHARACTERS USED IN ANALYSIS	8, 9, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.0000	100.00	0.7071

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.5000	1.733	3	0.6297

CHARACTER 30
"PATELLAR GROOVE"

Character thirty was determined using the genera ANCESTRAL, *Plesiadapis*,

Phenacolemur, *Cantius*, *Notharctus*, *Smilodectes*, and *Pteropus* and traits one through

nine, eleven through fourteen, sixteen through eighteen, twenty-three, and twenty-

eight. Scores for twenty-six taxa were determined through the use of five analyses. The

results of these analyses are listed below.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	99.99%	100.00%
Europolemur	1	100.00%	100.00%
Chiromyoides	0	100.00%	100.00%
Carpodaptes	1	97.19%	100.00%
Purgatorius	0	100.00%	100.00%
Palaechthon	1	97.19%	100.00%
Microsyops	1	100.00%	100.00%
Picrodus	1	97.19%	100.00%
Caenopithecus	1	97.19%	100.00%
Omomys	0	99.99%	100.00%
Saxonella	0	100.00%	100.00%
Navajovius	0	81.13%	100.00%
Ignacius	0	100.00%	100.00%
Mahgarita	1	100.00%	100.00%
Tetonius	1	97.19%	100.00%
Zanycteris	1	97.19%	100.00%
Pronycticebus	1	100.00%	100.00%
Microadapis	1	100.00%	100.00%
Leptadapis	1	100.00%	100.00%
Adapis	1	99.98%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 6, 8

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	8.4286	100.00	0.9455

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1061	5.609	5	0.3461

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	99.96%	85.71%
Tinimomys	0	99.46	85.71%
Micromomys	0	99.46%	85.71%

CHARACTERS USED IN ANALYSIS	2, 3, 5, 6, 8

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.4286	100.00	0.8416

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2917	3.080	5	0.6876

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	100.00%	100.00%

CHARACTERS USED IN ANALYSIS	1, 3, 4, 11, 18

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	5.8571	100.00	0.9242

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.1458	4.813	5	0.4391

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	100.00%	85.71%

CHARACTERS USED IN ANALYSIS	8, 9, 14, 15

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.4286	100.00	0.8416

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2917	3.696	4	0.4486

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	0	99.46%	85.71%

CHARACTERS USED IN ANALYSIS	8, 9, 11, 12

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	2.4286	100.00	0.8416

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.2917	3.696	4	0.4486

CHARACTER 31
"ASTRAGALAR TIBIAL TROCHLEA"

Missing scores for character thirty-one "astragalar tibial trochlea" were based on characters one through nine, eleven through eighteen, twenty-three, twenty-eight, and thirty-one of the genera ANCESTRAL, *Plesiadapis*, *Phenacolemur*, *Cantius*, *Notharctus*, *Smilodectes*, and *Pteropus*. Scores were determined for twenty-six genera using five analyses. The results follow.

Analysis #1

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Pronothodectes	0	99.94%	100.00%
Europolemur	1	100.00%	100.00%
Chiromyoides	0	99.94%	100.00%
Carpodaptes	1	92.41%	100.00%
Purgatorius	0	100.00%	100.00%
Palaechthon	1	92.41%	100.00%
Microsyops	1	100.00%	100.00%
Picrodus	1	92.41%	100.00%
Caenopithecus	1	92.41%	100.00%
Omomys	0	99.94%	100.00%
Saxonella	0	99.94%	100.00%
Navajovius	0	81.76%	100.00%

Ignacius	0	99.94%	100.00%
Mahgarita	1	100.00%	100.00%
Tetonius	1	92.41%	100.00%
Phenacolemur	0	99.94%	100.00%
Zanycteris	1	92.41%	100.00%
Pronycticebus	1	100.00%	100.00%
Microadapis	1	100.00%	100.00%
Leptadapis	1	100.00%	100.00%
Adapis	1	99.85%	100.00%

| CHARACTERS USED IN ANALYSIS | 1, 4, 6, 8 |

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	6.3333	100.00	0.9293

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1364	3.985	4	0.4081

Analysis #2

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Platychoerops	0	92.41%	83.33%
Tinimomys	0	62.25%	83.33%
Micromomys	0	98.80%	83.33%

| CHARACTERS USED IN ANALYSIS | 2, 5, 6, 8 |

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.6667	100.00	0.7906

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.3750	1.962	4	0.7428

Analysis #3

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Copelemur	1	100.00%	100.00%

| CHARACTERS USED IN ANALYSIS | 1, 4, 11, 17 |

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	4.3333	100.00	0.9014

AFTER FCTN.	WILKS Λ	x^2	df	SIGNIFICANCE
0	0.1875	3.348	4	0.5014

Analysis #4

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altanius	0	99.98%	83.33%

CHARACTERS USED IN ANALYSIS	8, 9, 14

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.6667	100.00	0.7906

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3750	2.452	3	0.4840

Analysis #5

GENUS	PREDICTED SCORE	PROBABILITY	ACCURACY
Altiatlasius	1	81.76%	83.33%

CHARACTERS USED IN ANALYSIS	8, 9, 11

FUNCTION	EIGEN VALUE	% OF VARIANCE	CANONICAL CORR.
1	1.6667	100.00	0.7906

AFTER FCTN.	WILKS Λ	X^2	df	SIGNIFICANCE
0	0.3750	2.452	3	0.4840

Table 3.1: Character State Matrix characters 1-16
(predicted scores presented in **bold** print)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
ANCESTRAL	0	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0
Pronothodectes	1	1	0	1	1	2	2	2	2,3	1	0	0	0	0	0	0
Plesiadapis	1	2	0	1	1,2	2	2	1	2	0	2	0	0,1	1	0	1
Platychoerops	1	2	0,1	1	2	2	2	1	3	0	0	0	1	1	0	0
Chiromyoides	1	2	1	1	2	2	2	2	2	2	0	1	0	1	0	0
Carpodaptes	1	1	0	1	2	1	2	1	0	1	2	0	0	0	0	1
Saxonella	1	2	1	1	2	2	2	1	0,2	0	1	1	0	0	1	0
Purgatorius	0	0	0	0	0	0	1	2	2,3	3	2	0	0	0	0	1
Palaechthon	1	1	0	1	1	1	1	0	2,3	1	2	0	0	0	0	1
Tinimomys	1	2	1	0	1	2	2	1	3	1	2	1	0	0	0	1
Micromomys	1	1	0	2	2	1	2	1	3	2	2	1	0	0	0	0
Navajovius	1	1	0	2	2	1	2	0	3	1	2	1	0	0	0	0
Microsyops	2	2	1	0	1	2	2	0	3,4	1	2	1	0	1	0	0
Ignacius	1	1	1	1	2	2	2	0	2	0	2	1	0	0	1	1
Phenacolemur	1	2	1	1	3	2	2	0	2	0	2	1	0	1	1	1
Picrodus	1	1	0	1	2	1	2	0	2	1	0	0	1	0	0	0
Zanycteris	1	1	0	1	1	1	2	0	2	0	0	0	1	0	0	0
Cantius	1	1	0	0	0	1	0	1	2	0	2	0	1	1	0	1
Copelemur	1	1	0	0	0	0	1	1	2	1	2	0	1	0	0	0
Notharctus	1	1	0	0	0	0	0	0	2	1	3	0	1	1	0	2
Smilodectes	1	1	0	0	0	1	0	0	2	2	3	0	1	1	0	2
Mahgarita	1	1	0	1	1	0	1	1	2	3	3	1	1	1	1	0
Europolemur	1	1	0	0	0	0	0	1	1	1	3	1	1	1	1	0
Pronycticebus	1	1	0	0	0	0	1	1	1	3	3	1	1	0	0	0
Microadapis	1	1	0	0	0	0	1	0	3	3	3	1	1	1	2	0
Leptadapis	1	1	0	0	0	0	1	0,1	4	3	3	1	1	1	2	0
Adapis	1	1	0	0	0	1	1	1	4	3	3	1	1	1	2	0
Caenopithecus	1	2	0	1	1	1	1	1	2	1	3	1	1	1	1	0
Omomys	1	1	0	1	1	2	2	0	1,2	2	2	1	0	0	0	0
Tetonius	1	1	0	1	1,2	1	2	0	1,3	3	2	0	0	0	0	0
Altanius	0	0	0	1	2	2	2	2	2	1	0	0	0	0	0	1
Altiatlasius	1	1	0	2	1	0	2	0	2	1	2	1	0	0	0	0
Pteropus	1	1	0	2	2	0	1	0	1	0	0	0	0	0	1	0

Character State Matrix characters 17-32
(predicted scores presented in **bold** print)

