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A STUDY OF PHENETIC AND PHYLOGENETIC RELATIONSHIPS
AMONG THE MOCKINGBIRDS, THRASHERS AND THEIR
ALLIES.

The City University of New York, Ph.D., 1975
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**A STUDY OF PHENETIC AND PHYLOGENETIC RELATIONSHIPS
AMONG THE
MOCKINGBIRDS, THRASHERS AND THEIR ALLIES**

by

JAMES L. GULLEDGE

**A dissertation submitted to the
Graduate Faculty in Biology in
partial fulfillment of the
requirements for the degree of
Doctor of Philosophy, The City
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1975

This manuscript has been read and accepted for the Executive Committee in Biology in satisfaction of the dissertation requirement for the degree of Doctor of Philosophy.

June 28

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INTRODUCTION

This study represents an attempt to analyze various aspects of supraspecific relationships among the birds that comprise the currently recognized avian family Mimidae (Davis and Miller, 1960). There are two objectives: 1) To analyze phenetic similarities and differences among mimid species using numerical taxonomic procedures; 2) To develop an hypothesis of the supraspecific phylogenetic relationships among these species.

The mockingbirds, thrashers and their allies have not been comprehensively reviewed since Ridgway (1907). Since that time, however, there have been several studies of subgroups and individual species. These include Engels' (1940) analysis of the structural adaptations of Toxostoma and Zusi's (1969) study of ecological adaptations of Cinclocerthia. Sheppard (1973) gives a detailed account of the ecology of Toxostoma lecontei. Bent (1946) provides natural history surveys of the North American taxa and Skutch (1950, 1968), reports on the natural history of Melanotis and Donacobius.

Current views of phylogenetic relationships among the various mimid taxa are vague and imprecise, especially among what are currently recognized as genera. This is reflected in the fact that the thirty one species recognized by Davis and Miller (1960) are grouped into thirteen genera, eight of which are monotypic with only an

occasional hint as to possible affinities among them. The purely phenetic basis of this situation is clearly demonstrated in the phenetic analysis reported in chapter four of this study. It suggests that previous classifications of these birds represent little more than subjective and intuitive evaluations of overall similarities and differences among the taxa.

In this study, I have chosen to consider two aspects of evolutionary relationships, phenetic divergence and phylogenetic history, separately. The phenetic analysis consists of two sections. The taxa are analyzed first on the basis of similarities and differences derived from an extensive set of external characters that are observable in museum skins or obtainable from natural history studies of the species. The working hypothesis for the analysis of these characters is that the resulting groupings will closely match those suggested in traditional classifications. The character set is unweighted (other than in the choice of characters and the nature of the coding schemes) and reflects no phylogenetic assumptions. Subsets of these external characters are analyzed in order to try to identify which kinds of external characters are most strongly reflected in previous classifications of the mimids. A second phase of the phenetic analysis is the study of skeletal characters of the mimids and representative thrushes. This study represents one of the

first attempts in avian biology to use discriminant functions and generalized distance to analyze correlations among skeletal characters among species and to correlate these with ecological shifts among the taxa. The study is somewhat experimental and serves to suggest additional questions as to both methodology and interpretation rather than providing a detailed analysis of functional and ecological relationships.

Studies of functional morphology and ecology such as those of Engels (1940) and Zusi (1969) rely on either bivariate ratios or indices to analyze interspecific similarities and differences. The multivariate techniques used in this study make it possible to evaluate the similarities and differences of the taxa relative to one another on the basis of information from all of the variables taken simultaneously rather than on the basis of pairs of variables as is the case in previous analyses. In addition, certain of the procedures make it possible to remove most of the effects of correlation of characters both within and among the predefined groups (species) of the study.

In addition to the external and skeletal character sets, a limited number of species were analyzed in terms of egg white protein patterns. Egg white proteins have received great attention in recent years. Some biologists

look upon them as particularly unambiguous sources of phylogenetic information. Many, however, disagree. In this study, the egg white protein evidence is analyzed separately from the other character sets. Not enough species were available to make it possible to incorporate these characters into the more comprehensive phenetic analysis.

Inasmuch as an hypothesis of phylogenetic relationships among taxa is the primary reference for all comparative biological studies of a taxon or groups of taxa, phylogenetic analysis takes on special significance. Currently, there is considerable debate as to the nature, objectives, and the appropriate logical framework in which to conduct such analyses. The use of shared derived characters as opposed to common possession of primitive characters as the only basis for establishing meaningful groupings of taxa is becoming more widespread among systematists. This is especially true among Ichthyologists and Entomologists, many of whom go further and insist that the resulting classifications be direct reflections of the phylogenetic hypotheses proposed on the basis of systems of shared derived characters.

The methodology of Hennig (1966) and Brundin (1966, 1968) which requires that taxa or groups of taxa be associated only on the basis of shared derived characters

and that these groups must be monophyletic, not only in the sense that all included forms are derived from a common ancestor but must also include all descendents of that ancestor, however diverse, is in sharp contrast to the traditional approach to forming groups above the species level. The traditional rationale, as expressed by Mayr (1969: 92) is that: "A genus is a taxonomic category containing a single species, or a monophyletic group of species, which is separated from other taxa of the same rank by a decided gap". A similar rationale is applied in forming other higher categories. Such a subjective approach to evaluating similarities and differences and to the grouping of taxa cannot avoid obscuring, in the resulting classifications, what are thought to be the phylogenetic relationships of the taxa.

I have therefore chosen to present a strictly phylogenetic classification of the mimid taxa as the only means by which to adequately express hypotheses of phylogenetic relationships among them. Likewise I have chosen to present the results of multivariate statistical analysis of sets of characters as the best available means by which to express phenetic similarities and differences among the taxa.

For the sake of clarity, I follow currently accepted generic names (Davis and Miller, 1960) in the chapters that

follow. To do otherwise would make it more difficult for the reader familiar with these birds to follow the discussions. Species taxa are likewise those recognized by Davis and Miller (loc. cit.) with the exception that in the phenetic analyses of chapters 4 and 5, I follow Swarth (1931) with regard to the Galapagos mockingbirds.

It must be stressed that the traditional generic names are merely convenient labels and my use of them in no way implies that I attach phylogenetic significance to them, nor are they meant to convey subjective evaluations of degrees of phenetic difference.

TAXONOMIC HISTORY

The birds currently recognized as the avian family Mimidae have had a long and varied taxonomic history. The first prominent mention of any members of the group occurred in Catesby's Natural History of Carolina, Florida and the Bahama Islands (1731). In this work the Mockingbird (Mimus polyglottos), the Brown Thrasher (Toxostoma rufum) and the Gray Catbird (Dumetella) were figured and descriptions of their behavior and remarkable singing abilities were given. Since Catesby's work antedates Linnaeus and the Systema Natura, it cannot be considered as part of the formal taxonomic history of the group.

From the time of Linnaeus's introduction of the binomial system of nomenclature in the tenth edition of the Systema Natura (1758) until now, the taxonomic history of the mimids has been closely bound to the history of the various views that have prevailed regarding passerine systematics and especially with regard to views of relationships among what are referred to as "ten primaried, Old World insect eaters." This is because of the affinities of mimids to two other important groups of ten primaried insect eaters, the thrushes and the wrens.

Linnaeus, according to Newton (1893), based his ornithological decisions on John Ray's 1713 work, Synopsis Methodica Avium. Using characters from the bill, nares, and the presence or absence of rectal bristles, Linnaeus

placed the then known mimids in his genus Turdus (Linnaeus, 1758). In the last Linnaean edition of the Systema Natura (Linnaeus, 1766), the Gray Catbird was placed in Muscicapa (Muscicapa carolinensis) and another bird currently considered to be a mimid, Donacobius atricapillus, which had been described by Brisson was added to Turdus.

Until the middle 1820s newly discovered mimids were placed in either Turdus or Muscicapa. P. L. S. Muller (1776) described Muscicapa fusca (Allenia fusca). (When necessary to avoid confusion, current names will be placed in parentheses following synonyms.) Vieillot (1807) added Muscicapa fuscatus (Margarops fuscatus) and Turdus gilvus (Mimus gilvus). Vieillot (1807) also transferred Muscicapa carolinensis (Dumetella carolinensis) to the genus Turdus. In 1818 Vieillot described and added Turdus brachyurus (Ramphocinclus brachyurus). Other mimids were added to the genus Turdus by Molina (1782) (Mimus thenca), Vieillot (1818) (Mimus triurus), and Lichtenstein (1823) (Mimus saturninus).

The work of sorting the large Linnaean genera such as Turdus into groups of supposedly related species and diagnosing genera in the modern sense did not get underway until the middle and late 1820s. During this period, much of systematic thinking was dominated by the views of Cuvier, as expressed in the Regne Animal. This great work

was translated into English and supplemented by Griffith and Pidgeon with additions by Gray (Cuvier, 1829). Cuvier, although a master anatomist, based his avian genera and families upon characters derived, in the main, from bills and feet. His views and influence show prominently in the series of works by Gray (1840; 1841; 1849; 1869) enumerating the genera of birds.

As far as the mimids are concerned, their separation from the Linnaean genus Turdus commenced with Boie (1826) and Swainson (1827a). Boie resurrected an old name from Brisson and established the genus Mimus, based on Turdus polyglottos. He placed the genus in the thrush family Merulidae. Swainson (1827a) erected the genus Orpheus within the Merulidae for Turdus polyglottos and for two new mimids from Mexico, Orpheus curvirostris (Toxostoma curvirostre) and Orpheus caerulescens (Melanotis caerulescens) (Swainson, 1827b). Swainson, in Swainson and Richardson (1831), then added Turdus carolinensis (Dumetella) and Turdus rufus (Toxostoma rufum) to Orpheus.

Swainson was either not aware of Boie's paper or felt no obligation to grant priority. He felt that too many genera were being established without proper analysis with regard to the "Natural System", especially in Germany and France and that he could therefore ignore them (Swainson, 1836:241). Swainson had become a follower and champion of

the Quinary system which had been strongly advocated by his predecessor Vigors. The Quinary system was a heavily metaphysical conception of the interrelatedness of organisms, graphically depicted as sets of closed circles with one group of organisms merging with another. In Newton's view (1893), the time spent expounding a system that was based more on philosophy and argument than on facts observed from study and comparison greatly inhibited the development of English ornithology.

There were of course workers in England (Macartney and Macgillivray for example) and in France and Germany who, in the words of Newton (1893:25) "--were content to prosecute their labors in a plain fashion consistent with common sense, plodding steadily onwards in their efforts to describe and group the various species as one after another they were made known." With regard to diagnosing mimid genera, Wagler (1831) proposed the genus Toxostoma to accomodate Orpheus curvirostris, feeling that because of its bill characters, it should be separated.

The continental workers, continuing in the traditional comparative anatomical approach were beginning to focus attention on a problem that was to remain the subject of the most intensive work in ornithology until the beginning of the Twentieth Century, namely, diagnosing the limits of the various orders of birds and the groups within

what are now the Passeriformes and Piciformes. These workers were beginning to recognize morphological structures other than bills and feet that could be of importance in sorting out and grouping birds into more "natural" arrangements.

Johannes Muller and Jean Cabanis are of special interest. Muller was the first anatomist to study the passerines in terms of the muscles of the syrinx. He also noted that there was a correspondance between the state of syrinx musculature and the condition of the planta of the tarsus. This last character, according to Newton (1893), had been noted by Keyserling and Blasius some years before Muller's work as being of importance in identifying certain groups, especially the larks. Cabanis, who had also done work on the muscles of the syrinx, made further correlations between the scutellation of the foot, the syrinx musculature and the number of primaries found in various groups.

Systematic arrangements based upon these correlations were first published by Cabanis (1847) and formed the basis for the classification used in his Museum Beineanum (Cabanis, 1850). In this work, the limits of the oscines within the Passeriformes are as they are today.

Cabanis transferred the mimids from their traditional

association with the thrushes and included them in the subfamily Troglodytinae of the family Liotrichidae which he established to encompass the babblers, wrens, and a few other Old World groups. He placed the thrushes in another family, the Rhacnemididae. The views of Cabanis were highly regarded and influenced Baird who adopted the family Liotrichidae and its subgroups (Baird, 1858). Baird elevated the mimids to subfamily rank however, rather than leaving them as a subgroup of the subfamily Troglodytinae.

The English workers, still strongly under the influence of Gray and others of the Cuvierian tradition did not accept this transfer and Sclater (1859) in his comprehensive review of the New World thrushes retains the mimids among them. He notes that in many details, including tarsal scutellation, the mimids do differ from thrushes. However, because of the transitional forms, such as the Gray Catbird (Dumetella) and the manner of nesting of mimids as well as the color of their eggs, they are still best associated with the thrushes.

Shortly after Sclater's review, Baird (1864) reversed himself and returned the subfamily Miminae to the Turdinae. As justification, he gave: "----among other reasons, on the ground of their more deeply cleft toes, and the greater extension forward of frontal feathers." He also included Donacobius in the Miminae because of the deeply cleft toes,

despite its wren-like character. Baird's arrangement was to hold sway among American ornithologists for some time as reflected in the early works of Coues (1872, 1878) and was used for A History of North American Birds (Baird, et. al. 1874). However, in the second edition of the Key to North American Birds, Coues (1884) took pains to point out that the mimids, as thrushes, are "Aberrant Turdidae, departing from the prime characteristic of the family in having the tarsi scutellate in front---."

In England, the last of the series of lists by Gray (1869) was continuing the traditional arrangements. The mimids remained in the family Turdidae, except for Donacobius which was placed with the wrens. Sclater and Salvin (1873), although following a new classification proposed by Huxley (1867) regarding major groups of birds, retained the mimids within the Turdidae, not even setting them apart as a subfamily. Donacobius remained among the wrens.

During the 1870's and 1880's, great progress was made in anatomical studies of birds. Huxley (1867) had worked out the palatal anatomy of most major groups and presented his results along with a new classification. He was followed by Garrod and Forbes, both of whom published many papers on various aspects of avian anatomy. The primary focus of these researches was not, however, on family

diagnosis and arrangement. Instead, they were addressed to the great problem of diagnosing the limits of the orders, especially the limits of the Passeriformes and Piciformes and within the Passeriformes, the major subdivisions.

After the last hand-list of Gray (1869), which was the last major listing of the world's birds in the Cuvierian tradition, the next effort is that of Sharpe (1874) who began The Catalogue of Birds in the British Museum. In volume III, Sharpe (1877) begins the catalog of the Passeriformes and states that he will follow the views of Garrod as to the organization of the higher groups. However, for the lower divisions, he proposed to base the classification on the work of Sundevall (1872).

Sundevall's system of classification is the last one of major significance which is based primarily, if not in most cases entirely, on external characters. Regarding choice of characters upon which to base a classification, Sundevall said:

"---the characters, especially of the groups inferior to Classes (viz. Families and Genera), should be such that they can always be examined in ordinary specimens-- that is to say, that they should be derived from the external parts of the body----" (Sundevall, 1872:21)

With regard to internal or anatomical characters, he said:

"It is a common notion, but one which is entirely false that anatomical or internal characters are always better and more certain than external ones. "----- Thus the form of the internal parts is generally very variable, and is not in any way preferable as a character to the external form. As, moreover, it is often inaccessible and cannot be examined, we ought to avoid making use of it." (Sundevall, 1872:22)

Sundevall grouped the mimids with other forms in a "Cohort" called the Cichlomorphae (thrush-forms). This group consists of the "Old World insect eaters." Sundevall separated the thrushes from the other members of the Cichlomorphae on the basis of the booted tarsus. He placed the mimids immediately after the wrens in the second division of the Cichlomorphae which he established on the basis of the size of the wing, it being short and rounded in these groups. Because of the fact that some mimids have longer wings, what Sundevall called moderate, it was necessary to establish two families for them, straddling the end of the "Brevipennes" and the following group the "Aequiparatae". These longer-winged mimids included the genera Mimus, Oreoscoptes, and Margarops.

Sharpe (1881), in his modification of Sundevall's classification, placed the subfamily Miminae in sequence after the subfamily Troglodytinae, both being included in the family Timaliidae (Babbling-thrushes). Regarding the Miminae, he said:

"The Mocking-Thrushes of America appear to form a very natural group representing in the New World the strong-legged Babbling-Thrushes of the Old. ---some of the genera of Miminae, such as Cinclocerthia, Ramphocinclus, and Rhodinocincla, appear to connect the Mocking-Thrushes with the Wrens, as does also the genus Harporhynchus." (Sharpe, 1881; 332)

Stejneger (1883), although very critical of the treatment of the thrushes in the Catalogue of the Birds in the British Museum (Seebohm, 1881) and the placement of Cichlherminia in the Miminae (Sharpe, 1881), agreed with the limits set by Seebohm (1881) for the thrushes which excluded the mimids. As Stejneger (1883) expressed it: "The peculiar spotted first plumage of the Turdidae is a very striking feature, and its coincidence with booted tarsi very remarkable." Stejneger (1883) believed that the mockingbirds are so closely allied to the wrens, that they should be included with them in a single family, the Troglodytidae.

In discussing Cichlherminia, Stejneger (1883) notes that it especially has been regarded as an intermediate link between thrushes and mockingbirds. However, the birds within the genus Cichlherminia which had previously been separated as Margarops (Sclater, 1859) are undoubtedly mimids and the remaining ones are unquestionably thrushes and should be so separated.

Stejneger (1885) restates his belief that the mimids are closely allied to the wrens. Although he calls them a family (Mimidae) he states that they hardly deserve family rank separate from the wrens, from which they differ chiefly in having well developed bristles at the mouth and in being somewhat larger (Stejneger, 1885).

At about this time, 1883, the American Ornithological Union began to organize its first check-list. The committee on nomenclature and classification produced a scheme which placed the mimids as a subfamily within the Troglodytidae. The first edition of the check-list provides little information as to why the Oscine families were arranged as they were, having, instead, many pages devoted to questions of proper nomenclatural procedure. However, the committee was composed of Coues, Allen, Ridgway, Brewster, and Henshaw and the classification used for the check-list no doubt reflected the current thinking among American ornithologists. With regard to the mimids, this was to associate them quite closely with the wrens.

The second check-list (AOU, 1885) maintained the arrangements of the first with regard to the mimids and wrens. This was done despite the work of Lucas (1888), who analyzed the skeletons of many mimids, thrushes, and wrens and concluded that the mimids should be separated from the others as a distinct family. He said that the mimids

cannot be included in a sharply defined family Troglodytidae. Further, he pointed out the striking similarities between the thrushes and Galeoscoptes (Dumetella) and suggested that the Gray Catbird may be a link between the two groups. In general, Lucas believed that the mimids fall mid-way between the thrushes and wrens.

The third edition of the check-list (AOU, 1910) reflects the views of Lucas. The mimids are elevated to family status, adjacent to the wrens. Because of conflicts within the committee on classification, (Wetmore and Miller, 1926) the third edition of the check-list does not reflect the latest views on Passerine classification, specifically those of Gadow, and the old sequence of groups was retained. This included placing the Turdidae at the end of the list of Passerine families, far removed from the wrens and mimids. In the fourth edition of the check-list (AOU, 1931), Wetmore and Miller shifted the sequence of Passerine families and placed the family Mimidae between the wrens and thrushes, the thrushes having been ousted from the top of the Oscine sequence by the Fringillidae. This arrangement regarding the Mimidae has been maintained in nearly every classification proposed since. These include: Mayr and Amadon (1951); Van Tyne (1959); Wetmore (1960); Storer (1960); and Storer (1971). A rather different sequence was proposed by Delacour and Vaurie

(1957). These two authors shifted the wrens, dippers, and mimids to a position outside the Muscicapidae, the extensive family in which they left the thrushes and babblers. They gave no reasons for this arrangement.

Unfortunately, placing the mimids between the wrens and the thrushes in a check-list or in a sequence of families in a classification does not help answer the more difficult question as to which of the adjacent groups they are most closely related. American ornithologists have generally championed the view that the mimids are closer to the wrens than the thrushes. This seems to stem primarily from the views of Coues and Stejneger. As Sibley (1970) says: "The Mimidae have long been thought to be allied to the wrens on the one hand and to the thrushes on the other. The actual evidence for a wren-mimid relationship is more difficult to find." On the other hand, Ripley (1952) said that the differences between the mimids and the thrushes "are no more compelling than those between other subfamilies of the Muscicapidae."

Even during the period when the views of Stejneger and Coues were being promulgated with such vigor, not all went along to the point of making the mimids a subfamily of the wrens. Ridgway (1907) cites Lucas and says that although occupying a position between the thrushes and wrens, the mimids are more closely related to the former,

and that they are apparently most closely related to the true thrushes. (Ridgway, 1907:182)

The Europeans were also inclined to maintain a close association between the mimids and thrushes. Evans (1899), noting that Gadow did not propose a classification for the families of the Oscines, proceeds to follow the order of Stejneger (1885) but not to necessarily adhere to his families. Evans groups the mimids as a subfamily in the Turdidae. Reichenow (1914) does not discuss the relationships among Muscicapid groups, simply listing them. He places the subfamily Miminae between the Troglodytinae and the Turdidinae within the family Sylviidae. Neither does Stresemann (1934) discuss the relationships among Oscine families. He places the family Mimidae between the wrens and thrushes. Berlioz (1950) places them adjacent to the thrushes and points out their resemblances to that group. He does not mention the supposed relationships to the wrens.

Two recent major investigations have tackled the problem of Oscine relationships. Beecher (1953) examined the jaw musculature of many species in nearly all groups. Sibley (1970) surveyed the egg white protein patterns of the Oscines.

Beecher, on the basis of the patterns of jaw

musculature would place the mimids as a subfamily within the Turdidae, which is placed in a superfamily, the Sylvioidea. The wrens are quite far removed in another lineage in the superfamily Timalioidea (Beecher, 1953). Beecher revives the suggestion that the mimids may stem from the thrushes via Margarops.

Sibley (1970), on the basis of egg white protein patterns cannot find a close link between the mimids and wrens. On the contrary, the protein patterns seem more like those of thrushes. They are even more similar to the egg white patterns found in the Sylviidae. Sibley (1970:67) says that it seems reasonable to conclude that the wrens and mimids are not closely related. Regarding the thrushes and mimids, he feels that a close relationship between them seems less certain than that between the thrushes and dippers and further evidence is needed. He suggests that an alliance of the mimids with groups such as the Sylviidae should be considered as a possibility for further study.

Morioka (1967) carried out an extensive survey of the anatomy of the thrushes, mimids, dippers, and wrens and reviewed other sources of characters such as tarsal scutellation, juvenal plumage, nidification and distribution. His object was to determine the relationships between the four groups. He concluded that

the wrens are far removed from the other three groups, which show strong affinities to each other. He believes that the thrushes, mimids and dippers form a monophyletic group within the Old World insect eater complex.

It would appear that the wheel has turned full circle with regard to the position of the mimids vis-a-vis the thrushes. In the early and middle Nineteenth Century, the weight of opinion was that they were closely related to the thrushes, with some wren affinities. In the late Nineteenth and early Twentieth Century, opinion, especially American, shifted and the mimids were thought to be quite close to the wrens. At present, most research indicates that the mimids do not have close ties to the wrens and are indeed much more closely related to the thrushes.

FAMILY AND GENERIC LIMITS

As mentioned before, the mimids were long ago recognized as a particular group within the the Old World insect eaters, the "Dentirostres" of the early naturalists and taxonomists. Diagnosing the limits of this group and sorting out the currently recognized genera was not completed until the beginning of the present century. The basic groupings began to appear consistently during the 1850's in the works of Cabanis (1850), and Bonaparte (1850). The first use that I have found of a formal

subfamily designation (Miminae) is in Baird (1858).

Sclater (1859) did not separate the mimids from the thrushes as Baird had done. He simply listed them after the various New World thrush genera. Sclater included all of the birds now recognized as mimids with the exception of Donacobius. This genus was consistently placed among the wrens by English taxonomists.

The first major work to include all of the mimids as Miminae or Turdidae was Baird (1864). Although he included Donacobius in the Miminae, he placed Ramphocinclus in the Turdinae because the specimen(s) he examined showed little if any tarsus scutellation. Gray (1869) did not separate the mimids as a group, leaving them interspersed among various thrush genera with Donacobius placed among the wrens. Sclater and Salvin (1873) grouped the mimids together but did not designate them as a subfamily within the Turdidae. Donacobius remained with the wrens.

Sundevall (1872) grouped all of the mimids into two adjacent families because of the demands of the characters upon which he based his classification (see above). Beginning with Sharpe (1881), the mimids recognized today, including Donacobius, are always found grouped together. (Sharpe (1903); Ridgway (1907); Hellmayr (1934); Davis and Miller (1960))

Certain genera have been particular problems as to proper placement. Donacobius was consistently placed among the wrens after its early history of being considered a thrush. Baird (1864), among later workers was the first to associate Donacobius with the mimids in the Turdidae. However, it was not until Sundevall (1872) and Sharpe (1881) that Donacobius was finally stabilized as a member of the Mimidae.

Ramphocinclus and Cinclocerthia were shifted about somewhat more than Donacobius. Besides being frequently combined (see synonymies in Ridgway (1907)), they have been placed in various other group. Ramphocinclus was placed among the ant thrushes (Gray, 1849:210) in the genus Formicarius. Later he placed it along with Cinclocerthia in the wrens (Campylorhynchus) (Gray, 1849: app. p.7). Bonaparte (1850) also placed Ramphocinclus among the wrens. Cinclocerthia, at one point was even placed among the oven-birds (Furnariids) Gray (1846). Sclater (1859) finally placed both of these genera among the mimids where they have remained since.

The problem of diagnosing family limits also involved removing various genera that are not now accepted as mimids. Two of the most frequently involved groups were the red-legged thrushes (Mimocichla) and the forest thrushes (Cichlherminia). The red-legged thrushes were

frequently placed in either the genus Mimus (Gray, 1849; Bonaparte, 1850) or Galeoscoptes (Dumetella) (Cabanis, 1850; Sclater, 1859). By 1870, these birds had been separated from the mimids by nearly all except Gray (1869) who kept some of them in Mimus.

Cichlherminia and Margarops were linked in close association even longer. Bonaparte (1854) established Cichlherminia for the Forest Thrush of the Lesser Antilles and the Lesser Antillean form of the Pearly-eyed Thrasher. He subsequently separated them (Bonaparte, 1857) erecting the genus Cichlhalopia for the thrasher. Sclater (1859) changed the name of Cichlhalopia to Margarops. He later combined Cichlherminia with Margarops (Sclater, 1871). Sclater (1880) described and named the St. Lucia Forest Thrush as Margarops sanctae luciae. Sharpe (1881) left the thrushes mixed with the thrashers but changed the name of all back to Cichlherminia. Stejneger (1883) emphatically argued for the separation of the thrushes and thrashers in the genus Cichlherminia (see above). Despite Stejneger's views, Newton (1893:959) wrote regarding Margarops "---and no one who has made its acquaintance in life can doubt that form being a true thrush." The separation of the two groups was accepted, however, and Sharpe followed suit in his 1903 hand-list.

Other than the thrushes discussed above, the bird

most often placed in the Mimidae and since removed was Rhodinocichla rosea. As early as Sundevall (1872), this bird was placed in his "Toxostominae". Baird (1864) believed it to be a wren and said that Sclater concurred and suggested that it should be placed near the genus Helodytes. Sclater and Salvin (1873) however, moved Rhodinocichla to the Turdidae, immediately following Harporhynchus (Toxostoma). The bird remained there (Sharpe, 1881; 1903) until Ridgway (1902) placed it among the wood warblers (Parulidae). Clark (1913) argued convincingly that Rhodinocichla is in fact a tanager. It has not been included among the Mimidae in systematic listings since. Recently, however, Skutch (1962) raised doubts about the matter and reopened the question of possible mimid affinities. Eisenmann (1962) examined the evidence and concluded that Rhodinocichla is indeed a tanager and has no relationship to the mimids.

Calyptrophilus, originally described as a tanager, is the only other bird to have been included among the mimids and since removed. Ridgway (1907) added it, although with some hesitation. Miller (1918) studied the case and returned Calyptrophilus to the tanagers.

Refinement of generic limits within the family Mimidae occurred over a period of about forty years. By 1859, when Sclater published his review of the New World Turdidae, all mimids which were destined to have a new

genus established for them had been discovered with the exception of Harporhynchus graysoni (Mimodes). The genus Mimus was relatively stable, although there was a tendency to make it very broad and include Galeoscoptes, (Dumetella) (Gray, 1849; 1869; Coes, 1872; 1878). Baird (1864) said that except for coloration, he could see little to set Galeoscoptes apart from Mimus. Dumetella, other than being placed in Mimus, has remained monotypic (disregarding the red-legged thrushes which some workers added). The genus Melanoptila has long been thought to be closely related to Dumetella (Sclater, 1859). Paynter (1954) advocates that the two genera should be combined. This view is endorsed by Mayr and Short (1970).

There was some effort to divide the thrashers (Harporhynchus) into two genera with Harporhynchus containing only H. redivivum, H. lecontei, and H. crissalis. The others were to be placed in the genus Methriopterus (Reichenbach, 1850). Ridgway (1882) reviewed the problem and rediagnosed the characters which can be used to separate the two groups. Among other things, these include the lack of spots in the ventral plumage. Engels (1940) noted that the Toxostoma redivivum group is indeed sharply marked off from other thrashers by the characters noted by Ridgway and in addition, by having brown or reddish brown irises instead of yellow; whitish mouth linings instead of yellow; and the most extreme

modifications of the skull and musculature to be found among the thrashers. Despite their differences, however, few accepted separating the thrashers generically, preferring at most to recognize two subgenera. Because of the intermediate Toxostoma species, the subgeneric separation was dropped by the time of Ridgway's Birds of North and Middle America (1907).

The bird now known as Mimodes graysoni was first assigned to Harporhynchus (Lawrence, 1871). Ridgway (1882) concluded that it was not properly placed and although on the basis of general appearance, it seemed intermediate between the two extremes of Harporhynchus, it was in reality more nearly related to Mimus. Ridgway felt, however, that it was distinctive enough to require a new genus, Mimodes.

Ridgway (1890) also established the genus Nesomimus for the mockingbirds of the Galapagos Islands. He thought that their tarsi were too long and the base of their bills too compressed for them to be rightfully included in Mimus. Swarth (1931) in his revision of Nesomimus recognized four species. Davis and Miller (1960) recognized only one, Nesomimus trifasciatus.

The genus Oreoscoptes was established by Baird (1858). It has been of little concern since, although Mayr

and Short (1970) suggest that given the variation found within Toxostoma, Oreoscoptes is doubtfully separable from it.

The problem of diagnosing the limits of Margarops was primarily that of sorting it out from the forest thrushes (Cichlherminia). In addition, Cory (1891) decided that the Scaly-breasted Thrasher, Cichlherminia montana, should be separated from the forest thrushes. He proposed the genus Allenia. He left the Pearly-eyed Thrasher with the forest thrushes. Some feel (Bond, 1961) that Allenia is a doubtful genus and suggest that Allenia is synonymous with Margarops.

The diagnoses of Melanotis and Donacobius have presented no problems. Therefore, with the proposal of Allenia, all of the currently recognized mimid genera had been established. The result, after the removal of Rhodinocichla and Calyptophilus is the family as known today: thirteen genera, ten of which are monotypic (Davis and Miller, 1960).

RELATIONSHIPS AMONG THE MIMID GENERA

Views regarding the phylogenetic relationships among the genera of mimids, although not often specifically expressed can be deduced in some measure from the

arrangements and groupings found in the major systematic works. Sclater (1859) was the first to discuss such relationships among the mimids. He felt that because of their intermediate character, the forest thrushes (Cichlherminia) and Margarops served to link the turdids and mimids. He felt that the "Mock-bird" series should commence with Dumetella, followed by Melanoptila and then Melanotis which he felt was hardly separable from Dumetella. Sclater then shifted to the most aberrant genera, Ramphocinclus and Cinclocerthia, which in structure and bill lead to some species of Toxostoma. He felt that these birds are connected by Oreoscoptes to the genus Mimus. To summarize, Sclater's groups are:

1) <u>Margarops</u>	2) <u>Dumetella</u>	3) <u>Ramphocinclus</u>	4) <u>Toxostoma</u>
	<u>Melanoptila</u>	<u>Cinclocerthia</u>	<u>Oreoscoptes</u>
	<u>Melanotis</u>		<u>Mimus</u>

Although additional genera were established in following years, Sclater's basic groups remain relatively intact throughout later systematic treatments. Margarops and its offshoot Allenia are always paired, as are Ramphocinclus and Cinclocerthia. Dumetella, Melanoptila, and Melanotis remain together in Baird (1864), Sclater and Salvin (1873), and Davis and Miller (1960). Ridgway (1907) and Hellmayr (1934) (who follows Ridgway completely with regard to the mimids) insert Mimodes between Melanoptila

and Dumetella, despite Ridgway's earlier argument (Ridgway, 1882) that Mimodes is most closely related to Mimus.

The last of Sclater's groups, Toxostoma, Oreoscoptes, and Mimus are less consistently grouped together. Sharpe (1881) inserted Dumetella between Oreoscoptes and Mimus then lists Toxostoma. He follows much the same pattern in his hand-list (Sharpe, 1903). (Sharpe's arrangements of the mimid genera are the most aberrant when compared to those of other systematists.) Ridgway (1907) begins the Mimidae with the specialized genus Toxostoma then shifts to the generalized Melanotis then Melanoptila.

Miller (1949) in a discussion of the adaptive radiation of the mimids stated: "the genus Toxostoma-- is obviously derived from the mockingbirds, diverging in the direction of stouter hind limbs, reduced flight equipment, and longer, heavier bill---". Mayr and Short (1970), as already noted, suggest that Oreoscoptes is "doubtfully separable" from Toxostoma.

Views regarding the relationships between Dumetella and Melanoptila have been discussed above.

The endemic West Indian mimids have traditionally been separated into two groups. One consists of Margarops and Allenia, the other consists of Ramphocinclus and

Cinclocerthia. No doubts have ever been expressed regarding the Margarops-Allenia association, indeed their generic distinctness has been questioned. Regarding their connections to continental groups, however, no proposals have been made. In a recent review, Bond (1963) could find no evidence to suggest possible links.

Regarding Ramphocinclus and Cinclocerthia, Bond (1963) suggests that they are a group related to the genus Melanotis. Zusi (1969) states that Ramphocinclus shows resemblances to Melanotis and to Toxostoma in its skull morphology and that, in its plumage pattern, it resembles Melanotis.

Of all the mimids, the genus Donacobius has received perhaps the least attention from recent systematists. Baird (1864) included it in his Miminae on the basis of its rictal bristles, notched beak, and its deeply cleft inner toes. Ridgway (1907) does not discuss it as it is extralimital to his work, although he points out several characters which make it unique among the mimids. Skutch (1968), in a life history study, describes a number of ways in which Donacobius differs from all other mimids. Zusi (1969) notes major differences in the skull morphology of Donacobius as compared to other mimids and dismisses it as a special offshoot of the group. In all of the literature reviewed, I have have found no suggested affinities between

Donacobius and any other mimid. Donacobius stands alone.

To summarize, it appears that most workers would group the currently recognized mimid genera into complexes as follows:

1) Margarops-Allenia with a tentative link to Cinclocerthia

2) Dumetella-Melanoptila-Melanotis with a tentative link to Ramphocinclus

3) (Mimus-Nesomimus-Mimodes) - (Toxostoma-Oreoscoptes)

4) Ramphocinclus-Cinclocerthia (instead of above suggestions) with a tentative link to Melanotis

5) Donacobius

There seems to be a general consensus, reflected in Davis and Miller (1960), that the Dumetella - Melanoptila - Melanotis group is the most primitive and that the sickle-billed Toxostoma thrashers are the most specialized.

NUMERICAL METHODS

The numerical methods used to analyze the data derived from the various sets of characters considered in this study can be grouped into four basic categories. These are: 1) Principal components analysis; 2) Discriminant functions analysis; 3) Cluster analysis; and 4) Network analysis. These four methods will be described from the point of view of a practicing systematist attempting to understand and use the results to interpret biological relationships of the taxonomic units he is studying. No attempt will be made to explain the mathematical and statistical procedures of the various kinds of analysis. The object of this chapter is, instead, to enable the reader to understand and interpret some of the phenetic and phyletic relationships among the taxa on the basis of the graphical displays and tables of values.

For detailed mathematical and statistical information about principal components analysis, discriminant functions and related techniques one can refer to Cooley and Lohnes (1971) and Van de Geer (1971). Cluster analysis is discussed in Sneath and Sokal (1973). Network analysis, at least from the point of view of research in systematics, is best investigated through papers published in recent volumes of the journal Systematic Zoology. These include Parris, Kluge, and Fckardt (1970), Parris, (1969, 1970), Kluge and Parris (1969), Lundberg (1972), Bades (1970) and others. An excellent general review of many of these

methods is given in Ornard (1973) .

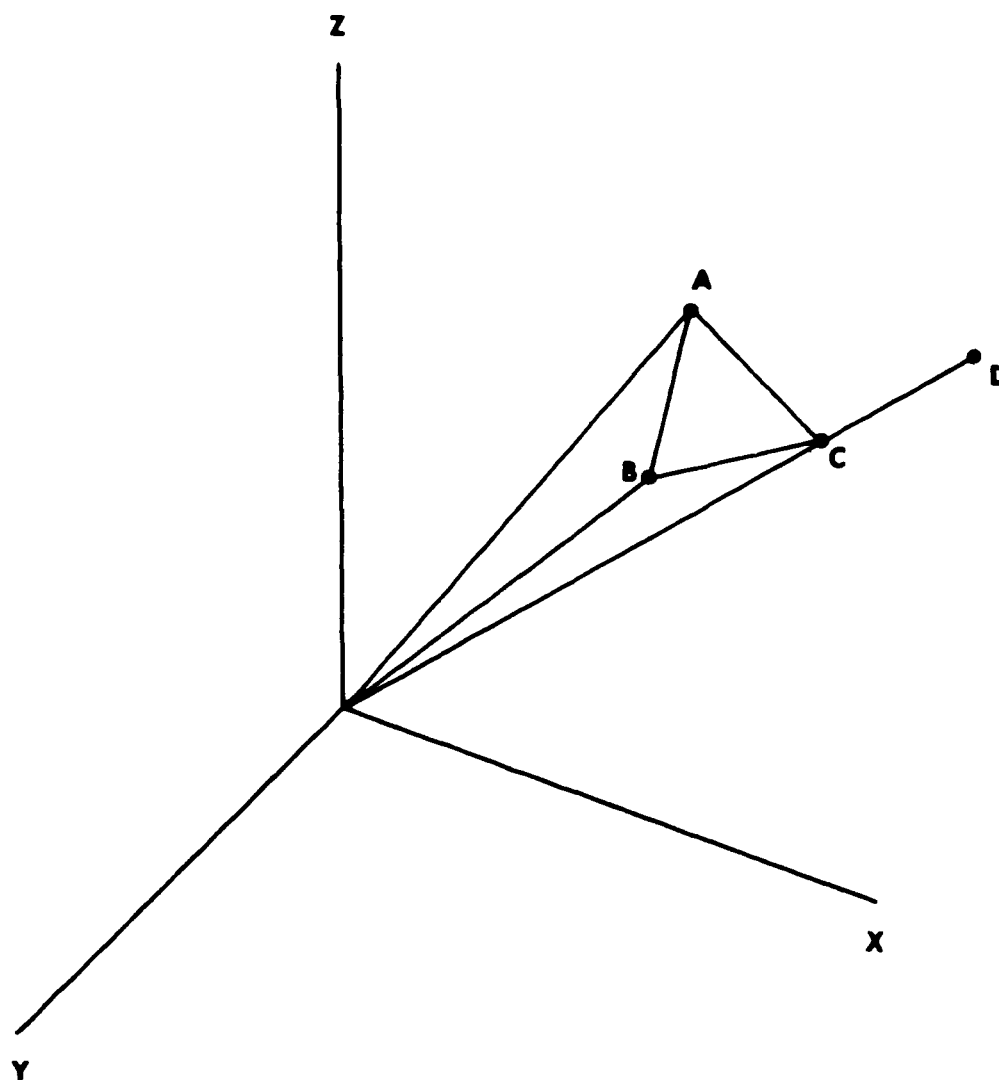
Each of these methods is suitable for certain questions and not others. Principal components analysis and a related technique, factor rotation, are very good for investigating the relationships among widely dispersed taxa or groups of taxa.

Cluster analysis, of which there are many varieties, is particularly good when the researcher is investigating the relationships among very similar taxa or groups of taxa. Cluster analysis is less satisfactory in discerning groups among phenetically diverse taxa.

Finally network analysis is best suited to finding most parsimonious connections among the taxa. The kinds of networks used depend upon the logical framework in which the researcher wishes to place the taxa he is studying and the criteria used to determine most parsimonious relationships.

All these methods operate upon similarity coefficients among the taxa (Cluster analysis), coefficients of correlation among the characters (Principal components) or coefficients of distance among the taxa (Cluster analysis and Network analysis). The relationships of two basic coefficients, correlation and distance, can be illustrated

FIGURE 2.1. FOUR OBJECTS: A, B, C, D POSITIONED IN SPACE BY THREE VARIABLES: X, Y, Z.



by the positioning of four taxa A, B, C, and D in a three dimensional space by three variables X, Y, and Z. (figure 2.1) .

The distance between any pair of points is the length of a line that would connect them. It can be calculated according to the multidimensional extension of the classical Pythagorean theorem for the relationship of sides of a triangle (Sneath and Sokal, 1973). The same logic applies for three or thirty characters. Since the coefficient of distance is additive over the number of characters, the coefficient is usually inversely weighted by the number of characters used. (Sneath and Sokal, 1973) .

The correlation coefficient used in systematic studies is the classical Pearson product moment correlation coefficient (Sneath and Sokal, 1973). This coefficient takes into account the variances of the taxonomic units about the mean of each variable. Since this coefficient is a measure of co-variation of the taxa, in other words how closely the variables of one taxon vary in conjunction with the same variables of another taxon, it is particularly good at representing shape information. (Rohlf and Sokal, 1965). In geometric terms, (see figure 2.1) the correlation coefficients may be represented by the cosine of the angles between the lines connecting the taxa to the

origin of the graph.

Figure 2.1 also illustrates an important relationship between the two coefficients. Notice that taxon D is positioned by the three variables X, Y, and Z so that the line connecting it with the origin of the graph is coincident with the line connecting taxon C to the origin. Therefore, there is no angular difference between the two lines (vectors) and the two taxa would have a correlation coefficient of 1.000 (the cosine of 0 degrees). However, the points themselves are not coincident and there is some distance between taxon C and taxon D. Therefore if two taxa have zero distance between them, they are coincident and must have the same correlation coefficient. However, two taxa may have the same correlation coefficient and yet not be coincident. This is of course what happens when two taxa are identical except for size, and is the reason why the correlation coefficient is often preferred when strong size problems exist in the data describing taxa.

The illustration in figure 2.1 is of taxa positioned by variables, with the correlation coefficients representing relationships among the taxa (Q analysis (Sneath and Sokal, 1973)). The calculations can also be done for correlations among the variables to give a matrix of character correlation coefficients (R analysis (loc. cit.)). It is this matrix of correlation coefficients

among the characters that is analyzed with principal components techniques.

PRINCIPAL COMPONENTS

In systematic studies, collected data usually consist of scorings or measurements of a set of variables that the researcher feels in some fashion describes the taxa. Within limits of practicality, time, and effort, researchers often try to include as many variables as possible. It would be useful if the total variation among the taxa in the study could be summarized in as small a number of variables as possible. Principal components analysis accomplishes this by constructing a set of new variables that describe the position of the taxa relative to each other in multidimensional space. The first new variable must explain as much of the variability among the taxa (as expressed in the matrix of correlation coefficients) as is possible for any single variable to explain. The second new variable must explain the largest amount of the remaining variability among the taxa and so on through the entire set of new variables. The result of this requirement is to nearly always reduce the number of variables needed to describe the original relationships among the taxa. The new variables are known as factors and the entire set of them is known as the factor structure of the matrix of correlation coefficients (the similarity

matrix).

The new variables are constructed at right angles to each other and are uncorrelated. They therefore help overcome problems of correlation which, when only the original variables are used, hinder attempts to discern fundamental patterns of similarity and difference.

Just as it is possible to plot the taxa with reference to pairs of original variables, for example wing length against tail length, the taxa can be plotted on the basis of the new variables. If they are plotted against three of the new variables, the three dimensional projections presented in this study will result. The significant thing about plotting the taxa in terms of the new variables is that we know that the first three new variables, the X, Y, and Z axes of the three dimensional projections express the largest amount of the variance contained in the original matrix that it is possible for any three orthogonal variables to express. The exact amount of the variance expressed in each new variable is dependent on how correlated the original variables were and is in addition influenced by the number of original variables. For example, if a large number of uncorrelated characters are included in the original data, it will be less possible to summarize them into many fewer new uncorrelated variables. If on the other hand, the original data includes many

highly correlated characters, these can be summarized into a much smaller set of new, uncorrelated variables. The percent of the variance of the relationships among the characters represented by each new variable (factor) will always be given in the tables of the distribution of the variance among the new variables.

By examining the elements that make up the new variables, it is possible to discover the relative influence of various original variables in determining the relationships among the taxa. The elements of the new variable or factor are in reality correlation coefficients between the new variable and the original variables. These observations can be illustrated best with an example. Table 4.7 is the factor structure, or set of new variables (also known as eigenvectors) obtained from the matrix of correlations among the 13 miscellaneous external characters. The plot of the 34 mimid taxa using the first three of these new variables is given in figure 4.11.

The first factor has high positive correlations with tarsus scutellation (.860), spotting of eggs (.791), and tail shape (.710). It has high negative correlations with toe scutes (-.857), the subterminal notch (-.836), and egg color (-.746). As can be seen in the three dimensional plot, this new variable places all the species (figure 4.11, species no's. 5-29) with spotted eggs, single toe

scutes, and slight or no subterminal bill notch at one end of the 1st axis and those with two toe scutes, slight tarsus scutellation and ungraduated tails (tail shape) at the other. Similar interpretations can be made for the relationships of the other factors with the original variables. Because the new variables are orthogonal and therefore uncorrelated with each other, one can be confident that there is no interactive effect between them. Therefore, the relationships of the original variables to each new variable are independent and can be interpreted unambiguously.

A refinement of the above methodology is to "rotate" the factors, or new variables. Once the new variables have been determined, they may be rigidly shifted in space to maximize their alignment with the taxa or groups of taxa. The uncorrelated relationships and the relative amount of variance explained by the rotated set remains fixed. But the relationship of the factors to the multidimensional space and consequently the taxa positioned in it by the original variables is changed. The object is to maximize the high and low correlations of some of the original variables with the new variables and to minimize the correlations of others.

When this procedure is applied to the factor structure (only the first three are rotated since they are the ones

of greatest interest and the ones that are being plotted) the rotated factors of table 4.7 result. Interpretation of the elements is done in exactly the same manner as described before. But notice that in the rotated factors, there are many more very high positive and negative elements and likewise many more elements that are near 0.0. When these three rotated variables are used to plot the 34 species of mimids from which the 13 characters were derived, figure 4.11B results. The groups are now even more sharply aligned with respect to the three new axes and our interpretation of their placement with regard to the various original characters is enhanced.

A three dimensional object can be viewed from an infinite number of points in space. The perspectives presented in this study were chosen to most clearly show the positions of the taxa relative to one another.

DISCRIMINANT FUNCTIONS

A particularly useful multivariate technique for investigating relationships among similar groups is discriminant functions. Discriminant functions and principal components share several features, being different only in the kind of information maximized in the factors (functions). Whereas principal components are constructed to reflect the maximum amount of variance in

the original matrix of character correlations, in as few new variables as possible, discriminant functions are constructed to reflect the maximum amount of intergroup variability in as few new variables as possible. In other words they are constructed to separate, better than any other set of possible variables, the groups in the study.

In this study the groups from which the discriminant functions are derived consist of collections of individuals grouped as to species. This is in contrast to the principal components analysis in which only the previously determined mean values of the characters of each species are used in the analysis. However, in each case the analysis is done in terms of species.

Procedurally, the discriminant function analysis weights the functions determined on the basis of intergroup (interspecies) variability by the amount of variability within groups (species). Because of this, discriminant functions are especially effective at dealing with all kinds of problems of correlation among variables describing groups, including size. The elements of the new variables (the functions or factors) are, as in principal components, correlation coefficients between the original variables and the new. These characteristics of discriminant functions will be elaborated upon in chapter five where they are used as the primary tool in analyzing intergroup relationships

among the taxa of this study, based on skeletal data.

CLUSTER ANALYSIS

Whereas principal components analysis is concerned with the problem of finding sets of uncorrelated variables that will describe the position of the taxa in a multidimensional space with no assumptions with regard to the nature of groups of taxa, or even that there are groups, cluster analysis starts from the basic assumption that there are clusters to be discerned. In addition, the most commonly used procedures produce hierarchical nests of clusters.

Of the many kinds of cluster analysis that various researchers in many fields have developed, two are most frequently used in taxonomic research. These are the unweighted pair group method using arithmetic averages (UPGMA) and single link (sometimes called nearest neighbor clustering) (Sneath and Sokal, 1973). The two kinds of procedures give different results and each has its advocates. Jardine and Sibson (1971) think that on conceptual and logical grounds, single link clustering is to be preferred. Others, including Sneath and Sokal (1973) feel that the results of a cluster analysis should retain as much of the "information" of the original similarity or dissimilarity matrix as possible. The UPGMA procedure

consistently proves to be better in that respect than other methods (Parris, 1969) .

In this study of mimic relationships, I have chosen to present only the phenograms produced by the UPGMA method. This method in every case had the highest correlation with the original similarity/dissimilarity matrix. Secondly, since minimum spanning trees (see below) contain all of the information necessary to draw a phenogram using single link criteria and approximate them, and since these minimum spanning trees are fitted to the three dimensional plots of the taxa, I felt it unnecessary to present the phenograms of single link cluster analysis as such.

CLUSTER ANALYSIS VERSUS FACTOR ANALYSIS

One might ask the question "Why do both a cluster analysis and a factor analysis on the same data?" Some reasons are evident in the above descriptions of the nature of the two basic classes of procedures. In addition when one is attempting to study relationships of taxa on the basis of many variables, the two kinds of analysis are better for answering different questions. Factor analysis is better than cluster analysis at representing relationships among widely separated taxa or groups of taxa. Relationships among taxa that are quite similar are distorted, sometimes considerably so, in factor analysis.

On the other hand, cluster analysis represents these close relationships quite well and badly distorts the relationships among taxa and groups that are quite different.

For these reasons, one will usually wish to investigate the relationships among taxa using different techniques. The results must then be interpreted on the basis of the distortions the procedures are known to have on the displayed relationships of the taxa as compared to the actual relationships contained in the similarity matrix.

From the point of view of interpretation, factor analysis is markedly superior to cluster analysis. In factor analysis it is possible to study and interpret the contribution of each of the original variables to the positioning of the taxa relative to one another in the multidimensional space. In cluster analysis, however, there is no way to tell what characters are most influential in generating the correlation or distance coefficients upon which the cluster analysis and resulting phenograms are based. Therefore a factor analysis can be used to help determine how characters and sets of characters relate to each other in describing the phenetic relationships of the taxa. Cluster analysis can not be used in this fashion. Factor analysis is, then, an

analytical tool whereas cluster analysis can usually be only used for descriptive purposes.

NETWORK ANALYSIS

Network analysis falls into two basic categories, depending upon the assumptions that the researcher wishes to make about taxonomic relationships. The kinds that are of interest with regard to this study are minimum spanning trees and Wagner trees.

Minimum spanning trees are sets of links connecting the taxa of a study and which form the shortest possible connecting network among them. The sum of the lengths of the links in taxonomic distance units is minimized. This suggests the fundamental similarity between these trees and the single link cluster analysis mentioned above. Although not coincident with a single link phenogram, the minimum spanning tree will reflect the same associations of taxa and thus can be used to construct one. When fitted to a three dimensional projection of the first three factors of a principal components analysis, they help clarify some of the problems of distortion among closely placed taxa by indicating the nearest neighbors. Minimum spanning trees also indicate distortions which result from using only three factors instead of the entire set to plot the positions of the taxa relative to one another.

Wagner networks (undirected trees) were first developed to help investigate problems of relationships among lower vascular plants (Farris, 1970). They differ from the minimum spanning tree in that hypothetical taxa are created to form the nodes of a branching, cladistic network that connects the "real" taxa. The total length of the network and of course its connecting links are minimized in terms of character state changes from node to node rather than in terms of taxonomic distance (Farris, 1970).

These procedures have attracted the attention of many systematists in as much as they are logically coincident with the methodology of Hennig and Brundin. (Farris, Kluge, and Eckardt, 1970). In that these procedures can analyze large sets of variables simultaneously, they theoretically should be well suited to investigations of problems of phylogenetic relationships in difficult groups. In the present state of development of computer algorithms, they are not altogether successful. The networks that resulted when these algorithms were used to analyze the data of this study were unstable. Minor alterations of procedure such as changing the sequence in which the taxa were input caused significant variation in the suggested relationships. I therefore chose to perform a more traditional phylogenetic analysis following the

procedures of Hennig (1966) and Brundin (1966, 1968).

COMPUTATIONAL METHODS

The various numerical procedures discussed above were carried out using the following data processing systems.

1) MTSYS (Late 1973 version). A system of multivariate analysis programs developed by F. James Rohlf, John Kishpaugh and David Kirk. The system and its documentation is available from F. James Rohlf, State University of New York, Stony Brook.

2) MULDIS. A system of routines to perform multiple discriminant function analysis, based on routines in Cooley and Lohnes (1971). These were modified by Leslie P. Marcus and the author to provide extended analytic, rescaling, and graphic output capabilities.

3) Univariate analysis routines from Sokal and Rohlf (1969).

4) CLADOS. A system of programs to perform cladistic analysis. These routines were obtained from James S. Parris, State University of New York, Stony Brook.

5) GRAFPAC. A system of plotting routines. (Rohlf, 1969)

These systems were used on an IBM 370/168 computer at the university computer center of The City University of New York and on a Xerox Sigma 7 computer at Queens College of The City University of New York.

EGG WHITE PROTEINS

The egg white proteins of the mockingbirds and thrashers have been examined prior to this study by Sibley (1970) in his review of the egg whites of passerine families. Sibley's 1970 work was based on results obtained from starch gel techniques, the best methods and procedures then available. As can be seen in the plates of that work, (for example figs. 12, 13), it is most difficult to discern detailed patterns of similarity and difference. Starch gel techniques do not allow for precise resolution of many complex mixtures of proteins that are extremely similar in size and electrical charge, such as egg whites. At most, one can see broad bands, and judgments of similarity can only be based on long and careful evaluation of the electrophoretic patterns.

The present study is based upon data obtained from a process with much greater resolving capacity, isoelectric focusing. Isoelectric focusing, although an old concept, has only in recent years been developed and refined for general laboratory use. Details of the methodology can be found in Vesterberg (1973), Wellner and Hayes (1973) and the specific procedures used in this study can be found in Sibley and Prelin (1972).

In studies of protein mixtures using conventional electrophoretic methods, the solution containing the proteins is placed on or in some substrate through which

the proteins can freely move. These materials include starch gel, sucrose columns, and in recent years acrylamide gels. The system is placed in an appropriate buffer solution and subjected to a low ampere, high voltage electric current.

Proteins in solution exist as "zwitterions" and thus possess an electric charge. They act as natural buffers and as a result the net charge exhibited by a protein in solution is a function of the pH of the solution. The pH point at which the net charge of a protein is neutralized is known as the isoelectric point of the protein. In conventional electrophoretic analysis, the buffer solution is chosen to facilitate movement of the particular proteins being studied in response to an applied electric voltage. The proteins will move towards the anode if the pH of the solution is above their isoelectric point and towards the cathode if the pH is below their isoelectric point. The distance the proteins move is a function of several factors but primarily the net charge of the protein in the particular pH environment, the potential difference of the two poles and the time to which the solution is exposed to the electric field.

Isoelectric focusing procedures differ in that the protein solution is placed in a mixture that is able to form a continuous pH gradient between two buffer solutions,

one very acidic, and the other very basic. If proteins in such a system are subjected to an electric voltage, they will move, but since their movement is relative to the net charge of the protein in a particular pH environment, they will move to a point in the pH gradient at which they are "neutral" and stop. They will not move away from that point regardless of the time of exposure to the electric field. The proteins have been "focused" at their respective isoelectric pH values.

Resolving power of an isoelectric focusing system can be quite fine. Westerberg and Svensson (Rilbe, 1973) found that they could resolve myoglobins that differed by as little as .02 pH units. The resolving capacity of the system can be adjusted in that the materials used to create the pH gradient, the carrier ampholytes, can be chosen to span small sections of the pH scale, thus spreading out the gradient over the entire physical base. Typical ranges presently available are pH 3-10, pH 4-6, pH 5-8. These allow detailed studies of the proteins in a particular pH range. In this study of the egg whites of the mimids, samples were run in ranges pH 3-10, pH 4-6 and a few at pH 5-8. Because the majority of the egg white proteins are isoelectric in the range pH 4-6, this report is restricted to an analysis of the samples run in that range.

Isoelectric focusing is not without its problems.

Preparation of the acrylamide gel is tedious, requiring great precision in procedure; purity of chemicals must be very high; and careful provisions for cooling the gel must be made. Cooling is a particular problem because once the proteins have focused they become quite resistant to current flow, generating heat.

A particular difficulty occurs in comparing samples run in different gels and buffer solutions at different times, and was a serious problem in this study. The problem stems from the fact that the pH gradients established in different runs are not identical and vary in the distribution of the pH points in the gradient. This manifests itself by slight shifts of position of the same proteins run in different gels. Detailed comparisons of the positions of proteins in the different gels is quite unreliable. It is not unusual for the gradient to be different in different parts of the same gel. This phenomena is evident in plate A-1694, fig. 3.2. Fortunately, some gels are quite close in the gradients formed and are comparable. The general problem of pH gradient instability and its theoretical aspects are discussed in Chrambach et al. (1973).

AVIAN EGG WHITE PROTEIN STUDIES

Charles Sibley has been the leading exponent of

isoelectric focusing techniques in analyzing avian egg white proteins. Sibley and Prelin (1972) reported on their studies of relationships of the ratites. Following this, reports of studies of other intriguing problems in avian systematics have been published. These include Sibley and Ahlquist (1973) on the relationships of the Hoatzin; Sibley (1973a) on the relationships of the Silky Flycatchers; and Sibley (1973b) on the relationships of the Swallow-tanager.

In the studies listed above, attention has been focused on the higher categories of birds, families and above. I have attempted to use the results of isoelectric focusing analysis to examine relationships among birds at a somewhat lower level, limiting my analysis to birds currently recognized as the family Mimidae with some attention paid to closely associated groups, the thrushes and wrens.

Once an electrophoretic separation has been accomplished, the resulting gel, or thin layer slab can provide only two kinds of information about each protein that has been separated. These are: 1) the pH at which the protein is isoelectric; and 2) the amount of the protein present, relative to other proteins in the sample. It is by the comparison of these two characters of each protein between species that taxonomic judgements are made. Inasmuch as the information is fundamentally numeric,

i.e. pH values and relative amounts, the comparison is essentially an exercise in numerical taxonomy, whether accomplished by subjective evaluation or by computer.

MATERIALS AND METHODS

Samples of egg white from 13 species of mimids representing 8 of the 13 mimid genera were available for this study. I collected samples of the egg whites of Melanoptila glabrirostris and Melanotis hypoleucus in June 1972. I collected samples from Allenia fusca, Cinclotheria ruficauda, and Ramphocinclus brachyurus on St. Lucia West Indies in 1971. Samples from the other species of mimids and related groups were from the egg white collection at Yale University, where the electrophoretic separations were performed.

In the present study, it was not possible to quantitatively measure either pH values or density. It was therefore necessary to develop an indirect method of evaluating these two characteristics of each protein band visible in the photographic plates. In most cases the egg white samples were run in polyacrylamide gels a number of times. Each electrophoretic run was from the same egg white sample. That being the case, I assumed that the patterns of a single egg should be consistent between runs. Grossly, that was true. However, for quantitative

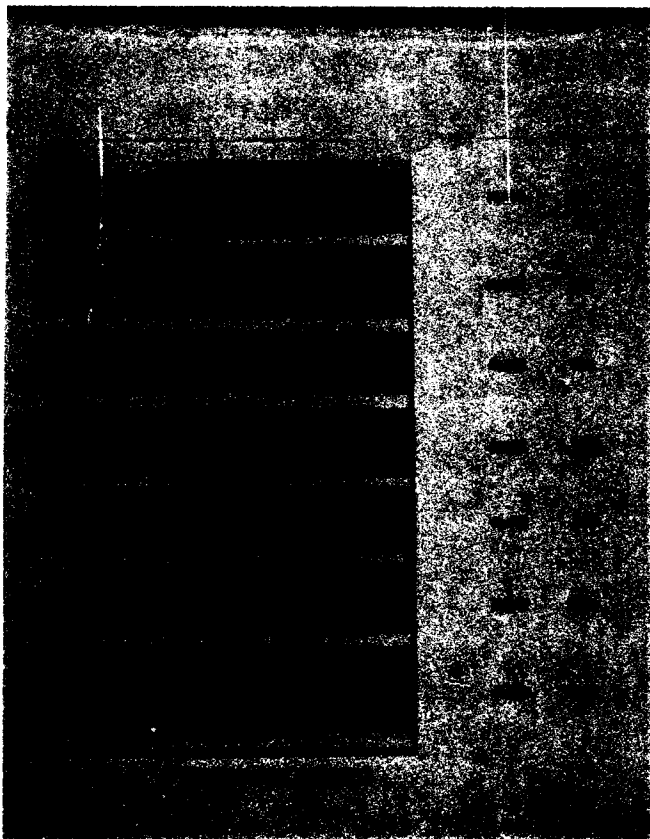
evaluation it proved to be impossible to compare the same egg white sample in different gels on the basis of the physical position of the bands in the gels. The problem is evident in Figure (3.1A) which shows the patterns of egg white proteins in Ramphocinclus brachyurus. These examples are all from two eggs collected in 1971 from the same nest, immediately after the second egg was laid. The difficulty in comparing the precise position of the proteins in the various gels is apparent.

The primary cause of differences between the gels seems to be instability of the pH gradient and slight differences in the pattern of the gradient in different runs. There are differences between regions of the same gel as can be seen in plate A-1694, figure 3.1B. However, in some gels, the gradient seems to be uniform throughout-at least to the extent that it can be determined without actual pH measurements.

The causes of the instabilities of the pH gradients are several and have been discussed at length in Chrambach et al. (1973). Whatever the cause, the end result is to make it most unreliable to try to make detailed comparisons of samples run in different gels. One way to avoid the problem is to run all possible combinations of pairs of samples side by side and visually evaluate the results. This is an extremely time consuming and financially costly

FIGURE 3.1A and 3.1B. PHOTOGRAPHS OF ELECTROPHORETIC GELS

A



B

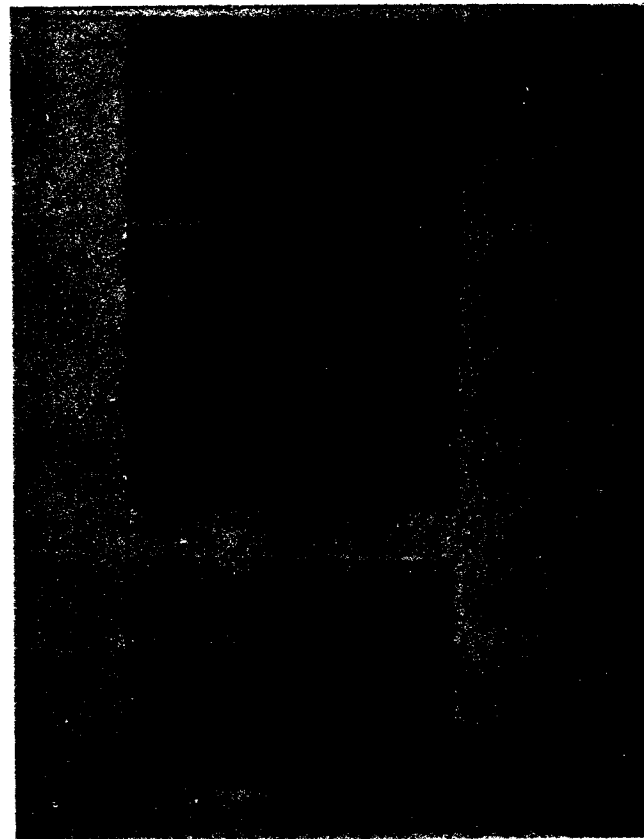
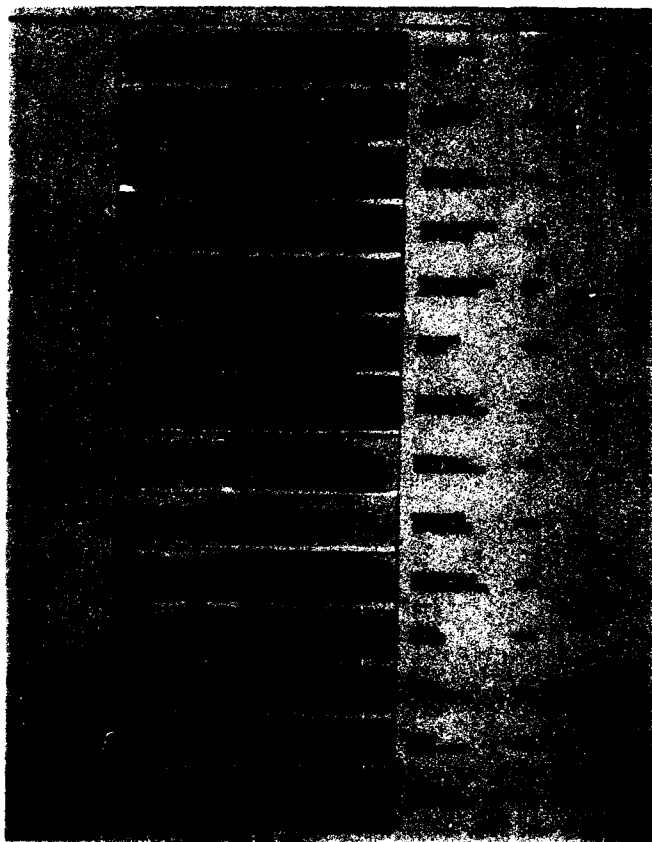
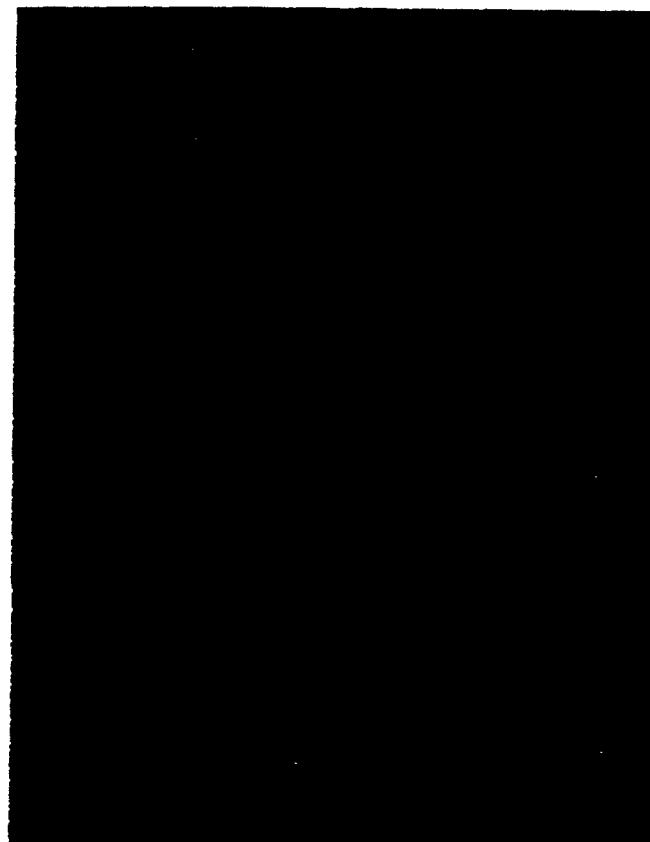


FIGURE 3.2A and 3.2B. PHOTOGRAPHS OF ELECTROPHORETIC GELS

A



B



solution to the problem. The researcher is still faced with the task of mentally integrating all of the comparisons of interest among the species being studied.

Several methods can be used to precisely measure pH values in the gel. One way is to slice the gel into thin layers, elute the slices in distilled water and then measure the pH of the solution. Another is to use a micro pH probe and touch the gel along its length, registering the pH values along the way (Charnbach et al, 1973; Radola, 1973). The concentration of the proteins can be measured by standard densitometry techniques and the relative intensity of the proteins calculated.

I attempted several approaches to comparing samples in different gels in lieu of actual measurements. Inasmuch as there was no standard reference mark in the gels, the first problem was to determine some common point that could be used as a reference. For this I chose a protein band that is present in every sample tested and in addition is in nearly exactly the same position in all the samples, regardless of species. This indicates that this protein's isoelectric point is nearly, if not exactly, identical in all the species studied.

The measured positions of the bands are given in appendix table 1. These positions were based on the

assumption that the band on the reference line in the plates, arbitrarily set at 30 mm, was homologous and identical in isoelectric point in all of the species in the study. Using a transparent millimeter ruler, with the 30 mm. mark centered on the reference band, the centers of the bands of the other proteins in the sample were measured to the nearest 1/2 mm.

As can be seen in plates 1076 and 1077, figure 3.2A, the 30 mm. reference band is not really at precisely the same position in the various samples, consequently, I made Toxostoma curvirostre, the only bird common to the two plates, the overall reference species and determined the variation of the positions of the 30 mm. bands in all the samples with reference to those of T. curvirostre. The adjustment values for each specimen are given in col. 11 of appendix table 1. Visually, Toxostoma, Mimus saturninus and Melanoptila are quite closely aligned. Mimus polyglottos and Mimus gilvus are shifted slightly to the right with Dumetella and Cinclocerthia somewhat more so. Ramphocinclus and Donacobius are shifted even more. Other plates confirmed these relative positions of the reference band at 30 mm.

Density information was coded by evaluating the relative intensity of each band within its sample. Three levels were used, light, medium and dark. The position reference band at 30 mm. and those at 37 mm. and 47 mm. were

in nearly all cases level 3, with the others varying. Overall there is much less variation in intensity than in position, as can be seen both in the plates and in the tabled values in appendix table 1.

If the gels had been uniform, the measurements of the same sample in different gels would have been the same, or nearly so. As pointed out above, they were not. I therefore calculated corrections needed to adjust each band in each sample to a single plate, that plate being the one which was most uniform and in which the bands were most sharply resolved. This effort ended in failure when I found that if I made the corrections on the basis of one species, and then with another, as the reference species, the resulting adjusted values did not agree. After many such efforts, I concluded that it was not possible to make detailed, precision comparisons of samples that were not at least run simultaneously in the same electrophoretic system, as some pairs of gels fortunately were.

Gels S-1076 and S-1077 (figure 3.2A) are such a simultaneously processed pair. They are very similar in the nature of the pH gradient and both contain samples from the same species, facilitating the comparison of samples between the two plates. These two plates include all of the currently available minid material with the exception of Minus thenca. Unfortunately, they do not include a

representative of the thrushes or wrens to which the mimids have on occasion been linked.

POLYMORPHISMS

The problem of polymorphisms of proteins is one that has complicated many studies of protein patterns in birds. This is especially true of blood serum proteins (Sibley and Hendrickson, 1970). In fact it has generally been concluded that serum proteins are not usable in many systematic studies because of their extreme variation, even within populations (Peduccia, 1970). In the case of egg whites, no comprehensive study of polymorphisms has been made. Therefore, it is not possible to evaluate the extent of the problem. To make such an evaluation, a researcher would have to systematically sample populations and carefully measure isoelectric points and the density of the protein bands.

Polymorphisms do not appear to be a serious problem in this study. As can be seen in any of the figures, especially figure 3.2A, the protein bands are aligned not only within a genus (Mimus, Toxostoma) but are in close alignment across the entire group. This would argue against significant numbers of polymorphisms in the egg white protein patterns in the 6-4 pH range. In the plates available for this study, there is no case in which

a polymorphic protein is clearly present, and only one in which it possibly is a problem.

SUBJECTIVE ANALYSIS

The first question to be reviewed is that of the position of the mimids versus the thrushes and wrens. As noted in the introduction and review of the groups, current views are strongly against close ties between the mimids and the wrens. Evidence from plate 665, (figure 3.2B), in which a wren Campylorhynchus rufinucha was compared to two mimids, Allenia and Cinclocerthia strongly supports this view. The patterns of the protein bands are strikingly different in the wren. As can be seen, there is a series of double bands at positions roughly equivalent to the protein bands in the mimid samples.

Although based on only one sample, the egg whites of mimids and wrens, as represented by Campylorhynchus rufinucha are quite different. It appears that egg white protein evidence supports the view that the two groups are not very closely related.

THRUSHES

The number of kinds of thrushes available for comparison in this study was also quite limited but does

include Turdus migratorius, Hylocichla mustelina, and Catharus fuscescens. In addition, a single sample of Myadestes ralloides and Muscicapa striata was available. Turdus migratorius is present in plate 665, figure 3.2B. Unfortunately, the proteins are not sharply focused. However, close examination shows that the alignment of the protein bands is extremely close between the mimids in the sample and the thrush. There is however, quite a dissimilarity in the density of the proteins. The thrush sample shows that the bands at higher pH values have considerably more protein than do those at low pH values, whereas the mimids have just the reverse situation.

Hylocichla mustelina was compared to Allenia fusca and Ramphocinclus brachyurus in plate 1443, figure 3.2B. Although basically similar to the mimids, the positions of the protein bands do not align themselves with those of the mimids very closely. However, from the relationship of Ramphocinclus proteins to those of the mimids in this plate, where the patterns are shifted slightly to the right, I would expect Hylocichla to match much more closely with members of Toxostoma and with Melanoptila. As can be seen in figure 3.2B, plate 1443, this is true. Hylocichla does align relatively closely with Allenia and with Mimus polyglottos.

Plate 1443, figure 3.2B also contains a sample of

Myadestes ralloides. This species, although possessing a basically similar pattern is different not only in the positions of the bands but also in the spacing of them, contributing to a quite different pattern when compared to the mimids and Hylocichla ustelina.

The most dramatic comparison of a thrush with mimids is illustrated in plate 1694, figure 3.1B. Here Catharus fuscescens can be compared to Ramphocinclus, Melanoptila and Dumetella. Without labels, the Catharus specimen cannot be distinguished from the mimids. This is true not only in the positions of the proteins and their pattern but also in the density of the bands. On the basis of plate 1694, Catharus fuscescens is in detail more like Ramphocinclus than are Melanoptila and Dumetella!

COMPARISONS AMONG THE MIMIDS

When the electrophoretic patterns of various mimids are examined, the similarity of the egg white patterns within the group is remarkable. The differences that can be observed and will be discussed below are all the more striking in this context. Plates 1077 and 1076, figure 3.2A show this quite well. In these two plates the pH gradients were very uniform and quite comparable in linear alignment, allowing the two plates to be used together in comparing patterns.

One of the most striking and immediately apparent variants within the mimid egg white patterns is the very dark band in the 20-25 mm. position of the gels. This band, although present in all of the mimids, is never as dense as in the genus Toxostoma. Within the mimids, it serves to immediately identify a member of this genus. Inspection of any of the plates which contain Toxostoma species clearly illustrates this unique feature of the egg white proteins of these species. It is all the more noteworthy as the three species of Toxostoma represented in this study represent a comprehensive cross section of the genus, based upon anatomical and ecological studies of the group. Among the mimids the distinctive Toxostoma density pattern is the most striking and discrete egg white protein character.

With regard to density estimates, analysis of the plates reveals another consistent pattern. In Cinclocerthia, Ramphocinclus, Dumetella, and Allenia, the density of bands from the 30 mm. to the 60 mm. positions are quite uniform. In all others the band at about 60 mm. tends to 'wash out' indicating somewhat lesser amounts of protein. In Toxostoma, the band at about 50 mm. is also weaker. As will be seen in the quantitative analysis, these patterns of density strongly clump groups of mimid species. In Melanoptila, the 60 mm. band is only slightly weaker than in Cinclocerthia, Ramphocinclus, Dumetella and

Allenia, although I coded it one step lower.

The Melanotis sample available was not the best quality and although the protein bands are evident, they are rather weak. Judging the density of these bands was difficult. However, they seem to be more like the patterns of Mimus, and Toxostoma, where the 50-60 mm. bands are significantly less intense. In fact, the 60 mm. band is relatively so weak that I coded it as level 1. With better material, this relative coding may indeed be different.

Donacobius atricapillus is best evaluated in plate 915, figure 3.1B. Its density pattern is different from all other mimids. It is strong at the 30 mm. position, becoming weak above that until the bands in the 60-70 mm. region where the density increases. This pattern distinguishes the species within the mimids.

NUMERICAL ANALYSIS

For numerical analysis, I restricted my data to that obtained from plates 1076 and 1077 because, as discussed above, these were the only two plates that I felt could be considered equivalent in the nature of the pH gradient through which the proteins were dispersed. Matrices of correlation coefficients and average taxonomic distance were computed between all species for protein density

codes, adjusted position codes, and the two combined. These matrices were analyzed with clustering procedures and by principal components analysis. The results of the principal components analysis are graphically depicted in figures 3.3-3.5. Minimum spanning trees are fitted to the projections.

Figures 3.3 and 3.4 give separate graphical representations of the two components of the data, density estimates and positions of the proteins in the gradients. As is evident, position information is more complex than is density. With regard to density Ramphocinclus, Cinclocerthia, and Alenia are coincident, as are Mimus gilvus and M. saturninus. A third coincident group consists of Toxostoma curvirostre and T. lecontei. Donacobius is placed some distance from its nearest neighbor.

The three dimensional projection of the principal components analysis of the adjusted positions (figure 3.3) shows no coincident groupings. One can, however, visually discern several discrete clusters. The two catbirds Dumetella (1) and Melanoptila (2) are closely associated, with the Blue-and-white Mockingbird (3) only a little more distantly located. The minimum spanning tree links these three to another rather coherent cluster, the three Toxostoma thrashers (7,8,9). Another cluster is formed in the center of the projection by two of the mockingbirds,

FIGURE 3.3. THREE DIMENSIONAL PROJECTION OF 13 MIMID SPECIES ONTO PRINCIPAL COMPONENT AXES DERIVED FROM EGG WHITE POSITION DATA.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	MELANOP (2)	0.573
MELANOP (2)	TOX CUR (8)	0.548
TOX CUR (8)	TOX LEC (9)	0.443
TOX LEC (9)	TOX RUP (7)	0.402
MELANOP (2)	MELANOT (3)	0.700
TOX LEC (9)	MIM SAT (6)	0.935
TOX LEC (9)	MIM POL (4)	1.158
MIM POL (4)	CINCLOC (11)	0.350
CINCLOC (11)	MIM GIL (5)	0.237
MIM POL (4)	ALLENIA (12)	0.540
MIM GIL (5)	DOWACOB (13)	0.768
DOWACOB (13)	RAPPHOC (10)	0.603

FIGURE 3.4. THREE DIMENSIONAL PROJECTION OF 13 MIMID SPECIES ONTO PRINCIPAL COMPONENT AXES DERIVED FROM EGG WHITE DENSITY DATA.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	RAPPHOC (10)	0.000
DUMETEL (1)	CINCLOC (11)	0.000
DUMETEL (1)	ALLENIA (12)	0.000
DUMETEL (1)	MELANOP (2)	0.903
MELANOP (2)	MIM POL (4)	0.000
MELANOP (2)	MEL HYP (3)	0.593
MELANOP (2)	MIM GIL (5)	0.806
MIM GIL (5)	MIM SAT (6)	0.000
MIM GIL (5)	TOX RUP (7)	0.931
TOX RUP (7)	TOX CUR (8)	1.087
TOX CUR (8)	TOX LEC (9)	0.000
MEL HYP (3)	DOWACOB (13)	1.622

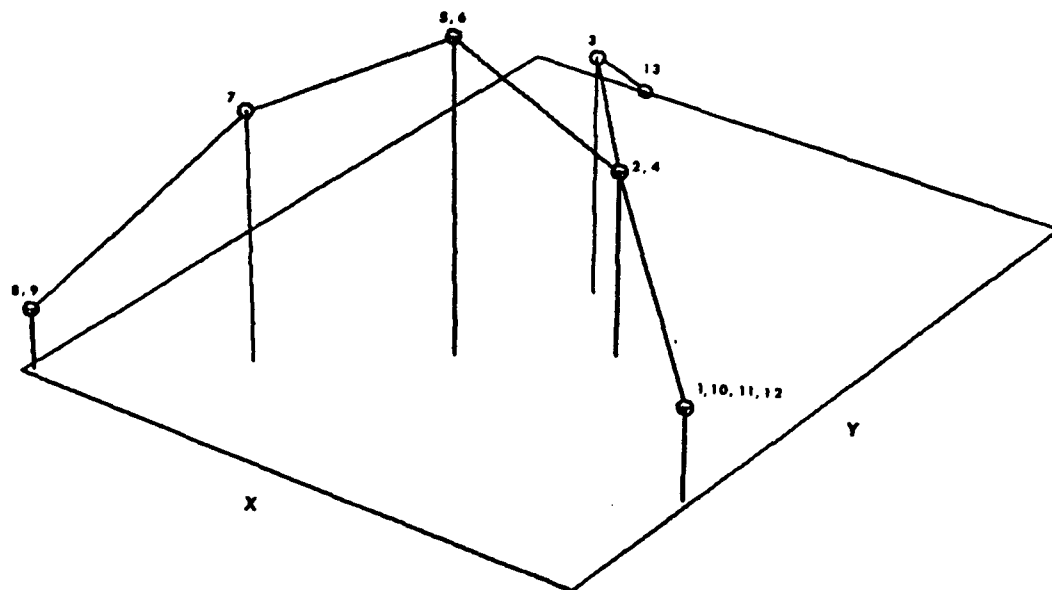
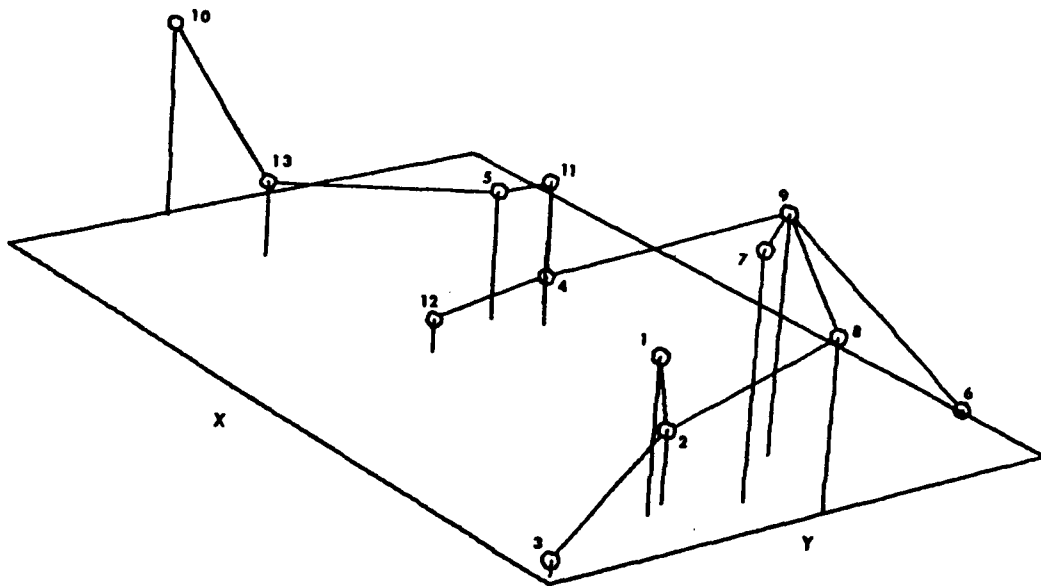
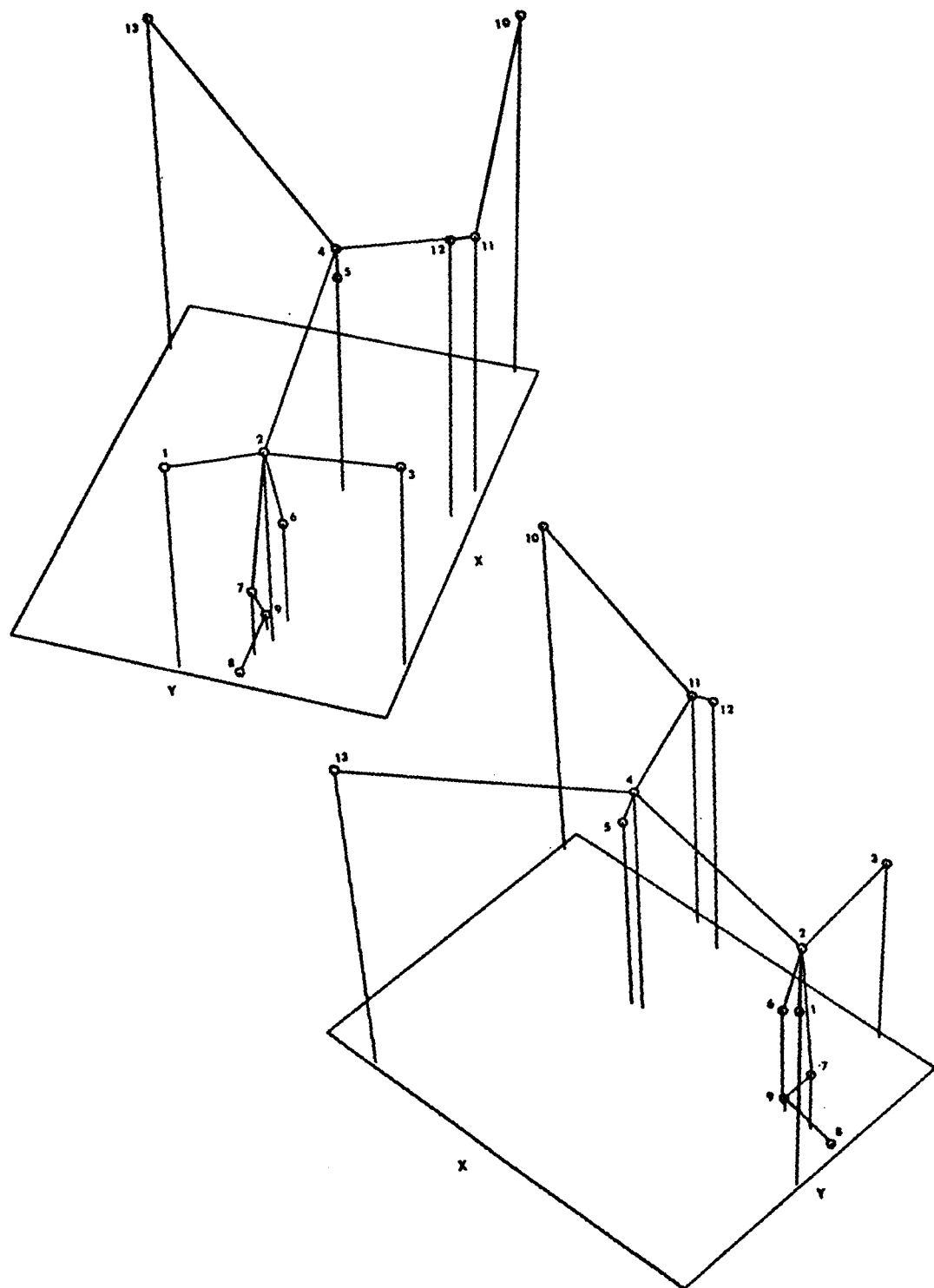


FIGURE 3.5. THREE DIMENSIONAL PROJECTION OF 13 MIMID SPECIES ONTO ROTATED PRINCIPAL COMPONENT AXES DERIVED FROM COMBINED EGG WHITE POSITION AND DENSITY DATA.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	MELANOP (2)	0.723
MELANOP (2)	MEL HYP (3)	0.659
MELANOP (2)	TOX RUF (7)	0.932
TOX RUF (7)	TOX LEC (9)	0.755
TOX LEC (9)	TOX CUR (8)	0.343
MELANOP (2)	MIM POL (4)	0.962
MIM POL (4)	MIM GIL (5)	0.585
MIM POL (4)	CINCLOC (11)	0.632
CINCLOC (11)	ALLENIA (12)	0.539
CINCLOC (11)	RAMPHOC (10)	0.947
MELANOP (2)	MIE SAT (6)	0.996
MIM POL (4)	DONACOB (13)	1.309



(Mimus polyglottos (4) , M. gilvus (5)), Allenia (12) and Cinclocerthia (11). Three species are oddly placed on the basis of the position data. Most peculiar is the placement of Mimus saturninus, (6). This bird is far removed from the other Mimus species to a position closer to the Toxostoma group.

Two things seem to contribute to the placement of M. saturninus. First, the lower bands are somewhat different in position compared to the other Mimus species. This is particularly true of the band at the 21 mm. position. In some of the plates available for this study, that band appeared to be doubled. Yet in the plates chosen for numerical analysis only a single band is clearly evident. If there are in actuality two bands, they may represent a polymorphism. Since it is not clear on plate 1076, and no procedure was developed to code for polymorphisms, the placement of the species must be viewed with suspicion. An additional factor contributing to the shift of this species towards the Toxostoma group was the adjustments applied to reflect the variation in the 30 mm. band. As can be seen in the table of data, appendix table 1, both M. polyglottos and M. gilvus were shifted whereas M. saturninus was not. The net effect was for the unshifted values for M. saturninus to be more similar to those of the Toxostoma species.

The other species that seems peculiarly placed is Ramphocinclus (10). This seems to be primarily due to the correction factor added to the position codes. It was shifted significantly, which sets this species apart from all the others. An examination of other plates indicated that the species is consistently shifted slightly in reference to other mimids although not quite as much as is suggested in plate 1077, figure 3.2A. Until such time as it is possible to accurately measure pH values, it is not possible to be more exact in analyzing the precise position of this species relative to other mimids on the basis of egg white data.

When adjusted position information and density information are combined, (figure 3.5) the basic organization suggested by the position data alone is retained with some shifts caused by adding the very sharply defined pattern of the density information. Basic groupings remain unchanged. The Toxostoma group is still together and better defined in that Mimus saturninus has been separated. The cause of this shift is the strong influence of the unusual nature of the density of the protein at the 25-27 mm. position of the Toxostoma specimens. The central cluster has been disassociated slightly, with the shift of the West Indian species (10-12) off to one side, although the minimum spanning tree still links them to M. polyglottos (4). Ramphocinclus (10) is

now linked to the other West Indian species through Cinclocerthia (11) and through it to the Mimus group.

Donacobius (13) is now distantly removed from the rest of the species. This is apparently the result of the peculiar density pattern present in the egg white of this species. This species was somewhat different in its protein pH values and that difference combined with the aberrant density pattern serves to separate it. Mimus saturninus (6) although still positioned in the multidimensional phenetic space near the Toxostoma group is different enough for the minimum spanning tree to link it to Melanoptila (2). If it were not for the peculiar pattern of the protein bands between 15 and 30 mm, M. saturninus would have clearly been linked to the other Mimus species.

If the correlation coefficients matrix and the matrix of average distances are analyzed with a hierarchical clustering procedure such as the unweighted pair group using arithmetic averages, a basically equivalent picture of phenetic relationships among these mimid species based upon egg white evidence emerges. The phenogram derived from the distance matrix (figure 3.7) does an excellent job of representing the groupings that can be seen in the three dimensional projection. In fact there is not a single discrepancy between the clusters formed by the UWPMA

FIGURE 3.6. PHENOGRAM FROM CORRELATIONS OF 13 MIMID SPECIES BASED ON EGG WHITE PROTEINS.