	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
ANCESTRAL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pronothodectes	0	**0**	**1**	**1**	**0**	**1**	**0**	**0**	**1**	**0**	**1**	**0**	**1**	**0**	**0**
Plesiadapis	0	0	0	0	0	2	0	1	1	0	0	0	1	0	0
Platychoerops	0	0	**0**	2	**0**	**0**	**0**	1	1	**0**	1	**0**	1	**0**	**0**
Chiromyoides	0	0	**0**	1	1	2	**0**	**0**	1	**0**	1	**0**	1	**0**	**0**
Carpodaptes	0	0	3	0	1	**1**	0	**0**	1	1	1	0	0	1	1
Saxonella	0	0	**0**	1	1	2	0	**0**	1	0	1	0	1	0	**0**
Purgatorius	1	0	**0**	1	**0**	2	0	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Palaechthon	0	0	1	1	1	1	**1**	0	**0**	1	1	0	0	1	1
Tinimomys	1	0	**0**	1	1	2	1	1	1	0	0	1	1	0	0
Micromomys	1	0	**2**	**0**	1	2	0	0	1	0	1	0	1	0	0
Navajovius	1	0	1	0	**0**	1	1	1	**0**	0	1	0	1	0	0
Microsyops	0	0	0	1	1	1	1	1	**1**	**1**	1	**1**	1	**1**	**1**
Ignacius	0	0	1	0	1	1	0	0	1	**0**	1	0	1	**0**	**0**
Phenacolemur	0	0	**0**	0	2	2	0	**1**	1	**0**	1	0	1	0	**0**
Picrodus	0	0	3	2	2	1	**1**	1	1	1	1	0	0	1	**1**
Zanycteris	**0**	**0**	1	2	**0**	1	1	0	**0**	1	1	0	0	1	1
Cantius	0	0	3	1	2	1	0	0	0	1	0	1	0	1	1
Copelemur	1	1	**0**	1	1	2	0	0	0	1	1	1	0	1	1
Notharctus	0,1	1	2	2	2	**0**	0	0	0	1	1	1	0	1	1
Smilodectes	1	0	3	2	2	**1**	1	**0**	0	1	1	1	0	1	1
Mahgarita	1	1	**1**	2	**1**	2	**0**	**0**	**0**	1	1	1	0	1	1
Europolemur	1	**1**	2	1	2	**0**	**0**	**0**	**0**	1	1	1	0	1	1
Pronycticebus	1	**1**	1	2	1	2	0	0	**0**	1	1	1	0	1	1
Microadapis	1	0	**2**	2	2	2	**0**	**0**	**0**	1	1	1	0	1	1
Leptadapis	1	1	1	2	1	2	0	0	**0**	1	1	1	0	1	1
Adapis	1	0,1	2	2	0	2	0	0	**0**	1	1	1	0	1	1
Caenopithecus	1	1	**0**	1	1	2	**0**	**0**	**0**	1	**0**	**0**	1	1	1
Omomys	1	0	**1**	**0**	**0**	1	1	**1**	**1**	0	1	0	1	**0**	**0**
Tetonius	1	0	3	2	2	**2**	1	**1**	**1**	1	1	0	0	1	1
Altanius	0	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
Altiatlasius	1	**0**	2	2	2	1	1	**0**	1	**0**	1	**0**	1	**0**	1
Pteropus	0	1	1	1	1	1	0	0	0	1	1	0	0	1	1

RESULTS OF PHYLOGENETIC ANALYSIS

Cladistic analyses were executed for both the original and predicted matrices, and the results appear below. Each set of results is given for the preliminary and final analyses prior to giving the next set of results. This will facilitate comparison between the analyses.

Search Results

Preliminary Analysis

Number of trees retained	108
Number of rearrangements tried	1,623,416
Length of shortest tree	12,388 (all 108 trees were this length)
Length of consensus tree	14,393

Final Analysis

Number of trees retained	1
Number of rearrangements tried	182,778
Length of shortest tree	15,618
Length of consensus tree	15,618

Consensus Statistics

Preliminary Analysis

Consistancy index	0.355
Homoplasy index	0.739
Retention index	0.590
Rescaled Consistancy index	0.209

Final Analysis

Consistancy index	0.327
Homoplasy index	0.759
Retention index	0.635
Rescaled Consistancy index	0.207

**Fig. 3.1: Preliminary Analysis
Consensus Cladogram**

Fig. 3.2: Final Analysis
Consensus Cladogram

- ANCESTRAL
- Pronothodectes
- Altanius
- Plesiadapis
- Ignacius
- Phenacolemur
- Tinimomys
- Microsyops
- Saxonella
- Chiromyoides
- Platychoerops
- Picrodus
- Zanycteris
- Pteropus
- Carpodaptes
- Micromomys
- Navajovius
- Omomys
- Tetonius
- Altiatlasius
- Palaechthon
- Cantius
- Notharctus
- Smilodectes
- Europolemur
- Mahgarita
- Caenopithecus
- Microadapis
- Adapis
- Leptadapis
- Pronycticebus
- Copelemur
- Purgatorius
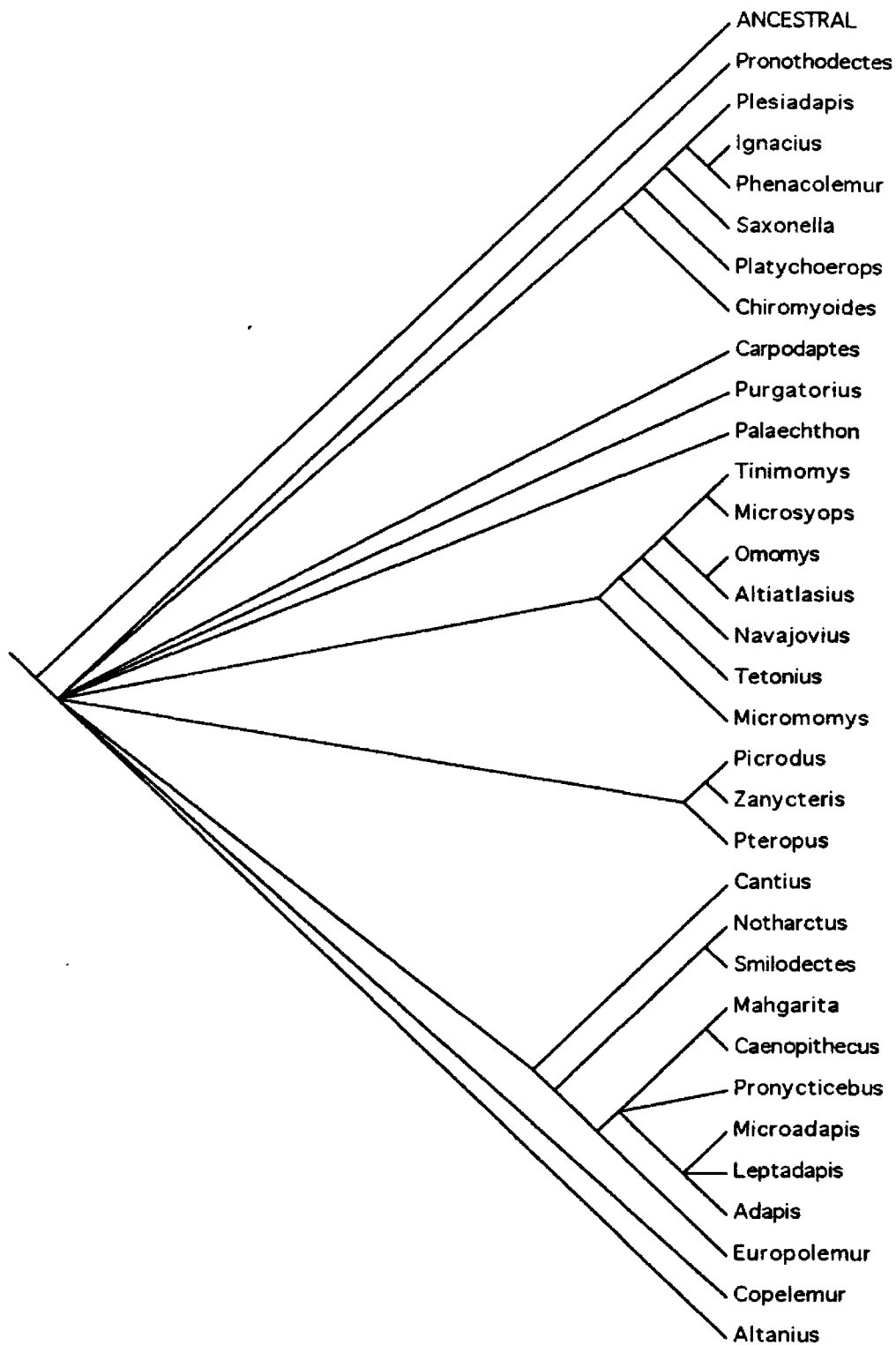
CHAPTER 4
DISCUSSION

Examining the results of the statistical analyses reveals varying degrees of success among the functions used to predict the missing character states. This is evident in the "before function" statistics Wilk's lambda and significance, as well as in the Eigen value, percent of variance, and canonical correlation that accompanies each function. Despite the extreme range of statistical results found among the 127 analyses performed, the 212 individual functions can be analyzed with reference to four types of results. These will be referred to as type 1, type 2, type 3, and type 4 functions.