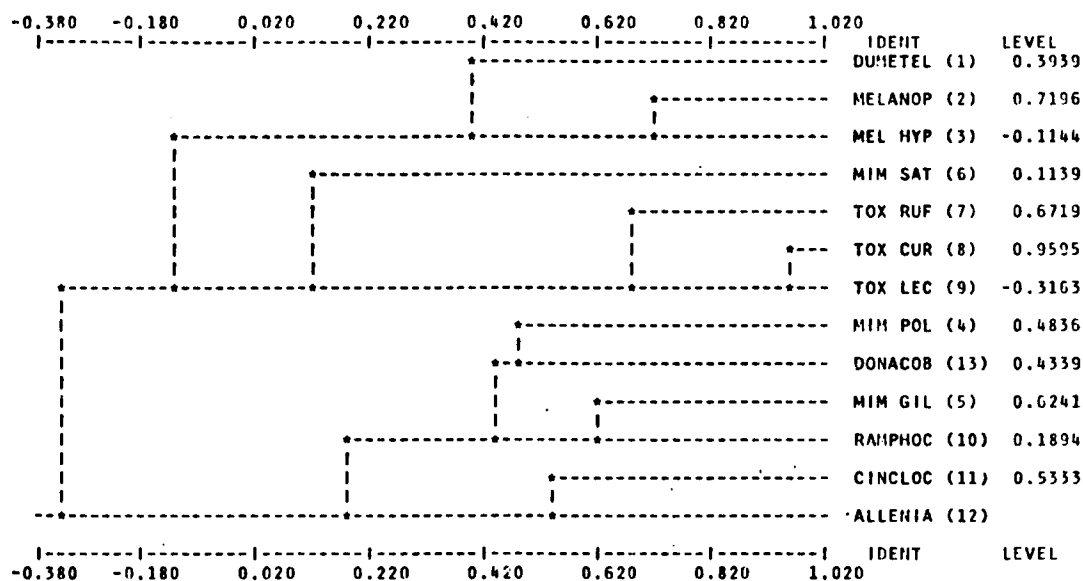
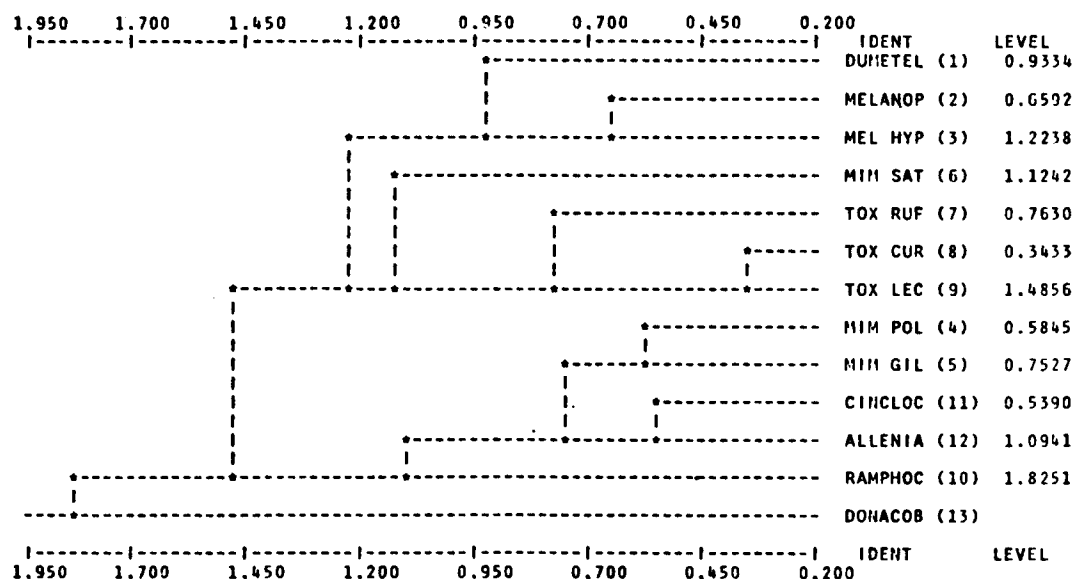


FIGURE 3.7. PHENOGRAM FROM DISTANCES AMONG 13 MIMID SPECIES BASED ON EGG WHITE PROTEINS.



procedure and those discernable in the three dimensional projection.

The phenogram derived from the correlation matrix (figure 3.6) shows some shifts in phenetic relationships among the species although only within the Mimus-West Indian cluster. Here M. polyglottos has been paired with Donacobius and M. gilvus with Ramphocinclus. These two (Ramphocinclus, and Cinclocerthia) are quite far removed from the Mimus-West Indian cluster in the three dimensional projections. Examination of the original data matrix in appendix table 1 and the factor structure of the correlation matrix (table 3.1) do little to help explain this association.

SUMMARY

The overall picture of the phenetic relationships of the mimid species based on egg white protein data is of two major clusters of species. One group consists of the catbirds and Blue-and-white mockingbird plus the Toxostoma thrashers. The second group includes the Mimus species (M. saturninus excepted) and the West Indian genera, including Ramphocinclus. In all analyses, with the exception of the unweighted pair group clustering of the correlation matrix, Donacobius is isolated from the rest of the group.

In comparing this picture of relationships with traditional groupings of mimid species, two major differences are apparent. The first is that Dumetella is probably not a sister species of the Black Catbird, Melanoptila, but is rather a sister species to the pair Melanoptila - Melanotis. In view of the less than high quality sample of Melanotis egg white, it may be wise to accept this arrangement of these three species with caution pending confirmation with additional egg white samples.

The second major difference between the results of this study and traditional views is the distinct separation of the Toxostoma thrashers from Mimus. These two genera have always been considered to be quite closely related. Although the unique quality of the density pattern of the Toxostoma species instantly sets them apart from other mimids, the position information alone separates them. In the three dimensional projection based on adjusted positions (figure 3.3) these three species (7-9) serve as a bridge between the catbirds (1-2), the Blue-and-white Mockingbird (3) and Mimus (4-5). The minimum spanning tree connects them to M. polyglottos. This arrangement is reflected in the phenogram derived from the correlation matrix of position data (figure 3.6). With the addition of the density information, this link is lost and Toxostoma is paired with Melanoptila in both phenograms and projections of the combined position and density information (figure

3.5).

A particularly interesting aspect of the egg white evidence is the consistent clustering of at least two of the West Indian mimid species with two species of the genus Mimus. No evidence has ever been offered to suggest possible links between these species and mainland species. In that light, the egg white evidence is intriguing, although the suggested affinity to Mimus contradicts the results of the phylogenetic analysis of chapter 6. The close pairing of Allenia and Cinclocerthia supports the suggestion of Zusi (1969) regarding relationships between these birds and agrees with the phylogenetic analysis.

EXTERNAL CHARACTERS

In avian systematics, at least below the family level, the primary characters that have been used to infer relationships have been characters of color, pattern, and miscellaneous features relating to bills, feet and other structures observable in museum skins. Miscellaneous characters include such things as relative size of rectal bristles, shapes of wings and tail, distinctive features such as crests, bare areas, and unusual bill morphology. All of these characters figure prominently in the diagnoses of avian genera, especially within the Passeriformes, an order noted for its lack of sharply delineated groups. In fact any character that exhibits discrete states is likely to have figured heavily in the diagnosis of some passerine genus.

No such discrete characters have been discovered for most passerine genera and we therefore find that many, if not most, are diagnosed on the basis of combinations of character states. Problems of borderline genera that cannot be assigned with precision to a particular group are inevitable. Genera and higher taxa have been formed on the basis of taxonomists' evaluations of overall similarity and dissimilarity between forms, a phenetic process. Occasional modifications of the phenetic groupings is made by an injection of opinions, feelings or assumptions about the phylogenetic relationships among the forms gathered together to constitute taxa above the species level.

A group that well illustrates the problems and the less than definitive results of traditional systematic methods is the complex to which the mockingbirds and thrashers belong, the "Old World insect eaters". The complex consists of four major divisions, the Sylviinae, the Timileiinae, the Muscipinae, and the Turdinae. The difficulties of sorting out discrete groups within the complex are so great and the similarities between many of the members of the groups so high that, in Peters' Checklist of Birds of the World (Mayr and Paynter, 1964), the entire complex is considered as a single family, the Muscicapidae. Many of the genera that are of a particularly generalized nature within the complex have often been moved back and forth between the subdivisions, especially between the Sylviinae and Turdinae and between the Timileiinae and Turdinae. Other smaller groups, including the wrens (Troglodytidae), the dippers (Cinclidae), and the mockingbirds and thrashers are usually considered to be closely allied to the Muscicapidae.

In order to evaluate directional changes in character states within a group being studied, it is necessary to have some opinion as to the group's most likely sister group. As reviewed in chapter 2, opinion has swung once again to the view that the mimids are most closely related to the thrushes. Although most of the external characters of the mimids have not been directly compared to thrush

groups in the phenetic analysis of external characters, certain ones of them that will figure in the phylogenetic analysis of chapter 6 are discussed.

The classic diagnostic characters of the Turdinae are the spotted plumage of the young birds and the booted tarsus (Seebohm, 1881). Unfortunately these are not consistently successful in assigning many species considered to be thrushes. For example, some of the scrub robins (Erythropygia) of Africa have quite distinct scutellation on the tarsus. They do have spotted young however (actually as much mottled and streaked as spotted). The presence of spotted or mottled plumage in young birds has fewer exceptions than the booted tarsus in the groups presently assigned to the Turdinae.

The mockingbirds and thrashers are somewhat equivocal in these two classical characters. In some mimids, the scutellation of the tarsus is so slight that only with close examination under magnification can hints of divisions between the scutes be seen. Many individual specimens of various thrush genera show as much scutellation as do the mimid specimens with minimum scutellation. The mimid species in which tarsus scutellation is particularly weak are Ramphocinclus brachyurus, Dumetella carolinensis, and Cinclocerthia ruficauda.

With regard to spotted plumages of the young, the general pattern is for young mimids to have ventral spotting. Dorsal spotting which is quite common in most but not all young turdines, is not evident. Dorsal markings in the young mimids are, if present, rather like the adults of the same species and are usually better described as streaks than spots. In addition, among thrushes, the streaks are usually formed by a light region along the shaft of the feather with a dark border. The dorsal streaks of young mimids that have such are the reverse with dark central regions with light borders.

Nearly all young mimids have ventral markings, either spots or streaks. The exceptions are the three sickle-billed Toxostoma thrashers, T. lecontei, T. redivivum and T. dorsale, and Donacobius. In the case of Melanoptila and Melanotis caerulescens, the coloration of the young birds is so dark that patterning is not apparent. The young of Melanotis hypoleucus show mottling very early as the white of the adult bird's breast is mixed in with the dark slaty blue.

The fact that of the thirteen genera recognized among the mimids, eight are monotypic and the literature indicates that only the vaguest notions of affinities among them have been given suggests that previous workers were unable to make rationally satisfying associations. I have

used numerical phenetic techniques to analyze an extensive set of external characters in an attempt to demonstrate the purely phenetic basis upon which mimid taxa are based and secondly to clarify and extend the phenetically based associations. A further objective is to discern, if possible, the kinds of characters that have been most influential in suggesting groupings of taxa.

COLOK

Color alone is not generally considered to be too useful in grouping birds into meaningful associations. Within a single genus, established on other grounds, can be found birds that differ quite strikingly in color. Among the mimids, color is a distinctive character in only two genera: Melanotis, the blue mockingbirds, and Melanoptila, the Black Catbird. Color is, however, useful in conjunction with pattern. It was therefore necessary to develop a method of coding the species as to color.

Unfortunately, colors in birds change during the course of the annual cycle. I therefore arbitrarily chose representatives of each species that were in the freshest possible plumage. These specimens were all from the collection of the American Museum of Natural History. In most cases the birds were collected shortly after the postnuptial molt. It was occasionally necessary to use

TABLE 4.1. COLOR CODES FOR BODY REGIONS.

REGIONS:

1	2	3	4	5
CROWN	BACK	RUMP	THROAT	BREAST
6	7	8	9	
CRISUM	FLANKS	WING	TAIL	

COLOR SCALES FOR EACH BODY REGION:

VALUE	GREY	BROWN	BLUE	COLOR INTENSITY
0		ABSENT	ABSENT	
1	WHITE	CREAMY	BLUISH WHITE	LIGHT
2	GREY CAST	BROWN CAST	BLUE CAST	MEDIUM
3	LT. GREY	LT. BROWN, BUFF	LT. BLUE	STRONG
4	MED. GREY	RUFUS, CINNAMON	INDIGO	
5	DARK GREY	MED. BROWN	MED. BLUE	
6	BLACK	DARK BROWN	DARK BLUE	

birds that were slightly worn. However, I did not attempt to code subtle differences of coloring and therefore feel that I obtained a reasonable measure of color characteristics of each species.

The coding system used to evaluate color in the mimids is given in table 4.1. The grey scale is used twice in each body area because of patterns. It is not so much a color as a measure of the darkness of a region of the body or a feather. One of the two grey characters pertains to the dark markings in an area. The other pertains to the light. These two grey characters occasionally caused some confusion because a decision had to be made as to whether an area was light with dark trim or the reverse. Usually there was little difficulty in making the decision. Sometimes, the balance is about even and admittedly there is some arbitrariness involved. On top of the grey foundation, colors are applied. In the case of the mimids, there are only two, browns and blues. Since the same shade of a color can occur in various intensities, I added a character to each area to code for three levels of color intensity. This logical framework is not meant to correlate with the way in which color is actually formed in feathers but rather to code its visual appearance. The color codes for all of the species are given in appendix table 2.

The coding system can be illustrated using the crown of Mimus saturninus as an example. In this species, the crown feathers are centrally quite dark. They are edged with a lighter border. Using the grey scale in Palmer (1962) as a guide, I coded the crown of the species as: Gray I = 5; Gray II = 4. There is an overlay of color which I coded as Brown = 5. The intensity of this color is low therefore it was coded as 1. The color codes for the crown of M. saturninus are therefore:

Gray I	Gray II	Brown	Blue	Intensity
5	4	5	0	1

It is necessary to include blue as a character for each area because of the blue mockingbirds.

NUMERICAL ANALYSIS OF COLOR DATA

Color is primarily useful in conjunction with patterns in grouping species of birds. In order to better understand what information color contributes, the associations of species on the basis of color alone will be given.

The matrix of color information has a built in difficulty in that there are considerable amounts of redundancy and character correlation present. This is a

particular problem in clustering using distance measures since distances are additive over characters. The correlation matrix derived from such a character set is less subject to this effect (see chapter two).

The high correlation between characters is reflected in the eigenvalues extracted from the matrix of character correlations. The original taxon by character matrix is 34 (34 taxa) by 45 (45 characters). Extracting the principal components from the 45 X 45 matrix of correlations between the characters gives the factors in table 4.2. The eigenvalues associated with the factors show that 85 of the variance contained in the original 45 X 45 matrix can be summarized in a matrix of 45 characters X 9 factors.

The 34 taxa were projected onto the principal components factor structure. The graphic representation of the first three axes (factors) is given in figure 4.1. The three axes contain 27, 18, and 12 percent respectively of the total variance of the original 34 X 45 data matrix. (Percentages are from table 4.2.) Three basic groupings are clearly detectable. A group of birds with little or nothing other than greys is formed by Dumetella (1), Melanoptila (2), and two Mimus species, M. polyglottos (5) and M. gilvus (6). This group connects to a large assemblage of grey-brown species through M. longicaudatus (9) the "greyest" of the South American species. The two

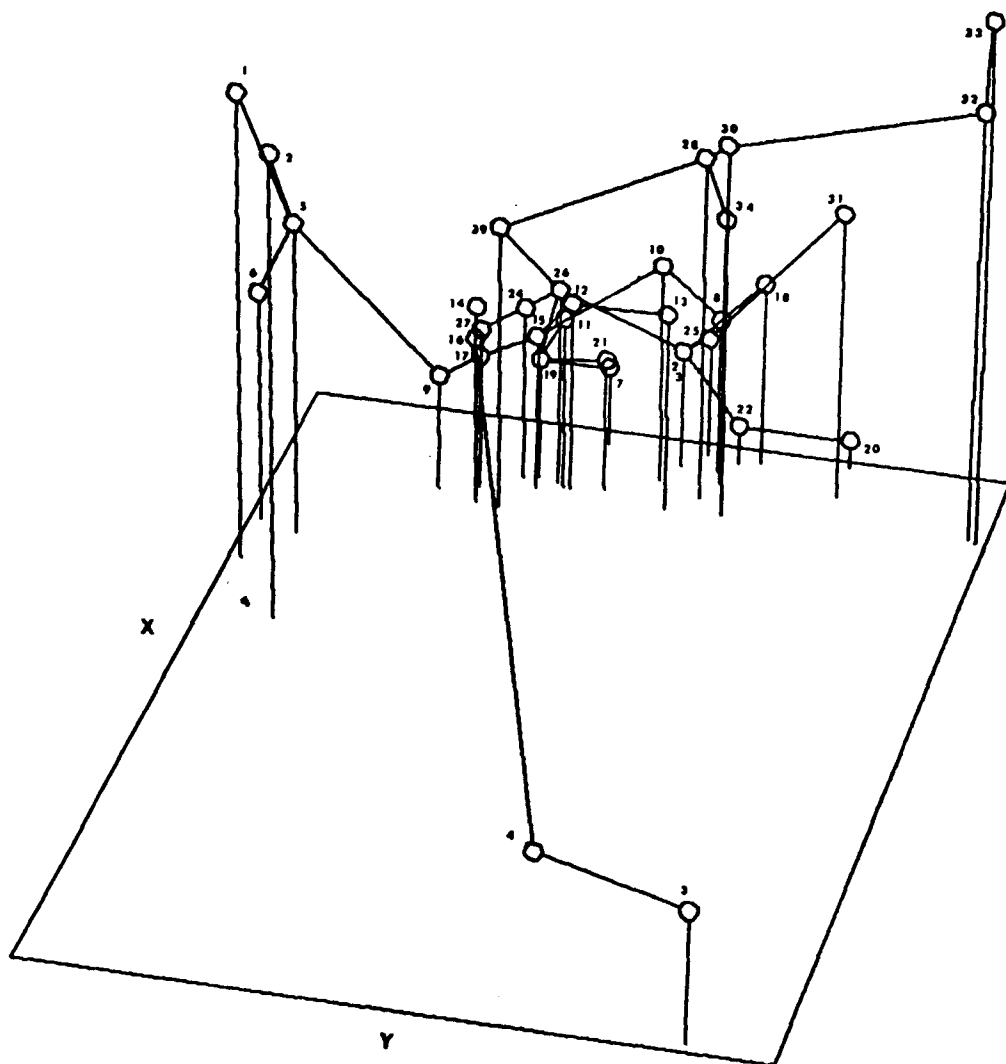
TABLE 4.2. EIGENVALUES AND PERCENT TRACE FOR FACTORS
DERIVED FROM 45 COLOR CHARACTERS.

TRACE = 45.000000

FACTOR NUMBER	EIGEN VALUE	PERCENT OF TRACE	ACCUM. PERCENT
FACT0001	12.03772	26.75	26.75
FACT0002	8.26521	18.37	45.12
FACT0003	5.35747	11.91	57.02
FACT0004	4.01180	8.92	65.94
FACT0005	2.42946	5.40	71.34
FACT0006	1.99834	4.44	75.78
FACT0007	1.56844	3.49	79.26
FACT0008	1.30897	2.91	82.17
FACT0009	1.25176	2.78	84.95
FACT0010	0.94418	2.10	87.05

FIGURE 4.1. THREE DIMENSIONAL PROJECTION OF 34 HIRID SPECIES ONTO PRINCIPAL COMPONENT AXES DERIVED FROM COLOR CHARACTERS.

THE MINIMUM SPANNING TREE		
I	J	LENGTH
DUMETEL (1)	HIM POL (5)	0.983
HIM POL (5)	HIF GIL (6)	0.655
HIM POL (5)	HIM LON (9)	0.881
HIM LON (9)	NES HAC (17)	0.461
NES HAC (17)	NES MEL (15)	0.346
NES HAC (17)	NES PAR (16)	0.476
NES PAR (16)	NES TRI (14)	0.401
NES MEL (15)	HIF TRI (12)	0.660
HIM TRI (12)	HIM DOR (13)	0.620
NES MEL (15)	HIF PAT (11)	0.695
HIM PAT (11)	OREOSCO (19)	0.609
OREOSCO (19)	TOX LON (21)	0.695
OREOSCO (19)	TOX CUR (26)	0.696
TOX CUR (26)	TOX CIN (23)	0.685
TOX CIN (23)	TOX GUT (22)	0.623
TOX CIN (23)	TOX OCE (25)	0.685
TOX CIN (23)	HIMODES (18)	0.710
NES MEL (15)	HIF SAT (10)	0.752
HIM SAT (10)	HIM THE (8)	0.577
TOX CUR (26)	TOX BEN (24)	0.753
TOX BEN (24)	TOX LEC (27)	0.722
TOX GUT (22)	TOX RUF (20)	0.795
TOX CUR (26)	TOX DOR (29)	0.875
TOX DOR (29)	TOX RED (28)	0.859
OREOSCO (19)	HIM GUN (7)	0.883
TOX RED (28)	CINCLOC (30)	0.903
HIM POL (5)	MELANOP (2)	0.915
CINCLOC (30)	MARGARO (32)	1.043
MARGARO (32)	ALLENIA (33)	0.690
TOX RED (28)	DOPACOB (34)	1.074
TOX OCE (25)	RAWPHOC (31)	1.109
NES PAR (16)	MEL HYP (4)	1.957
MEL HYP (4)	MEL CAB (3)	1.692



blue mockingbirds (3-4) form a distant cluster with no additional species. It connects into the main group among the greyer members of the grey-brown cluster. The second axis (Y) of the system distributes the birds in a dark brown to no brown, all grey pattern with Margarops (33) and Allenia (32) at one extreme and the catbirds and pure grey Mimus species at the other. The vertical axis (Z) represents primarily darkness with some interactive effects of color and intensity.

The details of the relationships within the tightly knit grey-brown cluster are best examined in the phenograms produced by clustering the matrices of correlations and average taxonomic distance between the taxa. As can be seen from figures 4.2 and 4.3, color alone does a relatively good job of grouping the species. The broad groupings are reasonably close to usually accepted views of associations of mimid species. However, there are many specific associations that are quite different. For example, in the clusters based on correlation coefficients, Oreoscoptes is paired with M. patagonicus. This pair is then clustered with M. gundlachi. M. triurus and M. dorsalis are paired, as would be expected, but the two are placed outside the bulk of the Mimus species, being clustered with the West Indian mimids. This is probably a result of the large amount of brown color found in these two Mimus species.

FIGURE 4.2. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF CORRELATIONS RESULTING FROM COLOR CHARACTERS.

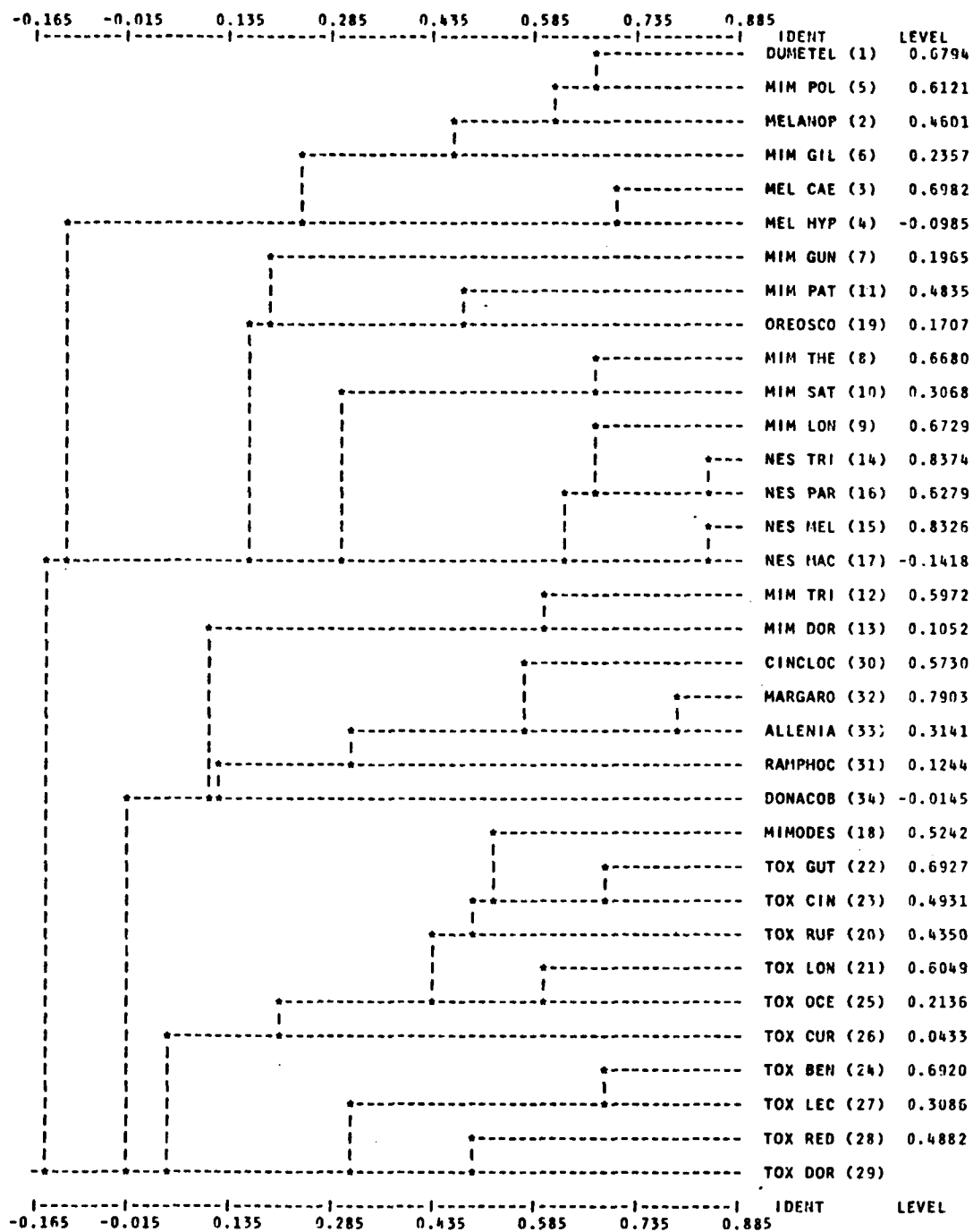
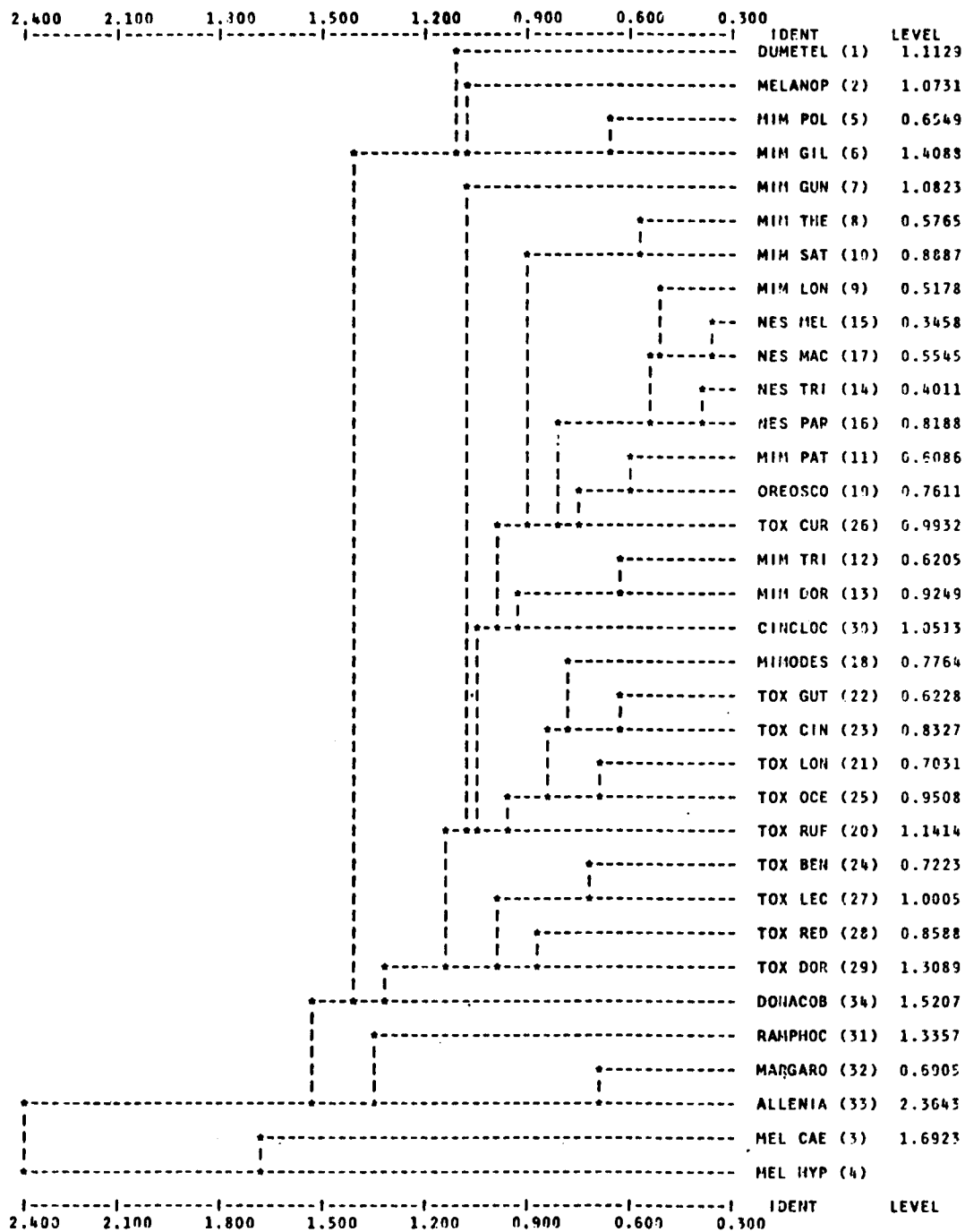


FIGURE 4.3. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF AVERAGE DISTANCE RESULTING FROM COLOR CHARACTERS.



The cluster analysis based on the distance matrix again is not grossly bad but as with clusterings based on the correlations among species, detailed placements are peculiar when compared to traditional views. For example, Toxostoma curvirostre is removed from the rest of Toxostoma and placed in the Minus-Nesomimus complex.

In conclusion, colors are able to suggest large clusters within the group that are reasonably consistent with current taxonomic views. Within the large clusters, however, the associations of species are not very successful in terms of currently accepted views of relationships.

PATTERNS

Patterns of birds are more often used as a source of characters than are colors alone. Patterns in conjunction with colors are one of the primary ways in which we identify species of birds. Very often birds which are closely related (or at least are assumed to be) share similar patterns. Unfortunately there are enough exceptions to make reliance on patterns, even in conjunction with color, risky when grouping species into higher taxa if the taxa are to represent monophyletic groups. A particularly dramatic case where color and pattern would lead one astray is the sharp contrast in

appearance of Turdus merula and Turdus philomelos. Among the mimids, the sickle-billed thrashers are quite different from the rest of the genus Toxostoma, especially in patterns.

Ripley's 1950 study of the thrushes illustrates the variable way in which such characters can be and are handled by most avian systematists. On the one hand he used color patterns and habits to synonymize the genus Tychaedon with Erythropygia. On the other, he disavowed distinctive pattern characters of various small or monotypic genera of thrushes, lumping them with what he considered to be allied groups. Similar examples can be found in the taxonomic treatment of many groups.

Among mimids, patterns can be used to group several species. The genus Mimus is consistent in having considerable amounts of white in both wings and tail when compared with other mimids. This pattern, in subdued form, is present in most of Toxostoma also. The bulk of the genus Toxostoma has spotted breasts as adults whereas T. redivivum, T. lecontei, and T. dorsale do not. Yet the monotypic genus Oreoscoptes also has a spotted breast and is not included in Toxostoma, although many taxonomists consider it to be closely related.

The numerical codes for patterns in the mimids are

given in appendix table 3. The same body regions coded for color were coded for pattern with the exception of the throat. Patterns in the wings and tails of the mimids are more complex than general body regions and therefore require a more elaborate coding scheme. Wing and tail feathers were coded to show reversal from the normal dark with light trim to white with dark trim because the color codes were not determined for the subdivisions of these regions as were the the pattern codes.

NUMERICAL ANALYSIS OF PATTERN DATA

Coding of the patterns of the mimids following the scheme outlined in table 4.3 results in 39 characters. The character matrix was analyzed using principal components procedures to produce the factor structure in table 4.4. The 34 X 39 matrix can be reduced to a 34 X 9 matrix containing 84 of the variance of the original. The first three factors account for 28.0, 12.3, and 10.7 percent of the variance respectively. A three dimensional plot of the projection of the taxa onto these factors is given in figure 4.4.

The taxa are separated into three distinct groups. One consists of the bulk of the genus Toxostoma, (20-25) plus Oreoscoptes (19). Another is composed of the members of the two mockingbird genera Mimus and Nesomimus (5-17).

TABLE 4.3. PATTERW CODES.

BODY REGIONS:

1	2	3	4
CROWN	BACK	RUMP	THROAT
5	6	7	8
CRISUM	FLANKS	WING	TAIL

CONTRAST SCALE:

1 = SLIGHT 2 = MEDIUM 3 = STRONG

PATTERNS AND MARKS:

STREAKS: FEATHERS WITH CONTRASTING AREA ALONG
SHAFT

SPOTS: PROMINENT MARKINGS ON OR NEAR ENDS OF
FEATHERS

BARRS: TRANSVERSE MARKINGS ALONG THENTH OF FEATHERS

SUPERCILLIARY LINE: LINE DORSAL TO EYE

SUB MALAR STREAK

MASKS: (CONSISTS OF FOLLOWING REGIONS)

LORES

POST ORBITAL: STREAK BEHIND EYE

AURICULAR AREA

STREAKS IN AURICULAR FEATHERS

BREAST BAND: CONTRASTING AREA BETWEEN ABDOMEN AND THROAT

COLLAR: CONTRASTING BAND CONTINUING UP AND AROUND LOWER
NECK

FIRST WING BAR

SECOND WING BAR

INNER WING

RECTRIX EDGES

RECTRIX TIPS

WING AND TAIL PATTERN CODES:

WINGS	TAIL
PRIMARY EDGES	RECTRIX I EDGE
PRIMARY TIPS	RECTRIX I TIP
SECONDARY EDGES	RECTRIX II-IV EDGES
SECONDARY TIPS	RECTRIX II-IV TIPS
PRIMARY COVERTS	RECTRIX V-VI TIPS

CODES

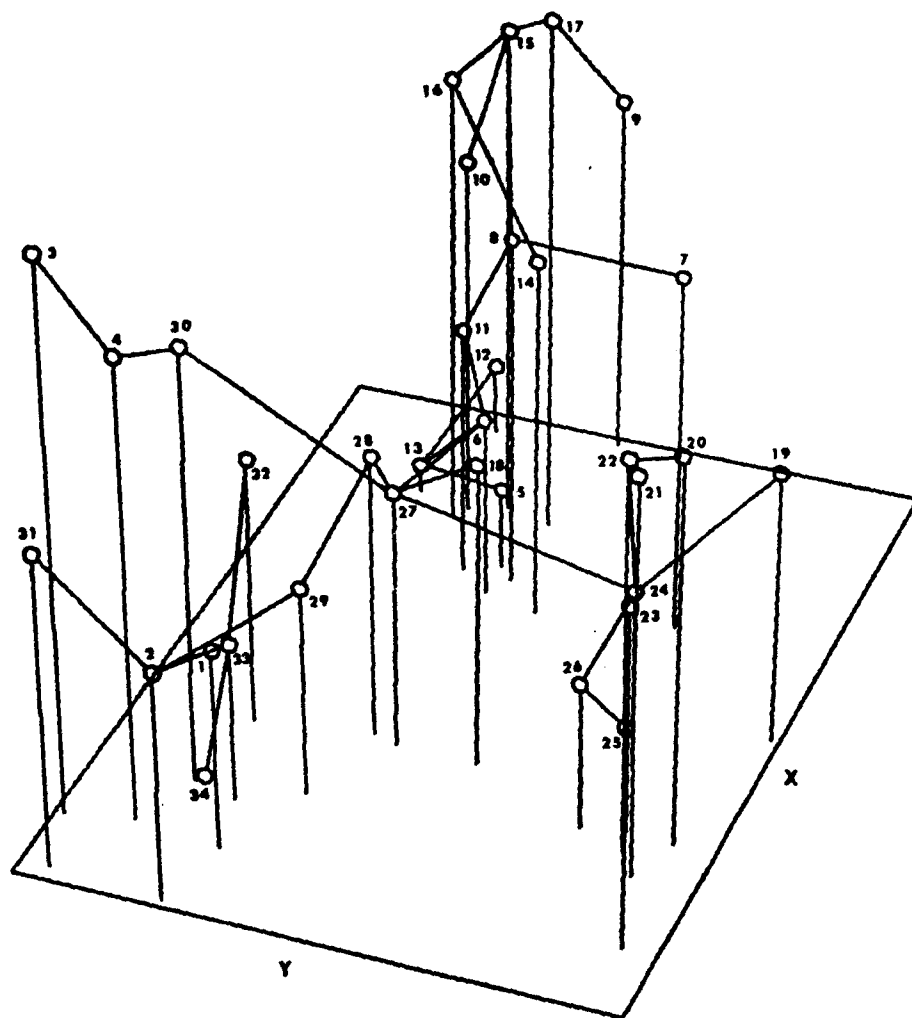
EDGES	TIPS
0 = NO EDGING	0 = SOLID (BLACK OR DARK)
1 = NARROW EDGING	1 = NARROW EDGING
2 = MODERATE EDGING (HALFWAY TO SHAFT)	2 = MODERATE TIPS
3 = BROAD (INTO SHAFT)	3 = DEEP TIPS
4 = ALL WHITE	4 = VERY DEEP (HALF OF LENGTH PLUS)
5 = BLACK EDGES ON WHITE	5 = ALL WHITE
	6 = BLACK TIPS ON WHITE

TABLE 4.4. EIGENVALUES AND PERCENT TRACE FOR FACTORS
DERIVED FROM 39 PATTERN CHARACTERS.

TRACE =		39.000000	
FACTOR NUMBER	EIGEN VALUE	PERCENT OF TRACE	ACCUM. PERCENT
FACT0001	10.91922	28.00	28.00
FACT0002	4.83992	12.41	40.41
FACT0003	4.16714	10.66	51.09
FACT0004	3.34887	8.59	59.68
FACT0005	2.00111	5.13	64.81
FACT0006	1.99846	5.12	69.94
FACT0007	1.71843	4.41	74.34
FACT0008	1.64792	4.23	78.57
FACT0009	1.33325	3.42	81.99
FACT0010	0.98641	2.53	84.51

FIGURE 4.4. THREE DIMENSIONAL PROJECTION OF 34 MIMID SPECIES ONTO FACTORS DERIVED FROM PATTERN CHARACTERS.

THE MINIMUM SPANNING TREE		
I	J	LENGTH
DUEETEL (1)	MELANOP (2)	0.593
MELANOP (2)	TOX DOR (29)	0.642
TOX DOR (29)	TOX RED (28)	0.593
TOX RED (28)	TOX LEC (27)	0.532
TOX LEC (27)	TOX BEN (24)	0.671
TOX BEN (24)	TOX CIN (23)	0.507
TOX BEN (24)	TOX CUR (26)	0.805
TOX BEN (24)	OREOSCO (19)	0.835
TOX LEC (27)	CINCLOC (30)	0.671
CINCLOC (30)	MEL HYP (4)	0.380
MELANOP (2)	ALLENIA (33)	0.890
TOX LEC (27)	MIM GIL (6)	0.900
MIM GIL (6)	MIM PAT (11)	0.565
MIM PAT (11)	MIM THE (8)	0.605
MIM GIL (6)	MIM DOR (13)	0.763
MIM DOR (13)	MIM TRI (12)	0.693
MIM THE (8)	NES MEL (15)	0.844
NES MEL (15)	MIM SAT (10)	0.787
MIM DOR (13)	MIM POL (5)	0.850
MIM THE (8)	MIM GUN (7)	0.886
NES MEL (15)	NES MAC (17)	0.901
NES MAC (17)	MIM LOW (9)	0.838
TOX CUR (26)	TOX OCE (25)	0.907
TOX BEN (24)	TOX GUT (22)	0.912
TOX GUT (22)	TOX RUF (20)	0.389
TOX GUT (22)	TOX LOW (21)	0.532
TOX LEC (27)	MIMODES (18)	0.927
NES MEL (15)	NES PAR (16)	0.931
MEL HYP (4)	MEL CAE (3)	0.969
ALLENIA (33)	MARGARO (32)	0.990
MELANOP (2)	RANPHOC (31)	1.018
NES PAR (16)	NES TRI (14)	1.093
ALLENIA (33)	DOWACOB (34)	1.213



The third is a rather loose association of the West Indian endemics, the two catbirds (1-2) and the blue mockingbirds (3-4). The central links are through the sickle-billed species of Torostoma (27-29). Donacobius (34) is in the third group but separated considerably on the vertical axis, although no more so than the blue mockingbirds (3-4) and Cinclocerthia (30).

The values of the elements comprising the factors (table 4.5), which represent correlation coefficients between the characters and the factor, show which characters are being most strongly influential in determining the axes (factors) of the system. The first factor is strongly determined by wing and tail patterns. Additionally, head patterns, the breast band and the collar contribute. This entire complex of characters is associated with the genus Mimus. As can be seen in the three dimensional projection (figure 4.4), the X axis places the members of the genus Mimus at one end and the unmarked species at the other. On the X axis, the Torostoma species and Oreoscoptes range along the middle of the axis.

The Y axis (Factor 2) shows high positive correlations with breast spotting. It is also relatively highly correlated with streaked flanks, streaked auricular feathers and the submalar line. This axis is negatively

TABLE 4.5. FIRST NINE PRINCIPAL COMPONENTS FACTORS DERIVED FROM CORRELATIONS OF PATTERN CHARACTERS.

	FACT0001	FACT0002	FACT0003	FACT0004	FACT0005	FACT0006	FACT0007	FACT0008	FACT0009
CRO ST	0.488	-0.034	0.422	-0.172	0.456	-0.368	0.287	-0.078	0.171
CRO SC	0.235	-0.049	0.218	-0.146	-0.413	0.435	-0.465	-0.042	-0.397
BAK ST	0.212	0.315	0.960	0.033	0.219	0.336	0.555	-0.318	0.042
BAK SC	0.432	-0.207	0.369	-0.589	0.084	-0.019	-0.218	-0.017	-0.127
RUMP ST	0.390	-0.174	0.455	-0.067	0.061	0.291	-0.152	-0.544	0.010
RUMP SC	0.358	-0.057	0.242	-0.459	-0.133	-0.254	0.032	0.555	0.233
BRES ST	-0.202	-0.282	0.343	0.289	0.073	-0.100	-0.032	-0.194	0.229
BRES SC	0.407	-0.189	0.216	-0.700	0.079	-0.158	0.141	0.267	0.015
BRES SP	-0.291	0.856	0.008	0.046	0.105	-0.181	-0.229	-0.072	0.006
CRIS ST	0.022	0.275	0.123	0.078	0.290	0.415	0.482	0.039	-0.104
CRIS SC	-0.404	0.101	-0.120	-0.587	0.126	-0.433	-0.051	-0.209	-0.196
FLANK ST	0.394	0.556	0.508	-0.075	0.118	0.377	-0.022	0.111	-0.080
FLANK SC	-0.254	-0.311	0.018	-0.463	0.142	-0.225	0.220	-0.037	-0.415
FLANK SP	-0.229	0.358	-0.137	-0.228	-0.133	-0.356	-0.208	-0.489	0.167
FLANK BR	-0.140	-0.170	-0.361	-0.135	0.239	0.438	-0.309	0.110	0.521
SHAPE SP	-0.243	0.793	-0.144	-0.097	-0.105	-0.194	-0.054	-0.356	0.101
SUPCILLN	0.842	-0.034	0.090	0.057	0.095	-0.120	-0.047	-0.243	0.123
MASK	0.582	-0.589	0.380	0.131	0.020	-0.152	0.122	-0.195	0.101
AURIC ST	0.480	0.555	-0.053	0.174	-0.176	-0.276	0.119	0.229	0.169
AURIC AR	0.311	-0.153	0.658	0.217	-0.412	-0.015	0.030	-0.130	0.061
MASKER	0.153	0.735	0.211	-0.104	-0.371	0.003	0.201	0.078	0.249
BRES MID	0.670	-0.008	-0.053	0.035	-0.435	-0.045	0.153	0.059	0.039
COLLAR	0.575	-0.106	0.423	-0.263	-0.282	0.021	-0.308	0.098	0.073
POB STP	0.483	-0.575	0.321	0.278	-0.083	-0.246	-0.015	-0.239	0.160
PRIM EDG	-0.022	0.431	0.553	0.454	0.226	-0.213	-0.234	0.203	0.351
PRIM TIP	0.844	0.133	-0.002	0.056	-0.145	0.118	0.156	0.060	-0.006
SEC EDG	0.075	0.016	0.459	0.615	0.401	-0.159	-0.252	0.194	-0.092
SEC TIP	0.847	0.087	-0.125	-0.015	0.061	-0.105	0.048	0.002	-0.199
WNG BR1	0.719	0.495	0.218	-0.018	0.174	-0.017	-0.095	0.048	-0.218
WNG BR2	0.743	0.502	0.144	0.040	0.212	0.011	-0.141	0.003	-0.202
PRIM COV	0.802	-0.159	-0.341	0.232	0.026	-0.206	0.003	-0.002	-0.128
IM WNG	0.667	-0.177	-0.420	0.203	0.289	0.046	-0.244	0.115	0.123
REC1 EDG	0.439	0.026	-0.546	0.332	-0.392	-0.180	0.132	0.026	-0.070
REC1 TIP	0.654	-0.055	-0.380	-0.220	0.152	0.133	-0.101	-0.061	0.212
REC2-4ED	0.622	-0.138	-0.455	0.345	0.074	-0.175	-0.049	0.015	-0.279
REC2-4TP	0.717	-0.045	-0.594	-0.005	0.176	-0.014	-0.142	-0.048	0.000
REC4-4TP	0.739	-0.129	-0.141	-0.348	0.113	0.148	0.087	-0.016	0.141
RECEDCON	0.888	0.108	-0.085	0.066	-0.221	0.118	0.132	-0.143	-0.057
RECTPCON	0.670	0.393	-0.275	-0.365	0.100	0.032	-0.196	-0.123	0.102

correlated with postorbital stripes and the presence of a mask. The result is to place most of the members of the genus Toxostoma at one end of the axis and the birds with little patterning except masks (the blue mockingbirds (3-4)) at the other. Those birds such as the members of Mimus and some of the thrashers which have a mixture of the characters are ranged along the middle of the axis.

The Z axis, (Factor 3), has its highest positive loadings on dorsal and flank streaking, with the auricular area, and secondary and primary edging also showing some positive correlations. The strongly negative correlations of the Z axis are with tail markings. These combine to place Donacobius (34) at one extreme and the blue mockingbirds (3-4) along with Cinclocerthia (30) at the other. Some of the members of the genus Nesomimus plus Mimus longicaudatus (9) are placed above the rest of the genus.

Inasmuch as the phenograms obtained from the pattern data (figures 4.5 and 4.6) strongly reflect the associations seen in the three dimensional plots of the taxa positioned in space by these characters, they will not be analyzed in detail. It is sufficient at this point to say that patterns alone serve to group the species of mimids into associations that are reasonably consistent with traditional views. The primary discrepancy noted, one

FIGURE 4.5. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF CORRELATIONS RESULTING FROM PATTERN CHARACTERS.