For the purpose of delineating between the four function types, the discriminating power of the variables prior to the execution of the function is considered to be high if the Wilk's lambda is 0.250 or lower. Those functions with a Wilk's lambda greater than 0.250 are considered to have little discriminating power. The second statistic used to divide the functions into the four types is the significance. A function with a "before function" significance of 0.0500 or less is considered significant. This is to say that the discriminating power of the variables prior to the function's execution has only a 5% chance of occurring randomly due to chance. A function with a "before function" significance greater than 0.0500 is considered insignificant.

Function type one has a high discriminating power with a high significance (< 0.0501). These prove to be the best discriminators and will be discussed in more detail later. Type 2 functions have a high discriminating power but are not statistically significant. Type 3 functions have little "before function" discriminating power but are statistically significant. Type 4 functions possess little discriminating power with little statistical significance. By referring to these four function types, the results of the statistical analyses can be interpreted without referring to each analysis individually.

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The results of the discriminant function analyses express mixed degrees of success in predicting character states effectively. Of the 212 functions executed in 127 analyses, 35 of them were powerfully discriminating, statistically significant, type 1 functions, 65 were type 2 functions, 8 were type 3, and 104 were type 4. The degrees of success become evident through closer examination.

All but two type 1 functions are the first functions of the analysis, and because SPSS-X lists functions from most to least important (SPSS-X, 442; 442), it is understandable that the most significant, best predicting type 1 functions would appear first. The two type 1 functions that are not the first function of the analysis are found in the first and sixth analyses for character 20. In these instances, the "before function" statistics show that, as is the case with the first function, the second functions of these analyses are also type 1, though they possess a slightly lower degree of discriminating power with less significance.

Those first functions, with high degrees of discriminating power and statistical significance, are responsible for over 70% of the variance within the analyses in which they exist. This high percentage of variance is coupled with a relatively high Eigen value and a large canonical correlation. Each of these statistics, in conjunction with the "before function" statistics for the next function, demonstrate little need for following functions. This is to say that those functions following type one functions possess little discriminating power with lower eigen values and less correlation. It is evident that type 1 functions are capable of delineating the majority of variability leaving little need for further functions to be executed.

There are two occasions where type 1 functions do not account for over 70% of the variance, and there is clearly need for following functions in order to delineate between character states. The first of these occurs in character 20, analysis 6, where function one (a type 1 function) accounts for 65.51% of the variance, and the second

function (also type 1) accounts for the remaining 34.49%. The other exception occurs in analysis 2 for character 22 where function 1 (type 1) accounts for 64.27% of the variance and the second (type 2) function accounts for the remaining 35.73% of the variance. These two analyses are important due to the necessity of multiple functions to delineate between groups. However, it must be noted that in this case function 2 has a relatively high significance when compared with other type 2 functions.

Analyses beginning with type 2 functions also tend to show the need for following functions due to the low percentage of variance that these functions account for. However, there are also instances where, following a type 2 function, the necessity for other functions to account for the remaining variance is quite small. As is the case with type 1 functions, type 2 functions tend to account for more of the variance when their "before function" Wilk's lambda is low. This can be seen in character 19, analysis 3. These functions are not considered to be successful first functions of an analysis primarily due to the low significance of their discriminating power. When used as second functions however, they may prove to be beneficial when accounting for the remaining variance despite their failure to pass the pre function chi square test for significance.

Type 3 functions are considered successful due to their statistical significance. Despite their low discriminating power, it is evident that these functions demonstrate the power necessary to account for the majority of the variation in the two analyses for character 2. In these instances, type three functions are the first of two functions accounting for over 70% of the variance. As is the case with most type 1 functions, type 3 functions leave little need for further functions.

Perhaps the least successful of the analyses are those that begin with a type four function. Forty-one analyses begin with type four functions, suggesting that the discriminating characters used for the analyses were unfit for discriminating between

groups. In many cases (e.g.. character 1, analysis 3) type 4 functions prevail where the characters chosen for the analysis do possess a significant discriminating power but the taxon being analyzed does not have all of the desired variables. In these cases, it is clear that the variables available for the analysis (in most cases, dental characters) are not the best discriminators for the character in question (in most cases, postcranial characters) . The other analyses that tend to begin with type 4 functions are those that deal with cranial or post-cranial characters for which the majority of the available (dental) characters are unfit for determining the condition of other characters.

Through this investigation of the various types of functions and their roles as discriminators in the prediction of the character states in question, it becomes clear that some characters are better predictors than are others. For example, those functions which have a statistically high discriminating power are those for which the best predicting variables were present for the analysis. Some analyses show that the best predicting variables have been used in discriminating scores for some taxa, but the absence of those variables in other taxa results in less successful analyses. The analyses used in the prediction of character 1 scores demonstrates this where it is clear that scores pertaining to the number of certain teeth offer high discriminating power to the functions, and their absence leads to insignificant low discriminating values.

The results of the statistical analyses offer mixed signals as to their success. On one hand, those analyses that begin with type 1 functions are successful in creating statistically significant, powerful discriminations of character states. These demonstrate the ability to make statistically significant decisions regarding those characters missing in the fossil record. However, with few exceptions (mentioned previously), this demonstrates that perhaps the same results could have been reached using linear rather than multidimensional models. These few exceptions do, however, demonstrate the advantages of discriminant function analysis in performing morphometric analyses.

Those functions for which the discriminating variables were of little significance demonstrate the shortcomings of canonical discriminant function analysis for determining character states not yet known from the fossil record. While discriminant function analysis possesses the power to derive a score for each analysis, the insignificance of the conclusions renders them only marginally reliable. This does not suggest, however, that other statistical methods would offer more significant results.

The significance of the results does not necessarily guarantee that the predicted scores for any particular taxon are correct. While the actual state for any unknown character can not be positively determined without fossil evidence, some indication of the success of the discriminant function analyses may be detected by examining the placement of each character within the consensus cladogram. By comparing the preliminary analysis, conducted without statistically derived character scores, with the final analysis, which used the complete, character matrix with statistically predicted scores for the missing data, the success of using predicted character states can be evaluated.

P.A.U.P. provides general statistics, which reveal the extent to which the use of predicted character states reduced the number of trees saved during the heuristic tree search. The preliminary analysis tried 1,623,416 different arrangements and retained 108 trees with lengths of 12,388 each. The consensus tree based on these 108 trees produced a tree of length 14,393. This analysis contrasts with the final analysis in which only one tree of length 15,618 was saved. In this examination of statistical character state prediction, it is evident that, by creating a complete character matrix prior to cladistic analysis, the number of most parsimonious trees is drastically reduced.

Differences in the lengths of consensus trees between the preliminary and final analyses creates the illusion that the preliminary, incomplete data set created a better tree due to its shorter length. This difference in tree length, however, is a result of

another possible improvement created by statistically determining character scores prior to the cladistic analysis. In this instance, variation in tree length is the result of differences in resolution of the consensus cladogram. While the preliminary consensus has 56 nodes resulting in a tree length of 14,393, the final analysis possesses 65 nodes for a tree length of 15,618. This increase in tree length can be accounted for by the increase in character changes which accompanies the increase in character states. For example, the consensus cladogram from the preliminary analysis has a tree length of 18,785 if examined under the assumptions produced by the predicted data matrix. In this instance, it becomes clear that the difference in tree lengths relates directly to the number of missing character states present in the preliminary analysis. Because missing character states add no information concerning character state change, the tree length is minimized by their presence.

Other statistics stemming from the consensus cladograms offer further information concerning the differences between the preliminary and final analyses. Consistency indices for the two analyses are relatively similar scoring 0.355 and 0.327 for the preliminary and final analyses respectively. These correspond with homoplasy indices of 0.739 for the preliminary analysis and 0.759 for the final analysis. While the consistency indices are low and the homoplasy indices are high for both analyses, they are quite similar between the two. While the statistical results of the two analyses show little difference, the slightly better indices for the preliminary analysis may lead to the conclusion that the preliminary analysis is more successful due the higher degree of consistency and the lower percentage of homoplasy. However, this may not be the case.