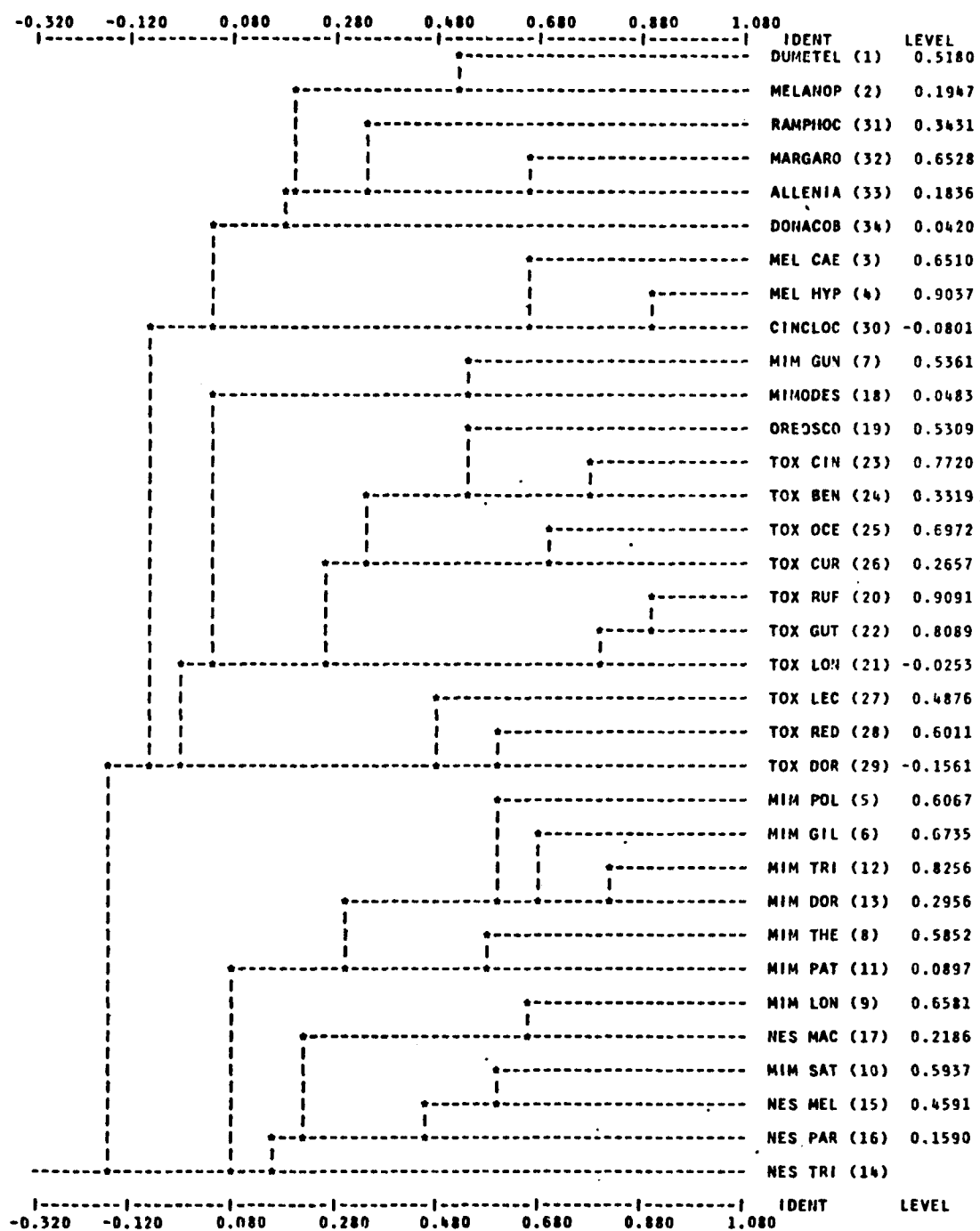
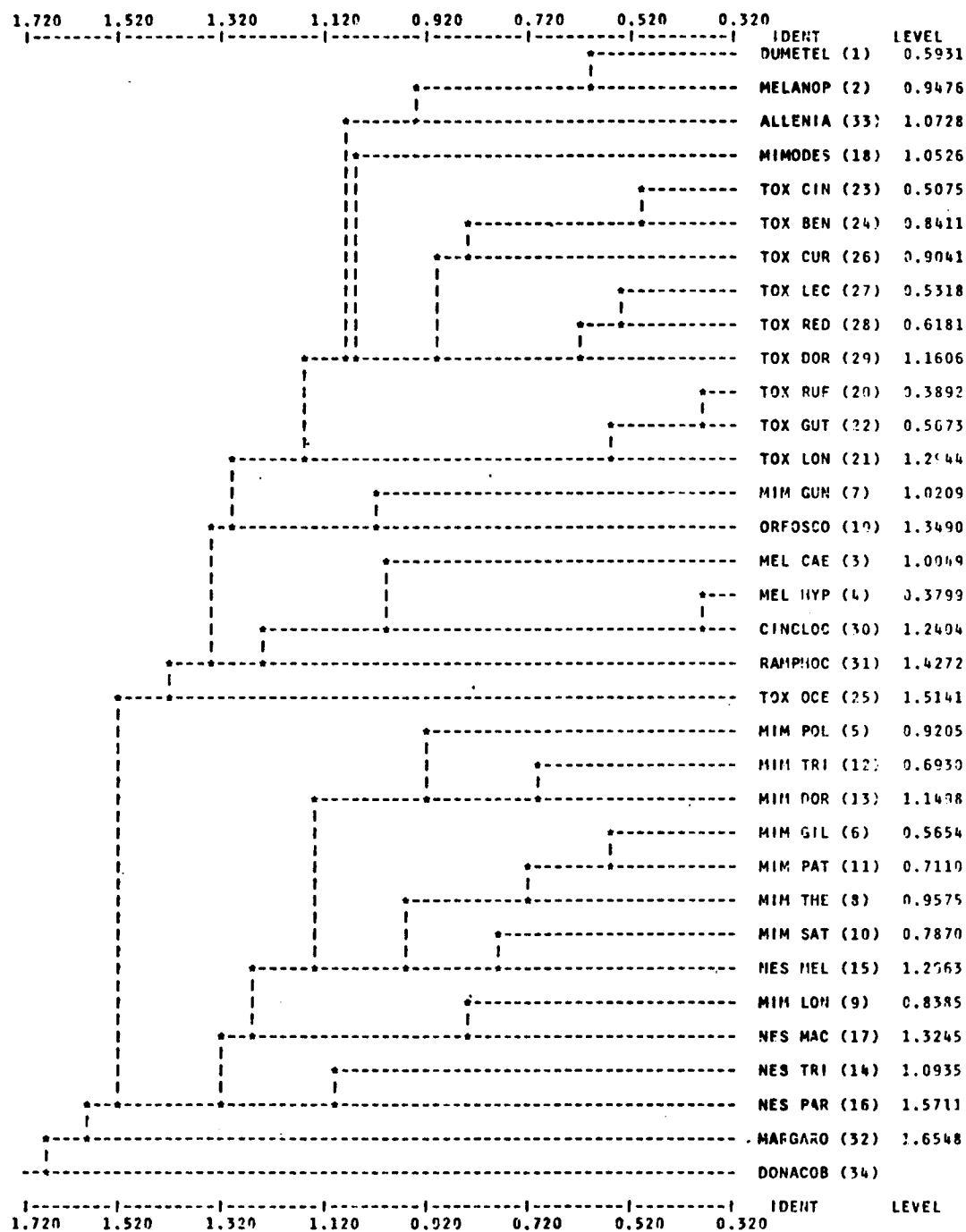


FIGURE 4.6. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF AVERAGE DISTANCE RESULTING FROM PATTERN CHARACTERS.



that does not occur in the phenograms, is the rather wide separation of the spotted breasted species of Toxostoma from the unmarked ones. In the phenogram that is derived from the correlation matrix (figure 4.5), all of the species of Toxostoma are clustered in a single branch of the diagram, while the catbirds and others of the unmarked group in the three dimensional plot (figure 4.4), branch from it. All of the mockingbirds form another group in the diagram.

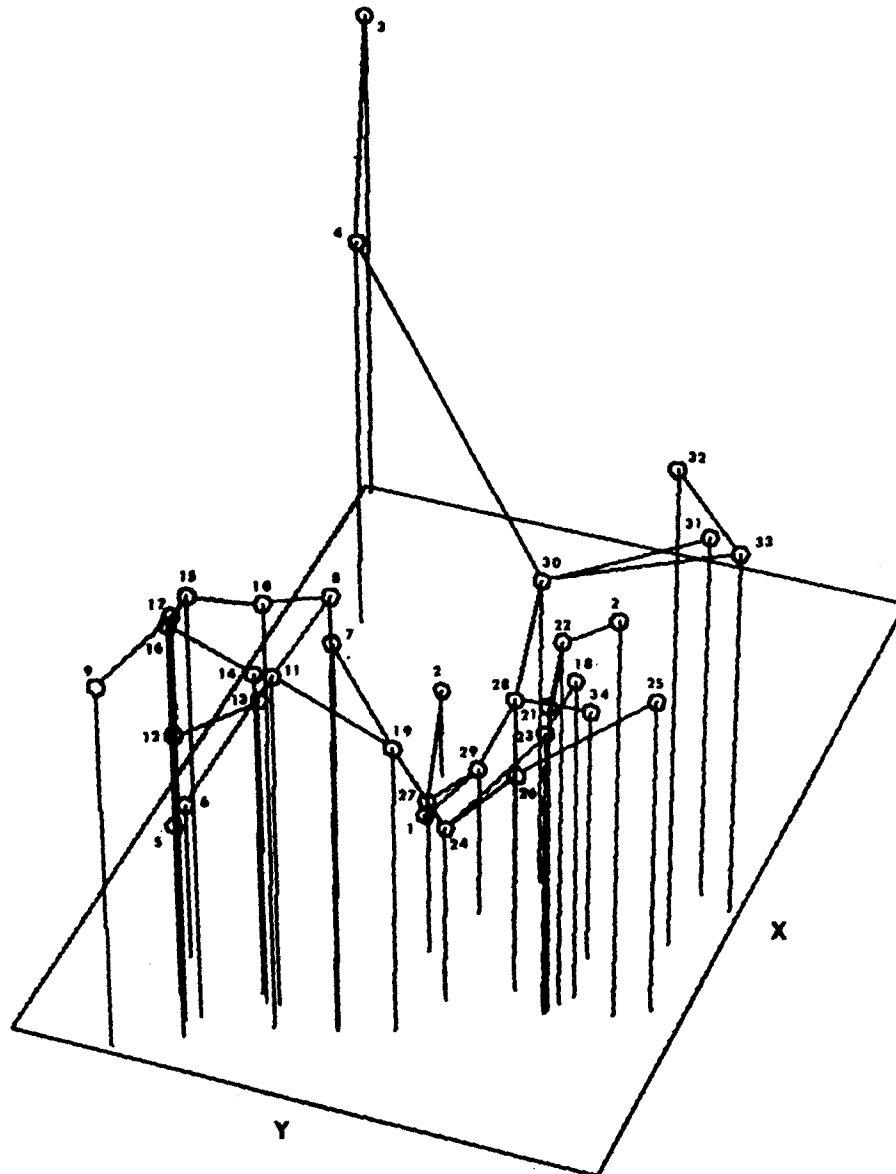
COLORS AND PATTERNS

Before considering the last of the external character sets, the miscellaneous characters, it seems appropriate to examine the effect of combining the two previous character sets, color and pattern. This is so in as much as the two do overlap and are usually considered in conjunction with each other in taxonomic studies of avian groups.

The high correlation of the characters is reflected in the fact that the 34 taxon X 84 character multidimensional space can be reduced to a 34 taxon X 16 factor space, retaining 90.5 percent of the total variance in the original. Forty five per cent of the total variance is retained in the first three axes. The three dimensional plots of the taxa projected onto these axes can be seen in figure 4.7.

FIGURE 4.7. THREE DIMENSIONAL PROJECTION OF 34 MIMID SPECIES ONTO PRINCIPAL COMPONENT AXES DERIVED FROM COLOR AND PATTERN CHARACTERS.

THE MINIMUM SPANNING TREE			
I	J	LENGTH	
DUMETEL (1)	MELANOP (2)	0.955	
DUMETEL (1)	TOX DOR (29)	1.087	
TOX DOR (29)	TOX RED (28)	0.747	
TOX DOR (29)	TOX LEC (27)	0.782	
TOX LEC (27)	TOX BEN (24)	0.699	
TOX BEN (24)	TOX CIW (23)	0.735	
TOX BEN (24)	TOX CUR (26)	0.777	
TOX CIN (23)	TOX GUT (22)	0.784	
TOX GUT (22)	TOX RUF (20)	0.640	
TOX GUT (22)	TOX LON (21)	0.730	
TOX BEN (24)	OREOSCO (19)	0.811	
TOX CUR (26)	TOX OCE (25)	0.833	
OREOSCO (19)	MIM PAT (11)	0.859	
MIM PAT (11)	MIM THE (8)	0.761	
MIM THE (8)	MIF SAT (10)	0.730	
MIM SAT (10)	NES MEL (15)	0.766	
NES MEL (15)	NES MAC (17)	0.664	
NES MAC (17)	MIF LON (9)	0.664	
NES MEL (15)	NES PAR (16)	0.750	
NES PAR (16)	NES TRI (14)	0.801	
MIM PAT (11)	MIM GIL (6)	0.828	
MIM GIL (6)	MIF POL (5)	0.756	
MIM PAT (11)	MIF DOR (13)	0.863	
MIM DOR (13)	MIF TRI (12)	0.655	
TOX CIN (23)	MIFODES (18)	0.871	
TOX RED (28)	CINCLOC (30)	0.899	
OREOSCO (19)	MIF GUF (7)	0.950	
CINCLOC (30)	ALLENIA (33)	1.120	
ALLENIA (33)	MARGARO (32)	0.843	
CINCLOC (30)	RAEPHOC (31)	1.160	
TOX RED (28)	DONACOB (34)	1.299	
CINCLOC (30)	MEL HYP (4)	1.555	
MEL HYP (4)	MEL CAE (3)	1.404	



Factor 1 (X axis) is highly correlated positively with the color blue, and the grey I codes for flanks, crissum, and throat. High negative correlations are with grey II in the flanks and the following pattern characters: supercilliary line, auricular area, submalar line, breast band, and wing and tail patterns. The effect of this factor is to place the blue mockingbirds (3,4) at one end of the axis and the other mockingbirds (5-17) at the other, with the thrashers (19-29) not far from the mockingbirds. The two catbirds (1-2) are placed about halfway along the axis.

Factor 2 (Y axis) is highly correlated with the brown color codes, grey II of the flanks and crissum, breast spots, and the crissum scaly patterns. It is highly correlated negatively with head pattern markings such as the mask, postorbital stripe, and markings of the primary tips and coverts. In addition it is negatively correlated with contrast codes of the edge of the rectrices. The result is to place the blue mockingbirds and the other mockingbirds at one end of the axis and the Toxostoma thrashers plus the West Indian genera Allenia, Margarops and Ramphocinclus at the other. Again, the two catbirds and the relatively unpatterned grey-brown sickle-billed thrashers are in the middle, with Cinclocerthia.

The Z axis (Factor 3) is strongly determined by dorsal

body patterns, such as streaked feathers in the crown and back. This is reflected in the correlations of this factor with the appropriate pattern codes as well as with the grey 2 color codes. Scaly breast patterns and the mask are also positively correlated with this factor. The highest negative correlations are with grey II in the wings and the codes for edge patterns in Rectrice I. The effect is to again leave the relatively unpattered birds at one end of the axis and place the others at the other end.

The net result of the interaction of the three factors is to form two major groupings. One consists of the mockingbirds of Mimus (5-13) and Nesomimus (14-17). The other group, not as tightly integrated as the first, consists of the Toxostoma thrashers (19-29), plus the West Indian endemics (30-33). The minimum spanning tree computed on the basis of distance shows the West Indian endemics branching off of the Toxostoma group from the sickle-billed thrasher, T. redivivum (28). The blue mockingbirds link through Cinclocerthia (30) to the sickle-billed thrashers (27-29). The two catbirds (1-2) are also depicted as a small cluster branching off of the sickle-billed thrashers.

The fact that on the basis of color and pattern, the sickle-billed thrashers (27-29) serve as a focal point for these various "branches" of the complex, is intuitively

appropriate inasmuch as they are generally unpatterned and quite intermediate in color. One interesting note is that Oreoscoptes, despite its spotted breast, is placed nearly as close to the Mimus cluster as to the Toxostoma. The minimum spanning tree links the thrashers to the mockingbirds through Oreoscoptes (19). The effect of combining the colors and patterns can be seen by comparing figures 4.1, 4.4, and 4.7. The colors have shifted the West Indian endemics over to a position near the Toxostoma thrashers and has caused the two blue mockingbirds to become more isolated than they were on the basis of pattern alone.

Turning to cluster analysis (figures 4.8 and 4.9) which puts the groups into a hierarchical system, the basic groupings apparent in the three dimensional projections are repeated. However, there is considerable difference between the phenograms based on correlations and those based on average taxonomic distance. This is due to the way in which correlated and redundant characters differentially affect the two kinds of similarity measures. In both phenograms, the Toxostoma and Mimus-Nesomimus clusters are similarly treated. The major difference is the placement of Oreoscoptes and Mimus gundlachii. On the basis of correlation coefficients, these two species are placed in the Toxostoma cluster. On the basis of average distance, they are placed in the Mimus group. The

FIGURE 4.6. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF CORRELATIONS RESULTING FROM COLORS AND PATTERNS.

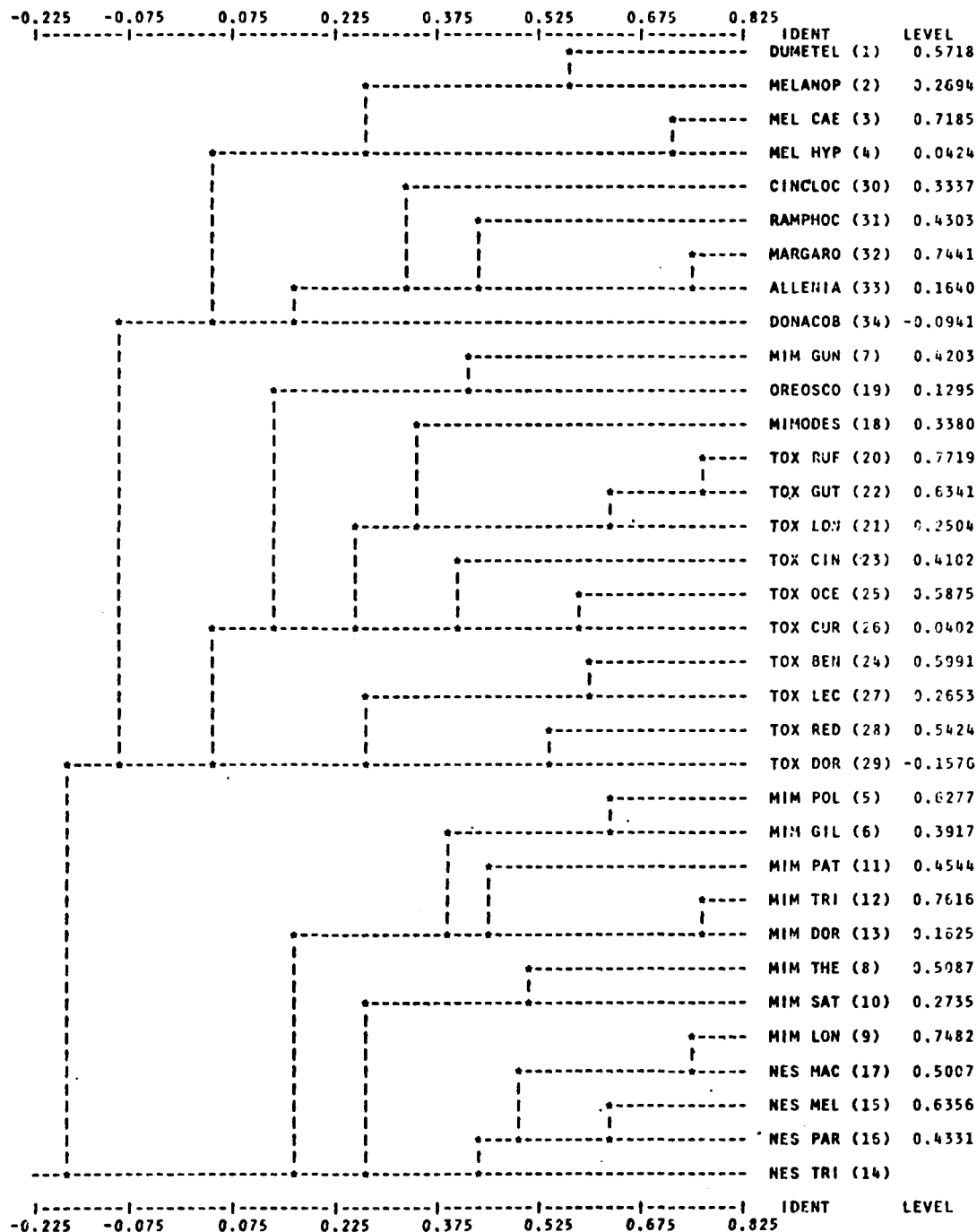
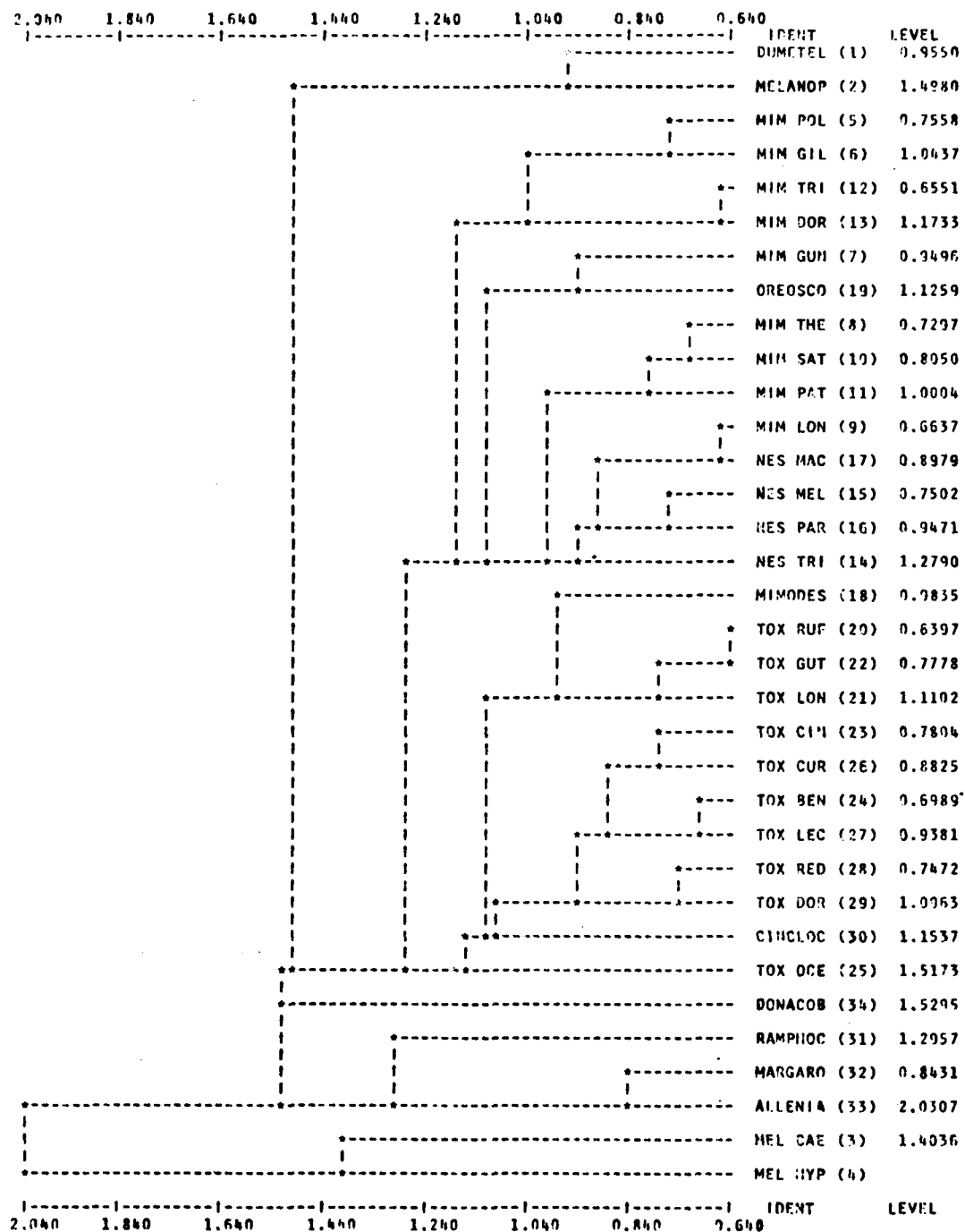


FIGURE 4.9. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF AVERAGE DISTANCE RESULTING FROM COLORS AND PATTERNS.



phenogram based on correlations also maintains the unpatterned species in a better organized cluster than does average distance. On the basis of distance, Cinclocerthia is placed in the Toxostoma cluster and the two catbirds are set off as a cluster opposed to both Toxostoma and Mimus.

The comments above about the phenograms of color plus pattern information serve to illustrate one of the major problems in interpreting phenograms. Loosely knit clusters are poorly and variably placed by different procedures. By examining the three dimensional projections of the same character set, it is apparent that the birds that are placed differently in the two kinds of phenograms are not closely associated with other species or, as in the case of Oreoscoptes (19) and M. gundlachii (7), are on the edges between two major clusters. If the phenograms are studied in conjunction with the three dimensional projections, a reasonably good picture of phenetic relationships can be obtained. Admittedly, a certain amount of subjectivity is introduced in the process of deciding on the preferred interpretation of the results of not just one, but all of the various procedures.

MISCELLANEOUS CHARACTERS

The set of miscellaneous characters is of quite a different nature than those discussed so far. It is a

heterogeneous collection of various characters gleaned from the birds external anatomy plus characters selected from the natural history of the birds. These characters are generally of a discrete nature, or at most are coded in only a few states.

The characters are:

Eye color: Basically three colors of the iris are found in mimids. These are dark brown, red, and yellow. Brown irises are found in Dumetella, Melanoptila, Mimodes and in two of the sickle-billed thrashers. Red irises are found only in Melanotis and Ramphocinclus. All of the rest of the species have yellow irises, although the shade of yellow varies from the bright golden yellow of Cinclocerthia to the pale straw color of some Toxostoma thrashers and the greenish yellow of the South American Mimus patagonicus and M. triurus.

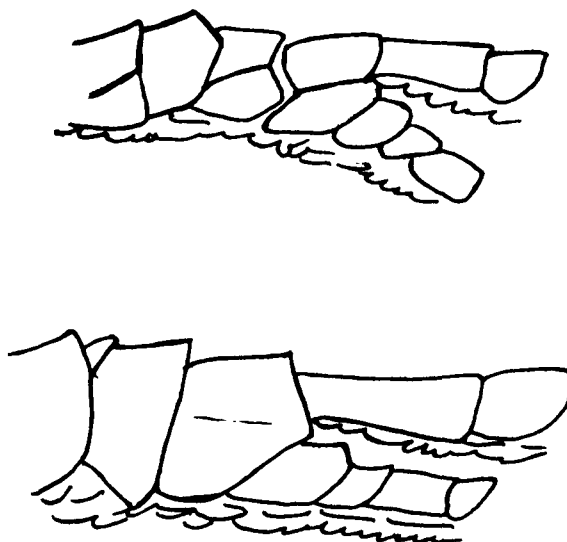
bill notch: Among most of the so-called "Old World insect eater" assemblage, a subterminal notch is characteristically present. Among the mimids, this character varies from prominent to absent. It is often slightly developed in members of Mimus and is absent in all members of Toxostoma. Two members of the genus Mimus, M. dorsalis and M. triurus show only the barest hint of a notch and by rights could also be said to lack one. In the

other mimids, the notch is at least moderately developed and is prominent in Melanotis, Melanoptila, and the West Indian endemics.

Bill curvature: This character represents an estimate of the degree of curvature of the mandibles of the species. It does not pertain to the tip of the bill which is nearly always decurved, but rather to the rest of the bill from the base to a point just anterior to the external nares. It ranges from straight in some long billed forms (such as Cinclocerthia and Ramphocinclus) and some short billed forms (such as Dumetella) to highly curved as in the sickle-billed thrashers.

Basal toe scutes: These scutes (Clark 1972) are those distal to the tarsometatarsus, at the base of the two outer toes, (see figure 4.10). In all of the Old World insect eaters examined, there are two scutes at this point of junction of the toes to the tarsus-metatarsus. However, in all of the members of the two genera Mimus and Toxostoma, plus Mimodes and Oreoscoptes, there is but one. In addition, Melanoptila has but one in most cases. However, in this monotypic genus, the character is variable. Seventy percent of the fifty specimens examined had only one basal toe scute. Fifteen percent had two and fifteen percent had one scute on one foot and two on the other. I coded Melanoptila as having one basal toe scute,

FIGURE 4.10. SCUTES AT BASE OF OUTER TOES OF DUMETELLA (TOP) AND TOXOSTOMA (BOTTOM). ADAPTED FROM CLARK (1972).



despite the small number of two scuted specimens found.

Tarsal scutellation: Most birds have a series of scutes along the anterior surface of the tarsus. In some groups, notably the thrushes, these scutes are lacking and the entire anterior surface is faced with a single sheath of scutellate material. This is the booted tarsus that has been a traditional diagnostic character of the thrushes. It is however not universally diagnostic in that some presumed thrushes have scutellate tarsi. This is particularly true of some groups such as the scrub robins (Erythropygia) of Africa which have quite well defined scutes on the tarsus.

Among the mimids, the scutellate tarsus is a problem. In most species, particularly those in Mimus, and Toxostoma, the scutes are usually well developed. However, in some species, notably Ramphocinclus, the scutes are often effectively lacking. This is also true of some individuals in Cinclocerthia, Allenia, and Dumetella. In some specimens, the scutellation is so completely diminished that considerable magnification is needed in order to detect any sign of a scute. Generally, this character sets off the West Indian endemics and the two catbirds from other mimids. In an intermediate condition, are Melanotis, Oreoscoptes and a few of the Toxostoma thrashers. The distribution of the states of this

character can be seen in appendix table 4.

Wing shape: In lieu of measuring the lengths of wings, primaries, and secondaries, with the associated problems of size corrections, I coded the species into three categories on a visual basis. There are: 1) short round wings; 2) moderate wings; 3) long pointed wings. Generally, sedentary, non-migratory species have shorter, rounder wings. The most extreme is Donacobius. Others with short round wings include Melanoptila and several members of Toxostoma, where running is a more frequent mode of locomotion than is flight. Most mimid species fall into the intermediate category. Only two, Oreoscoptes which is very migratory and Allenia, which is highly arboreal, have relatively long, pointed wings. I expected Dumetella to have relatively pointed wings on the basis of its migratory nature, but this was not the case, this species having only moderately pointed wings.

Tail shape: Among mimids, tail shapes vary in the degree of graduation of the length of the outer to the central rectrices. At one extreme is, again, Donacobius which has outer rectrices barely half as long as the central rectrices. Oreoscoptes and Allenia are at the other extreme with outer rectrices 9/10 the length of the central rectrices. The coding ranged from 1 for essentially square tails to 4 for extreme graduation.

Rictal bristles: The development of rictal bristles is variable among the thrushes and is also variable among the mimids. In some species, such as Cinclocerthia and Melanoptila, the bristles are quite diminished. In others such as Dumetella, Melanotis caerulescens and M. hypoleucus, they are strongly developed. I coded this development on a 1 to 3 scale.

Egg color: Color in birds' eggs has on occasion been considered as a potential taxonomic character. In a review of the possibilities of using color and spotting of eggs for taxonomic purposes, Lack (1958) concluded that neither was particularly reliable. He based his conclusions on the results of his survey of color and spotting within the old world insect eaters, primarily the Turdinae and Sylviinae. Lack found that these two characters reflected nest site choice and the exposure of eggs to possible predation rather than phylogenetic relationships. He essentially dismissed egg color and markings as keys to relationships. Lack's conclusions seem quite reasonable. However, he was primarily devoting his attention to relationships at a relatively high taxonomic level within this large complex. I do not think that the evidence warrants total dismissal of egg color and markings as characters within what appear to be closely knit subgroups within the greater complex.

Egg color and markings among the mimids together make

a dichotomy within the group that is generally consistent with groupings suggested by color and patterns. Color ranges from a pale bluish-white to quite deep blue-green as found in Dumetella. The pale colored eggs belong to the genus Mimus and most of the Toxostoma thrashers. A somewhat deeper shade of blue-green is found in Oreoscoptes, and Toxostoma ocellatum, curvirostre, and lecontei. Deeper still are the eggs of all the West Indian endemics, Melanotis, Melanoptila, and two of the Toxostoma species, T. redivivum and T. dorsale.

Turning to markings, all of the species with deep blue eggs are unmarked with the exception of T. redivivum. It is interesting that within the Toxostoma complex, the species that are most specialized in feeding adaptations share a number of characteristics with the more generalized mimids. In a genus with conspicuous plumage patterns, with pale eggs that are marked, the sickle-billed thrashers are unpatterened in their plumage; have relatively deeply colored eggs and one of them, T. dorsale has unmarked eggs.

The eggs of Donacobius are, as with so many other characteristics of the species, unusual. Rather than being bluish, they are reddish in tone. The eggs are marked with very fine speckles that appear so dense as to be a solid coloration (Skutch, 1968).

Nest sites: Realizing the variability that can occur in the choice of places to build nests, I have coded in a general way the basic habitat preferences of the various species for nest building. Most species of mockingbirds and thrashers build nests in shrubs, bushes, or small trees. None build on the ground and very few build at any great height in trees. The exceptions are Margarops, Allenia and Cinclocerthia which all build at heights that are considerably above the average. Allenia, the most arboreal member of the family prefers, (at least on St. Lucia, West Indies where I studied it) the outer branches of trees such as a mango, or various other trees with even more open foliage. The shift to arboreal locations has been accompanied by a reduction in the bulkiness of the typical mimid nest. There are considerably fewer heavy sticks built into the framework of the nests of this species.

Margarops is particularly unusual in that it likes to build nests in holes in trees. Where such a site is not available, this species will use other "holes". Wetmore (1918) found a pair nesting on a ledge in a small, shallow cave in the islet of Desecheo near Puerto Rico.

Cinclocerthia is somewhat in between these last two species in its choice of nest site. It is arboreal and likes to place a nest at the base of the fronds of various

palms. Such a site approaches a hole in character.

The only other major peculiarity in choice of nest sites is that of Donacobius. This species, a lover of reeds and swampy spots, builds a nest in the reeds over or very near water (Skutch, 1968).

I coded these various sites as follows: 1) marshy, reeds for Donacobius; 2) the typical shrub, brush, small tree sites of most mimid species; 3) arboreal-cavity sites of Margarops and Cinclocerthia; 4) the truly arboreal sites of Allesia.

Spotting of young: The spotted plumage of young birds is one of the two principal characters used to distinguish thrushes from other members of the Old World insect eater group. As with tarsus scutellation, the other primary character which was discussed above, spotting of the young is not infallible in diagnosing a thrush.

Spotted plumages in young mimids is variable, as was true with tarsal scutellation. In none of them is the dorsal plumage spotted, as is typical of many thrushes. However, they typically have either spotted or mottled ventral plumage. All of the species of Mimus and Nesomimus as well as the species Toxostoma have spotted breasted young. This is also true of Dumetella where, because of

the general dark coloration of the plumage, the spots are not prominent. The young of Cinclocerthia, Margarops and Allenia are mottled or streaked. The young of Melanoptila, Melanotis caerulescens, and the three sickle-billed Toxostoma thrashers are unmarked. The breasts of the young of Melanotis hypoleucus are mottled with the white of the adult plumage.

The codes for spotted juvenal plumage are: 0 = unmarked; 1 = streaked; 2 = spotted.

Foraging: As was true with the nest site preference character, this character represents an over simplified evaluation of the locations that the species prefer to forage in or on. The species fall into four categories. 1) Ground foragers. This group includes the species of Mimus and Toxostoma as well as Nesomimus and the two blue mockingbirds. One could argue that Mimus species are less rigidly ground foraging than Toxostoma species. This is true but, despite the fact that the various Mimus species do feed in shrubs and bushes on fruits and berries and no doubt find some insects there, they are primarily ground foragers. (Bent, 1948, Hudson, 1920); 2) Brush and shrub foragers include the two catbirds; 3) Arboreal foragers include Cinclocerthia, Margarops and Allenia. Some populations of Cinclocerthia do forage at times at low levels and on the ground. (Zusi, 1969); 4) Marsh and

swampy area foraging is unique to Donacobius.

NUMERICAL ANALYSIS OF MISCELLANEOUS CHARACTERS

The characters of the miscellaneous data set (appendix table 4) are of intrinsic interest since they, more than any characters so far considered (with the exception of the peculiar density pattern of the egg white proteins of Toxostoma) form sharply distinct clusters among the mimids. For that reason, they have great appeal as possible indicators of relationships beyond the mere phenetic. Some of these characters will be used in the phylogenetic analysis of chapter six. For the present, they will only be considered within the framework of traditional phenetic analysis.

The three dimensional projections of the taxa onto the factors and rotated factors (see chapter 2,) extracted from the matrix of character correlations is given in figure 4.11. The three axes of the projection sum up 70.67 of the variance among the taxa resulting from these miscellaneous characters (table 4.6). Two groups are formed. One is composed of the West Indian endemics, the two blue mockingbirds (3-4) and the two catbirds (1-2). The other is composed of the species of Mimus and Toxostoma with Oreoscoptes (19) and Mimodes (18) as relatively closely associated outliers. Mimodes is a particular

problem in this set of characters because there are four characters, egg color, egg spotting, nest site choice, and the plumage of the young about which no information was available. The placement of the species is therefore not nearly as reliable as could be wished. The only other species in this data set with a missing character is Ramphocinclus. Information about the nature of the juvenal plumage is not available. The single missing character probably has little effect on Ramphocinclus but in as much as there are four out of thirteen characters missing for Mimodes, its placement in the phenetic multidimensional space is subject to considerable error.

Analysis of the correlations between the characters and the rotated factors (table 4.7) indicate that the X axis of the projections (Factor 1) is positively correlated with the spotting of eggs, the shape (graduation) of the tail, and the development of rictal bristles. This axis is negatively correlated with choice of nest site. The Y axis (Factor 2) has a high positive correlation with egg color. Its high negative correlations are with eye color and wing shape. The Z axis shows especially high positive correlations with the subterminal notch of the bill and the number of scutes at the base of the outer toes. It is strongly correlated negatively (-0.822) with the degree of curvature of the bill, and to a lesser degree (-0.650) with tarsal scutellation.

FIGURE 4.11. (A) THREE DIMENSIONAL PROJECTION OF 34 MINID SPECIES ONTO FACTORS DERIVED FROM MISCELLANEOUS EXTERNAL CHARACTERS. (B) FACTORS ROTATED.

THE MINIMUM SPANNING TREE		
I	J	LENGTH
DUMETEL (1)	RANPHOC (31)	0.741
RANPHOC (31)	MEL CAE (3)	0.891
MEL CAE (3)	MEL HYP (4)	0.716
MEL HYP (4)	MIMODES (18)	1.218
MIMODES (18)	TOX RED (28)	0.962
TOX RED (28)	TOX LEC (27)	0.549
TOX RED (28)	TOX DOR (29)	0.932
MIMODES (18)	TOX LOW (21)	1.039
TOX LOW (21)	TOX RUP (20)	0.326
TOX LOW (21)	TOX GUT (22)	0.326
TOX LOW (21)	MIM DOR (13)	0.603
MIM DOR (13)	MIM TRI (12)	0.246
MIM TRI (12)	MIM SAT (10)	0.000
MIM TRI (12)	MIM LOW (9)	0.000
MIM TRI (12)	MIM PAT (11)	0.000
MIM TRI (12)	MIP THE (8)	0.000
MIM TRI (12)	NES TRI (14)	0.394
NES TRI (14)	NES MEL (15)	0.000
NES TRI (14)	NES PAR (16)	0.000
NES TRI (14)	NES MAC (17)	0.000
NES TRI (14)	TOX CIN (23)	0.408
TOX CIN (23)	TOX CUR (26)	0.250
MIM TRI (12)	MIM POL (5)	0.417
MIM POL (5)	MIM GUN (7)	0.000
MIM POL (5)	MIM GIL (6)	0.000
NES TRI (14)	TOX BEN (24)	0.430
TOX CUR (26)	TOX OCE (25)	0.628
MIM POL (5)	OREOSCO (19)	0.774
MEL CAE (3)	MELANOP (2)	1.288
MELANOP (2)	CINCLOC (30)	1.262
CINCLOC (30)	ALLEWIA (33)	1.031
CINCLOC (30)	MARGARO (32)	1.107
MIMODES (18)	DOWACOB (34)	1.833

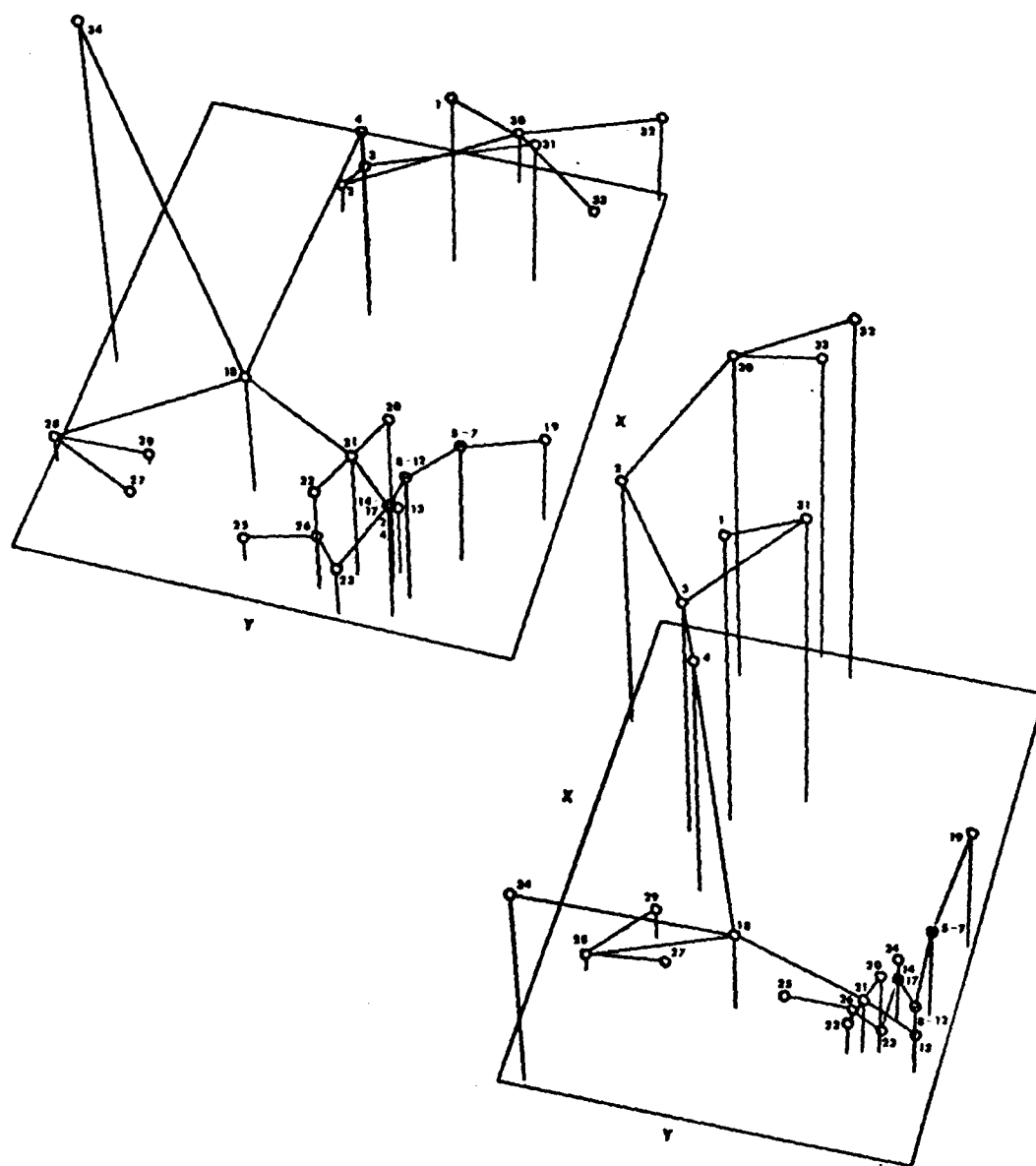


TABLE 4.6. EIGENVALUES AND PERCENT TRACE FOR FACTORS DERIVED FROM 13 MISCELLANEOUS EXTERNAL CHARACTERS.

TRACE = 13.000000			
FACTOR NUMBER	EIGEN VALUE	PERCENT OF TRACE	ACCUM. PERCENT
FACT0001	5.41555	41.66	41.66
FACT0002	2.37949	18.30	59.96
FACT0003	1.39171	10.71	70.67
FACT0004	1.13095	8.70	79.37
FACT0005	0.79441	6.11	85.48

TABLE 4.7. (A) FIRST FOUR PRINCIPAL COMPONENTS FACTORS DERIVED FROM CORRELATIONS OF MISCELLANEOUS EXTERNAL CHARACTERS.

	FACT0001	FACT0002	FACT0003	FACT0004
EYE COLR	0.348	-0.581	0.097	-0.611
B NOTCH	-0.836	-0.197	0.239	0.044
B CURV	0.567	0.480	-0.461	-0.217
TOE SCUT	-0.857	0.044	0.328	-0.139
TAR SCUT	0.860	0.185	0.066	-0.134
WING SHP	-0.001	-0.640	-0.147	-0.106
TAIL SHP	0.710	0.434	0.304	-0.098
RICT BRI	0.263	-0.276	0.690	0.331
EGG COLR	-0.746	0.541	0.197	-0.130
EGG SPTS	0.791	0.060	0.330	-0.354
NEST	-0.560	-0.429	-0.440	-0.160
YNG SPOT	0.513	-0.753	0.112	0.057
GRND/ARB	-0.684	0.131	0.239	-0.608

TABLE 4.7. (B) FIRST THREE FACTORS ROTATED.

	RFAC0001	RFAC0002	RFAC0003
EYE COLR	0.096	-0.674	-0.069
B NOTCH	-0.329	0.098	0.823
B CURV	0.092	0.283	-0.822
TOE SCUT	-0.201	0.320	0.838
TAR SCUT	0.578	-0.146	-0.650
WING SHP	-0.304	-0.579	0.058
TAIL SHP	0.755	0.117	-0.448
RICT BRI	0.603	-0.417	0.290
EGG COLR	-0.096	0.752	0.559
EGG SPTS	0.710	-0.262	-0.407
NEST	-0.778	-0.153	0.250
YNG SPOT	0.148	-0.895	-0.144
GRND/ARB	-0.150	0.346	0.632

The result of the analysis of the data by means of cluster techniques also indicates two basic groupings of the species (figures 4.12 and 4.13). The primary difference between the results of clustering the taxa on the basis of correlations versus taxonomic distance is to shift the position of the three sickle-billed thrashers, Donacobius and Mimodes. On the basis of correlations, these taxa are grouped with the catbirds, blue mockingbirds, and the West Indian endemics. On the basis of distance, they are placed as an arm of a large cluster including the Mimus-Toxostoma complex. The intermediate placing of these taxa in the principal components analysis suggests the rather equivocal nature of their phenetic relationships with regard to this character set. Some caution is therefore in order when interpreting the results of the numerical analysis.

In summary, this set of relatively dichotomous characters again divides the mimids into groups that are consistent with those suggested by analysis of color and pattern characters and are reasonably consistent with the relationships suggested by the egg white protein data.

COMBINED EXTERNAL CHARACTERS

The effect of combining the data on miscellaneous characters with that from color and pattern is apparent in

FIGURE 4.12. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF CORRELATIONS RESULTING FROM MISCELLANEOUS EXTERNAL CHARACTERS.

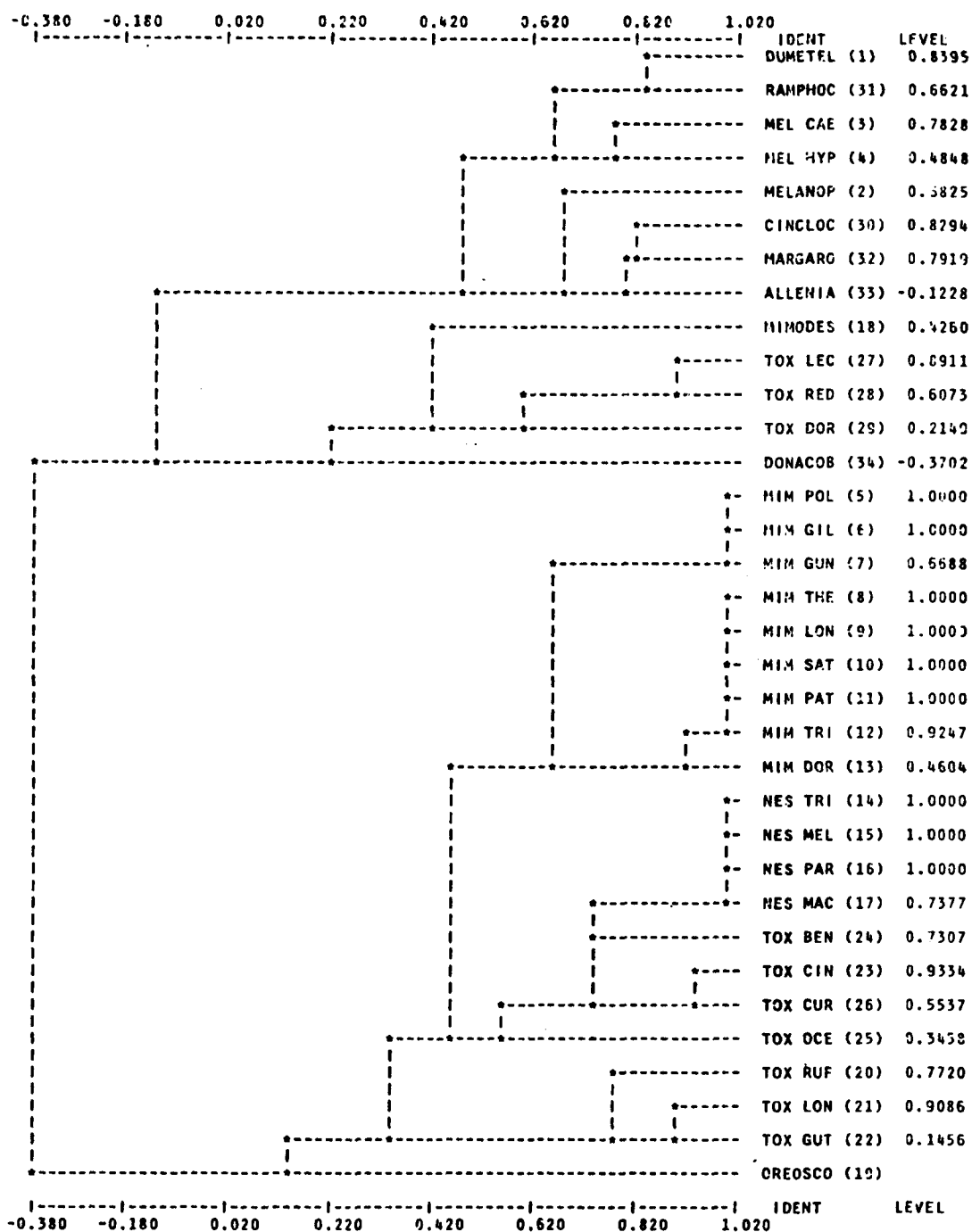
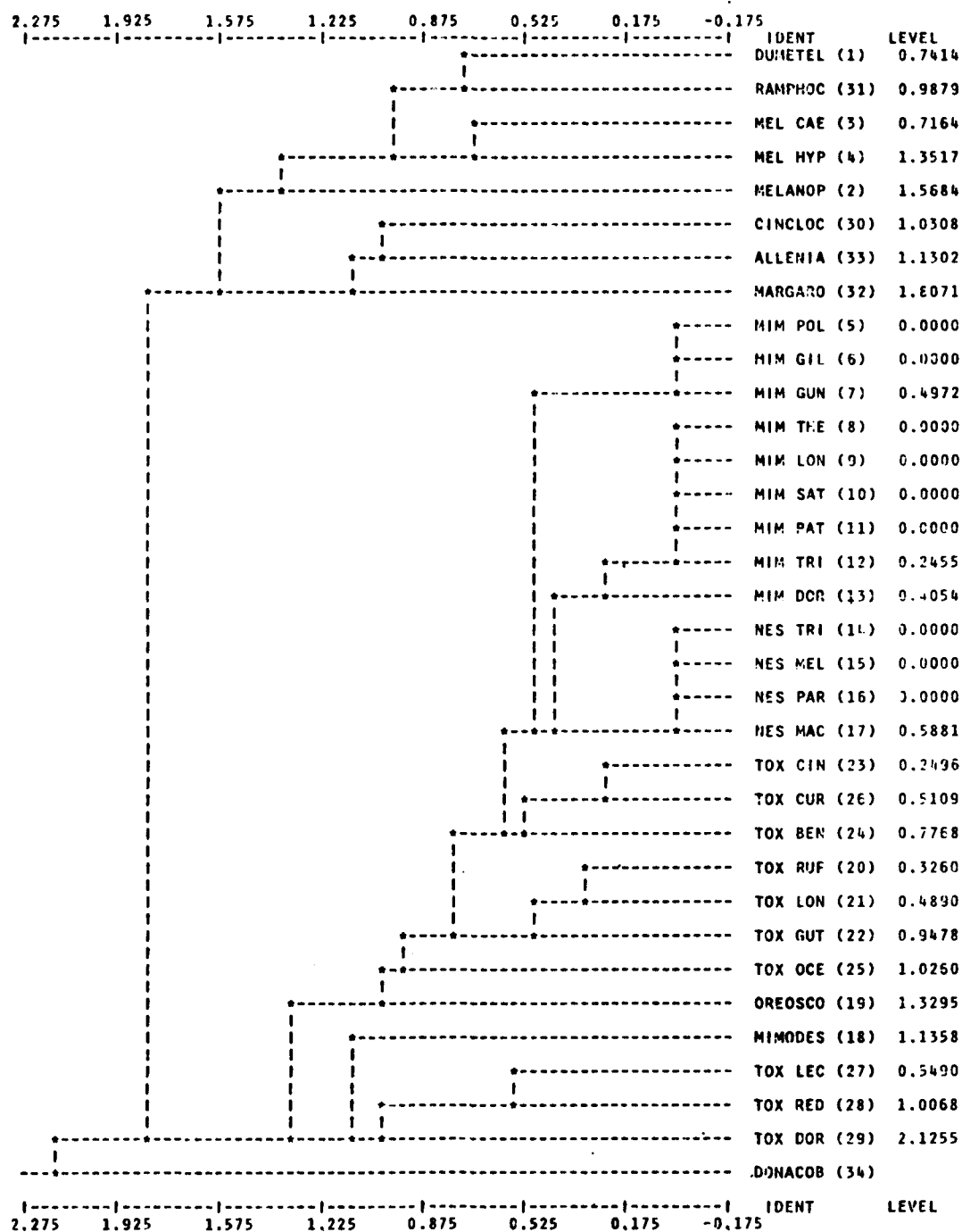


FIGURE 4.13. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF AVERAGE DISTANCE RESULTING FROM MISCELLANEOUS EXTERNAL CHARACTERS.



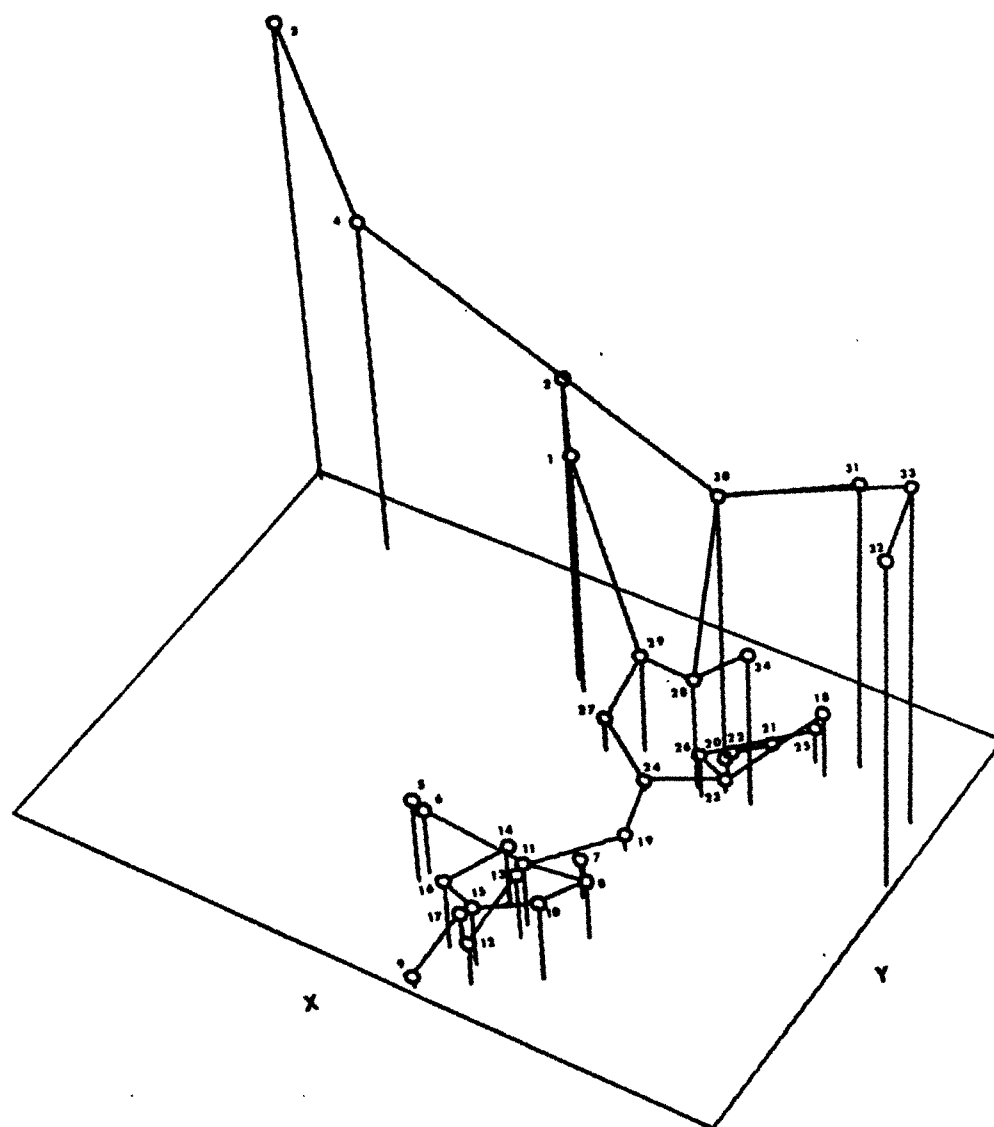
the three dimensional projection of the taxa in figure 4.14. The large elongated cluster that the color and pattern characters positioned at right angles to the two catbirds (1-2) and the blue mockingbirds (3-4) in figure 4.7 has now been sorted out into discrete subunits. Although the mockingbirds (5-17) were reasonably distinct as a group in the color and pattern projection, their cluster has become even more tightly organized. The Toxostoma thrashers, which on the basis of color and pattern are a confused conglomeration, are now clearly separated into two subgroups, the sickle-billed species (27-29) and all of the others. The distinct nature of Donacobius (34) on the basis of the miscellaneous characters serves to move it further away from the Toxostoma complex.

The projection in figure 4.14 of the 34 birds onto the factors derived from the correlation matrix of the original variables shows groupings that are strikingly similar to groupings of these birds implied in the classifications produced by other taxonomists. These results demonstrate how completely phenetic the traditional arrangements are and suggests that these arrangements have been based on little other than external characters.

Examination of the correlation coefficients that make up the rotated factors (table 4.6) indicate that the

FIGURE 4.14. THREE DIMENSIONAL PROJECTIONS OF 34 MIMID SPECIES ONTO FACTORS DERIVED FROM ALL EXTERNAL CHARACTERS.

THE MINIMUM SPANNING TREE		
I	J	LENGTH
DUMETEL (1)	MELANOP (2)	0.999
DUMETEL (1)	MIM POL (5)	1.217
MIM POL (5)	MIM GIL (6)	0.703
MIM GIL (6)	MIF PAT (11)	0.785
MIM PAT (11)	MIM THE (8)	0.708
MIM THE (8)	MIM SAT (10)	0.679
MIM SAT (10)	NES MEL (15)	0.729
NES MEL (15)	NES MAC (17)	0.618
NES MAC (17)	MIM LOW (9)	0.634
NES MEL (15)	NES PAR (16)	0.696
NES PAR (16)	NES TRI (14)	0.745
MIM PAT (11)	MIM DOR (13)	0.808
MIM DOR (13)	MIF TRI (12)	0.616
MIM PAT (11)	OREOSCO (19)	0.867
OREOSCO (19)	TOX BEN (24)	0.833
TOX BEN (24)	TOX CIN (23)	0.706
TOX CIN (23)	TOX CUR (26)	0.729
TOX BEN (24)	TOX LEC (27)	0.766
TOX CIN (23)	TOX GUT (22)	0.775
TOX GUT (22)	TOX RUP (20)	0.641
TOX GUT (22)	TOX LOW (21)	0.690
TOX LEC (27)	TOX DOR (29)	0.804
TOX DOR (29)	TOX RED (28)	0.751
TOX CUR (26)	TOX OCE (25)	0.809
MIM THE (8)	MIM GUN (7)	0.921
TOX RED (28)	CINCLOC (30)	1.138
CINCLOC (30)	ALLENIA (33)	1.108
ALLENIA (33)	MARGARO (32)	0.867
CINCLOC (30)	RAMPHOC (31)	1.257
TOX RED (28)	DONACOB (34)	1.330
TOX CIN (23)	MIWODES (18)	1.339
CINCLOC (30)	MEL HYP (4)	1.543
MEL HYP (4)	MEL CAE (3)	1.327



position of these factors in the multidimensional space is being determined largely in the following manner. The X axis (Factor 1) is negatively highly correlated with the pattern characters of the tail and wings and in addition by the mask elements. The breast band and collar also contribute significantly. The positive end of this axis is correlated with spotted breasts, egg color and the intensity of color in the tail. These characters serve to set the mockingbirds apart from other mimids.

The second factor (Y axis) is sharply polar with regard to the two colors, being positively correlated with brown and negatively correlated with blue. In addition the scaly breast and streaking characters are influential, as is the presence of a scaly pattern in the crissum. These characters place the blue mockingbirds at one end of the axis and the patterned, dark brown West Indian endemics at the other.

The third axis (Factor 3) has high positive correlations with the grey I color codes and especially high correlations with the subterminal notch and number of toe scutes. The ground versus arboreal character is also relatively strongly correlated with this character. The effect of these correlations is to place the Mimus and Toxostoma groups at one end of this axis and the West Indian endemics and blue mockingbirds at the other with the

TABLE 4.8. FIRST THREE PRINCIPAL COMPONENTS DERIVED FROM COMBINED EXTERNAL CHARACTERS ROTATED TO SIMPLE STRUCTURE.

	RFAC0001	RFAC0002	RFAC0003		RFAC0001	RFAC0002	RFAC0003
CRN GRY1	-0.014	0.046	0.711	RUMP SC	-0.406	0.080	0.075
CRN GRY2	-0.087	0.107	-0.220	BRES ST	0.200	-0.553	0.378
CRN BRN	0.139	0.748	-0.004	BRES SC	-0.527	0.348	0.290
CRN BLU	0.275	-0.713	0.425	BRES SP	0.502	0.137	-0.583
CRN INT	0.343	-0.020	0.197	CRISS ST	0.152	0.140	-0.204
BAK GRY1	-0.123	0.353	0.572	CRISS SC	0.289	0.531	0.230
BAK GRY2	-0.651	0.152	0.014	FLANKST	-0.213	0.070	-0.532
BAK BRN	0.045	0.777	-0.036	FLANKSC	0.076	0.429	0.439
BAK BLU	0.275	-0.713	0.425	FLANKSP	0.257	0.134	-0.200
BAK INT	0.406	0.192	-0.007	FLANKBR	0.078	0.133	0.056
RMP GRY1	-0.007	0.188	0.508	SHAPE SP	0.404	0.138	-0.512
RMP GRY2	-0.654	0.071	-0.026	SUPCILLN	-0.796	-0.063	-0.257
RMP BRN	0.115	0.792	-0.018	MASK	-0.638	-0.276	0.295
RMP BLU	0.275	-0.713	0.425	AURIC ST	-0.212	-0.043	-0.725
RMP INT	0.247	0.263	0.081	AURIC AR	-0.257	-0.450	-0.033
THR GRY1	0.209	-0.049	0.761	WHISKER	0.106	0.093	-0.727
THR GRY2	0.162	-0.148	0.638	BRES BND	-0.633	-0.108	-0.254
THR BRN	0.033	0.574	0.459	COLLAR	-0.602	-0.111	-0.089
THR BLU	0.200	-0.553	0.378	PORR STP	-0.514	-0.363	0.210
THR INT	0.223	0.114	0.443	PRIM EDG	0.254	-0.356	-0.377
BRE GRY1	0.074	-0.160	0.519	PRIM TIP	-0.713	-0.123	-0.414
BRE GRY2	-0.007	0.172	-0.624	SEC EDG	0.046	-0.511	-0.063
BRE BRN	0.027	0.094	0.094	SEC TIP	-0.756	0.109	-0.263
BRE BLU	0.200	-0.553	0.378	WNG BR1	-0.510	0.069	-0.608
BRE INT	0.187	0.317	-0.074	WNG BR2	-0.551	0.006	-0.631
CRS GRY1	0.396	-0.273	0.670	PRIM COV	-0.737	-0.149	-0.189
CRS GRY2	0.387	0.348	-0.189	IWNG	-0.644	-0.079	-0.172
CRS BRN	0.317	0.671	0.339	REC1 EDG	-0.330	-0.172	-0.359
CRS BLU	0.173	-0.582	0.300	REC1 TIP	-0.504	0.325	-0.202
CRS INT	0.356	0.190	-0.139	REC2-4ED	-0.571	-0.134	-0.124
FLN GRY1	0.352	-0.158	0.794	REC2-4TP	-0.678	0.133	-0.205
FLN GRY2	-0.268	0.133	-0.603	REC4-6TP	-0.773	0.179	-0.042
FLN BRN	-0.089	0.799	0.201	RECECON	-0.814	-0.154	-0.409
FLN BLU	0.275	-0.713	0.425	RECTPCON	-0.585	0.351	-0.443
FLN INT	0.093	0.256	-0.000	EYE CLR	-0.415	0.227	-0.238
WNG GRY1	-0.401	-0.043	0.606	B NOTCH	-0.040	-0.079	0.878
WNG GRY2	0.083	0.040	-0.273	B CURV	0.085	0.103	-0.573
WNG BRN	0.164	0.816	-0.043	TOE SCUT	0.306	0.050	0.811
WNG BLU	0.275	-0.713	0.425	TAR SCUT	-0.426	-0.186	-0.626
WNG INT	-0.023	0.290	-0.362	WING SHP	-0.502	0.082	0.145
REC GRY1	-0.331	-0.055	0.546	TAIL SHP	-0.046	-0.304	-0.541
REC GRY2	0.235	0.137	-0.412	RICT BRI	-0.223	-0.056	-0.210
REC BRN	0.391	0.744	-0.064	EGG CLR	0.470	0.161	0.336
REC BLU	0.275	-0.713	0.425	EGGSPTS	0.084	0.177	-0.335
REC INT	0.464	0.361	-0.217	NEST	0.176	0.298	0.082
CRO ST	-0.454	-0.074	0.031	YNG SPOT	0.049	0.321	-0.083
CRO SC	-0.299	-0.064	-0.024	GRND/ARB	0.072	0.359	0.616
BAK ST	-0.160	0.034	-0.181				
BAK SC	-0.546	0.189	0.186				
RUMP ST	-0.423	-0.145	0.064				

catbirds placed in an intermediate position.

CLUSTER ANALYSIS

The phenograms produced by the UPGMA cluster analysis are given in figure 4.15 and 4.16. These both reflect the discrete groupings of the taxa that are visible in the three dimensional projections. The integrity of the clusters is maintained and the only problems occur in the connections of the groups at low correlation levels and/or high distance values. This is again the problem of distortion in phenograms at these levels. Since the position of the major clusters is apparent in the projections, I will not attempt to reconcile the differences between the two phenograms. Certain points are however worth attention.

Oreoscoptes is a particularly difficult species to place. The phenogram based on correlations places it as a member of the Mimus complex. On the other hand, the distance coefficient places it well within the Toxostoma cluster. This is one of those cases where the taxonomist must resort to one of two courses. He must either look for some more characters which may help resolve the placement of the species, or he must make a subjective decision. The borderline nature of the phenetic placement of the species is evident in the three dimensional plot of figure 4.14.

FIGURE 4.15. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF CORRELATIONS RESULTING FROM ALL EXTERNAL CHARACTERS.

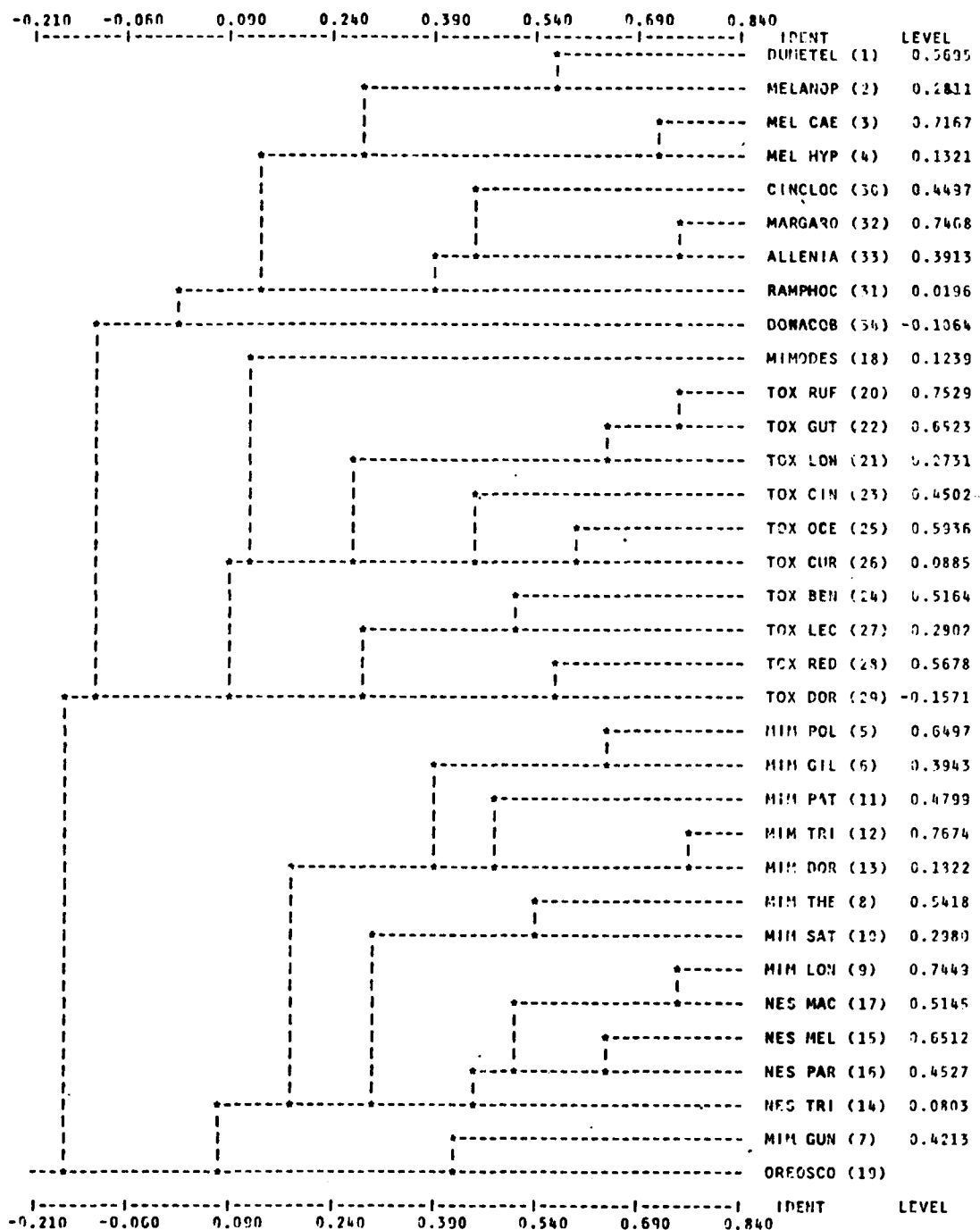
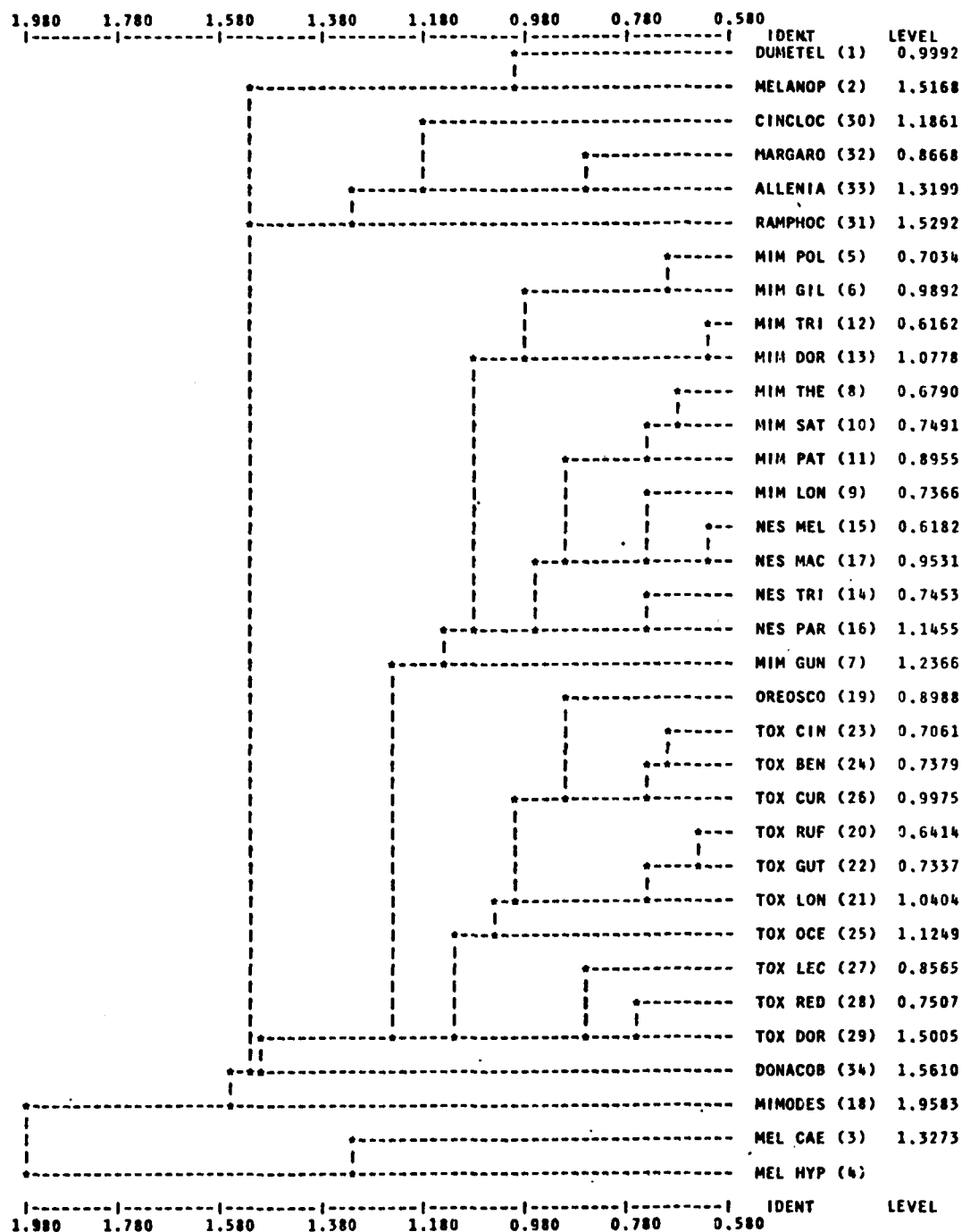


FIGURE 4.16. PHENOGRAM OF TAXA CLUSTERED ON THE BASIS OF AVERAGE DISTANCE RESULTING FROM ALL EXTERNAL CHARACTERS.



The equidistant position of this bird (19) relative to the nearest Mimus and Toxotoma species is emphasized by the lengths of the minimum spanning tree links that connect them. In terms of taxonomic distance, Oreoscoptes is .833 units from Toxostoma bendirei and .867 units from Mimus patagonicus. On an arbitrary basis then, the species must be associated with Toxostoma.

The other noteworthy problem is the placement of the blue mockingbirds, and Donacobius. The cluster analysis of the distance coefficients (figure 4.16) places these birds on branches of the phenogram opposed to all of the other species and groups of species. In the case of the blue mockingbirds, this is probably due to the additive nature of some of the highly correlated characters. Therefore, the clustering of the correlation coefficients, figure 4.13, may be a better summary of phenetic relationships of these two species to other birds than the clustering based on distance. The three dimensional projections suggest as much. In them, the blue mockingbirds are clearly associated on the Z axis with the West Indian endemics and the catbirds. This is also the association produced by the cluster analysis of the correlation coefficients.

The position of Donacobius and Mimodes, which is rather ambivalent in the two cluster analyses, is likewise ambivalent in the three dimensional projection. Mimodes does tend in both cluster analyses and the three

dimensional projection to associate with Toxostoma. Since Minodes has such a high percentage of missing miscellaneous characters, there is little reason to prefer any other association.

SKELETONS

Skeletons, next to external characters, represent the most accessible and frequent source of taxonomic characters. They have received special attention from both functional anatomists and systematists. In this chapter skeletal data will be analyzed to show phenetic relationships among the taxa and to suggest some general correlations among the variables and known ecological differences among the taxa. The study will attempt to demonstrate that discriminant functions and generalized distances are useful tools with which to study these facets of avian biology and have certain advantages over other numerical methods.

MATERIALS AND METHODS

A total of 253 skeletons of 32 species of mimids and 54 skeletons of 14 species of thrushes were examined for this study (table 5.1). Each skeleton was measured and coded for 65 variables. For most of the analyses only 57 variables were used and only 184 skeletons were included due to large numbers of missing characters in many of the skeletons. The samples are listed in table 5.1. The variables are distributed according to anatomical region as follows: skull 30; pectoral assemblage 16; pelvic assemblage 10; axial 1.

The skeletal characters were measured in one of three

TABLE 5.1 TAXA AND NUMBER OF SKELETONS AVAILABLE

TOTAL AVAIL	NO MISS DATA	TAXA	FIGURE LABELS	EXT CHAR
25	10	<u>DUMETELLA CAROLINENSIS</u>	DUMETEL	YES
11	5	<u>MELANOPTILA GLABRIROSTRIS</u>	MELANOP	YES
5	4	<u>MELANOTIS CAERULESCENS</u>	MEL CAE	YES
4	4	<u>MELANOTIS HYPOLEUCUS</u>	MEL HYP	YES
22	9	<u>MIMUS POLYGLOTTOS</u>	MIM POL	YES
9	4	<u>MIMUS GILVUS</u>	MIM GIL	YES
5	2	<u>MIMUS GUNDLACHII</u>	MIM GUN	YES
4	2	<u>MIMUS THENCA</u>	MIM THE	YES
7	3	<u>MIMUS LONGICAUDATUS</u>	MIM LOW	YES
4	2	<u>MIMUS SATURNINUS</u>	MIM SAT	YES
4	2	<u>MIMUS PATAGONICUS</u>	MIM PAT	YES
3	2	<u>MIMUS TRIURUS</u>	MIM TRI	YES
3	3	<u>NESOMIMUS TRIPASCIATUS</u>	NES TRI	YES
5	3	<u>NESOMIMUS MACDONALDI</u>	NES MAC	YES
8	5	<u>NESOMIMUS PARVULUS</u>	NES PAR	YES
1	1	<u>MIMODES GRAYSONI</u>	MIMODES	YES*
10	4	<u>OREOSCOPTES MONTANUS</u>	OREOSCO	YES
14	9	<u>TOXOSTOMA RUFUM</u>	TOX RUF	YES
4	3	<u>TOXOSTOMA LONGIROSTRE</u>	TOX LOW	YES
6	3	<u>TOXOSTOMA GUTTATUM</u>	TOX GUT	YES
1	1	<u>TOXOSTOMA CINEREUM</u>	TOX CIN	YES
3	3	<u>TOXOSTOMA BENDIREI</u>	TOX BEN	YES
2	2	<u>TOXOSTOMA OCELLATUM</u>	TOX OCE	YES
20	10	<u>TOXOSTOMA CURVIROSTRE</u>	TOX CUR	YES
2	2	<u>TOXOSTOMA LECONTEI</u>	TOX LEC	YES
7	5	<u>TOXOSTOMA REDIVIVUM</u>	TOX RED	YES
5	4	<u>TOXOSTOMA DORSALE</u>	TOX DOR	YES
17	12	<u>CINCLOCERTHIA RUFICAUDA</u>	CINCLOC	YES
2	2	<u>RAMPHOCINCLUS BRACHYURUS</u>	RAMPHOC	YES*
18	13	<u>ALLENIA FUSCA</u>	ALLENIA	YES
12	9	<u>MARGAROPS FUSCATUS</u>	MARGARO	YES
8	3	<u>DONACOBIVUS ATRICAPILLUS</u>	DONACOB	YES
2	1	<u>COSSYPHA CYANOCAMPTER</u>	COS CYA	NO
1	1	<u>COSSYPHA CAPFER</u>	COS CAP	NO
2	2	<u>COSSYPHA HUMERALIS</u>	COS HUM	NO
4	3	<u>COSSYPHA NIVEICAPILLA</u>	COS NIV	NO
1	1	<u>ALETHE POLIOCEPHALA</u>	ALE POL	NO
1	1	<u>COPSYCHUS SAULARIS</u>	COP SAU	NO
5	4	<u>COPSYCHUS MALABARICUS</u>	COP MAL	NO
3	2	<u>MYADestes GENIBARRIS</u>	MYA GEN	NO
3	2	<u>NOTICOLA SOLITARIUS</u>	NOT SOL	NO
4	3	<u>CATHARUS FUSCESCENS</u>	CAT FUS	NO
9	7	<u>CATHARUS USTULATA</u>	CAT UST	NO
7	5	<u>HYLOCICHLA MUSTELINA</u>	HYL MUS	NO
6	4	<u>TURDUS PHILOMELUS</u>	TUR PHI	NO
15	5	<u>TURDUS MIGRATORIUS</u>	TUR MIG	NO

*MIMODES GRAYSONI HAS 4 MISSING EXTERNAL CHARACTERS

RAMPHOCINCLUS BRACHYURUS HAS 1 MISSING EXTERNAL CHARACTER

ways: 1) Dial calipers, read to the nearest .1 mm. (DC in table 5.2). 2) Ocular micrometer mounted in a Bausch and Lomb dissecting microscope. (OM in table 5.2). 3) Angles were measured with an ocular protractor installed in the dissecting microscope. (PR in table 5.2).

I did not routinely measure the left and right side for a character, except for the angles which were more variable. I did however, measure both sides for a character in enough specimens to be confident that I was obtaining an accurate evaluation. Where both sides were measured the average was recorded. Some structures that were measured across a medial line, for example pelvic widths, were damaged on one side. In those cases, I measured from the unbroken edge to the medial line and doubled this to represent the full measurement. I checked this procedure carefully on undamaged specimens. I felt that possible errors introduced by the procedure were more than compensated for by not having to eliminate the specimen because of missing characters. For a very few characters such as the length of the premaxilla, some reconstruction was employed. Very often when the ramphotheca is removed from the underlying bone, the soft spongy tip is broken off. It is not difficult, on the basis of experience with undamaged specimens to extrapolate the position of the final, terminal tip. These are perennial problems for anyone attempting to accumulate

information from a sizable number of specimens. These problems are discussed and a similar rationale for dealing with them is proposed by Howells (1973) in a study of cranial variation in man.

Whenever many thousands of measurements are being taken errors inevitably are made. These involve errors in reading dials, errors in entering data on data sheets and finally errors made in entering the data into the computer. In this study the primary check, beyond simple remeasuring of all entries that appeared peculiar, was to calculate the basic univariate statistics (Sokal and Rohlf, 1969) for all of the characters by taxon and examine the coefficients of variation of the characters. This allowed me to detect and remove most, if not all of the grossly erroneous measurements. Whenever a coefficient of variation seemed inconsistent with coefficients of variation for the same character in other taxa, the specimens contributing the excessive variation were identified and the character was remeasured. Summary tables of the basic statistics for all the taxa included in this study are given in appendix table five.

NUMERICAL PROCEDURES

Univariate statistics of all skeletal measurements and codes were examined. Means, standard deviations, and

coefficients of variation for each character, by taxa are given in appendix table 5. The taxa were not separated by sex in as much as sex information was not available for many of the specimens. In a few samples there were enough of each sex to make it worth while to process each separately. There were no statistically significant differences between the males and females in all except one case. What slight differences may in reality exist were thought not to be important in the context of this study. The only bird in which significant differences did occur was Cinclocerthia ruficauda, and then only in measures of bill length. As can be seen in the appendix tables, the coefficients of variation are little different for this species with the exception of the two measures of premaxilla length SK 11 and SK 12. Initially it was feared that interpopulation variation among the subspecies of Cinclocerthia would also cause problems. This also proved to be unfounded, and although four of the subspecies are represented in the 17 specimens measured, the coefficients of variation are not particularly inflated. In summary, it appears that intersex and interpopulation differences among mimids are not great.

When analyzing morphometric data for a number of related organisms, a problem that must be quickly faced is that of size. In animals such as birds and mammals that attain a fixed adult size one does not have to contend with

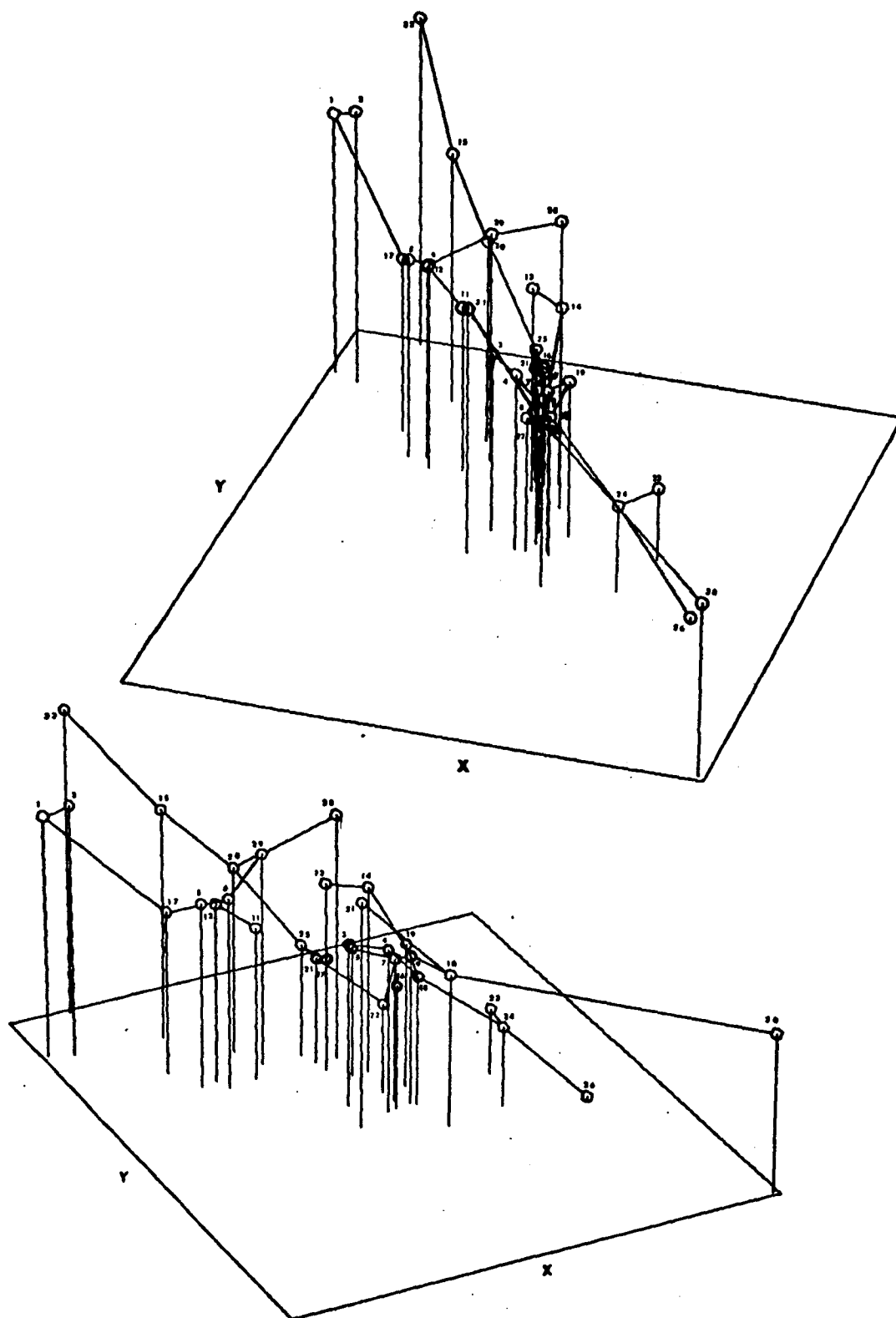
problems encountered by workers studying such groups as fishes and others which exhibit more or less continuous growth. As only adult specimens were used in this study, growth problems were not considered significant and were not studied. There is, however, a problem in comparing different species. For example, Allenia fusca and Margarops fuscatus are considered to be sister species, yet they are quite different in size. The question is how to remove size differences so that more meaningful comparisons of shape and structural relationships can be discerned. There have been many approaches to the problem. These have been reviewed by Sneath and Sokal (1973) among others.

In this study two approaches to the problem were tried. (That there is a problem can be seen in figure 5.1 which shows projections of the taxa onto the first three rotated principal components before any form of rescaling was attempted). The first method was the classic one of choosing a variable and expressing every other variable as a ratio to it. This was the approach used by Schnell (1970) in his study of the Laridae. As a reference variable, I initially chose trunk length because it appears to be a variable that is inherently less subject to the more obvious selective forces that affect locomotory systems such as the sternum, or limb measurements. Likewise most skull variables would seem to be too closely connected with feeding mechanisms to be reliable indicators

FIGURE 5.1. THREE DIMENSIONAL PROJECTION OF 32 MIMID SPECIES ONTO ROTATED PRINCIPAL COMPONENT AXES, DERIVED FROM UNSCALED SKELETAL VARIABLES.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	MPLANOP (2)	0.461
DUMETEL (1)	OREOSCO (17)	0.856
OREOSCO (17)	MIM POL (5)	0.537
MIM POL (5)	MIM GIL (6)	0.293
MIM GIL (6)	MIM TRI (12)	0.382
MIM TRI (12)	MIM PAT (11)	0.560
MIM GIL (6)	RAMPHOC (29)	0.786
RAMPHOC (29)	TOX GUT (20)	0.647
TOX GUT (20)	TOX LFC (25)	0.799
TOX LEC (25)	TOX DOR (27)	0.582
TOX LEC (25)	TOX CIN (21)	0.763
TOX CIN (21)	TOX BEN (22)	0.766
TOX BEN (22)	MIM GUN (7)	0.753
MIM GUN (7)	MIM GHE (8)	0.578
MIM GUN (7)	MIM LOW (9)	0.615
MIM LOW (9)	TOX LOW (19)	0.700
TOX LOW (19)	TOX RUP (18)	0.505
TOX RUP (18)	TOX CUR (24)	0.690
TOX CUR (24)	TOX OCE (23)	0.720
MIM LOW (9)	MIM SAT (10)	0.730
TOX RUP (18)	MEL HYP (4)	0.739
MEL HYP (4)	MEL CAE (3)	0.420
MIM LOW (9)	NES MAC (14)	0.790
NES MAC (14)	NES TRI (13)	0.548
TOX GUT (20)	NES PAR (15)	0.810
MIM GUN (7)	EIMODES (16)	0.827
RAMPHOC (29)	CIMCLOC (28)	0.885
TOX CUR (24)	TOX RED (26)	0.942
MIM SAT (10)	ALLENIA (31)	1.029
NES PAR (15)	DONACOB (32)	1.151
MIM SAT (10)	MARGARO (30)	1.788



of pure size relationships. Trunk length has been used previously by Zusi (1969) to accomplish similar objectives.

When a single variable is used as a reference variable to generate ratios with all other characters as was done by Schnell (1970), no consideration is taken of the amount of correlation the variable has with other variables. Therefore, ratios between it and uncorrelated variables are affecting components other than the common size component. In fact artificial variability is introduced for characters which are uncorrelated with the reference variable. In order to avoid these difficulties variables were rescaled using regression coefficients between the reference variable and all others (Vandermeer, 1967). In this case, variables that are uncorrelated with the reference variable will be affected slightly, if at all, and their variability cannot increase.