Because unknown data are not figured into the consistency and homoplasy indices, scores for these statistics in the preliminary analysis are based on many fewer character changes than is true for the final analysis. The fact that the final analysis uses 348 character states that were missing during the preliminary analysis offers

another reason for the slightly lower consistency index and slightly higher homoplasy index of the final analysis consensus cladogram. With so many more character states present, the chance of homoplasy increases dramatically. This is due to the increased number of conflicting character state changes that do not exist with large amounts of missing data.

The statistics accompanying the two analyses demonstrate the effectiveness of applying a complete data set to cladistic analysis for the purpose of reducing the number of trees saved during a heuristic tree search. Additionally, differences in the consistency and homoplasy indices are explainable by realizing the increased number of possible character changes which accompanies fewer missing data. However, the effect of statistically determined character states can best be seen through close examination of the consensus cladograms.

One glance at the consensus cladograms confirms the hypothesis that more resolution results from the utilization of a more complete character matrix. Simply counting the nodes demonstrates that the final analysis, with 65 nodes, yields a more refined consensus than does the incomplete data set used in the preliminary analysis. Because each of the nodes represents a common ancestor between two lineages, the increase in nodes can be interpreted as an increase in the definition allotted by the complete character matrix used in the final analysis. For example, the preliminary analysis shows lack of resolution where *Copelemur, Altanius, Palaechthon, Purgatorius,* and *Carpodaptes* all share node 54. The corresponding node (64) in the final analysis designates a split between one taxon, *Purgatorius,* and the rest of the taxa used in the analysis. This demonstrates the ability of the complete data matrix to further resolve the relationships between *Copelemur, Altanius, Palaechthon, Carpodaptes,* and the rest of the genera. However, this increase in resolution does not necessarily infer an accurate account of archontan evolution.

In order to interpret the results of the final analysis as valuable to the understanding of early archontan evolution, it is necessary to demonstrate the extent to which the positioning of the well known taxa is altered by incorporating quantitatively determined character states into the analysis. Because the less known characters were weighted less in the analyses, the preliminary consensus should possess the generality expected from lack of a complete character matrix without terribly obscuring the placement of the well known taxa. This allows for a comparison, through which the extent that the final consensus retains the accuracy of well know taxa can be evaluated.

Generally, the positioning of those taxa for which resolution could be determined in the preliminary analysis is preserved in the final analysis. This can be seen in the close affinity between *Plesiadapis* and the Paromomyidae *Ignacius* and *Phenacolemur*, the ancestral positioning of *Purgatorius*, the primitive condition of *Palaechthon* when compared with the position of other microsyopids, the close affinity of the picrodonts with the outgroup *Pteropus*, the close positioning of the omomyids *Altiatlasius*, *Tetonius*, and *Omomys*, and the clade containing the family Adapidae. Certainly there are some differences concerning the exact placement of some of the genera, but the statistically determined data set does succeed in preserving the general placement of those taxa for

The moderate success of the discriminant analyses in creating statistically significant functions in conjunction with the outstanding success of the complete character matrix in reducing the number of equally parsimonious trees and improving the resolution of the consensus cladogram leaves questions regarding the accuracy of the final analysis. Of predominant concern is the accuracy of the consensus cladogram, considering the likelihood of inaccurate character state determination. Because many of the functions used to determine the states used in the phylogenetic analysis are not

statistically significant, the scores produced by these analyses may not be accurate. This could lead to the misplacement of certain taxa despite the fact that the positions of well known taxa are retained.

In order to assess this problem, the results of a consensus cladogram must be observed in relation to the significance and discriminating power of the variables used to derive missing character scores. By examining the character changes, occurrences of homoplasy, and any statistically derived scores which may correspond to these changes, the consensus cladogram can be analyzed in reference to what has been hypothesized about primate origins. In general, the success of the statistical analyses, the statistically derived character states, and the imposed taxonomic position of each taxon makes isolating possible inaccuracy in the consensus cladogram possible.

When the occurrence of homoplasy, in the forms of convergence and reversal, is examined in reference to the occurrence of statistically determined character states, a general pattern is revealed. The occurrence of predicted character states directly associated with homoplasy increases dramatically from the dental and mandibular characters to the cranial and post-cranial characters. Characters one through eighteen (those characters dealing with dental and mandibular traits) have a total of seven occurrences of homoplasy that are directly associated with statistically derived scores. The remaining fourteen characters (those dealing with cranial and post-cranial traits) show correlation between predicted character states and fifty occurrences of homoplasy.

This dramatic increase in the frequency of homoplasy can be explained through the methods used in performing this analysis. First, the dental characteristics used in this analysis were present for more taxa than were the cranial and post-cranial characters. Therefore, the occurrence of homoplasy among statistically determined scores may simply be a result of the increase in the number of predicted states required for cranial and postcranial traits. Additionally, because there were fewer missing

character states for the dental characters, weights were greater for characters one through eighteen. This would cause P.A.U.P. to assign these characters more importance in creating the cladogram, thus avoiding homoplasy amongst these highly weighted characters. The final reason for the significant increase in homoplasy and statistically derived scores is the significance of the functions used to derive the scores. Because there is greater correlation between dental characters and other dental characters than there is between dental characters and cranial and post-cranial characters, the insignificance of the functions in which dental traits were used as the discriminating variables for cranial and post-cranial traits may cause more "incorrect" predictions thus leading to more occurrences of homoplasy in the consensus cladogram.

On a more specific level, the questionable placement of certain genera within the cladogram can be traced to insignificant functions and the occurrence of homoplasy. To begin, the genus *Altanius* is grouped with *Pronothodectes* rather than the omomyids. If *Altanius* is actually an omomyid as has been suggested (Szalay and Delson, 1979;223), then the cladistic analysis should recognize this. However, this clearly did not happen. The inconsistency between what is known about *Altanius* and its affinities with the family Omomyidae can be traced to the results of the statistical analyses used to determine the missing character states for the genus.

Tracing the occurrence of homoplasy that directly involves *Altanius* exposes possible errors in the statistical analyses performed to designate certain character states. For the case of *Altanius*, nine occurrences of homoplasy correspond with statistically determined character states. Eight of these occurrences of homoplasy are reversals in which the assigned character state is more primitive than those of the omomyids *Tetonius*, *Omomys*, and *Altiatlasius*, and all of these are the result of either insignificant functions or significant functions with little discriminating power. In fact, the majority of the character states assigned to *Altanius* are the result of unsuccessful discriminant

functions. This is primarily due to the fact that few character states were present for *Altanius* at the onset of this research leaving only poor discriminating variables for analysis. Additionally, those character states that were known were not sufficient for discerning between *Altanius* and certain genera of Plesiadapiformes. This resulted in statistical character state predictions that mirrored those of the plesiadapids, of which there were more genera for comparison.

Other elements of inconsistency can be traced through the occurrence of taxonomic placement based on scores generated by insignificant or weak discriminant functions. While they don't necessarily agree, published phylogenies concerning Plesiadapiformes show clean separations between lineages of Plesiadapidae, Saxonellidae, Corpolestidae, Microsyopidae Paromomyidae, and Primates (see Beard, 1993 and MacPhee, Cartmill, and Gingerich, 1983). Although these trees delineate between taxa on the family level rather than the genus level, it would seem appropriate that the genera belonging to these families would be grouped more closely than they would with other genera. While some members of certain families are grouped closely, others clearly are not.

Among those genera whose placement in the final cladogram is in agreement with what is commonly hypothesized about their family relationships are the Paromomyidae, in which *Phenacolemur* and *Ignacius* share a last common ancestor, the picrodonts *Picrodus* and *Zanycteris*, and the Adapidae. Because only one genus from each of the families Saxonellidae and Carpolestidae were used in this analysis, it is difficult to discern discrepancies among those taxa. It has been suggested that these families share a common ancestor (Beard, 1993: 132), but this result waas not obtained in this analysis. This leaves the families Plesiadapidae and Microsyopidae containing the majority of the genera that are not grouped at the family level.

The first observable problem with the positioning of Plesiadapid genera is the positioning of *Pronothodectes*. With the removal of *Altanius* from this branch (a possibility previously discussed), the positioning of *Pronothodectes* reflects what is commonly hypothesized about the genus being a good ancestral candidate to other members of the family Plesiadapidae. However, the positioning of this genus in the final cladogram suggests that it may be ancestral not only to Plesiadapidae but to members of the families Paromomyidae, Microsyopidae, and Saxonellidae. This is a good possibility when the primitive character states of *Pronothodectes* (Szalay and Delson, 1979; 75) are considered along with the fact that only one occurrence of homoplasy (a convergence) coincides with a predicted character state. This leaves the conclusion that the microsyopids *Tinimomys* and *Microsyops*, and the paromomyids *Ignacius* and *Phenacolemur* may be misplaced in the final cladogram.