Using regression coefficients to rescale the variables suggests that the choice of the reference variable can then be made on the basis of the degree of correlation of variables with each other. Those that are highly correlated with many other variables in different sections of the skeleton quite likely contain considerable size information and are thus likely possibilities as reference variables for rescaling. In the taxa considered in this study, 32 mimids and 14 turdines, that variable which was

most highly correlated with many others in all regions of the skeleton was SK 4, Cranium width 1, the width of the cranium at the level of the dorsal process of the exoccipital wing (figure 5.1 and table 5.2). Regression coefficients were computed for all variables relative to it and the original values scaled accordingly. (See Vandermeer, 1967 for a detailed discussion and formula). Log transformations can also be used to help remove certain aspects of size differences, especially those resulting from growth. These were tried and found to make little if any difference in the analysis when compared to the results obtained using the untransformed data.

A particularly good approach to dealing with problems of correlated variables resulting from any component, not only size is the use of generalized distances. This procedure was developed by Mahalanobis to overcome the problems of distortion in measures of taxonomic distance (Howells, 1973). Generalized distances are obtained by a deliberate weighting of the means of the variables for each taxon by the pooled within group variance. The concept bears a strong relationship to an approach suggested by Farris (1966). Farris advocated weighting characters on the basis of their relative constancy within, versus their variance among the groups of a study. The generalized distance accomplishes much the same thing. It was only possible to compute generalized distance on the basis of

the skeletal data, however, since individuals were not scored for the external characters. As a result, there was no pooled within group variance with which to weight. A theoretical question of some importance is whether it is really desirable to remove all correlation between characters in a study. In this study this was desired, based on the assumption that the residual information is likely to better suggest functional, ecological and hopefully some phylogenetic relationships than when the correlating elements, particularly size, are not removed from the variables.

Closely related to the generalized distance concept are discriminant functions (see chapter two). These functions are "new variables", consisting of a weighted combination of original variables that best serve to distinguish predefined groups, in this case the species of minids and thrushes. The relationship between the generalized distance and the discriminant function is that generalized distances calculated between taxa projected onto the discriminant functions are Euclidean distances in terms of these new axes (Van de Geer, 1972). In a manner akin to principal components analysis discussed previously, the first few axes summarize more of the intergroup differences as measured by distance than any other orthogonal (uncorrelated) axes that can be constructed.

The problems most frequently investigated with discriminant functions have been those where an attempt was made to discern affinities between phenetically very similar groups, usually populations. An excellent example and one of the most lucid demonstrations of these techniques is the study by Howells (1973) of seventeen human populations, using cranial measurements. Rohwer (1972) used discriminant function techniques to estimate the degree of interbreeding between the Eastern Meadowlark (Sturnella magna) and the Western Meadowlark (Sturnella neglecta).

Some have claimed that in studies of species and higher taxa discriminant functions are of little use in as much as the groups are so distinct that little can be gained. Among the mimids however, there are two quite troublesome monotypic genera, Mimodes and Oreoscoptes. On the basis of most characters analyzed so far, the position of these two taxa relative to other members of the group are equivocal, especially so in the case of Oreoscoptes.

On the basis of the combined external characters, (figure 4.14) Mimodes is clearly in the Toxostoma cluster, although slightly set apart. Oreoscoptes occupies a position nearly equidistant from the Mimus and Toxostoma clusters. I therefore hoped that the use of discriminant functions to analyze the skeletal characters would more

accurately suggest the phenetic affinities of these two taxa to other mirds.

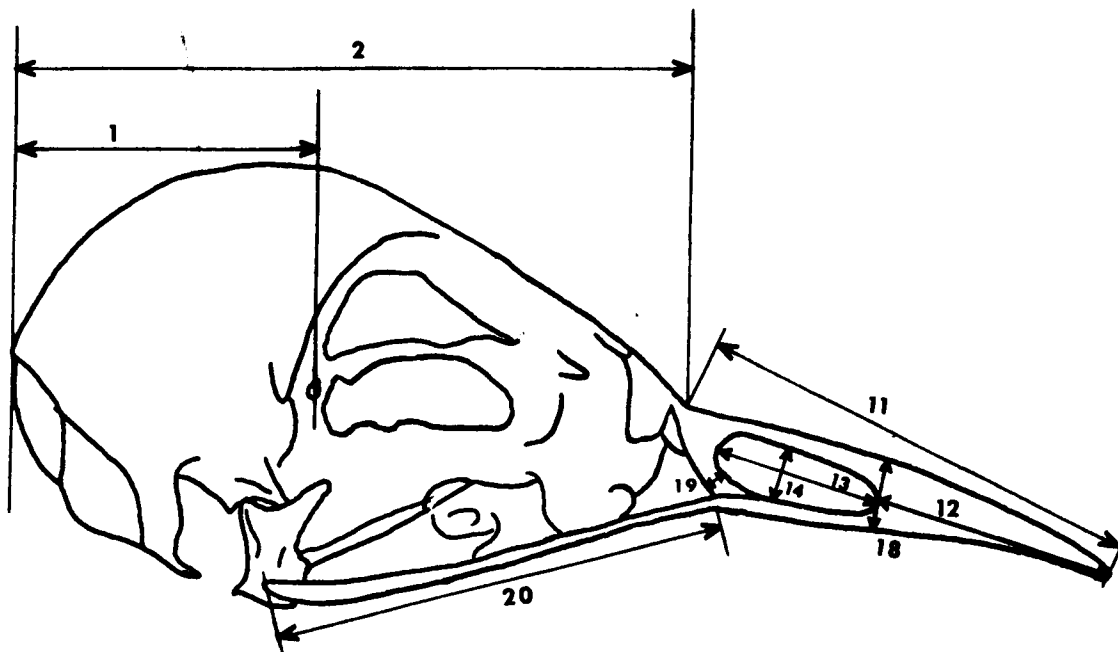
CHARACTERS AND CHARACTER COMPLEXES

Many of the characters used in this study (figures 5.2 - 5.5; table 5.2) have no special significance, being basic, repeatable measurements of various body skeletal features that have traditionally been used to represent various aspects of morphological structures. Lengths and widths of appendicular bones fall into this category. For characters of this type little can be said prior to graphical and numerical analysis, after which some of their relationships become interesting. Many of these characters are the standard ones long used to calculate ratios between limb elements and to evaluate limb to limb functional relationships (Engels, 1940; Zusi, 1969). Other guides in the selection of characters were Schnell (1970) and Robins and Schnell (1971).

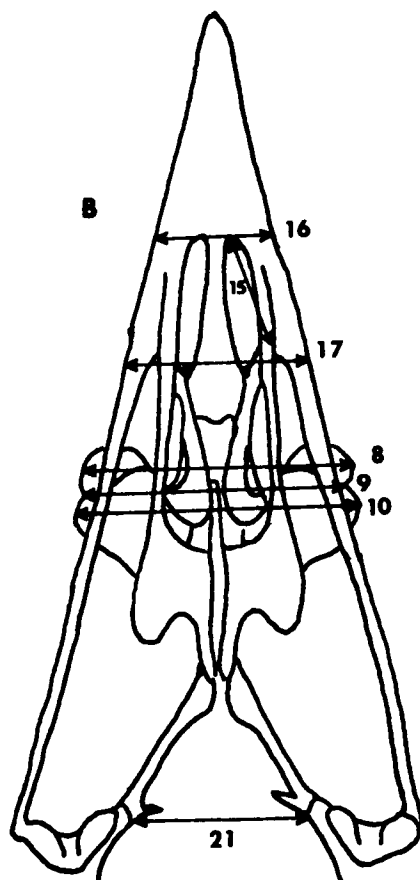
CRANIAL CHARACTERS

The choice of characters in the skull presents a challenging problem. Here one is dealing with extremely complex shapes and a few simple measurements will hardly suffice to even minimally represent them. The researcher must try within practical limits to include enough data

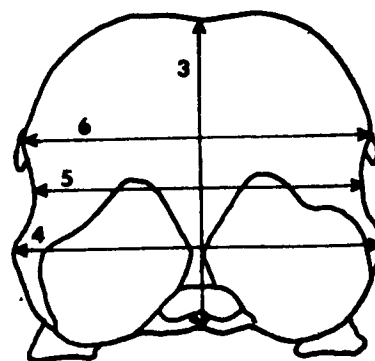
FIGURE 5.2. THREE VIEWS OF A TYPICAL MIMUS SKULL
ILLUSTRATING VARIOUS CRANIAL MEASUREMENTS. NUMBERS REFER
TO SKELETAL VARIABLES IN TABLE 5.2. (A) LATERAL VIEW. (B)
VENTRAL VIEW OF ANTERIOR REGIONS. (C) POSTERIOR VIEW.



A



B



C

FIGURE 5.3. DETAILS OF MIMID CRANIAL REGIONS ILLUSTRATING VARIOUS CRANIAL MEASUREMENTS. NUMBERS REFER TO SKELETAL VARIABLES IN TABLE 5.2. (A) AND (B) LATERAL VIEWS OF TYPICAL MIMUS TYMPANIC AND TEMPORAL REGIONS, (C) VENTRAL VIEW OF TYMPANIC REGION OF ALLENIA, (D) VENTRAL VIEW OF TYMPANIC REGION IN MIMUS, (E) VENTRAL VIEW OF TYPICAL MIMID MAXILLOPALATINES, (F) LATERAL VIEW OF TYPICAL MIMID DESCENDING PROCESS OF NASAL AND LACRIMAL.

(a) Suprameatic fossa. (b) Zygomatic ridge. (c) Suprameatic ridge. (d) Exoccipital wing. (e) Quadrate. (f) Maxillopalatine. (g) Ectethmoid plate. (h) Descending process of nasal. (i) Lacrimal. (j) Postorbital process.

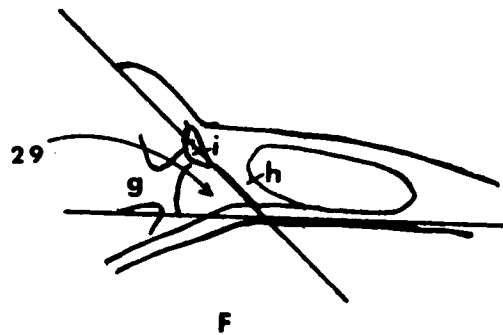
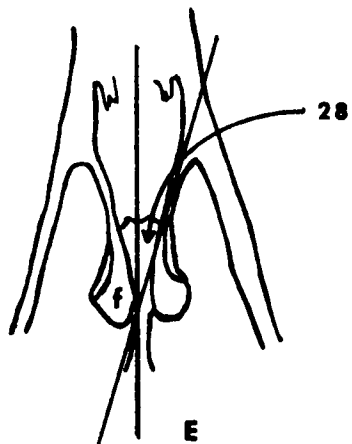
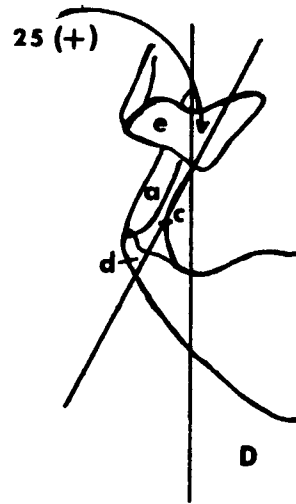
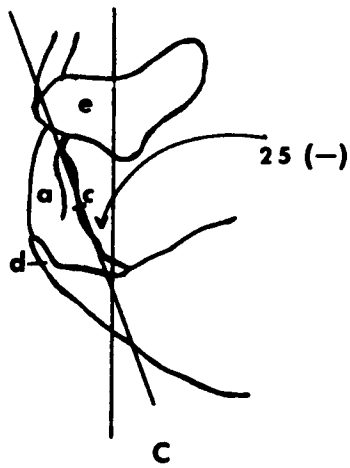
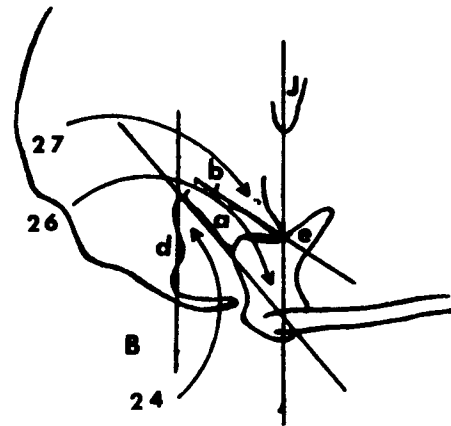
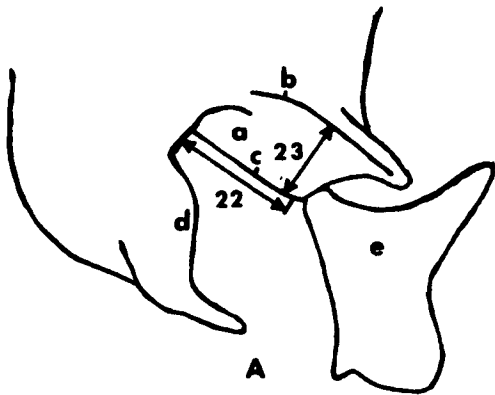


FIGURE 5.4. (A) VENTRAL VIEW OF ANTERIOR FACE OF THE ECTETHMOID PLATE OF DUFETELLA. (B) POSTERIOR VIEW OF ECTETHMOID PLATES OF A TYPICAL MINID (LEFT) AND THRUSH (RIGHT). (a) Olfactory process (SK 64). (b) Lateral ectethmoid foramen (SK 65).

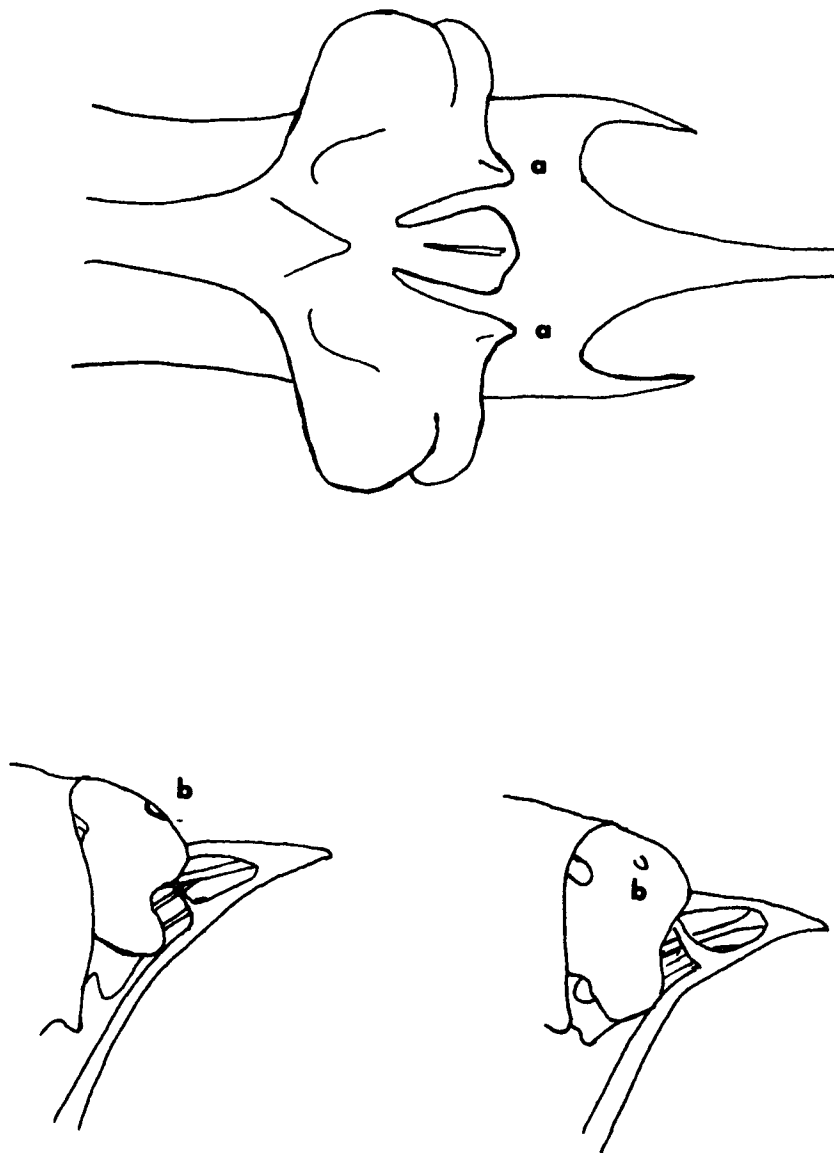


FIGURE 5.5. ILLUSTRATIONS OF TYPICAL MIMID POST CRANIAL SKELETAL STRUCTURES (DRAWN TO VARIOUS SCALES). NUMBERS REFER TO SKELETAL VARIABLES IN TABLE 5.2. (A) LATERAL VIEW OF STERNUM. (B) LATERAL (TOP) AND POSTERIOR (BOTTOM) VIEWS OF PYGOSTYLE. (C) VENTRAL VIEW OF STERNUM. (D) HUMERUS. (E) ULNA. (F) CORACOID. (G) TIBIOTARSUS. (H) TARSOMETATARSUS. (I) DORSAL VIEW OF PELVIS. (J) FEMUR. (K) CARPOMETACARPUS. (L) PHALANX I. (M) PHALANX II, DIGIT III.

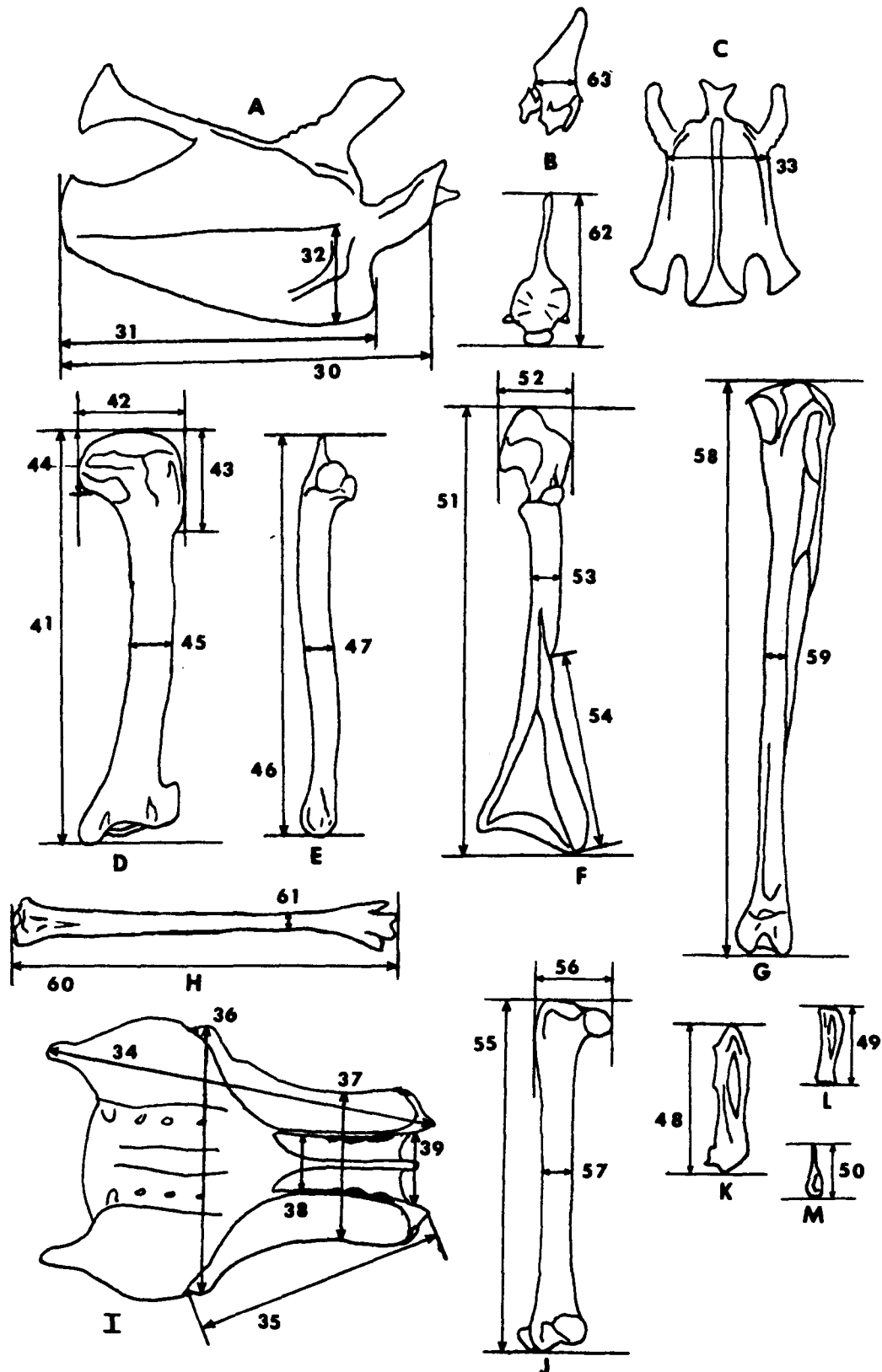


TABLE 5.2. SKELETAL CHARACTERS. "V" NUMBERS REFER TO LABELS OF VARIABLES IN APPENDIX TABLE 5. "*" SIGNIFIES CHARACTERS THAT WERE NOT INCLUDED IN THE DISCRIMINANT FUNCTIONAL ANALYSIS BECAUSE OF EXCESSIVE MISSING DATA. DC = DIAL CALIPER; OM = OCULAR MICROMETER; OP = OCULAR PROTRACTOR.

SK 1 Cranium length I (V8) DC: Medial distance from posterior of supraoccipital to edge of optic foramen in the laterosphenoid.

SK 2 Cranium length II (V13) DC: Medial distance from posterior of supraoccipital to nasal - frontal hinge.

SK 3 Cranium height (V9) DC: Medial distance from basioccipital to frontal.

SK 4 Cranium width I (V10) DC: Distance between the supratympanic processes of the squamosal (dorsal processes of the exoccipital wing).

SK 5 Cranium width II (V11) DC: Minimum distance across cranium in frontal plane between postorbital and zygomatic processes.

SK 6 Cranium width III (V12) DC: Distance across cranium in frontal plane at level of postorbital processes

SK 7 Interorbital width (V15) DC: Minimum width across frontals between the orbits.

SK 8 Ectethmoid width I (V22) DC: Maximum transverse distance across dorsal wing of ectethmoid.

SK 9 Ectethmoid width II (V23) DC: Minimum transverse distance across ectethmoid at level of indentation

SK 10 Ectethmoid width III (V24) DC: Maximum transverse distance across ventral wing of ectethmoid.

SK 11 Premaxilla length I (V14) DC: Medial distance from frontal/nasal hinge to tip of premaxilla (ramphotheca removed)

SK 12 Premaxilla length II (V56) DC: Distance from anterior edge of nares to tip of premaxilla (ramphotheca removed)

SK 13 Nares length (V19) DC: Maximum distance from anterior to posterior borders of external nares.

TABLE 5.2. CONTINUED

SK 14 Nares width (V20) DC: Maximum width across nares from ventral to dorsal processes of the premaxilla.

SK 15 Pedicle distance (V21) DC: Distance from anterior edge of nares to midpoint of junction of the pedicle of the maxillopalatine to the maxilla.

SK 16 Bill width I (V16) DC: Transverse distance across bill at anterior end of nares.

SK 17 Bill width II (V17) DC: Transverse distance across bill at posterior end of nares.

SK 18 Bill Height (V18) DC: Dorsal - ventral distance across bill at front end of nares.

SK 19 Descending process of premaxilla, width (V25) OM: Minimum longitudinal distance across the process.

SK 20 Jugal bar length (V30) DC: Distance from posterior end of jugal bar to its junction with the descending process of the nasal.

SK 21* Interpterygoid width (V28) OM: Distance between ends of the two pterygoid bars.

SK 22 Suprameatic ridge length (V27) OM: Distance from posterior edge of articular facet of the squamosal - quadrate articulation to exoccipital wing. (In cases where the suprameatic fossa extends under the exoccipital wing, the distance is to a point perpendicular to the edge of the exoccipital wing.)

SK 23 Suprameatic fossa width (V26) OM: Distance from ventral edge of the fossa to the zygomatic ridge at the level of the posterior edge of the quadrate - squamosal articulation.

SK 24 Angle (V49) OP: Ventral edge of suprameatic fossa relative to anterior edge of exoccipital wing.

SK 25 Angle (V51) OP: Ventral edge of suprameatic fossa relative to anterior/posterior axis of skull.

SK 26 Angle (V54) OP: Ventral edge of suprameatic fossa relative to a perpendicular dropped from the postorbital process to the jugal.

TABLE 5.2. CONTINUED

SK 27 Angle (V53) OP: Zygomatic ridge relative to a perpendicular dropped from the postorbital process to the jugal.

SK 28 Angle (V52) OP: Pedicles of the maxillopalatines relative to the posterior/anterior axis of skull

SK 29 Angle (V50) OP: Descending process of nasal relative to ventral edge of the premaxilla.

SK 30 Sternum length (V36) DC: Medial distance from posterior edge of sternum to anterior edge of manubrium.

SK 31 Keel length (V39) DC: Distance from posterior edge of sternum to anterior edge of the keel

SK 32 Sternum depth (V37) DC: Maximum distance from ventral edge of keel to base of manubrium.

SK 33 Sternum width (V38) DC: Transverse distance between lateral edges of sternum immediately posterior to sternocostal processes.

SK 34 Pelvis length I (V31) DC: Maximum distance from posterior to anterior iliac processes.

SK 35 Pelvis length II (V32) DC: Distance from posterior edge of supraacetabular process to anterior process of the ilium.

SK 36 Pelvis width I (V33) DC: Maximum distance between lateral edges of the supraacetabular processes.

SK 37 Pelvis width III (V35) DC: Minimum distance between lateral edges of the ilia between the acetabulum and the anterior processes of the ilium.

SK 38 Pelvis width IV (V72) DC: Minimum distance between the medial dorsal ridges of the ilia, anterior to the acetabula.

SK 39* Pelvis width V (V73) DC: Distance between the medial dorsal ridges of the ilia at the anterior edge of the iliac fossa.

SK 40 Trunk length (V55) DC: Medial distance from posterior edge of centrum of last thoracic vertebra to anterior edge of first thoracic vertebra (6).

TABLE 5.2. CONTINUED

SK 41* Humerus length (V43) DC: Maximum length from proximal edge of head to distal edge of the medial epicondyle.

SK 42 Humerus head width (V44) DC: Maximum distance between medial edge of head and lateral edge of the deltoid crest, perpendicular to axis of shaft.

SK 43 Humerus deltoid crest length (V45) OM: Distance from plane at end of head, perpendicular to axis of shaft, to distal edge of deltoid crest.

SK 44 Humerus head depth (V46) OM: Distance from plane at end of head, perpendicular to axis of shaft, to distal border of the bicipital crest.

SK 45 Humerus shaft width (V62) DC: Minimum transverse medial - lateral distance across shaft.

SK 46 Ulna length (V47) DC: Distance from proximal end of ulna to end of the olecranon process.

SK 47 Ulna shaft width (V61) DC: Minimum transverse anterior - posterior distance across shaft.

SK 48 Carpometacarpus length (V63) DC: Maximum length of carpometacarpus.

SK 49 Phalanx I of digit III (V64) DC: Maximum length.

SK 50* Phalanx II of digit III (V65) DC: Maximum length.

SK 51 Corocoid length (V66) DC: Maximum length from distal edge of the coraco - humeral surface to proximal edge of sterno - coracoidal process.

SK 52 Corocoid head width (V67) DC: Maximum distance between medial and lateral surfaces of the proximal end of the corocoid.

SK 53 Corocoid shaft width (V68) DC: Minimum transverse medial - lateral distance across shaft.

SK 54 Corocoid flange length (V69) OM: Length of ventro - lateral flange from lateral sterno - coracoidal process to anterior crest of the flange.

SK 55* Femur length (V40) DC: Distance from proximal side of trochanter to distal edge of external condyle.

TABLE 5.2. CONTINUED

SK 56 Femur head width (V41) DC: Maximum width from medial surface of head to lateral surface of the shaft, perpendicular to shaft axis.

SK 57 Femur shaft width (V59) DC: Minimum transverse medial - lateral shaft distance.

SK 58* Tibiotarsus length (V42) DC: Maximum dimension from proximal articular surface to most distal edge of distal condyles.

SK 59 Tibiotarsus shaft width (V60) DC: Minimum transverse medial - lateral shaft distance.

SK 60 Tarsometatarsus length (V57) DC: Maximum dimension from proximal process to distal edge of trochlea for the third digit.

SK 61 Tarsometatarsus width (V58) DC: Minimum transverse medial - lateral shaft distance.

SK 61* Pygostyle height (V70) DC: Distance from ventral surface of centrum to dorsal edge of pygostyle.

SK 63* Pygostyle width (V71) DC: Anterior - posterior distance across blade of pygostyle just dorsal to terminal plate.

SK 64 Olfactory process (V75) DC: Degree of development of finger like process on anterior dorsal face of the ectethmoid. Coded 0, 1, 2, 3.

SK 65 Lateral ectethmoid foramen (V76) DC: Relative position of the dorso - lateral ectethmoid foramen. Coded: 1 = completely inside orbit; 2 = along edge of frontal - ectethmoid juncture; 3 = outside the orbit, on top of the ectethmoid plate.

points to allow some assessment of complex relationships. The only alternatives, and alternatives not yet fully developed, are methods of pattern recognition and optical data analysis where the entire object is evaluated at once. Only with these methods can one avoid the problems inherent in choosing only a few reference points to represent what are in reality complex curvilinear relationships (Oxnard, 1973). For these reasons, I included four separate measures of skull length; from the occipital to the optic foramen to indicate one dimension of the brain case itself; from the occipital to the frontal-nasal hinge to assess length of the skull proper; the distance from the frontal-nasal hinge to the tip of the premaxilla; and the distance from the anterior of the nares to the tip of the premaxilla. Hopefully the multivariate analysis will detect shifts in the relative proportions of sections of the skull along the anterior-posterior axis.

Other sets of measurements that were chosen to try to summarize complex interrelationships are the three skull widths and the three ectethmoid widths. In each case, there is considerable variation among the taxa in the relative proportions of these elements. In the case of the ectethmoid, the mimids have sharper and deeper indentations than do their relatives the thrushes (figure 5.4). Likewise, the width of the skull at the three points measured (figure 5.2) is also quite variable. In fact one

of the most striking features of a turdine thrush skull is the extreme relative width of the skull at the dorsal end of the exoccipital wing (SK 4) .

In hopes of better understanding the relationships of structures in the skulls of the mimids and thrushes, I have included six angles. Four of these are associated with the complex relationships of the structures that make up the temporal region of the skull, just dorsal to the tympanic fossa .

A similar rationale guided the choice of several measurements (figure 5.5) beyond the basic ones in the post-cranial skeleton. For example, the several pelvic measurements should reflect shifts in proportions of the regions anterior to the acetabulum, relative to overall length. The two measures of distance between the dorsal ridges of the ilia should indicate the degree to which the two are parallel. The seemingly large number of measurements of such bones as the humerus and coracoid should reflect what, subjectively, seem to be significant variations among the taxa.

In the analysis of the skeletal material, I have not included indices such as ratios of one element to another in as much as the multivariate techniques construct linear combinations of all of the variables taken simultaneously.

In studies using pairs of variables such as that of Engels (1940), such indices were the only means available to evaluate relationships among the characters and to evaluate significant shifts in the morphology of the birds. For this reason I will not attempt to interpret the biological significance of any of the variables or combinations of them at this point, rather I will later attempt to relate available knowledge of the biology of the taxa in terms of the factors obtained from the analysis.

TEMPORAL COMPLEX

The temporal region of the skulls of the mimids and thrushes deserve special mention with regard to variability. It is striking that, within a small group of passerines such as the mimids, such major variation should occur. This is especially so since most passerine groups are generally so uniform.

One part of the temporal complex seems intimately involved in the shifts made by many mimids in diets and foraging techniques. A principal result is the weaker development of the muscle that arises from the temporal fossa, the M. adductor externus complex (Morioka, 1967). As analyzed and illustrated in Engels (1940), a shift in the orientation of the zygomatic ridge is correlated with a decrease in the mass of the muscle. In most mimid and

thrush species, the ridge is essentially parallel to the ventral border of the suprameatic fossa. In the sickle-billed Toxostoma thrashers, its posterior end is shifted dorsally. This shift is reflected in the relationship of the two variables SK 26 and SK 27.

The region between the zygomatic ridge and the dorsal border of the tympanic fossa, posterior to the articulation of the squamosal with the quadrate, is the suprameatic fossa (figure 5.3). As pointed out above, its shape and area are variable in response to the position of the zygomatic ridge. The point of the posterior termination of its ventral border, the suprameatic ridge, is also variable. In most minids the suprameatic ridge terminates at the dorsal process of the exoccipital wing (figure 6.7). In Allenia, Margarops, Cinclocerthia and often in Melanotis, it continues in under the exoccipital wing forming a broad post tympanic shelf. The only other Old World insect eaters to exhibit this condition are some of the turdine thrushes (figures 6.4 and 6.5). Among the minids, Melanotis represents an intermediate condition (see figure 6.6). Here the suprameatic ridge continues under the exoccipital wing, but often there is a slightly raised strut curving up and out to the dorsal process of the exoccipital wing. The prominence of this strut is variable.

The functional aspects of the relationships of the suprameatic fossa and ridge are unknown. There are no muscle fibers that arise from the fossa (Morioka, 1967). One aspect of the area, the posterior strut of the suprameatic fossa (figure 6.7), may be involved in the transmission of forces from the quadrate-squamosal articulation to the rest of the brain case. Whatever its functional roles, the region serves to unmistakably identify Allenia, Cinclocerthia, and Margarops and some specimens of Melanotis among the mimids.

Another feature of the suprameatic ridge was first pointed out by Zusi (1969), who noted that in mimids the angular relationship of the suprameatic ridge to the midline axis of the skull is quite variable (SK 25). In the genera Margarops and Allenia and in Turdus, the value is negative. In Cinclocerthia and Hylocichla, the angle approaches zero degrees. In all other mimids and thrushes examined, the angle is positive. (See illustrations of this region in figure 5.3.) The specific values for the various genera can be examined in appendix table five.

ECTETHMOID

Three ectethmoid plate measurements were included in the study. In combination, they reflect the degree of indentation of the central part of the plate (figures 5.2

5.4B). In mimids, the ratio of the indent width (SK 9) to the dorsal (SK 9) and ventral (SK 10) widths is low in comparison to the thrushes. In order to quantify the differences between the various taxa within the mimids and to contrast them to the thrushes, these three separate widths were measured.

Another important character is the relative position of the lateral ectethmoid foramen (SK 65, figure 5.4B). In most of the Old World insect eaters, a single foramen is present. In the turdines however, the foramen is divided. A medial foramen remains and the second, lateral to the first, shifts in different degrees towards the edge of the orbit. The split of the original foramen into two is barely complete in Donacobius. In all the other mimids and turdines examined, the lateral foramen is distinctly separate and can be coded as to its position: inside the orbit (1); on the edge of the frontal at its juncture with the ectethmoid plate (2); completely outside the orbit, on the anterior dorsal face of the ectethmoid plate (3). The significance of the shift in position of the foramen is unknown.

The anterior medio-dorsal face of the ectethmoid plate bears another feature that is variable within the taxa included in this study. This is the olfactory process, (SK 64). The process (figure 5.4A) is in the general region of

the sensory epithelium of the nasal chamber. Its function is not known. One could postulate that it serves to increase the surface area of the ectethmoid that bears the sensory opthalmic epithelium, however there is no anatomical evidence to support this. Bang and Cobb (1966), who described the opthalmic region of birds in some detail, make little mention of it.

DESCENDING PROCESS OF NASAL

The posterior region of the external nares offers a combination of several characters that have been traditionally used as part of the diagnosis of the mimids. These include the angle at which the descending process of the nasal meets the maxilla (SK 29 figure 5.3) and its width (SK 19). (Lucas, 1888; Ridgway, 1907). In general the angle is much smaller than in thrushes. Likewise, the width of the process is narrower in the mimids. It has been suggested (Morioka, 1967) that these two characters are correlated with the extension of the anterior part of the skull and the lengthening of the premaxilla. In the course of my numerical analysis of these characters, the correlation coefficients for all of the characters relative to each other were obtained. Using values that had been rescaled by regression to remove as much of an individual size component as possible, the coefficient between the angle of the descending process and the length of the

premaxilla was $-.669$, confirming Morioka's observation. It is interesting that there is no corresponding relative increase in cranium lengths. The correlation coefficient of the angle with cranium length II (SK 2), is only $-.289$, indicating a weak negative correlation. The width of the process bears little relationship to either premaxilla length or cranium length, the correlation coefficients being $.157$ and $.099$ respectively. These two values are not significant at the $.05$ level.

In this same area of the skull, the character labeled "pedorig" (SK 15) should be mentioned. In most mimids, the center of the base of the pedicle of the maxillopalatines is well within the opening of the external nares. In some birds however, such as Dumetella and Melanoptila, the origin of the pedicle is posterior to the opening of the nares, a condition typical of the thrushes.

NUMERICAL ANALYSIS OF SKELETAL CHARACTERS

The discriminant functions do an excellent job of sorting the species of mimids into clusters. The projections of the taxa onto the first three axes are presented in figure 5.6. Because of the congestion in the central part of the three dimensional projection, a bivariate plot of the first two axes is given in figure 5.7. The figures consist of essentially two perpendicular

FIGURE 5.6. TWO VIEWS OF THREE DIMENSIONAL PROJECTION OF 32 MIMID SPECIES ONTO FIRST THREE DISCRIMINANT FUNCTIONS DERIVED FROM SKELETAL VARIABLES.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	MELANOP (2)	130.532
DUMFTEL (1)	MIM POL (5)	177.192
MIM POL (5)	MIM GIL (6)	33.026
MIM GIL (6)	MIM TRI (12)	128.194
MIM TRI (12)	MIM PAT (11)	129.626
MIM POL (5)	OREOSCO (17)	175.868
MIM TRI (12)	MIM LON (9)	199.610
MIM PAT (11)	MIM THE (8)	208.678
DUMETEL (1)	MEL HYP (4)	211.029
MEL HYP (4)	MEL CAE (3)	127.616
MIM LON (9)	MIM GUN (7)	211.872
MIM GUN (7)	MIMODES (16)	176.653
MIM PAT (11)	NES MAC (14)	214.427
NES MAC (14)	NES PAR (15)	158.921
NES MAC (14)	NES TRI (13)	185.806
MIM GIL (6)	MIM SAT (10)	217.077
MIM SAT (10)	RAMPHOC (29)	187.436
MEL HYP (4)	TOX RUF (18)	223.787
TOX RUF (18)	TOX LON (19)	92.502
TOX LON (19)	TOX GUT (20)	185.565
TOX LON (19)	TOX CUR (24)	191.396
TOX CUR (24)	TOX DOR (27)	182.379
TOX DOR (27)	TOX LEC (25)	160.558
TOX LON (19)	TOX OCE (23)	242.850
TOX GUT (20)	TOX CIN (21)	246.015
TOX CIN (21)	TOX BEN (22)	150.214
TOX DOR (27)	TOX RED (26)	352.743
MIM GIL (6)	ALLENIA (31)	409.142
ALLENIA (31)	MARGARO (30)	267.522
RAMPHOC (29)	CINCLOC (28)	417.628
NES MAC (14)	DOWACOB (32)	670.025

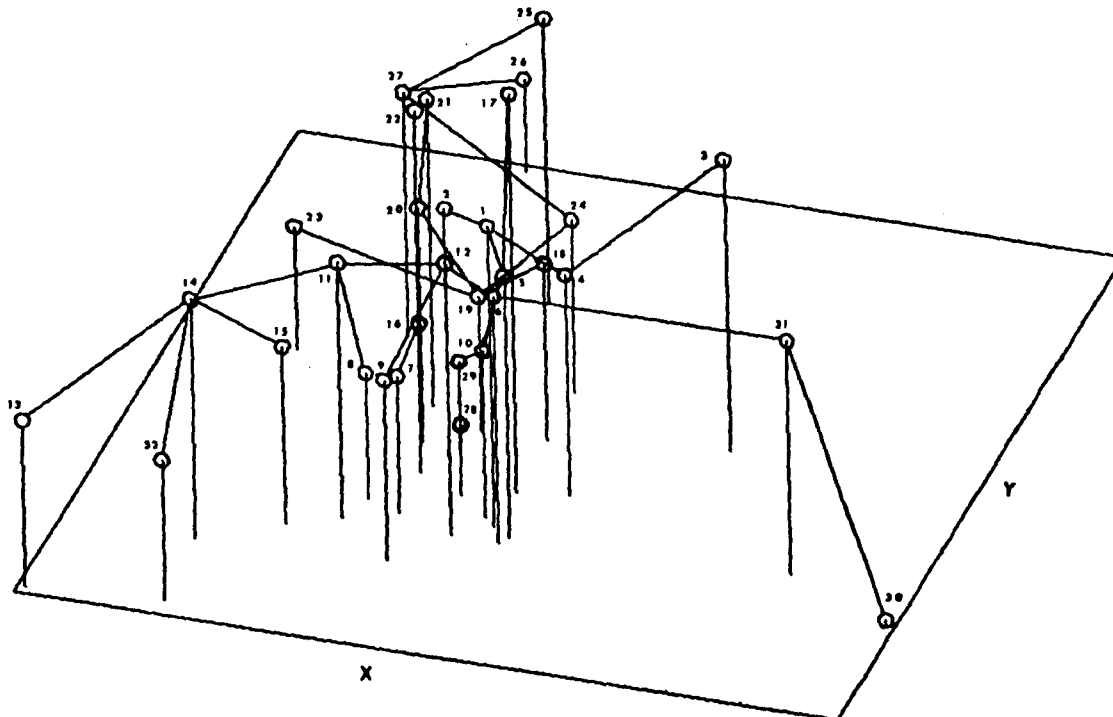
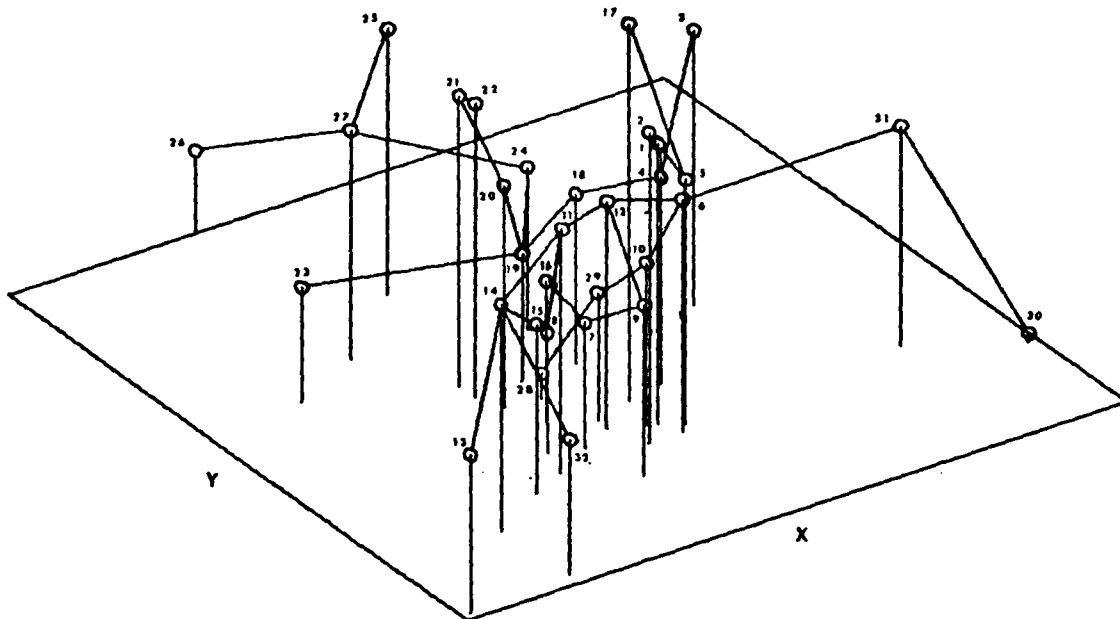


FIGURE 5.6. BIVARIATE PLOT OF 32 MIMID SPECIES PROJECTED ONTO FIRST TWO DISCRIMINANT FUNCTIONS DERIVED FROM SKELETAL DATA. NUMBERS FOLLOWING TAXA REFER TO NUMBERS IN THREE DIMENSIONAL PORJECTION, FIGURE 5.5.

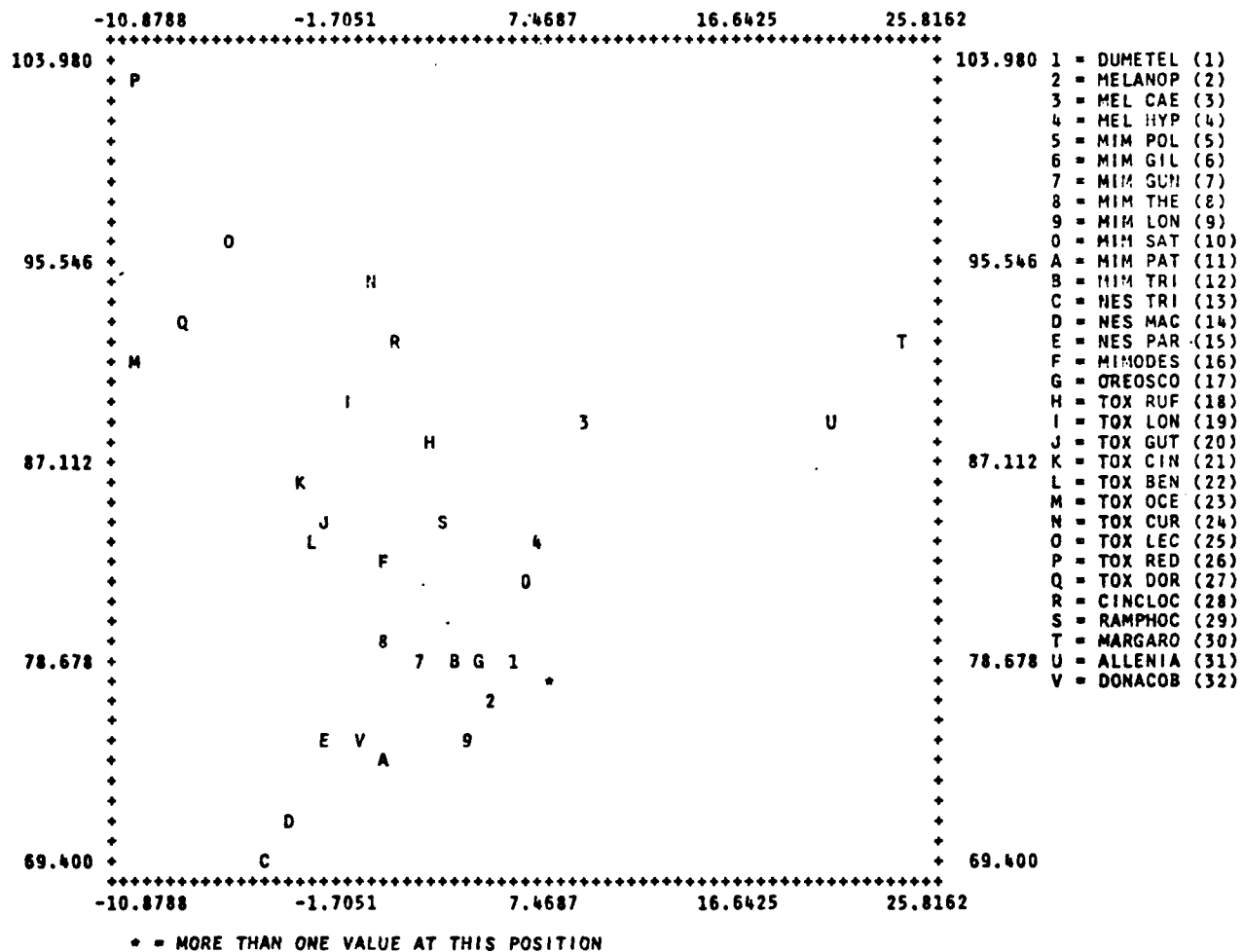
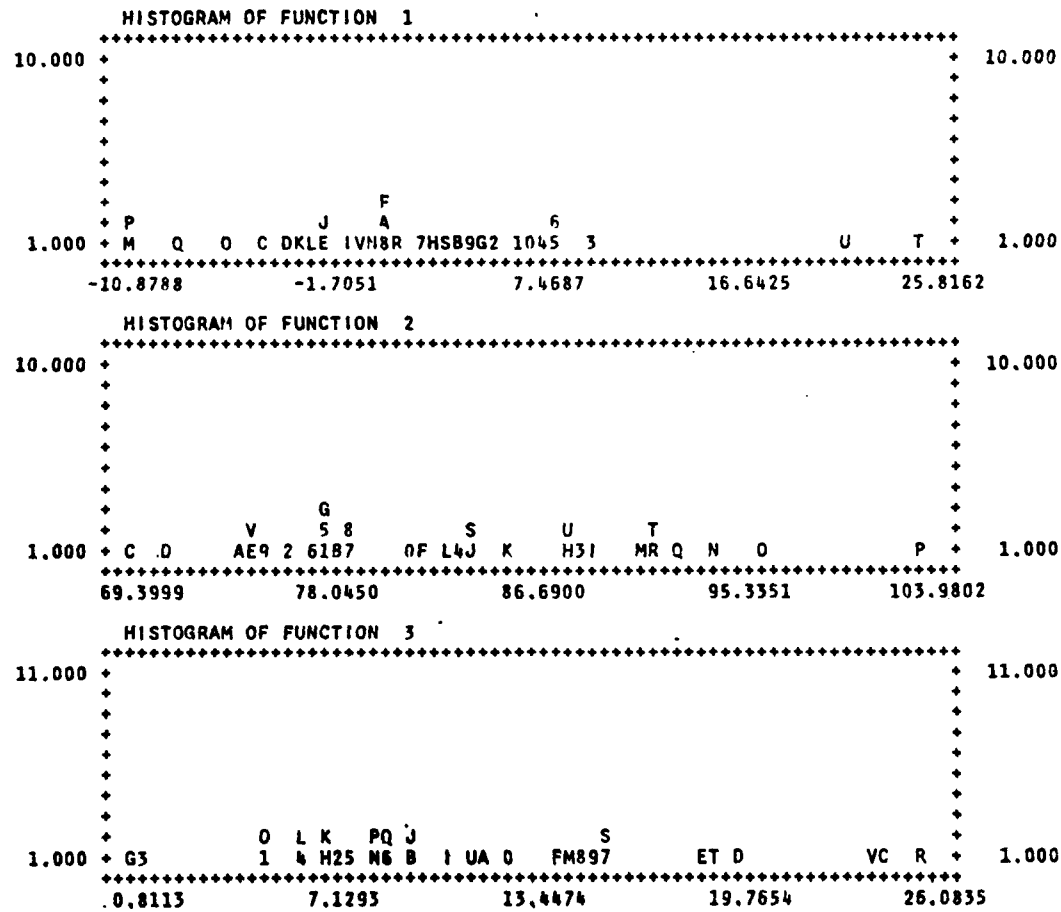


FIGURE 5.7. HISTOGRAMS OF 32 MIMID SPECIES PROJECTED ONTO FIRST THREE DISCRIMINANT AXES. SYMBOLS AS IN FIGURE 5.6



legs, one representing the Mimus complex and the other, beginning with Toxostoma rufum (18), the Toxostoma wing. The minimum spanning tree, which was computed from the generalized distance matrix, forms several nicely defined subclusters. The sickle-billed thrashers (25-27) form a subgroup within Toxostoma. The Galapagos mockingbirds (13-15) form a distinct group within the Mimus wing.

The aberrant Donacobius is placed near the Galapagos mockingbirds on the basis of the first three discriminant functions. The minimum spanning tree links it to Nesomimus macdonaldi (14). But note that the length of the link in generalized distance units is 670 whereas the next longest link in the tree (between Mimus gilvus and Allenia) is only 418 units. The placement of Donacobius reflects the loss of information which results from plotting the taxa only on the basis of the first two axes. Discriminant information contained in other axes is not visible. By examining the minimum spanning tree and the lengths of its links such distortions are easily detected.

At the other end of the second axis, Allenia (31) and Margarops (30) are placed. These last two are linked by the minimum spanning tree to Mimus gilvus (6). The two blue mockingbirds (3-4) are at the opposite end of the Mimus wing from the Galapagos mockingbirds, connecting to Dumetella (2) through Melanotis hypoleucus (4).

Of particular interest is that on the basis of skeletal morphology, Oreoscoptes (17 in figure 5.6 and "G" in figure 5.7) is associated with the central part of the Mimus cluster rather than with any part of Toxostoma. Mimodes (16 in figure 5.6 and "P" in figure 5.7) is placed relatively close to the Toxostoma wing by the first two axes.

Elements of the discriminant functions represent correlations between the original variables and the discriminant functions as was the case with the principal components of chapter 4. The following relationships may be determined with regard to the first function (table 5.3). Twenty three of the original variables are correlated with the first discriminant function (the X axis in figures 5.6 and 5.7) at a level of .5 or greater. Of these, fourteen are characters derived from the pectoral assemblage, three are from the bill, three are the ectethmoid plate measures, three are temporal angles and one is a pelvic measurement. There are only three characters that are highly correlated negatively ($<-.5$): the angle of the suprameatic ridge to the midline; the length of the suprameatic fossa; the length of the premaxilla anterior to the external nares.

Placement of the taxa relative to each other in terms of the first discriminant function can be clearly seen in

the histogram of figure 5.8. At one end are the two most arboreal species, Allenia and Margarops with their well developed flight mechanisms and at the other the most terrestrial of the Toxostoma thrashers, the sickle-billed group and Toxostoma ocelatum. As is indicated by the character correlations, the angles and the length of the bill anterior to the nares are negatively weighted on this axis.

Sixteen of the variables are highly correlated ($>.5$) positively with the second discriminant function (the Y axis in figures 5.6 and 5.7). Seven of these are pelvic assemblage measures, four are cranial lengths and widths, with four from other areas. The effect is to distribute the taxa with the ground dwelling and digging forms at one end of the axis and the small skulled birds with lightly built pelves and slight limbs at the other (figure 5.8). As can be seen in any of the graphic representations of these axes, the ground dwelling Toxostoma thrashers are placed at one end and the lightly built, ground foraging but non-digging Nesomimus group at the other.

The third discriminant function (the Z axis in figure 5.6) seems to primarily reflect elongation of the skull and bill. It is positively correlated with three bill length measures and the length of the jugal bar. It is negatively correlated with six characters, two from the descending

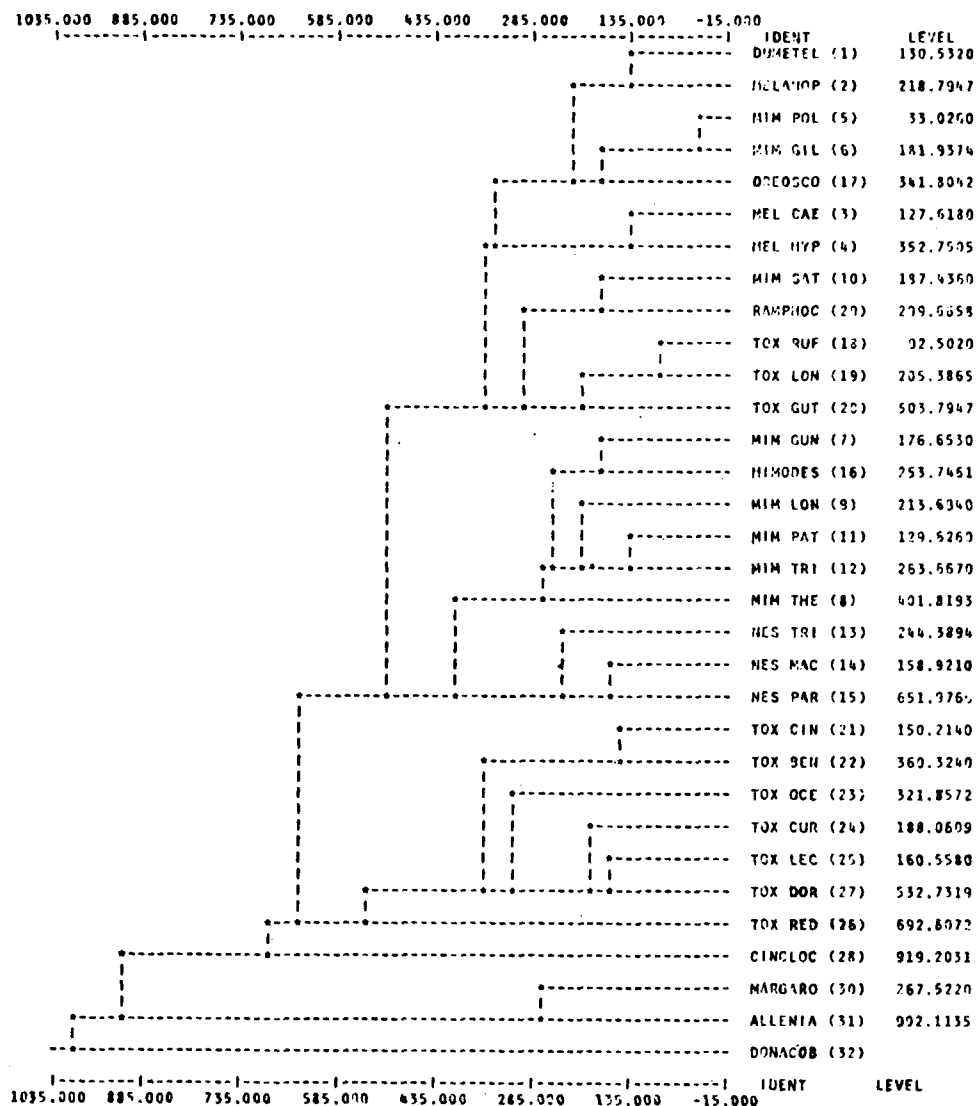
TABLE 5.3. FIRST 10 DISCRIMINANT FUNCTIONS FOR 32 MINID SPECIES DERIVED FROM SKELETAL DATA. (Variable Cran-W1 does not appear in table as it was used as the reference variable in regression analysis and rescaling of all other variables before they were analyzed with discriminant analysis procedures.)

	1	2	3	4	5	6	7	8	9	10
CRAN-L1	-0.378	0.762	0.324	0.213	-0.140	0.048	0.170	0.009	0.049	0.053
CRAN-H	-0.164	0.321	-0.477	0.567	0.227	-0.116	-0.114	0.054	0.265	-0.028
CRAN-W2	-0.452	0.716	0.266	-0.051	-0.191	-0.135	-0.174	0.107	-0.187	-0.027
CRAN-W3	-0.182	0.624	0.334	0.617	0.087	0.009	0.070	0.010	0.131	-0.133
CRAN-L2	0.065	0.655	0.434	0.303	0.257	-0.152	0.311	-0.066	-0.015	-0.190
PRAX-L1	-0.431	0.434	0.632	-0.252	0.128	-0.197	0.249	0.008	0.055	-0.023
INTORB-W	0.394	0.295	-0.441	0.012	0.427	0.001	0.160	0.234	0.026	-0.253
BILL-W1	0.005	0.633	0.155	0.150	0.269	0.097	-0.187	-0.145	0.344	0.001
BILL-W2	0.737	0.221	0.312	0.223	-0.057	0.021	-0.058	0.143	0.114	0.023
BILL-H	0.550	0.356	0.374	0.207	0.279	-0.237	0.200	-0.081	0.147	-0.239
NARES-L	0.199	-0.062	0.685	-0.104	0.339	-0.353	0.313	0.106	0.009	0.099
NARES-V	0.539	0.156	-0.333	0.156	0.156	-0.267	0.070	0.110	0.047	-0.117
PEORIG	0.164	-0.068	0.392	-0.311	0.645	-0.396	0.021	0.212	0.010	-0.016
ECTH-W1	0.542	0.404	-0.523	0.204	0.196	-0.020	0.079	-0.112	-0.000	-0.112
ECTH-W2	0.271	0.180	0.460	0.180	0.202	-0.068	0.066	-0.265	-0.068	-0.097
ECTH-W3	0.906	0.235	-0.001	0.122	0.111	-0.024	0.119	0.024	-0.097	-0.075
DPH-W	0.090	0.095	-0.504	-0.070	0.236	-0.378	-0.215	0.219	-0.248	-0.303
SF-U	-0.401	0.539	-0.393	0.237	-0.386	-0.247	-0.075	0.026	-0.133	-0.113
SF-L	-0.709	0.557	-0.475	0.110	-0.017	-0.117	-0.024	-0.085	-0.036	-0.058
JUGAL-L	0.178	0.468	0.750	0.139	0.203	-0.115	0.236	-0.052	0.127	-0.090
PELV-L1	0.279	0.688	0.284	0.480	0.173	-0.166	0.217	0.067	0.081	0.050
PELV-L2	0.360	0.517	0.246	0.392	0.317	-0.340	0.173	0.005	0.016	0.235
PELV-H1	0.430	0.429	-0.185	0.526	0.115	-0.432	0.142	-0.003	-0.265	0.075
PELV-W3	0.690	0.072	-0.289	0.303	0.171	-0.481	0.043	-0.010	-0.128	0.097
STERN-L	0.417	0.297	-0.553	0.410	0.368	-0.040	0.120	-0.060	-0.040	-0.048
STERN-D	0.559	0.114	-0.597	0.400	0.140	0.053	0.171	-0.108	0.051	-0.081
STERN-W	0.592	0.302	-0.125	0.412	0.372	-0.265	0.008	0.009	-0.659	0.037
STERN-KL	0.332	0.178	-0.699	0.385	0.325	0.088	0.192	-0.047	-0.039	-0.039
FEIUR-WH	-0.031	0.746	0.210	0.458	0.367	-0.147	0.019	0.009	0.056	0.062
HUM-HW	0.807	0.225	-0.150	0.211	0.222	-0.184	0.121	0.005	-0.029	-0.138
HUM-DCL	0.733	0.025	0.332	0.371	-0.060	-0.237	0.030	-0.035	0.056	-0.002
HUM-HD	0.719	0.081	-0.306	3.140	0.174	-0.217	0.111	-0.113	-0.019	-0.112
ULNA-L	0.811	-0.082	0.087	0.444	-0.096	-0.178	0.119	0.057	-0.031	-0.102
EOH-SF	0.813	0.309	0.335	0.101	0.016	0.132	-0.126	-0.115	-0.026	-0.025
CEPH	0.406	-0.288	-0.667	-0.118	0.008	-0.056	-0.198	0.119	-0.242	-0.107
SF-MID	-0.745	-0.400	-0.231	0.275	0.206	0.102	-0.107	0.139	0.168	0.044
HXP-MID	0.440	0.061	-0.165	-0.493	0.291	-0.074	-0.543	0.152	0.066	-0.068
ZY-POP	0.740	-0.156	0.484	-0.195	0.120	-0.102	0.155	-0.070	0.139	-0.033
SF-POP	0.718	0.351	0.338	-0.276	-0.104	-0.029	-0.046	-0.278	-0.040	-0.056
TRUNK-L	0.403	0.533	0.303	0.454	0.285	0.122	0.079	-0.060	-0.125	-0.054
PRAX-L2	-0.564	0.488	0.517	-0.278	0.000	-0.160	0.195	-0.019	0.057	-0.035
TARHET-L	-0.315	-0.422	0.141	0.730	0.348	-0.055	0.022	0.038	-0.072	-0.067
TARHET-W	0.035	0.774	0.444	0.115	0.153	0.015	0.023	0.012	0.067	-0.122
FEIUR-SV	0.002	0.753	0.049	0.332	0.426	-0.095	0.139	0.070	-0.040	-0.063
TIRIA-SW	-0.057	0.741	0.244	0.667	0.209	0.048	-0.035	0.003	-0.208	-0.085
ULNA-SV	0.847	0.226	0.145	0.266	0.103	-0.127	0.116	0.044	-0.002	-0.015
HUM-SW	0.351	0.351	0.010	0.339	0.185	-0.044	0.103	-0.005	0.139	-0.073
CARHET-L	0.809	-0.119	0.155	0.458	-0.143	-0.158	0.072	0.004	-0.010	0.044
PHALNX-L	0.726	-0.358	0.071	0.687	-0.224	-0.104	0.122	0.013	-0.006	0.096
CORAC-L	0.583	0.503	-0.012	0.329	0.545	-0.112	0.198	-0.026	0.046	0.039
CORAC-HW	0.841	0.062	-0.171	0.195	0.036	-0.091	0.166	0.052	-0.090	0.035
CORAC-SW	0.537	0.640	0.006	0.334	-0.005	-0.131	0.058	-0.049	0.099	-0.146
CORA-CRL	0.560	0.292	-0.073	-0.114	0.278	-0.053	0.102	-0.068	-0.251	-0.096
PELV-U5	0.111	0.577	-0.243	0.602	-0.022	-0.154	-0.006	0.008	0.015	-0.074
OLF PRO	-0.000	0.197	0.445	-0.304	0.451	0.175	-0.028	-0.230	0.197	-0.255
ECTH FOR	0.597	0.213	0.166	-0.100	-0.162	-0.379	-0.341	-0.200	-0.419	-0.160

process of the nasal, the dorsal width of the ectethmoid and three sternal measurements. It appears that within this group of birds, as bill length increases, the development of the sternum decreases.

The phenogram based on the generalized distance matrix which was in turn derived from the variables rescaled by regression to cranium width 1 (SK 4) is shown in figure 5.9. It reflects the major groupings that were visible in the three dimensional projection, bivariate plots and histograms. The most aberrant bird, Donacobius, is on a branch of the phenogram separate from all of the other taxa. Next most distant are Margarops and Allenia, and so on until Dumetella and Melanoptila form a cluster with two Mimus species and Oreoscoptes. The phenogram is consistent with the general placement of the birds in a transitional series from "specialized" to "generalized", as suggested in Peters' check-list (Davis and Miller, 1960). Certain small groups of what are generally considered to be closely related birds are evident. These include the two blue mockingbirds, the Toxostoma rufum group and the Galapagos mockingbirds, and Margarops-Allenia. Other groupings at a slightly greater distance are not so well represented however, at least when compared to traditional views of relationships within the family. For example, the genus Mimus is separated into three groups, each of which is intermingled with other groups. Mimus polyglottos and

FIGURE 5.9. PHENOGRAM DERIVED BY UWPGA FROM GENERALIZED DISTANCE MATRIX FOR 32 MIMID SPECIES.



Mimus gilvus are clustered with Oreoscoptes and this trio is in turn clustered with Dumetella and Melanoptila. The Toxostoma rufum group is separated from the rest of Toxostoma and clustered with Mimus saturninus and Ramphocinclus. Similar shifts, although not as dramatic occur within the major Toxostoma cluster.

Without the help of information equivalent to the correlations of characters with the discriminant functions, it is impossible to determine what character relationships cause the various taxa to cluster. This is of course a general problem in interpreting phenograms as representations of phenetic relationships. In general, however, grossly similar morphological types are being clustered; for example the Toxostoma rufum group and Ramphocinclus. But it is not clear why Mimus saturninus should also be clustered with this group and actually paired with Ramphocinclus. In as much as interpretation of the groups is so unclear, there seems little point in attempting to analyze the phenogram further. I believe that much more information can be gained from careful study of the discriminant functions and their correlation with the various original variables.

MIMID VERSUS THRUSH SKELETONS

Because of suggested affinities of the mimids to the

thrushes, I included fourteen thrush species (table 5.1) in the study of skeletal characters. These taxa were added to the mimids and processed in the same way as discussed previously. The graphic results are shown in the three dimensional plot in figure 5.10 and the bivariate plot of the first two axes in figure 5.11. Histograms of the first three axes are shown in figure 5.12. The phenogram based on generalized distance is given in figure 5.13.

The bivariate plot (figure 5.11) appears to be turned 90 degrees counterclockwise when compared to the bivariate plot of the mimids alone (figure 5.7). This is due to the fact that when the thrushes are analyzed with the mimids, the first discriminant function is being established by those characters and combinations of characters which best separate thrush taxa from mimid taxa. The second axis (Y) is comparable to the first axis (X) in figure 5.7 and is the one which reflects those characters and combinations of characters which, next to the combinations which determine the first discriminant function, best separate the taxa.

Examination of the correlations between the original variables and the first discriminant function in table 5.4 shows that most of the characters traditionally used by taxonomists to characterize a mimid versus a thrush are important in determining the "new variable" and the "mimid" end of the X axis in the graphs in figures 5.10, 5.11 and

FIGURE 5.10. THREE DIMENSIONAL PROJECTIONS OF 32 MINID SPECIES AND 14 SPECIES OF TURDIDAE ONTO FIRST THREE DISCRIMINANT FUNCTIONS DERIVED FROM SKELETAL DATA.

THE MINIMUM SPANNING TREE

I	J	LENGTH
DUMETEL (1)	MELANOP (2)	95.202
DUMETEL (1)	OREOSCO (17)	148.985
OREOSCO (17)	MIM POL (5)	147.175
MIM POL (5)	MIM GIL (6)	32.876
MIM GIL (6)	MIM TRI (12)	115.992
MIM TRI (12)	MIM PAT (11)	106.782
MIM PAT (11)	MIM THE (8)	133.677
DUMETEL (1)	MEL HYP (4)	176.656
MEL HYP (4)	MEL CAE (3)	97.937
MIM THE (8)	MIM GUN (7)	182.586
MIM GUN (7)	MIMODES (16)	176.731
MIM PAT (11)	NES MAC (14)	183.092
NES MAC (14)	NES PAR (15)	116.818
NES MAC (14)	NES TRI (13)	173.994
MIM TRI (12)	MIM LON (9)	184.633
MEL HYP (4)	TOX RUF (18)	191.843
TOX RUF (18)	TOX LOW (19)	92.198
TOX LON (19)	TOX GUT (20)	137.685
TOX LOW (19)	TOX CUR (24)	192.983
TOX CUR (24)	TOX DOR (27)	163.375
TOX DOR (27)	TOX LEC (25)	144.958
TOX CUR (24)	TOX BEN (22)	170.715
TOX BEN (22)	TOX CIN (21)	161.744
MIM GIL (6)	MIM SAT (10)	193.570
MIM SAT (10)	RAMPHOC (29)	177.875
TOX LOW (19)	TOX OCE (23)	214.964
MELANOP (2)	COS HUM (35)	221.037
COS HUM (35)	COS CYA (33)	201.357
TOX DOR (27)	TOX RED (26)	229.202
COS CYA (33)	COS CAP (34)	253.996
COS HUM (35)	COS NIV (36)	269.617
MELANOP (2)	ALP POL (37)	286.187
COS CYA (33)	COP HAL (39)	292.498
MIM GIL (6)	ALLENIA (31)	294.896
ALLENIA (31)	MARGARO (30)	230.017
COP HAL (39)	COP SAU (38)	318.671
DUMETEL (1)	CAT UST (43)	325.283
CAT UST (43)	CAT FUS (42)	52.438
CAT FUS (42)	HYL MUS (44)	252.818
HYL MUS (44)	TUP MIG (46)	256.916
TUR MIG (46)	TUR PHI (45)	199.395
COP HAL (39)	HOW SOL (41)	359.040
HOW SOL (41)	MYA GEN (40)	327.972
RAMPHOC (29)	CINCLOC (28)	423.730
COS NIV (36)	DOWACOB (32)	514.498

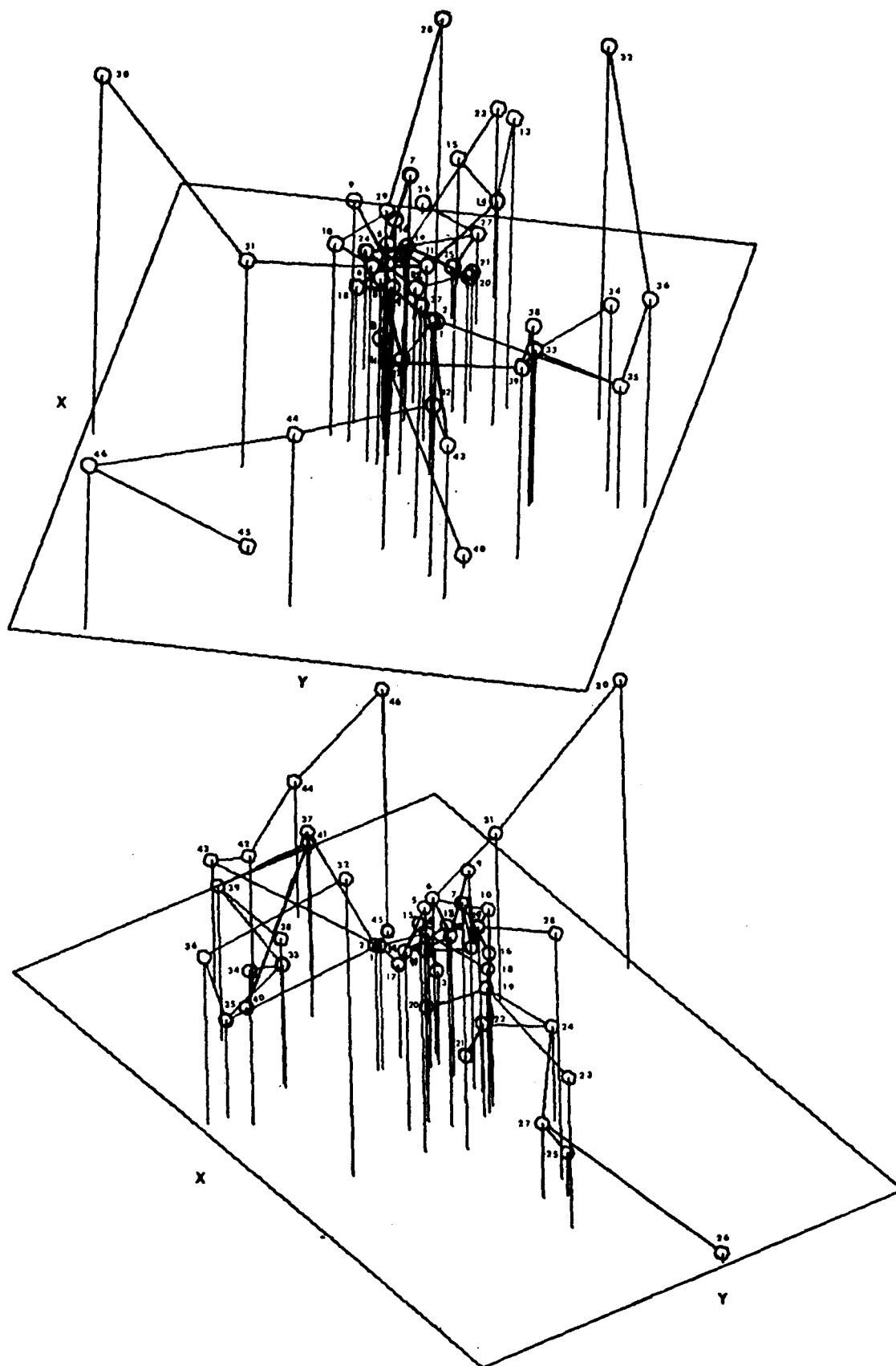


FIGURE 5.11 BIVARIATE PLOT OF 32 MIMID SPECIES AND 14 SPECIES OF TURDIDAE PROJECTED ONTO FIRST AND SECOND DISCRIMINANT FUNCTIONS DERIVED FROM SKELETAL DATA. NUMBERS FOLLOWING TAXA REFER TO NUMBERS IN THE THREE DIMENSIONAL PROJECTION, FIGURE 5.10.

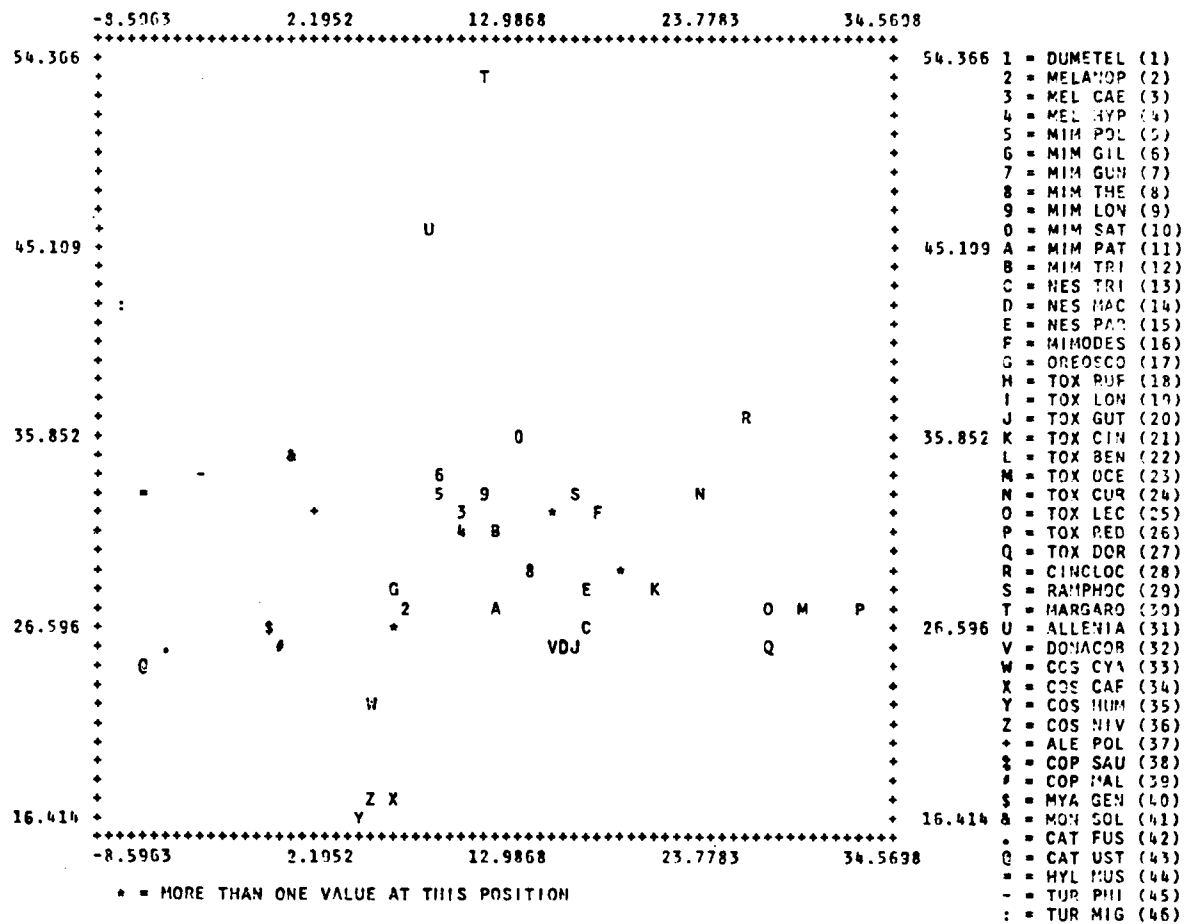


FIGURE 5.12. HISTOGRAMS OF 32 MIMID AND 14 THRUSH SPECIES PROJECTED ONTO FIRST THREE DISCRIMINANT AXES. SYMBOLS AS IN FIGURE 5.11.

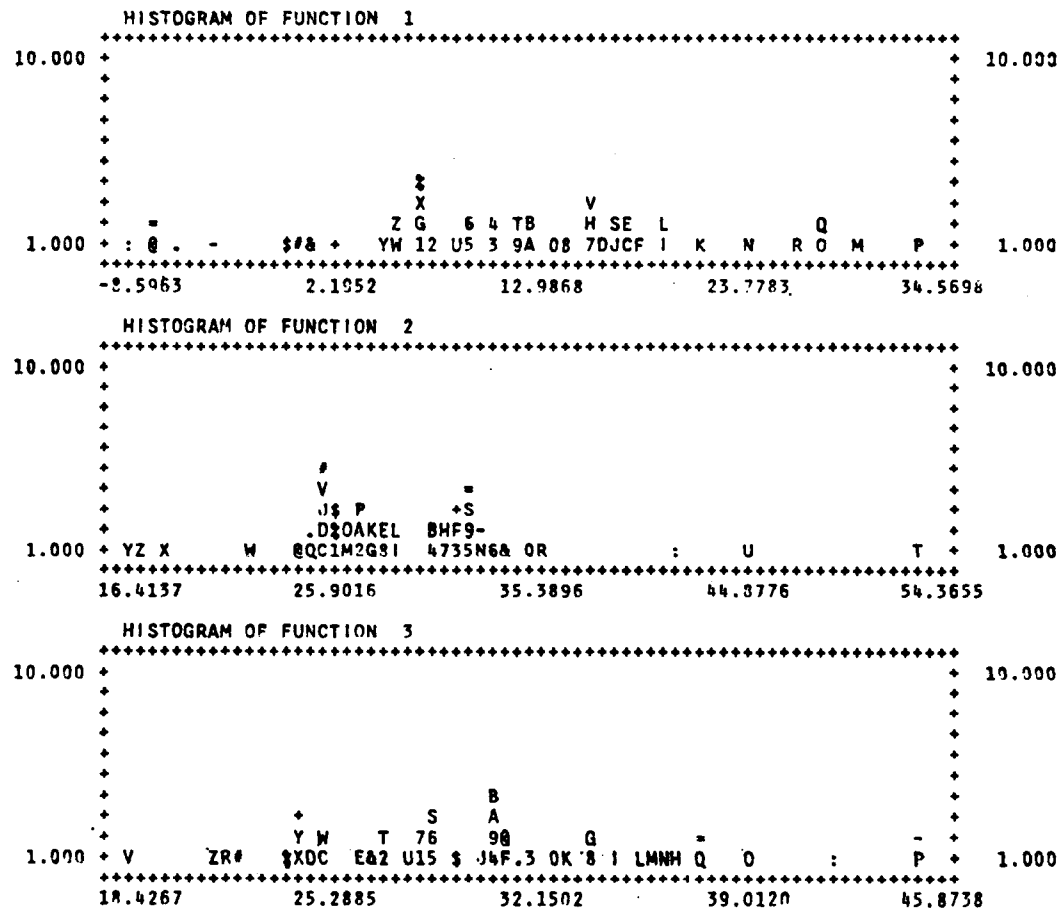


TABLE 5.4. FIRST 10 DISCRIMINANT FUNCTIONS FOR 32 MINID AND 14 THRUSH SPECIES DERIVED FROM SKELETAL DATA. (Variable Cran-W1 does not appear in table as it was used as the reference variable in regression analysis and rescaling of all other variables before they were analyzed with discriminant analysis procedures.)

CRAN-L1	-0.842	0.358	0.289	0.441	-0.062	-0.053	-0.095	-0.023	0.121
CRAN-M	-0.288	0.114	0.710	0.251	-0.321	-0.399	-0.010	-0.023	-0.121
CRAN-W2	-0.864	0.016	-0.130	-0.254	0.100	-0.004	0.009	-0.037	-0.013
CRAN-W3	-0.723	0.428	0.281	0.262	0.083	0.200	0.043	-0.154	0.017
CRAN-L2	-0.592	0.567	0.203	0.195	-0.154	0.209	0.194	-0.167	-0.103
PAAX-L1	-0.815	0.143	0.160	0.007	-0.405	-0.011	-0.206	-0.094	-0.050
INTOR3-W	-0.079	0.324	0.211	-0.205	-0.211	0.556	-0.046	-0.177	-0.009
BILL-W1	-0.249	0.215	0.181	-0.195	-0.197	0.343	-0.055	-0.154	-0.039
BILL-W2	-0.211	0.673	-0.221	-0.148	0.153	0.167	0.098	-0.154	-0.474
BILL-H	-0.212	0.720	-0.106	0.111	-0.085	0.369	0.220	-0.260	-0.368
MARES-L	-0.314	0.405	-0.437	0.217	-0.271	0.161	0.220	0.121	-0.013
MARES-W	0.522	0.319	0.519	0.101	-0.090	0.199	-0.379	-0.181	-0.228
PEDORIG	0.348	0.076	-0.156	-0.030	-0.563	0.310	0.202	-0.212	-0.062
ECTH-W1	0.327	0.469	0.510	-0.241	0.172	0.351	0.371	-0.317	0.161
ECTH-W2	0.636	0.361	0.389	-0.221	0.039	0.264	0.043	0.264	-0.004
ECTH-W3	0.436	0.033	0.393	-0.153	-0.065	0.217	0.103	0.196	-0.072
DPH-W	-0.689	-0.216	-0.026	-0.026	-0.362	-0.032	-0.092	-0.073	0.046
SF-W	-0.436	-0.089	0.678	-0.187	-0.225	-0.241	0.135	-0.058	-0.201
SF-L	-0.645	-0.348	0.428	-0.122	0.182	0.021	0.195	-0.058	0.142
UGAL-L	-0.671	0.506	-0.131	0.187	-0.145	0.165	0.139	-0.067	-0.114
PELV-L1	-0.408	0.685	0.428	0.274	-0.102	0.135	0.106	-0.081	-0.081
PELV-L2	-0.259	0.650	0.390	0.103	-0.174	0.168	0.216	-0.007	-0.034
PELV-W1	0.082	0.556	0.647	0.240	-0.006	0.047	0.311	0.067	0.019
PELV-W3	0.594	0.446	0.439	0.092	0.017	0.105	0.340	0.051	0.152
STERM-L	0.314	0.364	0.715	0.170	0.018	0.274	-0.046	0.153	0.056
STERM-D	0.637	0.591	0.627	0.138	0.025	0.087	-0.071	0.153	-0.164
STERM-W	0.128	0.607	0.449	0.190	0.018	0.332	0.252	-0.020	-0.165
STERM-KL	0.424	0.228	0.722	0.165	-0.055	0.220	-0.106	0.176	-0.042
FEMUR-HW	-0.631	0.474	0.399	0.204	-0.114	0.335	-0.105	0.159	0.128
MUM-HW	0.480	0.660	0.317	0.017	0.013	0.331	0.103	-0.013	-0.034
MUM-DCL	0.005	0.794	-0.146	0.272	0.226	0.080	0.176	0.076	-0.076
MUM-HD	0.501	0.544	0.356	0.036	0.065	0.140	0.141	0.199	0.199
ULNA-L	0.292	0.773	0.044	0.275	-0.348	0.041	0.164	-0.002	-0.190
<EDM-SF	0.416	0.704	0.126	0.123	-0.340	-0.037	-0.134	-0.002	-0.029
<DPN	-0.880	-0.189	0.192	-0.215	-0.028	-0.030	0.022	-0.021	-0.021
<SF-HID	-0.248	-0.762	-0.162	0.129	0.355	0.240	0.016	-0.116	-0.240
<MRP-HID	0.683	-0.122	-0.068	-0.331	-0.166	0.162	0.027	-0.314	-0.187
<ZF-POP	0.180	0.666	-0.537	0.067	-0.137	0.131	0.177	-0.115	-0.092
TRUHX-L	-0.309	0.708	0.381	-0.117	-0.451	-0.205	-0.014	0.181	-0.312
PAAX-L2	-0.838	0.018	-0.075	0.332	-0.110	0.158	-0.082	-0.004	-0.056
TARGET-L	-0.180	-0.240	0.024	-0.070	-0.409	-0.112	0.168	-0.062	-0.137
TARGET-W	-0.706	0.506	0.102	0.046	-0.138	0.317	0.068	-0.040	-0.162
FEMUR-SM	-0.520	0.445	0.451	0.119	-0.221	0.194	0.009	0.131	-0.076
TIBIA-SM	-0.611	0.466	0.403	0.166	-0.153	0.374	0.044	0.042	-0.051
ULNA-SM	-0.611	0.466	0.403	0.166	-0.153	0.258	-0.030	-0.079	-0.141
MUM-SM	0.272	0.844	0.161	0.130	0.015	0.175	-0.089	0.009	-0.016
MUM-SW	0.317	-0.023	-0.178	-0.061	-0.120	0.164	-0.188	0.086	-0.341
GAMLET-L	0.321	0.774	0.101	0.366	0.244	-0.056	0.114	-0.073	-0.124
PAALNX-L	0.626	0.491	0.136	0.407	0.157	-0.209	0.085	-0.143	-0.011
CORAC-L	0.112	0.694	0.492	0.162	-0.154	0.255	0.099	0.055	-0.128
CORAC-M	0.494	0.665	0.198	0.176	0.134	0.085	-0.033	0.124	-0.073
CORAC-SM	0.003	0.764	0.479	-0.011	0.002	0.126	0.121	0.000	0.006
CORAC-CRL	0.417	0.395	0.275	-0.025	-0.375	0.071	-0.030	0.249	0.027
PELV-W5	-0.384	0.461	0.604	-0.151	-0.329	0.133	-0.123	-0.032	0.069
OLE PRO	-0.024	0.240	0.008	0.041	-0.558	0.170	-0.044	-0.118	-0.306
ECTH FOR	-0.332	0.453	-0.149	-0.164	0.134	-0.027	0.124	-0.137	-0.307

5.12. These include the following: Narrow descending processes of the nasal (SK 19 (table 5.3 and figure 5.3): Cor. (correlation coefficient) with DF1 (first discriminant function) = .689); Deep indentation of the ectethmoid plate (SK 9: Cor. with DF1 = .636); Narrow angle between the descending process of the nasal and the premaxilla (SK 29: Cor. with DF1 = .880); Narrow angle of pedicles of the maxillopalatines relative to the midline (SK 28: Cor. with DF1 = .683).

Other characters not usually used to distinguish mimids from thrushes also contribute and would seem to be nearly as good as those listed above in characterizing mimids relative to thrushes. These include: The minimum distance between the crests of the ilia (SK 37: Cor. with DF1 = .594); The depth of the sternum (SK 28: Cor. with DF1 = .637); The depth of the head of the humerus (SK 44: Cor. with DF1 = .501); The length of the third digit (SK 49: Cor. with DF1 = .626)

Examination of the means for all of the characters by taxa showed that high positive correlations between the original variables and the first discriminant function indicates a smaller real value for the mimid variables when compared to those of the thrushes and vice versa. The values in table 5.4 therefore show that the features that establish the "thrush" end of the X axis in figures 5.10,

5.11, and 5.12 are those reflecting the smaller, less elongated skull and the thinner, relatively more delicate appendicular bones of the pelvic limb of thrushes. Examples are: The length of the premaxilla anterior to the external nares (SK 12) which has a negative correlation with the first discriminant function of $-.815$; The width of the cranium at the temporal fossa region is correlated with a value of $-.864$. (This reflects the sharp temporal indentation of the cranium in the turdine thrushes.); The width of the tarsometatarsus (SK 61) is negatively correlated with a value of $-.706$ and the width of the tibiotarsus (SK 59) with a value of $-.611$.

Many of these features of mimid skeletons relative to thrushes are subjectively apparent to anyone who has studied them. However, the discriminant functions allow a precise evaluation of the relationships of the variables and their interactions when they are combined to generate a function which will best separate the taxa.

When the first discriminant function in table 5.3, that one which best discriminates among mimid taxa, is compared to the second discriminant function in table 5.4, it is apparent that they are quite comparable as to the characters and groups of characters that are determining the functions. This is reflected in the positioning of the mimid taxa relative to one another in figures 5.7 and 5.11.

Although the graph which includes the thrushes (figure 5.11) compresses the mimids relative to one another, the taxa are, in most cases in essentially the same relative positions. This is reassuring with regard to the appropriateness of the generalized distance and multiple discriminant function methodology adopted in this study. If the relative position of the mimid taxa had changed greatly, it would suggest that the within covariance structure (variance and correlation) of the various groups was not in fact uniform and that by adding a number of new taxa with different character variance and covariance relationships, the weighting function would have been altered. The fact that this did not happen suggests that the variability and covariability of characters is relatively uniform in the various groups. Most significant shifts were among the more generalized forms. These were moved closer to the thrushes which of course changed their positions relative to the other mimids. Most mimids remained in relatively the same position.

It is noteworthy that on the basis of 57 skeletal variables surveyed over 32 mimid and 14 thrush taxa, the first discriminant function, the one which best separates the mimids from the thrushes (figures 5.11 and 5.12) is barely able to separate the Cossypha thrushes (W, X, Y, Z) and Copsychus saularis (%) on the one hand and the two catbirds (1, 2), two species of Mimus (5, 6), Allenia (U)

and Oreoscoptes (G) on the other. The second and third axes do not distinguish between mimids and thrushes to any great degree. In fact it is only when the first and second functions are plotted (figure 5.11) that a clear separation occurs and even then Copsychus saularis (%) is positioned very close to Oreoscoptes (G) (superimposed in figure 5.11) and the catbirds (1, 2). This emphasizes the close similarity in skeletal systems among the more generalized mimids and some of the thrushes.