Only one occurrence of homoplasy that is related to predicted characters for either of the paromomyids exists. This occurs as a convergence in character 21 "snout length" where *Phenacolemur* is predicted to have a short snout by a strong type one function. This converges with predicted states for *Platychoerops*, the *Picrodus/ Zanycteris* node, *Altiatlasius*, and some of the adapids. The placement of the paromomyids is of little surprise considering their close placement with Plesiadapids in other analyses (see Beard, 1993 and MacPhee et.al., 1983). Because the family Paromomyidae appears to have derived from the plesiadapids, there is little concern about the placement of other members of Plesiadapidae, for they are grouped together with the paromomyids, simply branching from them at the rise of the *Plesiadapis* lineage.

Members of the family Plesiadapidae are still separated by a node that contains two members of the family Microsyopidae *Microsyops* and *Tinimomys*. *Tinimomys* shows homoplasy directly related to two statistically derived character states. One of these is a reversal of character 27, and the other is a convergence at character 28 involving the

node from which *Tinimomys* and *Microsyops* split. *Microsyops* is involved in three other convergences which correspond to predicted character states.

The positioning of *Tinimomys* may support Beard's (1993) hypothesis that *Tinimomys* and *Micromomys* are not members of the family Microsyopidae but rather a new family Micromomidae. This family is thought to be relatively close to Plesiadapidae phylogenetically (Beard, 1993; 132). If this is the case, the results of this analysis may closely reflect the actual positioning of *Tinimomys*, in which case, the positioning of *Micromomys* with the microsyopid *Navajovius* should be questioned. *Micromomys* has four statistically determined character states which account for homoplasy. Of these, three are scores derived from insignificant functions. In addition, nine of the statistically determined character states for *Micromomys* were derived using insignificant variables, eight of which were responsible for different scores between *Micromomys* and *Tinimomys*. Through the tracing of character changes and statistical prediction of character states, some explanation regarding the positions of *Tinimomys* and *Microsyops* may be reached. The homoplasy associated with scores derived from insignificant functions offer some explanation regarding the possible misplacement of these taxa.

If *Micromomys* and *Tinimomys* are members of the family Micromomidae, then only three microsyopids *Microsyops*, *Navajovius*, and *Palaechthon* are left separated in the final consensus cladogram. Additionally, this analysis supports Scale's hypothesis regarding the placement of *Palaechthon* in the family Palaechthonidae (Beard, 1993; 145) by positioning this genus as the most primitive of the Plesiadapiformes. This leaves *Navajovius* and *Microsyops* as the only two microsyopids in need of closer examination.

As previously stated, *Microsyops* has four occurrences of homoplasy associated with statistically determined character states. *Navajovius* has three occurrences of homoplasy associated with predicted scores, two of which had little significance. The

comparable accounts of homoplasy and types of functions used in the prediction of scores for both *Microsyops* and *Navajovius* makes it difficult to draw any conclusions regarding possible misplacement of either genus of Microsyopidae.

The results of this analysis suggest that the omomyids *Altiatlasius, Tetonius,* and *Omomys* are closely related to the microsyopid *Navajovius*. The fact that these true primates are not grouped with the adapines and notharctines is not surprising but questionable. This type of arrangement is not surprising due to dental similarities between the primitive *Altiatlasius* and some members of the family Microsyopidae (Sigé et. al., 1990:1). Additionally, it has been proposed by Gingerich that some forms of Plesiadapiformes show dental and cranial similarities with tarsioids such as *Tetonius* suggesting phylogenetic relation between plesiadapids and omomyids (Gingerich, 1986:37-38). It has been suggested, however, that linking the omomyids with microsyopids, as is the case in this analysis, causes too many convergences between the omomyids and the adapids (Szalay, 1977:16). Again the placement of the omomyids among the microsyopids can be examined within the context of predicted states.

The omomyid lineage begins with *Altiatlasius* representing the most primitive of the three genera included within this clade. Because the majority of characters for this genus are statistically derived, and of these, few are the result of significant functions, it appears as though character states for *Altiatlasius* were statistically designated due to the existing similarities between itself, the other omomyids, and the genera *Navajovius* and *Micromomys*. Therefore, it is possible that the positioning of the omomyids may be the result of characteristics common between the omomyids *Tetonius* and *Omomys*, and *Micromomys,* and *Navajovius* linked by the statistically predicted scores of *Altiatlasius*. It is also possible that the dependency on dental traits for prediction of cranial and post-cranial character states linked the omomyids with the microsyopids due to dental similarities.

Phylogenetic relationships among the adapid primates are depicted in a form quite amenable to proposed relations between the Adapidae (See Szalay and Delson, 1979 and Fleagle, 1988) with few exceptions. Among the Notharctinae and the Adapinae, the only genus misplaced from its sub-family is *Europolemur*, but discrepancies are traceable through predicted character states. For example, despite the fact that the degree of post-orbital bar formation for all known adapid skulls is complete (suggesting the presence of a complete bony ring around the orbit), the predicted scores for *Europolemur*, *Cantius*, and *Copelemur* are "1" indicating partial closure. The primitive characteristics of *Copelemur* and *Cantius*, in conjunction with the predicted degree of post-orbital closure with *Europolemur*, places *Europolemur* within the more primitive sub-family Notharctinae.

The positioning of *Copelemur* as a possible ancestor to all later adapids (both notharctines and adapines) supports the fact that it was once grouped with *Cantius* under the genus *Pelycodus*. While *Cantius* was thought to be a candidate for the Adapidae ancestor (Rose and Walker, 1985:74), the close similarities between this genus and *Copelemur* in association with the dispersal of predicted character states, creates a situation where *Copelemur* is ancestral to all later Adapidae and *Cantius* is positioned as a possible ancestor to later notharctines.

By examining the use of statistically determined character scores and the placement in the cladogram that resulted from using these scores, potential errors in the consensus cladogram were detected. Because the statistical methods used in determining character states produced results with varying degrees of significance and discriminating power, questionable placement of certain taxa can be either supported or rejected based on the success of the functions used to derive missing scores. While no taxonomic relations were completely resolved using these methods, the statements made regarding genus placement and the characters used to determine that placement

reflected the statistical significance of the characters used in the analysis. Thus, a

model was created through which future fossil discoveries can be compared.

CHAPTER 5
CONCLUSIONS

Applying discriminant function analyses to the cladistic analysis of early Tertiary archontan evolution produces mixed results. The mixed nature of the results can be seen in the functions used to discern between character states as well as in the consensus cladograms from both the original analysis, in which predicted character states were not used, and in the final analysis, in which the complete set of statistically predicted character states was implemented. Through the examination of these results, avenues for future research are opened. This includes methodological considerations as well as applications to other areas of paleontology.

The results of the functions offer important information with regards to character choice, the effectiveness of discriminant functions, and the ways in which certain character state predictions are reflected by changes in the consensus cladogram. It is apparent that certain characters and character complexes are better for discerning between groups. This is evident in the "before function" statistics and the probability and accuracy accompanying each analysis. The Wilk's lambda and corresponding chi square and significance offer valuable information about the variables used to discriminate between groups. This offered insight into the accuracy of the predicted states.

Comparison of the consensus Cladograms from the preliminary and final analyses supports the hypotheses set forth at the onset of this investigation. It is apparent that the statistically predicted character matrix improves the resolution of the consensus cladogram while maintaining the general phylogenetic placements of well known genera. While there are slight differences between the relationships of some well

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known taxa, this is generally the result of more resolution and does not compromise the accuracy of the Method.

The improved resolution is clear in the reduction of polytomous branches. This improved resolution offers the opportunity to investigate the positioning of poorly represented taxa through tracing predicted character states and their changes. This becomes increasingly effective when trying to determine the source of contradiction between what is hypothesized about relationships in the literature and the positioning of specific taxa within the final cladogram. By examining the significance of the functions used to predict character states, answers regarding the likelihood of misplaced taxa can be reached.

Despite the high number of statistically insignificant discriminant functions used in this analysis, results show that applying morphometric techniques to intertaxonomic investigation can be useful for predicting missing morphological data. There are, however, limitations that were observed during this analysis. These limitations are primarily a reflection of methodologies that should be addressed prior to conducting future research using these methods.

Perhaps the biggest problem encountered was the tremendous lack of data. While the discriminant function analysis was powerful enough to produce scores for each character in question, in many cases, it could not do so with much statistical significance. This can be attributed to the enormous amounts of missing data in the data set. Possible resolutions to this problem of missing data include using only those data that are present for the majority of the taxa being analyzed, examining phylogenetic relations on the family level rather than the generic level, and incorporating character states from probable living descendants. There are problems with each of these approaches as well.

Since investigating Early Tertiary archontan evolution involves extensive amounts of missing data, reducing the number of characters used in the analysis to only those known for a majority of the taxa being analyzed would result in the use of only dental characters. This would compromise the existing knowledge for those genera that are well represented and would severely limit the number of distinct anatomical systems used in phylogenetic analysis.

Family level examinations could be accomplished with more success in the statistical prediction phase, but would pose great limitations when examining Early Tertiary archontans. Chapter 4 discussed the problems with the family Microsyopidae, where there is uncertainty as to what genus belongs within a given family. This could cause problems by including genera that do not belong, thus offering a false sense of relationship not only between members of the family but between families as well. This technique could prove more useful in research examining the relations of later primates whose family affinities are more certain.

The only living archontan used in this analysis was the outgroup *Pteropus*. *Pteropus* was used as an outgroup because it was a non-primate archontan and because of its dental similarities with the picrodonts. While more living genera could have been used, I chose not to use them, primarily because doing so would introduce the assumption that archontans and primates living 45 to 65 million years ago were generally the same anatomically as they are today. However, using living examples to increase the numbers of character states through which to predict missing data may have its place with more recent taxa.

Aside from the problems of large amounts of missing data, another methodological consideration should be discussed. The discriminant functions used in this analysis were constructed using the DIRECT method. This method enters all discriminating variables concurrently, using all variables in calculating the function.

Therefore, those variables omitted were those that did not pass tolerance when used in conjunction with all other discriminating variables. This method may not have been as affective as other techniques. While the direct method did produce scores for each analysis, it did so with many instances of low discriminating power and little significance. Stepwise methods, such as WILK'S, may have produced better results. By trying each variable independently, this technique may have retained those variables with the most discriminating power (resulting in a smaller Wilk's lambda), rather than selecting all variables at the risk of some of the "better predictors" failing tolerance.

Another methodological consideration for future research in the area of statistical character state recognition and its application to cladistic analysis is the problem of character weighting. While weighting was necessary in the preliminary analysis in order to insure that missing characters did not skew the phylogenetic positioning of the well known taxa, it may have hindered the results of the final cladistic analysis. Because dental characters were the best represented of the characters used, these received greater weights. This allowed for the fact that the majority of the cranial and post-cranial characters were statistically derived. However, because the dental characters were mostly used in predicting the cranial and post-cranial character states, a double weighting (in a sense) occurred. Because the predicted scores were a reflection of the dental scores, the dental scores received a disproportionate amount of weight. Not only were they given more weight in the analysis, but they were also responsible for the character states that they were used to predict.

This use of unequal weights caused problems in interpreting the occurrences of homoplasy in the final consensus cladogram. There were clearly more cases of homoplasy among the cranial and post-cranial characters, but it was difficult to locate the cause. This increase in the amount of homoplasy may have been caused by the greater number of predicted scores among the cranial and post-cranial characters.

However, it may have been the result of unequal weighting. Because the dental characters were weighted more heavily, the analysis may have put more emphasis on those characters thus assuring minimal amounts of homoplasy among them. Future attempts at this type of analysis should incorporate methods to protect the positions of well known taxa in the preliminary analysis while taking into consideration methods for equaling the weights between characters in the final analysis.

Despite the limited degree of success, this analysis supports the original hypotheses. The number of trees retained during the heuristic search methods was held to a minimum resulting in fewer best trees and more resolution in the consensus. This was accomplished without compromising the positions of well known taxa. In addition, by examining the significance of functions used to determine missing character states, questionable placements of taxa could be addressed. Through the use of statistically predicted character states, a model was developed through which future discoveries pertaining to primate origins can be compared, and a method was introduced for addressing other avenues of primate origins and evolution.

Appendix A
Source List of Character States

When possible, all character states were scored according to Szalay and Delson's

1979 book <u>Evolutionary History of the Primates</u>. The sources listed here refer only to

those characters for which scores were not found in the forementioned volume.

Pronothodectes
Character 10- Fox, 1990

Purgatoris
Characters 8, 10, and 18- Clemens, 1974

Navajovius
Characters 20, 25, and 30- Erwin, 1995

Microsyops
All characters- Szalay, 1969

Ignacius
Characters 19 and 22- Shipman, 1990

Altiatlasiuis
All characters- Sigé et.al., 1990

Pteropus
All characters- Mounted Specimine, University of Montana Bird and Mammal
Museum

APPENDIX B
CHARACTER CHANGE LISTS

Preliminary Analysis

Character	CI	Steps	Changes
1.	0.667	1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 0 Purgatorius
		1	node_41 1 --> 2 node_39
2.	0.333	1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 2 node_38
		1	node_34 2 ==> 1 Ignacius
		1	node_54 1 ==> 0 Purgatorius
		1	node_41 1 ==> 2 node_39
		1	node_48 1 ==> 2 Caenopithecus
3.	0.500	1	node_54 0 ==> 1 node_38
		1	node_35 1 ==> 0 Plesiadapis
		1	Platychoerops 1 --> 01 (within terminal)
		1	node_41 0 ==> 1 node_39
4.	0.250	1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 0 Purgatorius
		1	node_41 1 --> 0 node_39
		1	node_42 1 ==> 2 Navajovius
		1	node_46 1 ==> 2 Pteropus
		1	node_54 1 ==> 0 node_53
		1	node_50 0 ==> 1 node_48
		1	node_54 1 ==> 0 Copelemur
5.	0.357	1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 2 node_38
		1	Plesiadapis 2 --> 12 (within terminal)
		1	node_34 2 ==> 3 Phenacolemur
		1	node_54 1 ==> 2 Carpodaptes
		1	node_54 1 ==> 0 Purgatorius
		1	node_54 1 --> 2 node_44
		1	node_42 2 --> 1 node_41
		1	Tetonius 2 --> 12 (within terminal)
		1	node_54 1 --> 2 node_46
		1	node_45 2 --> 1 Zanycteris
		1	node_54 1 ==> 0 node_53
		1	node_50 0 ==> 1 node_48
		1	node_54 1 ==> 0 Copelemur
6.	0.200	1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 2 Pronothodectes
		1	node_54 1 ==> 2 node_38
		1	node_54 1 ==> 0 Purgatorius
		1	node_42 1 ==> 2 node_41
		1	node_46 1 ==> 0 Pteropus
		1	node_53 1 --> 0 node_52
		1	node_47 0 --> 1 Smilodectes
		1	node_48 0 ==> 1 Caenopithecus

Character	CI	Steps	Changes
		1	node_49 0 ==> 1 Adapis
7.	0.286	1	node_55 1 --> 2 node_54
		1	node_54 2 --> 1 Purgatorius
		1	node_54 2 --> 1 Palaechthon
		1	node_46 2 --> 1 Pteropus
		2	node_54 2 ==> 0 node_53
		1	node_51 0 ==> 1 node_50
8.	0.250	1	node_54 1 ==> 2 Pronothodectes
		1	node_35 1 ==> 0 node_34
		1	node_38 1 ==> 2 Chiromyoides
		1	node_54 1 ==> 2 Purgatorius
		1	node_54 1 ==> 0 Palaechthon
		1	node_44 1 ==> 0 node_43
		1	node_39 0 ==> 1 Tinimomys
		1	node_54 1 ==> 0 node_46
		1	node_52 1 ==> 0 node_47
		1	node_49 1 ==> 0 Microadapis
		1	Leptadapis 1 --> 01 (within terminal)
		1	node_54 1 ==> 2 Altanius
9.	0.688	1	Pronothodectes 2 --> 23 (within terminal)
		1	Saxonella 2 --> 02 (within terminal)
		1	node_37 2 ==> 3 Platychoerops
		1	node_54 2 ==> 0 Carpodaptes
		1	Purgatorius 2 --> 23 (within terminal)
		1	Palaechthon 2 --> 23 (within terminal)
		1	node_54 2 ==> 3 node_44
		1	Microsyops 3 --> 34 (within terminal)
		1	node_41 3 ==> 2 node_40
		1	Omomys 2 --> 12 (within terminal)
		1	Tetonius 3 --> 13 (within terminal)
		1	node_46 2 ==> 1 Pteropus
		1	node_52 2 --> 1 node_51
		1	node_50 1 --> 2 node_48
		1	node_50 1 ==> 4 node_49
		1	node_49 4 ==> 3 Microadapis
10.	0.214	1	node_55 0 ==> 1 node_54
		1	node_38 1 ==> 0 node_37
		1	node_38 1 ==> 2 Chiromyoides
		2	node_54 1 ==> 3 Purgatorius
		1	node_54 1 --> 2 node_44
		1	node_43 2 --> 1 node_42
		1	node_41 1 --> 2 node_40
		1	node_43 2 ==> 3 Tetonius
		1	node_54 1 --> 0 node_46
		1	node_45 0 --> 1 Picrodus
		1	node_47 1 ==> 2 Smilodectes
		2	node_51 1 ==> 3 node_50
11.	0.273	2	node_55 0 ==> 2 node_54
		2	node_54 2 ==> 0 Pronothodectes
		2	node_54 2 ==> 0 node_38

Character	CI	Steps	Changes
		1	node_37 0 --> 1 node_36
		1	node_36 1 ==> 2 node_35
		2	node_54 2 ==> 0 node_46
		1	node_53 2 ==> 3 node_52
12.	0.250	1	node_37 0 --> 1 node_36
		1	node_35 1 --> 0 Plesiadapis
		1	node_43 0 ==> 1 node_42
		1	node_52 0 ==> 1 node_51
13.	0.500	1	Plesiadapis 0 --> 01 (within terminal)
		1	node_37 0 ==> 1 Platychoerops
		1	node_46 0 ==> 1 node_45
		1	node_54 0 ==> 1 node_53
14.	0.167	1	node_54 0 ==> 1 node_38
		1	node_34 1 ==> 0 Ignacius
		1	node_36 1 ==> 0 Saxonella
		1	node_39 0 ==> 1 Microsyops
		1	node_54 0 ==> 1 node_53
		1	node_50 1 ==> 0 Pronycticebus
15.	0.400	1	node_35 0 ==> 1 node_34
		1	node_46 0 ==> 1 Pteropus
		1	node_52 0 ==> 1 node_51
		1	node_50 1 ==> 0 Pronycticebus
		1	node_50 1 ==> 2 node_49
16.	0.250	1	node_36 0 ==> 1 node_35
		1	node_54 0 ==> 1 Carpodaptes
		1	node_54 0 ==> 1 Purgatorius
		1	node_54 0 ==> 1 Palaechthon
		1	node_39 0 ==> 1 Tinimomys
		1	node_54 0 --> 1 node_53
		1	node_52 1 ==> 2 node_47
		1	node_52 1 --> 0 node_51
17.	0.400	1	node_54 0 ==> 1 Purgatorius
		1	node_54 0 ==> 1 node_44
		1	node_39 1 ==> 0 Microsyops
		1	node_53 0 ==> 1 node_52
		1	Notharctus 1 --> 01 (within terminal)
18.	0.333	1	node_46 0 ==> 1 Pteropus
		1	node_53 0 --> 1 node_52
		1	node_47 1 --> 0 Smilodectes
		1	node_49 1 --> 0 Microadapis
		1	Adapis 1 --> 01 (within terminal)
		1	node_54 0 ==> 1 Copelemur
19.	0.375	1	node_55 0 ==> 1 node_54
		1	node_35 1 ==> 0 Plesiadapis
		1	node_43 1 --> 0 node_42
		2	node_43 1 ==> 3 Tetonius
		1	node_52 1 ==> 2 node_47
		1	node_47 2 ==> 3 Smilodectes
		1	node_49 1 ==> 2 Adapis
20.	0.333	1	node_55 0 ==> 1 node_54

Character	CI	Steps	Changes
		1	node_54 1 --> 0 node_38
		1	node_54 1 ==> 0 Carpodaptes
		1	node_42 1 ==> 0 Navajovius
		1	node_43 1 ==> 2 Tetonius
		1	node_54 1 --> 2 node_53
21.	0.400	1	node_55 0 ==> 1 node_54
		1	node_35 1 ==> 0 Plesiadapis
		1	node_43 1 ==> 2 Tetonius
		1	node_52 1 ==> 2 node_47
		1	node_49 1 ==> 0 Adapis
22.	0.667	1	node_55 0 ==> 1 node_54
		1	node_34 1 ==> 2 Phenacolemur
		1	node_54 1 --> 2 node_53
23.	0.333	1	node_54 0 --> 1 node_44
		1	node_46 0 --> 1 node_45
		1	node_47 0 ==> 1 Smilodectes
24.	0.500	1	node_35 0 ==> 1 Plesiadapis
		1	node_54 0 --> 1 node_44
25.	1.000	1	node_54 0 --> 1 node_38
26.	0.500	1	node_55 0 --> 1 node_54
		1	node_54 1 --> 0 node_38
27.	0.333	1	node_55 0 ==> 1 node_54
		1	node_35 1 ==> 0 Plesiadapis
		1	node_53 1 ==> 0 Cantius
28.	1.000	1	node_54 0 --> 1 node_53
29.	1.000	1	node_54 0 --> 1 node_38
30.	0.500	1	node_55 0 --> 1 node_54
		1	node_54 1 --> 0 node_38
31.	0.500	1	node_55 0 --> 1 node_54
		1	node_54 1 --> 0 node_38

Final Analysis

Character	CI	Steps	Changes
1.	0.667	1	node_64 0 ==> 1 node_63
		1	node_34 1 ==> 0 Altanius
		1	node_37 1 ==> 2 Microsyops
2.	0.400	1	node_64 0 ==> 1 node_63
		1	node_34 1 ==> 0 Altanius
		1	node_42 1 ==> 2 node_41
		1	node_35 2 ==> 1 Ignacius
		1	node_56 1 ==> 2 Caenopithecus
3.	0.667	1	node_42 0 --> 1 node_41
		1	node_36 1 ==> 0 Plesiadapis
		1	Platychoerops 1 --> 01 (within terminal)
4.	0.333	1	node_63 0 ==> 1 node_52
		1	node_38 1 ==> 0 node_37
		1	node_44 1 ==> 2 Pteropus
		1	node_50 1 ==> 2 node_49
		1	node_47 2 ==> 1 node_46
		1	node_59 0 ==> 1 node_56
5.	0.500	1	node_63 0 ==> 1 node_52
		1	node_52 1 ==> 2 node_51
		1	node_34 2 ==> 1 Pronothodectes
		1	Plesiadapis 2 --> 12 (within terminal)
		1	node_35 2 ==> 3 Phenacolemur
		1	node_38 2 ==> 1 node_37
		1	node_43 2 ==> 1 Zanycteris
		1	node_48 2 ==> 1 node_47
		1	Tetonius 1 --> 12 (within terminal)
		1	node_59 0 ==> 1 node_56
6.	0.222	1	node_63 0 ==> 1 node_52
		1	node_45 1 ==> 2 node_42
		1	node_44 1 ==> 0 Pteropus
		1	node_46 1 ==> 2 Omomys
		1	node_47 1 ==> 0 Altiatlasius
		1	node_55 0 --> 1 node_54
		1	node_53 1 --> 0 Notharctus
		1	node_56 0 ==> 1 Caenopithecus
		1	node_57 0 ==> 1 Adapis
7.	0.667	1	node_52 1 ==> 2 node_51
		1	node_44 2 ==> 1 Pteropus
		1	node_61 1 ==> 0 node_55
8.	0.273	1	node_42 1 ==> 2 node_34
		1	node_36 1 ==> 0 node_35
		1	node_37 1 ==> 0 Microsyops
		1	node_40 1 ==> 2 Chiromyoides
		1	node_45 1 ==> 0 node_44
		1	node_49 1 ==> 0 node_48
		1	node_52 1 ==> 0 Palaechthon
		1	node_54 1 ==> 0 node_53

Character	CI	Steps	Changes
		1	node_57 1 ==> 0 Microadapis
		1	Leptadapis 1 --> 01 (within terminal)
		1	node_64 1 ==> 2 Purgatorius
9	0.647	1	Pronothodectes 2 --> 23 (within terminal)
		1	node_38 2 ==> 3 node_37
		1	Microsyops 3 --> 34 (within terminal)
		1	Saxonella 2 --> 02 (within terminal)
		1	node_41 2 ==> 3 Platychoerops
		1	node_44 2 ==> 1 Pteropus
		1	node_51 2 --> 0 node_50
		1	node_50 0 --> 3 node_49
		1	node_48 3 ==> 1 node_47
		1	Omomys 1 --> 12 (within terminal)
		1	Tetonius 1 --> 13 (within terminal)
		1	Palaechthon 2 --> 23 (within terminal)
		1	node_55 2 ==> 1 Europolemur
		1	node_59 2 ==> 4 node_58
		1	node_57 4 ==> 3 Microadapis
		1	node_60 2 ==> 1 Pronycticebus
		1	Purgatorius 2 --> 23 (within terminal)
10.	0.167	1	node_65 0 ==> 1 node_64
		1	node_51 1 --> 0 node_45
		1	node_42 0 --> 1 node_34
		1	node_38 0 --> 1 node_37
		2	node_40 0 ==> 2 Chiromyoides
		1	node_43 0 --> 1 Picrodus
		1	node_49 1 ==> 2 Micromomys
		1	node_47 1 ==> 2 node_46
		1	node_46 2 ==> 3 Tetonius
		1	node_54 1 ==> 0 Cantius
		1	node_53 1 ==> 2 Smilodectes
		2	node_61 1 ==> 3 node_60
		2	node_56 3 ==> 1 Caenopithecus
		2	node_64 1 ==> 3 Purgatorius
11.	0.375	2	node_65 0 ==> 2 node_64
		2	node_51 2 ==> 0 node_45
		1	node_40 0 ==> 1 node_39
		1	node_39 1 ==> 2 node_38
		1	node_62 2 ==> 3 node_61
		1	node_54 3 ==> 2 Cantius
12.	0.167	1	node_41 0 ==> 1 node_40
		1	node_36 1 ==> 0 Plesiadapis
		1	node_50 0 ==> 1 node_49
		1	node_46 1 ==> 0 Tetonius
		1	node_62 0 --> 1 node_61
		1	node_55 1 --> 0 node_54
13.	0.500	1	Plesiadapis 0 --> 01 (within terminal)
		1	node_41 0 ==> 1 Platychoerops
		1	node_44 0 ==> 1 node_43
		1	node_63 0 ==> 1 node_62

Character	CI	Steps	Changes
14.	0.167	1	node_42 0 ==> 1 node_41
		1	node_35 1 ==> 0 Ignacius
		1	node_37 1 ==> 0 Tinimomys
		1	node_39 1 ==> 0 Saxonella
		1	node_62 0 --> 1 node_61
		1	node_60 1 --> 0 Pronycticebus
15.	0.333	1	node_36 0 ==> 1 node_35
		1	node_39 0 ==> 1 Saxonella
		1	node_44 0 ==> 1 Pteropus
		1	node_55 0 ==> 1 Europolemur
		1	node_60 0 ==> 1 node_59
		1	node_59 1 ==> 2 node_58
16.	0.250	1	node_34 0 ==> 1 Altanius
		1	node_39 0 --> 1 node_38
		1	node_37 1 --> 0 Microsyops
		1	node_50 0 ==> 1 Carpodaptes
		1	node_52 0 ==> 1 Palaechthon
		1	node_55 0 ==> 1 node_54
		1	node_54 1 ==> 2 node_53
		1	node_64 0 ==> 1 Purgatorius
17.	0.333	1	node_65 0 --> 1 node_64
		1	node_63 1 --> 0 node_52
		1	node_37 0 ==> 1 Tinimomys
		1	node_50 0 ==> 1 node_49
		1	node_54 1 ==> 0 Cantius
		1	Notharctus 1 --> 01 (within terminal)
18.	0.333	1	node_44 0 ==> 1 Pteropus
		1	node_63 0 ==> 1 node_62
		1	node_55 1 --> 0 node_54
		1	node_53 0 --> 1 Notharctus
		1	node_58 1 --> 0 node_57
		1	Adapis 0 --> 01 (within terminal)
19.	0.176	1	node_64 0 --> 1 node_63
		1	node_45 1 --> 0 node_42
		1	node_34 0 --> 1 Pronothodectes
		1	node_35 0 ==> 1 Ignacius
		2	node_43 1 ==> 3 Picrodus
		1	node_51 1 ==> 2 node_50
		1	node_50 2 ==> 3 Carpodaptes
		1	node_48 2 ==> 1 Navajovius
		1	node_46 2 ==> 1 Omomys
		1	node_46 2 ==> 3 Tetonius
		1	node_61 1 ==> 2 node_55
		1	node_55 2 --> 3 node_54
		1	node_53 3 --> 2 Notharctus
		1	node_56 1 ==> 0 Caenopithecus
		1	node_58 1 ==> 2 node_57
		1	node_62 1 --> 0 Copelemur
20.	0.154	1	node_65 0 ==> 1 node_64
		1	node_34 1 ==> 0 Altanius

Character	CI	Steps	Changes
		1	node_38 1 ==> 0 node_36
		1	node_41 1 ==> 2 Platychoerops
		1	node_44 1 ==> 2 node_43
		1	node_51 1 ==> 0 node_50
		2	node_48 0 --> 2 node_47
		2	node_46 2 --> 0 Omomys
		1	node_54 1 ==> 2 node_53
		1	node_61 1 ==> 2 node_60
		1	node_56 2 ==> 1 Caenopithecus
21.	0.143	1	node_64 0 ==> 1 node_63
		1	node_45 1 --> 0 node_42
		1	node_41 0 --> 1 node_40
		1	node_36 1 ==> 0 Plesiadapis
		1	node_35 1 ==> 2 Phenacolemur
		1	node_43 1 ==> 2 Picrodus
		1	node_43 1 ==> 0 Zanycteris
		1	node_48 1 ==> 0 Navajovius
		1	node_48 1 --> 2 node_47
		2	node_46 2 ==> 0 Omomys
		1	node_61 1 ==> 2 node_55
		1	node_57 1 ==> 2 Microadapis
		1	node_57 1 ==> 0 Adapis
22.	0.154	2	node_65 0 ==> 2 node_64
		1	node_63 2 --> 1 node_52
		1	node_34 1 ==> 0 Altanius
		1	node_41 1 ==> 2 node_40
		1	node_35 2 ==> 1 Ignacius
		1	node_37 2 ==> 1 Microsyops
		1	node_41 1 ==> 0 Platychoerops
		1	node_49 1 ==> 2 Micromomys
		1	node_46 1 ==> 2 Tetonius
		1	node_61 2 --> 1 node_55
		1	node_53 1 ==> 0 Notharctus
		1	node_55 1 ==> 0 Europolemur
23.	0.200	1	node_38 0 ==> 1 node_37
		1	node_44 0 ==> 1 node_43
		1	node_49 0 ==> 1 node_48
		1	node_52 0 ==> 1 Palaechthon
		1	node_53 0 ==> 1 Smilodectes
24.	0.167	1	node_39 0 ==> 1 node_38
		1	node_35 1 ==> 0 Ignacius
		1	node_41 0 ==> 1 Platychoerops
		1	node_43 0 ==> 1 Picrodus
		1	node_49 0 --> 1 node_48
		1	node_47 1 --> 0 Altiatlasius
25.	0.200	1	node_52 0 --> 1 node_51
		1	node_34 1 --> 0 Altanius
		1	node_45 1 --> 0 node_44
		1	node_43 0 --> 1 Picrodus
		1	node_48 1 ==> 0 Navajovius

Character	CI	Steps	Changes
26.	0.200	1	node_64 0 ==> 1 node_63
		1	node_45 1 ==> 0 node_42
		1	node_37 0 ==> 1 Microsyops
		1	node_50 1 ==> 0 node_49
		1	node_46 0 ==> 1 Tetonius
27.	0.167	1	node_64 0 ==> 1 node_63
		1	node_34 1 ==> 0 Altanius
		1	node_36 1 ==> 0 Plesiadapis
		1	node_37 1 ==> 0 Tinimomys
		1	node_54 1 ==> 0 Cantius
		1	node_56 1 ==> 0 Caenopithecus
28.	0.333	1	node_38 0 ==> 1 node_37
		1	node_63 0 ==> 1 node_62
		1	node_56 1 ==> 0 Caenopithecus
29.	0.200	1	node_45 0 --> 1 node_42
		1	node_34 1 --> 0 Altanius
		1	node_50 0 ==> 1 node_49
		1	node_46 1 ==> 0 Tetonius
		1	node_56 0 ==> 1 Caenopithecus
30.	0.200	1	node_64 0 ==> 1 node_63
		1	node_45 1 ==> 0 node_42
		1	node_37 0 ==> 1 Microsyops
		1	node_50 1 ==> 0 node_49
		1	node_46 0 ==> 1 Tetonius
31.	0.167	1	node_64 0 ==> 1 node_63
		1	node_45 1 ==> 0 node_42
		1	node_37 0 ==> 1 Microsyops
		1	node_50 1 --> 0 node_49
		1	node_48 0 --> 1 node_47
		1	node_46 1 --> 0 Omomys

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