When the three dimensional graph of the first three discriminant functions (figure 5.10) and the minimum spanning tree computed from the generalized distance matrix (based on characters which have been adjusted to remove correlations both within and among taxa) are examined, additional insight as to the phenetic skeletal relationships between the mimid and thrush taxa is gained. Dumetella (1) and Melanoptila (2), two of the structurally most thrush like mimids serve as the connecting taxa between the mimids and the thrushes. Dumetella (1) is linked by the minimum spanning tree to Catharus ustulata (43) and Melanoptila (2) links to Cossypha humeralis (35) and Alethe poliocephala (37). It is interesting that in no case does a turdine thrush link directly to a saxicoline thrush. This demonstrates the intermediate position of the more generalized mimids in terms of structural similarities and differences when compared to the turdine and saxicoline

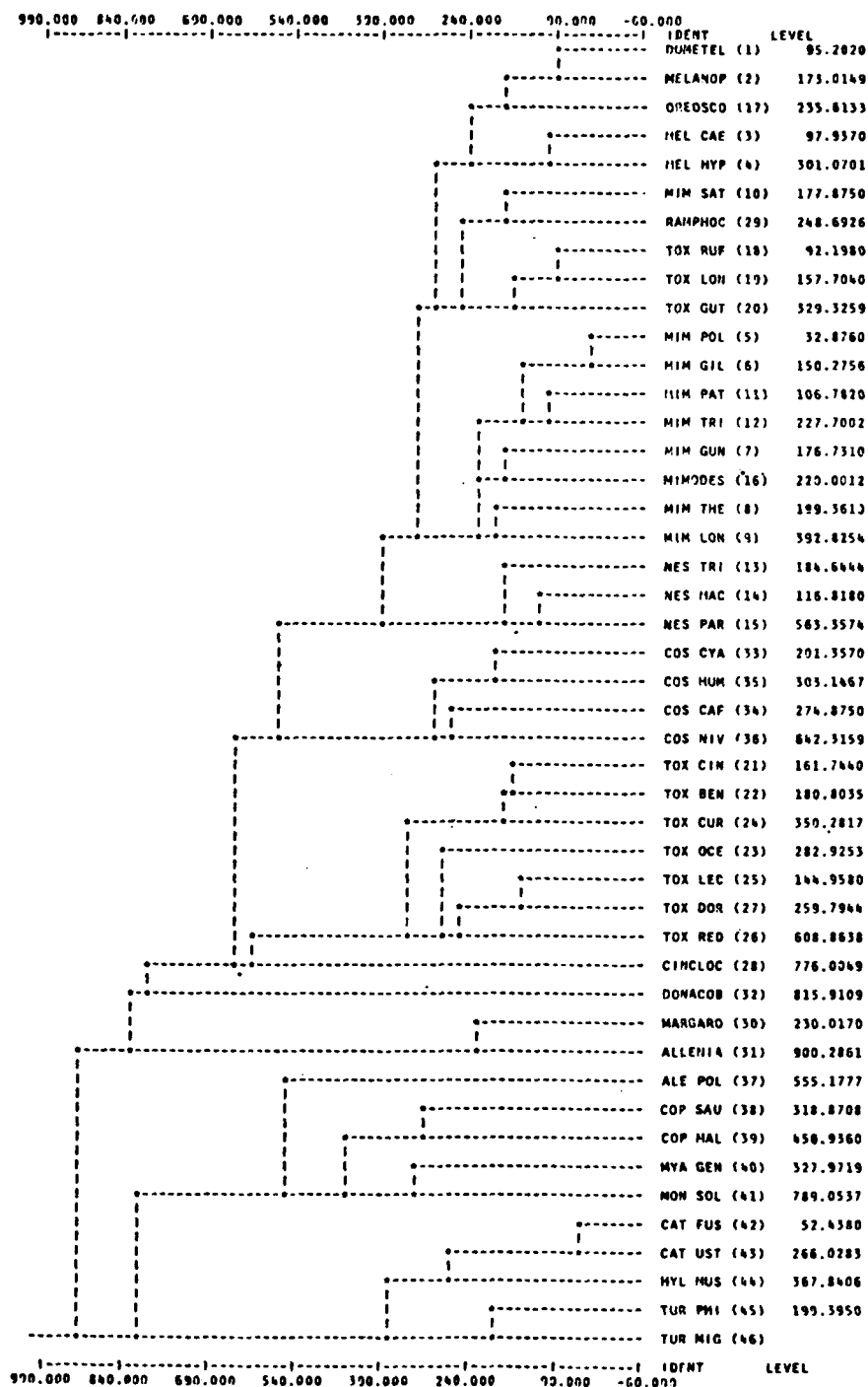
thrushes.

Donacobius (32) is linked to Cossypha niveicapilla (36). The link is nearly 100 generalized distance units longer than the next longest link in the tree. This suggests the peculiar skeletal organization of this bird in comparison to any of the thrush or mimid taxa. Although on the basis of only the first three (figure 5.10) or two (figures 5.11 and 5.12) discriminant functions Donacobius (32 and V) is placed close to the Galapagos mockingbirds (13, 14, 15 and C, D, E) and Toxostoma guttatum (20 and J), the species is in reality quite far removed from the other taxa in the full multidimensional space.

The phenogram derived from the generalized distance matrix of the skeletal data from both mimid and thrush taxa is given in figure 5.13. It demonstrates again the skeletal similarity of the Cossypha thrushes to the mimids. The UWPGMA cluster procedures separates all of the thrushes from the mimids with the exception of these four species.

Consideration of the known aspects of the natural history of the various taxa analyzed in this study and of the skeletal characters that are of primary importance in placing the taxa relative to each other in the multidimensional space suggests immediately that the discriminant functions are identifying functional types

FIGURE 5.13. PHENOGRAM DERIVED BY UWPGA FROM GENERALIZED DISTANCE MATRIX FOR 32 MIMID AND 14 THRUSH SPECIES.



rather than phylogenetic clusters. This becomes more convincing as the individual characters are examined relative to the discriminant functions. As was described above with regard to the placement of the various mimid taxa, the structural modifications that seem appropriate for certain modes of life are clustering the taxa and providing the basis for the minimum spanning tree linking them. In terms of traditional suggestions regarding relationships within the group, only the major clusters seem consistent.

The fact that structural relationships are so influential in placing the taxa in the multidimensional space suggests that phylogenetic information may be quite difficult to obtain, or at least difficult to separate from functional information. This is at once challenging and depressing. It is challenging in that the multivariate techniques used here might well be used to help go beyond the traditional use of indices and ratios in analyzing functional relationships, and may help to find better correlations between functional and ecological facets of a bird's biology. The depressing aspect of these conclusions is that one must be extremely careful in attributing phylogenetic significance to many, if not most morphological variables beyond the mere observation that similar taxa may be related. It suggests that one must be extremely careful in choosing morphological variables to be

used in studies of phylogeny.

SKELETAL AND EXTERNAL CHARACTERS COMBINED

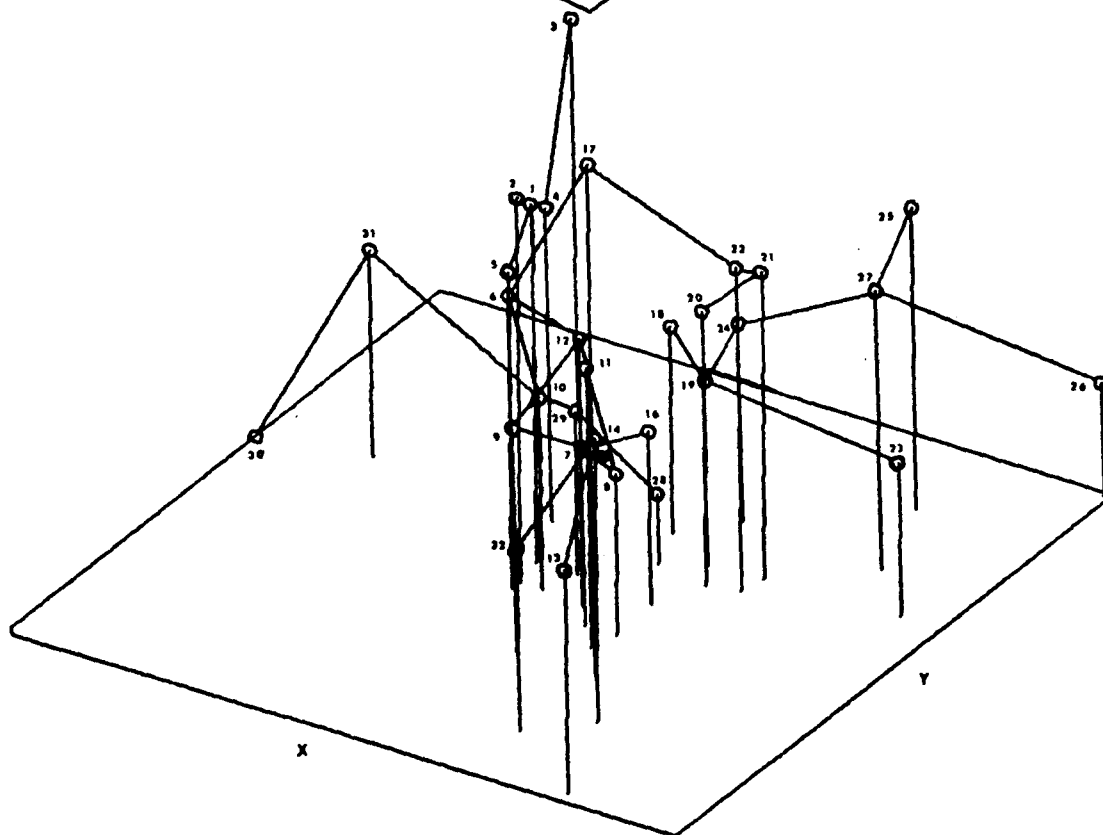
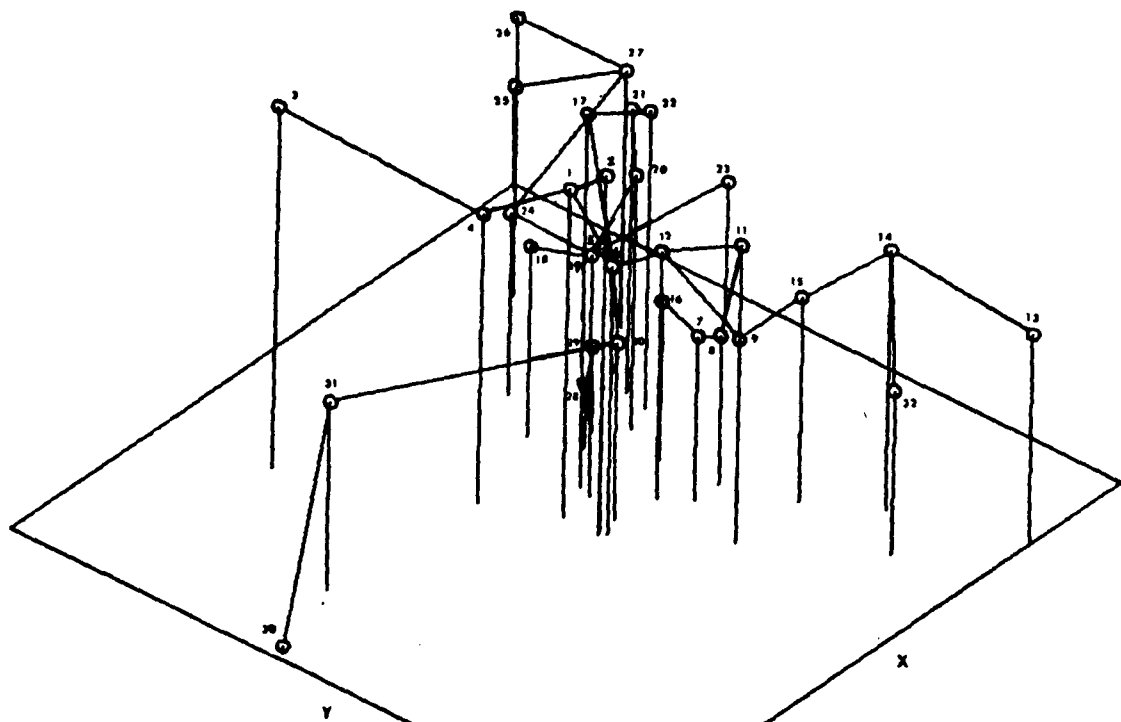
The external character set was combined with the skeletal data by adding the Euclidean distance matrix derived from the external character set to the generalized distance matrix derived from the skeletal characters. The principal coordinate axes, (Sneath and Sokal, 1973), of this total matrix were then computed and graphed (figure 5.14). The skeletal data seem to be dominant in the combined set. The basic structure of the relationships as expressed in the graph are essentially those visible in the graph of the skeletal data alone (figure 5.6). For these reasons, I am not convinced that this process of combining the information from the two character sets is altogether satisfactory. This approach may not be giving proper weights to the respective character sets and warrants further study.

In comparing the placement of the taxa on the basis of the external character set (figure 4.14) and the skeletal data (figure 5.6) the results are so noncongruent that it is obvious that the external and skeletal character sets are not particularly compatible and should not be expected to complement each other. Such an interpretation would be consistent with the view that the analysis of skeletal data

FIGURE 5.14. TWO VIEWS OF THREE DIMENSIONAL PROJECTION OF 32 MINID SPECIES ONTO FIRST THREE PRINCIPAL COORDINATE AXES DERIVED FROM COMBINED EXTERNAL AND SKELETAL DATA.

THE MINIMUM SPANNING TREE

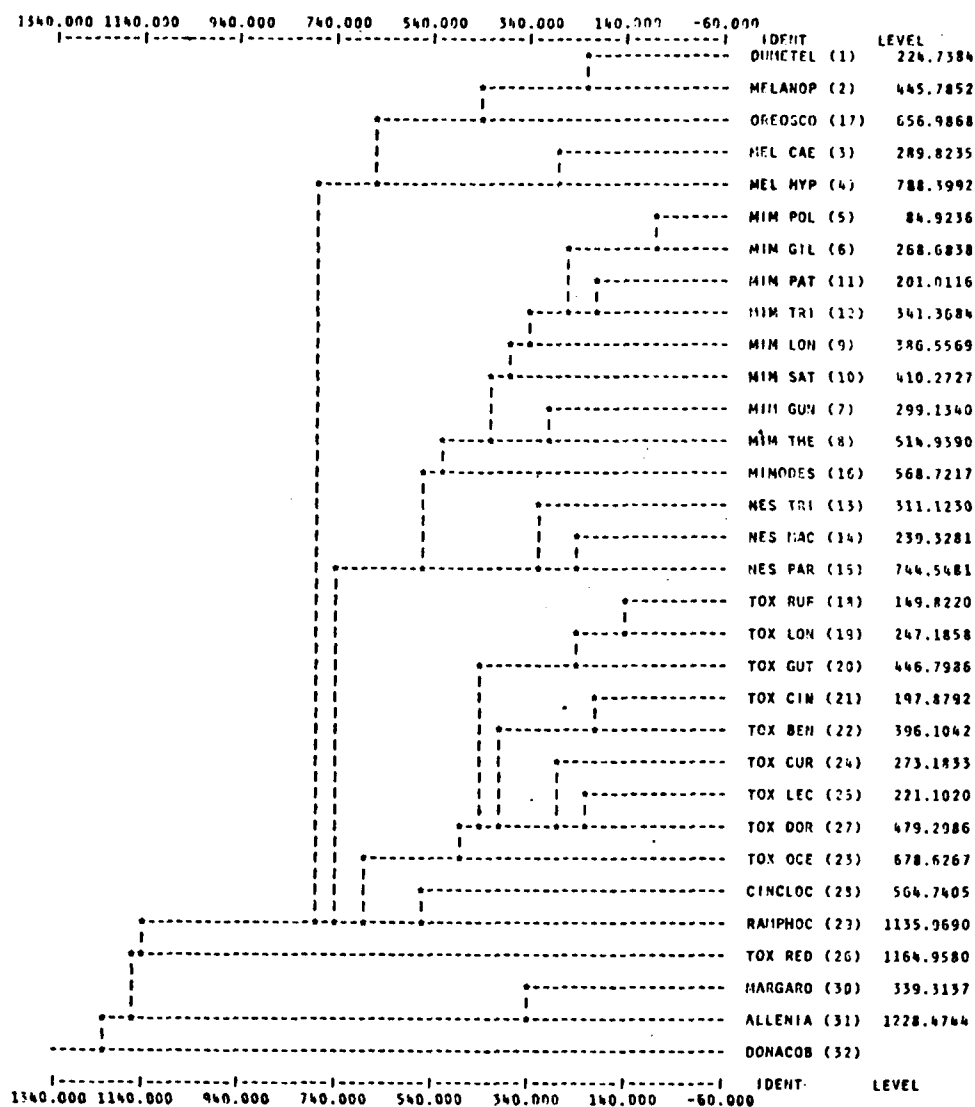
I	J	LENGTH
DUMETEL (1)	MELANOP (2)	224.738
DUMETEL (1)	MIM POL (5)	321.913
MIM POL (5)	MIM GIL (6)	84.924
MIM GIL (6)	MIM TRI (12)	223.940
MIM TRI (12)	MIE PAT (11)	201.012
MIM PAT (11)	MIE THE (8)	256.155
MIM GIL (6)	OREOSCO (17)	286.731
MIM THE (8)	MIM GUN (7)	299.134
MIM TRI (12)	MIM LON (9)	300.010
MIM LON (9)	NES PAR (15)	283.298
NES PAR (15)	NES MAC (14)	239.328
NES MAC (14)	NES TRI (13)	243.809
MIM GIL (6)	MIM SAT (10)	322.221
OREOSCO (17)	TOX BEN (22)	371.061
TOX BEN (22)	TOX CIN (21)	197.879
TOX CIN (21)	TOX GUT (20)	303.426
TOX GUT (20)	TOX LON (19)	230.562
TOX LON (19)	TOX RUP (18)	149.822
TOX LON (19)	TOX CUR (24)	279.737
TOX CUR (24)	TOX DOR (27)	258.766
TOX DOR (27)	TOX LEC (25)	221.102
TOX LON (19)	TOX OCE (23)	333.823
MIM GUN (7)	MIMODES (16)	377.158
TOX DOR (27)	TOX RED (26)	405.975
MIM SAT (10)	RAMPHOC (29)	436.413
DUMETEL (1)	MEL HYP (4)	469.768
MEL HYP (4)	MEL CAE (3)	289.823
RAMPHOC (29)	CINCLOC (28)	564.740
MIM SAT (10)	ALLENIA (31)	679.451
ALLENIA (31)	MARGARO (30)	339.314
NES MAC (14)	DONACOB (32)	936.824



reflects essentially functional and ecological rather than phyletic relationships among the taxa. Since the groups formed by the external characters do not appear to exhibit very strong correlations with obvious ecological and functional adaptations known to exist within the group, the external character set may be a better indicator of phyletic relationships. In fact on the basis of external characters, the most specialized group, the sickle-billed thrashers associate with some of the most generalized members of the family. For whatever reason, the two character sets are not compatible and seem to be reflecting quite different aspects of the phenetic relationships among mimid species.

The phenogram derived from the combined distance matrix (figure 5.15) is simplified in comparison to that derived from the skeletal data alone. However, it is not very similar to those in figures 4.15 and 4.16. The two genera Mimus and Toxostoma are again integrated internally, apparently because of the strong cohesiveness these taxa exhibit on the basis of the external character set. The general pattern of the phenogram is rather like that observed in figure 5.9 where there is a trend from "specialized" to "generalized" from one side of the phenogram to the other.

FIGURE 5.15. PHENOGRAM DERIVED BY UNPGA FROM GENERALIZED DISTANCE MATRIX FOR 32 MIMID SPECIES, COMBINED EXTERNAL AND SKELETAL CHARACTERS.



PHYLOGENETIC ANALYSIS AND CLASSIFICATION

In analyses of the character sets discussed earlier, various references were made to the difficulty and/or unreliability of trying to infer phylogenetic (in the sense of Hennig, 1966) relationships on the basis of phenetic comparisons. One way around this problem is to carry out a cladistic analysis of the taxa. For this study the cladistic methodology used is that of Hennig (1966) as elaborated by Brundin (1966, 1968). Fundamentally, the approach is to determine sister groups on the basis of shared derived characters. The groups formed are monophyletic by definition, and must include all descendents of the ancestral taxon. This is a much more restrictive requirement than the monophyly discussed by such workers as Simpson (1961) or Mayr (1969). There are of course many additional facets of phylogenetic systematics as espoused by Hennig and Brundin but these are the core of the approach. The rationale has been widely debated in various papers, for example Darlington (1970), Mayr (1974), Cracraft (1972), and many others. In avian systematics, the principal exponent of phylogenetic analysis in the sense of Hennig has been Cracraft (1972a, 1972b).

To carry out a phylogenetic analysis, it is necessary to determine the primitive versus derived state of various characters. This is best done by examining the state of characters in the organisms that are of primary interest as well as in those that may be allied. Characters and

character states that are shared by many varied taxa are likely to be primitive. Subgroups that share peculiar variations of the characters (derived or synapomorph conditions) usually become evident. Theoretically, on the basis of the patterns of occurrence of derived conditions, pairs of taxa can be assembled. One member of each pair will usually exhibit fewer derived conditions than the other. This one is referred to as the pleisiomorph or primitive sister group and the other the synapomorph sister group. In actual practice, it is sometimes impossible, on the basis of available information, to resolve some associations of taxa. In such cases, multichotomous sections of the cladistic network will remain. Hopefully, further study or additional information will permit such associations to be resolved into simple dichotomous relationships. It is of course theoretically possible for the multichotomous branchings to reflect the true nature of the phylogenetic relationships among the taxa in question, although such an hypothesis cannot be tested.

Figures 6.1, 6.2, and 6.3, illustrate the hypothesis of phylogenetic relationships among the mimids which is developed in this chapter. The branching sequences of these figures are based upon the shared derived characters which are summarized in tables 6.1 - 6.3. The hierarchical categories used in this chapter are those of the family Muscicapidae in table 6.1.

FIGURE 6.1. PHYLOGENETIC RELATIONSHIPS AMONG THE GENERA OF THE TRIBE MIMINI.

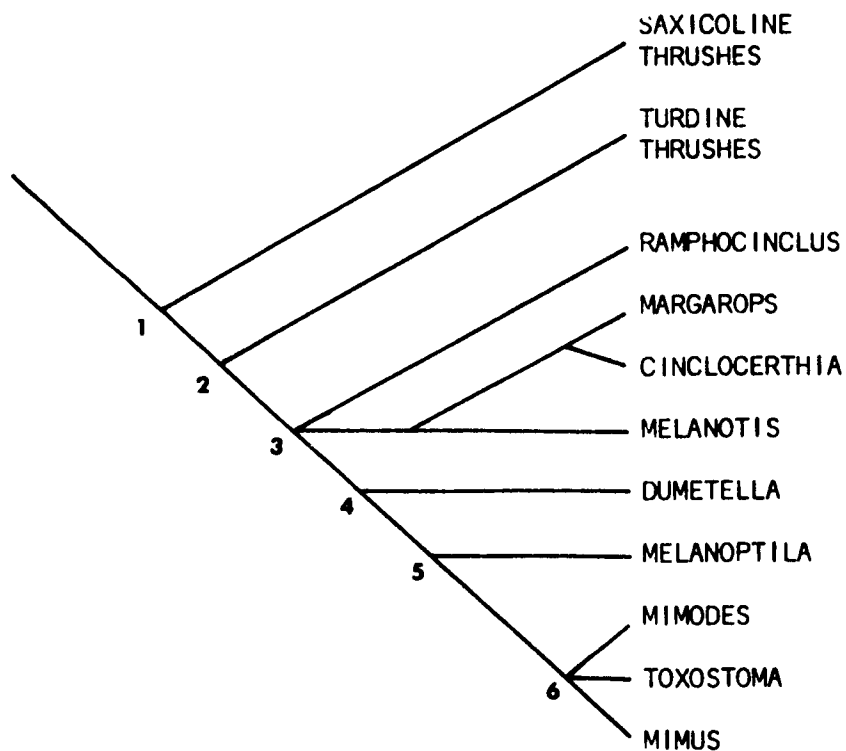


FIGURE 6.2. PHYLOGENETIC RELATIONSHIPS AMONG THE SPECIES OF THE SUBTRIBE CINCLOCERTHIAE.

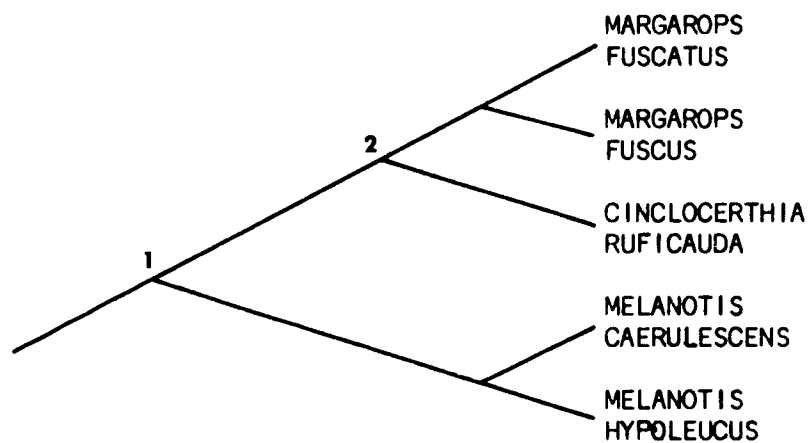


FIGURE 6.3. PHYLOGENETIC RELATIONSHIPS AMONG THE SPECIES OF THE SUBTRIBE MINAE.

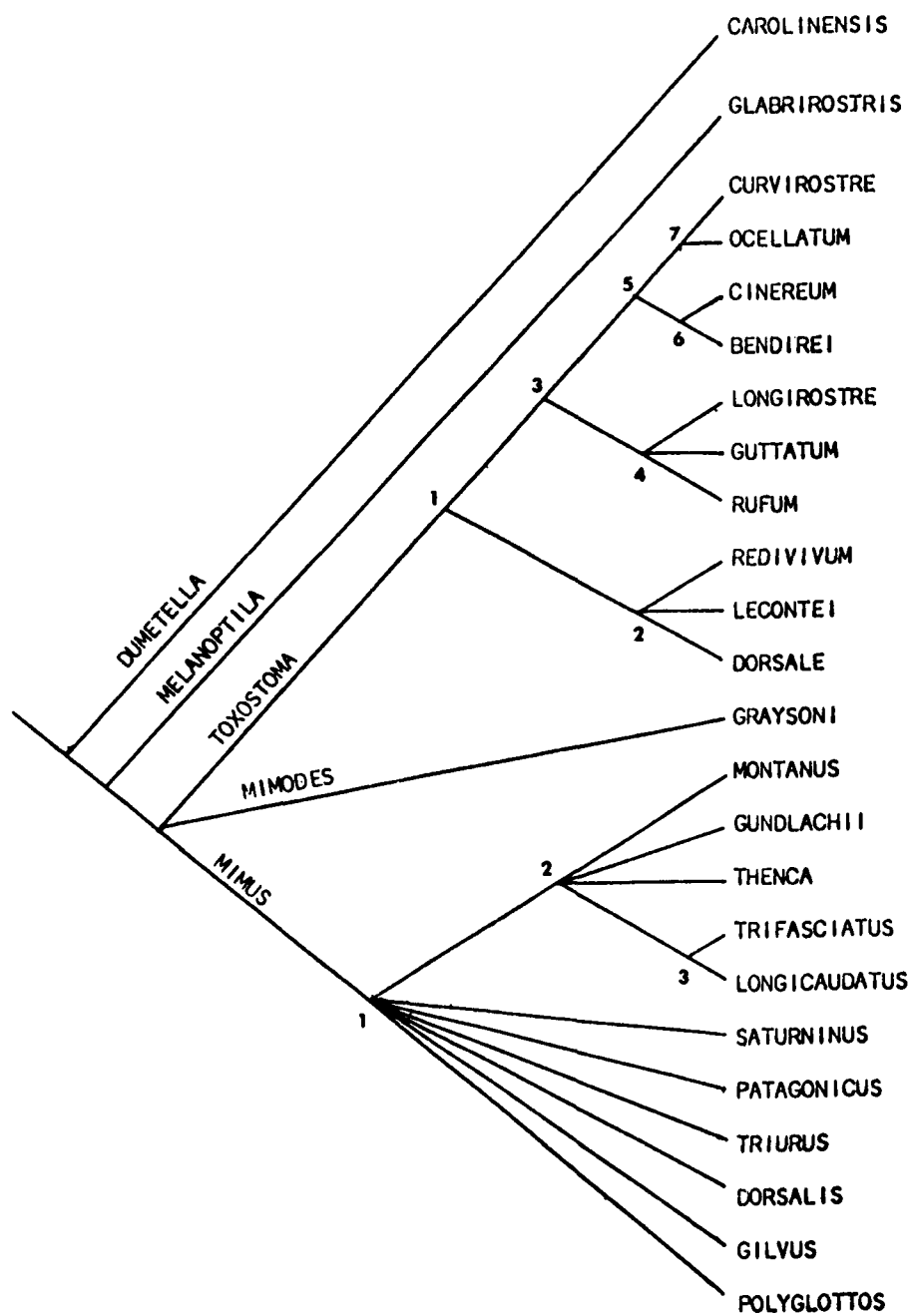


TABLE 6.1. CHARACTERS AND DERIVED CONDITIONS SUPPORTING BRANCHING POINTS OF PHYLOGENETIC DIAGRAMS IN FIGURE 6.1.

Branch Point (BP) 1: Saxicolini-Turdini

Supertribe Saxicolini

Shared derived characters not analyzed

Supertribe Turdini

1. Suprameatic ridge connects, if at all, to the dorsal end of the exoccipital wing by means of a broad strut
2. No ossification of alinasal turbinals and nasal septum

BP 2: Turdini-Mimini

Tribe Turdini

1. Inflation of exoccipital wing

Tribe Mimini

1. Wedge-shaped lacrimal inserted at junction of ectethmoid plate, frontal and descending process of nasal
2. Ectethmoid plate deeply winged

BP 3: Ramphocinclae-Cinclocerthiae-Mimae

Subtribe Ramphocinclae

Species autapomorphies (Derived conditions unique to the species)

Subtribe Cinclocerthiae

1. Loss of posterior suprameatic strut
2. Well developed post suprameatic shelf
(For details of this subtribe see table 6.2)

Subtribe Mimae

1. Differential shading of outer webs of outer rectrices
2. Rufous, cinnamon, or pinkish buff coloration of under tail coverts and often posterior flanks and abdomen

BP 4: Dumetelles-Mimes

Infratribe Dumetelles

Species autapomorphies

Infratribe Mimes

1. Fused, single scute at base of outer toes

(TABLE 6.1 CONTINUED ON FOLLOWING PAGE)

TABLE 6.1 CONTINUED

BP 5: Melanoptila-Mimus

Supergenous Melanoptila
Species autapomorphies

Supergenous Mimus

1. Linear streaks in flank feathers
2. Spotted eggs
3. Reduced amounts of blue-green egg color

BP 6: Mimodes-Mimus-Toxostoma

Genus Mimodes
Species autapomorphies

Genus Mimus

1. Lateral edges of primaries, secondaries, and rectrices edged with white, outer rectrices often all or nearly all white

Genus Toxostoma

1. Loss of subterminal notch of maxillary tomium
2. Heavy egg white protein concentration in band immediately preceding 30 mm. reference band (this study)

TABLE 6.2 CHARACTERS AND DERIVED CONDITIONS SUPPORTING BRANCHING POINTS OF PHYLOGENETIC DIAGRAM IN FIGURE 6.2

Branch Point (BP) 1: Melanotes-Cinclocerthies

Infratribe Melanotes

1. Blue plumage

Infratribe Cinclocerthies

1. Loss of posterior suprareatic strut
2. Extreme development of postympanic shelf

BP 2: Cinclocerthia-Margarops

Genus Cinclocerthia
Species autapomorphies

Genus Margarops

1. Arboreal habit and accompanying structural modifications
2. Scaly ventral feather patterns

TABLE 6.3 CHARACTERS AND DERIVED CONDITIONS SUPPORTING
BRANCHING POINTS OF PHYLOGENETIC DIAGRAMS IN FIGURE 6.3

Toxostoma Branch Point (TBP) 1

TBP 2

1. Total loss of spotting in all plumages
2. Extreme structural modifications for digging
(Shared skull and pelvic skeletal modifications
reflected in discriminant functions of chapter 5)

TBP 3

1. Spotted ventral plumage

TBP 3

TBP 4

1. Ventral spots linear in shape
2. Rufous shade of brown in plumage

TBP 5

1. Ventral spots not linear in shape

TBP 5

TBP 6

1. Ventral spots wedge shaped

TBP 7

1. Ventral spots round

Mimus Branch Point (MBP) 1

MBP 2

1. Prominent streaks in dorsal plumage

MBP 2

MBP 3

1. White collar at base of neck

THRUSHES (SUBFAMILY TURDINAE)

There is no one key character that will diagnose the thrushes, the subfamily Turdinae. Generally however, they are Old World insect eaters that have a fully developed double humeral fossa (Eock, 1962), and have spoon, slipper, or club shaped maxillopalatines that are always inflated (Morioka, 1967). In addition they nearly all possess the classic characters proposed by Seebohm (1898) to diagnose the group, the booted tarsus and a spotted juvenal plumage.

TURDINE THRUSHES (TRIBE TURDINI)

Within the large, diverse subfamily Turdinae one quite well defined subgroup consists of the "true" or turdine thrushes. These can be distinguished by the following characters: (See figure 6.4.)

1) The exoccipital wing is inflated and forms a spacious tympanic cavity. (An autapomorphic character of the tribe.)

2) The exoccipital wing and suprameatic ridge are connected weakly, if at all, by a raised strut at the point where the suprameatic fossa passes medially to the

FIGURE 6.4. ANTERIOR LATERAL OBLIQUE (I) AND VENTRAL (II) VIEWS OF THE TEMPORAL AND TYMPANIC REGIONS OF THE SKULLS OF: (A) COPSYCHUS MALABARICUS (AMNH 2497), (B) MONTICOLA SOLITARIUS (USNM 292720), (C) CATHARUS USTULATA (AMNH 8077). (a) Zygomatic process. (b) Suprameatic fossa. (c) Suprameatic ridge. (d) Posterior suprameatic strut. (e) Exoccipital wing. (f) Post tympanic shelf. (g) Dorsal process of exoccipital wing. (h) Quadrate.



I



II

A



I



II

B



I



II

C

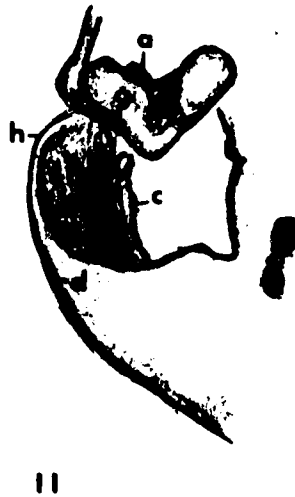
FIGURE 6.5. ANTERIOR LATERAL OBLIQUE (I) AND VENTRAL (II) VIEWS OF THE TEMPORAL AND TYMPANIC REGIONS OF THE SKULLS OF: (A) HYLOCICHLA MUSTELINA (AMNH 7965), (B) TURDUS PHILOMELOS (AMNH 8144), (C) MARGAROPS (ALLENIA) FUSCUS (AMNH 7845). (a) Zygomatic process. (b) Suprameatic fossa. (c) Suprameatic ridge. (d) Exoccipital wing. (e) Post tympanic shelf. (f) Dorsal process of exoccipital wing. (g) Quadrate.



A



B



C



FIGURE 6.6. ANTERIOR LATERAL OBLIQUE (I) AND VENTRAL (II) VIEWS OF THE TEMPORAL AND TYMPANIC REGIONS OF THE SKULLS OF: (A) MELANOTIS HYPOLEUCUS (AMNH 8123). (B) MELANOTIS CAERULESCENS (MVZ 153017). (C) MELANOTIS CAERULESCENS (MVZ 86202). (a) Zygomatic process. (b) Suprameatic fossa. (c) Suprameatic ridge. (d) Posterior suprameatic strut. (e) Exoccipital wing. (f) Post tympanic shelf. (g) Dorsal process of exoccipital wing. (h) Quadrate.



I

A



II



I

B



II



I

C



II

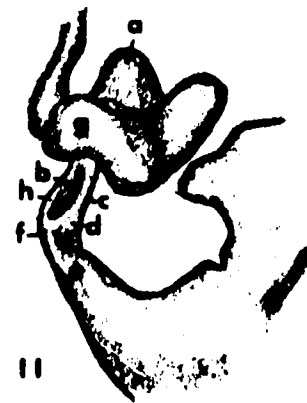
FIGURE 6.7. ANTERIOR LATERAL OBLIQUE (I) AND VENTRAL (II) VIEWS OF THE TEMPORAL AND TYMPANIC REGIONS OF THE SKULLS OF: (A) DUMETELLA CAROLINENSIS (AMNH 5450). (B) MINUS GUNDLACHII (USNM 17494). (C) TOXOSTOMA BENDIREI (AMNH 8139). (a) Zygomatic process. (b) Suprameatic fossa. (c) Suprameatic ridge. (d) Posterior suprameatic strut. (e) Exoccipital wing. (f) Dorsal process of exoccipital wing. (g) Quadrate.



A



B



C



exoccipital wing, forming a post tympanic shelf medial to the exoccipital wing (figure 6.4 - 6.5).

3) There is no ossification of the nasal septum or alinasal turbinals.

In addition, the following conditions are nearly always present in turdine thrushes:

1) A small lacrimal is always present in turdine thrushes (rarely among saxicoline thrushes). It is attached solely to the descending process of the nasal.

2) The postorbital process is smaller than the zygomatic process.

MIMIDS (TRIBE MIMINI)

A second distinct subgroup of the subfamily Turdinae consists of the mockingbirds, thrashers, and their allies, currently recognized as the family Mimidae. The group can be distinguished within the subfamily by the combination of two characters:

1) All mimids have a deep indentation between the dorsal and ventral wings of the ectethmoid plate. In all thrushes, with only an occasional exception among the

saxicoline thrushes, in which case the presence of the ossified nasal septum and alinasal turbinals would be diagnostic, the indentation of the ectethmoid is shallow (figure 6.11).

2) As pointed out above, all turdine thrushes have a small lacrimal. It is a small tab of bone attached to the upper sections of the descending process of the nasal (figure 7.1). All mimids also have a lacrimal. However, in all cases it extends dorsally along the edge of the descending process to form a wedge in the junction of the descending process, the frontal, and the ectethmoid plate.

ADDITIONAL FEATURES OF MIMIDS

1) The mimids have a narrow descending process of the nasal relative to that of turdine thrushes.

2) The angle formed by the descending process of the nasal and the maxilla is more acute than that in turdine thrushes.

3) The angle formed by the pedicels of the maxillopalatines and the cranial midline is more acute than that found in thrushes.

These three characteristics of mimids result from the

general elongation of the anterior part of the skull in mimids as compared to any of the turdine thrushes (chapter 5). It was not possible to resolve the primitive versus derived states of these conditions, although available evidence indicates that the elongation of the mimid skull is a derived condition.

Most mimids, with frequent individual exceptions among several species (Ramphocinclus, Cinclocerthia, Dumetella) exhibit a distinctly scutellate tarsus. This was the primary reason for their exclusion from the thrushes by late Nineteenth and early Twentieth century systematists (see chapter 1). As noted by Ripley (1952), there are many exceptions to the presence of a scutellate tarsus among thrushes. The ambivalent nature of the condition in the tribe Mimini makes it unreasonable to separate the mimids from the Turdinae on the basis of scutellation of the tarsi.

MIMIDS AND THRUSHES (SUPERTRIBE TURDINI)

The mimids and the turdine thrushes, with the exception of Donacobius which is neither a mimid nor a thrush and is discussed in chapter 7, share all basic features of cranial organization. Most of these features are common to not only turdine thrushes and mimids but also to most of the saxicoline thrushes. Since these characters

saxicoline thrushes, in which case the presence of the ossified nasal septum and alinasal turbinals would be diagnostic, the indentation of the ectethmoid is shallow (figure 6.11).

2) As pointed out above, all turdine thrushes have a small lacrimal. It is a small tab of bone attached to the upper sections of the descending process of the nasal (figure 7.1). All mimids also have a lacrimal. However, in all cases it extends dorsally along the edge of the descending process to form a wedge in the junction of the descending process, the frontal, and the ectethmoid plate.

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These three characteristics of mimids result from the

are generally present in many varied groups they are likely to be primitive and are therefore of no value in determining relationships within the complex. It is necessary to find at least one derived character that turdine thrushes and mimids share in common and in opposition to other groups within the complex. Only on the basis of such unique shared derived characters can phylogenetic hypotheses be based.

SKELETAL EVIDENCE

Convincing evidence as to mimid - turdine affinities is available from a detailed analysis of the cranial features of the various groups. My analysis of the skeleton system of the mimids and turdine thrushes was greatly facilitated by the comprehensive comparative study of the anatomical similarities and dissimilarities of these birds plus the wrens and dippers carried out by Morioka (1967). With regard to the mimids, Morioka considered only the question of whether they are more closely related to wrens or thrushes. He did not consider to which thrushes the mimids might be most closely related.

Since Morioka was primarily concerned with relationships at a somewhat higher level than those dealt with in the present study, he did not discuss several details of the temporal region of the cranium that are

crucial to the hypothesis of relationships proposed here. I therefore re-examined the skulls of all mimid species, except Mimus dorsalis which was unavailable, several species of the major turdine thrush genera and representatives of the major groups of saxicoline thrushes.

Postcranial elements were examined but in as much as they are so similar within all of these groups, with the exception of Donacobius, they are not discussed. Because previous studies by Engels (1940), Beecher (1953), and Morioka (1967) found that the musculature is so uniform in closely related groups of birds, I did not feel it worthwhile to repeat their dissections and consequently soft anatomy is not considered in this study.

TEMPORAL REGION

Morioka (1967) pointed out that the temporal region of the various thrushes shows a remarkable amount of variation for an avian family or subfamily. Even a casual survey of various genera confirms this. More remarkable yet is that within a small subgroup, such as the mimids, this region of the skull should exhibit such dramatic variation. Morioka did not analyze the variation found among the mimids. He lumped all of the forms he examined into a single category that he considered to be the Copsychus condition.

With regard to the exoccipital and auditory meatic regions which are particularly significant in this study, Morioka (1967:30) said:

"In Copsychus saularis the exoccipital wing extends upward - - - and meets the lateral zygomatic ridge which extends backward parallel to the free ventral edge of the suprameatic fossa. Hence the suprameatic fossa is a narrow oblong plate forming the upper boundary of the tympanic cavity. The tympanic membrane is more superficial than in the turdine condition." (See figures 6.4 and 6.5)

In addition to the mimids, Morioka attributed this condition to the turdine genus Catharus, to the saxicoline genus Monticola, and a few other saxicoline groups. A careful reappraisal of this region in the mimids, Catharus, Turdus, Hylocichla, Monticola, and Copsychus suggest that Morioka's "Copsychus condition" is not uniform and, as typified by the two species of Copsychus examined, can be distinguished from the other groups listed. A comparison of the temporal region of Copsychus malabaricus (figure 6.4A), Monticola solitarius (figure 6.4B), Catharus ustulata (figure 6.4C), Melanotis caerulescens and M. hypoleucus (figure 6.6), Margarops fuscus (figure 6.5C) and Dumetella carolinensis (figure 6.7A) demonstrate this.

The primary difference lies in the fact that only in Copsychus does the suprameatic ridge angle directly out to the junction of the exoccipital wing and zygomatic ridge.

In all of the others, the suprameatic ridge passes medially to this junction and the connection, if any, between the suprameatic ridge and the junction is by way of a broad, low strut across the posterior end of the suprameatic fossa. In two phylogenetic lines, the turdine thrushes and one group of mimids, there has been a reduction of the posterior strut of the suprameatic fossa. In the genus Turdus there is no trace of the strut. In Catharus and Hylocichla (more so in Hylocichla than Catharus) it is quite reduced and in Zoothera barely discernable. In the mimid genera Margarops and Cinclocerthia it also disappears. In the mimid genus Melanotis, the strut is absent in some specimens, clearly present in others, and barely evident in others (figure 6.6).

Among saxicoline thrushes, Monticola (figure 6.4B) exhibits a temporal region that is indistinguishable from that found in the more generalized turdine thrushes and mimids. Two species of Monticola (M. solitarius and M. saxatilis) were examined and no important variation was evident. Ripley (1952) began his enumeration of the "true" or turdine thrushes with Monticola, following the saxicoline genera Saxicoloides and Prunella and preceding the turdine genus Myiophoneus. This sequence implies that Ripley considered Monticola to represent the most primitive turdine condition. In the Checklist of Birds of the World, Ripley (1964) placed Monticola between Pseudocossyphus and

Myiophoneus.

Morioka (1967) rejected this view and argued that Monticola is rightfully a saxicoline genus primarily because these birds have ossified nasal septa and alinasal turbinals, in contrast to the condition of these structures in all turdine thrushes and mimids. If ossification of these structures is assumed to be primitive among thrushes, the loss of this ossification is a derived condition. Since shared derived characters are the only meaningful basis upon which to establish phylogenetic relationships among taxa, I would also exclude Monticola.

Two additional characters not shared by Monticola and turdine or mimid genera are: 1) Turdine thrushes and mimids characteristically nest in bushes and trees. Monticola species nest on the ground, in crevices. Such ground or hole nesting is characteristic of many saxicoline groups; 2) Monticola does not have a lacrimal, in contrast to all turdine thrushes and mimids.

On the basis of this discussion, I could propose Monticola as the saxicoline primitive sister group of the turdine - mimid complex. Without a more thorough survey of genera that may be related to Monticola, I would hesitate to take a very firm stand on the issue. However, the organization of the temporal region is such that no

distinction can be made between Monticola and several turdine and mimid genera. Other saxicoline thrushes have a different temporal arrangement. Therefore the temporal of Monticola must be considered as representative of a primitive turdine thrush - mimid condition.

THE TEMPORAL OF TURDINE THRUSHES AND MIMIDS

From the temporal condition exemplified by Monticola and some mimid genera, a parallel change has occurred in turdine thrushes and in one group of mimids. In each phylogenetic line there has been a reduction in the degree of development of the strut across the posterior end of the suprameatic fossa where it passes under the exoccipital wing and merges with the post suprameatic shelf. The extreme condition is found in Turdus and Hylocichla among the turdines and in Margarops and Cinclocerthia among the mimids (figure 6.5). The complete loss of the strut and a parallel development of the post tympanic shelf was not found in any other thrush group examined. Most turdine thrushes but no mimids exhibit the inflation of the exoccipital wing which makes the typical turdine skull unique among oscines that I have examined. Among the turdine thrushes, Catharus (figure 6.4C) exhibits the least inflation of the exoccipital wing and retains a weakly developed posterior strut across the suprameatic fossa.

EGG WHITE PROTEIN EVIDENCE

The egg white evidence also suggests a sister group relationship between the turdine thrushes and the mimids. However it is based upon a very small sample of turdine species. Among turdine egg whites samples available for comparison were Turdus migratorius, Hylocichla ustelina, and Catharus fuscescens. The only other thrush available was Myadestes raloides. Since, as discussed in chapter three, it was not possible to quantify the results of the protein analysis, which makes it impossible to make detailed interspecific comparisons, I considered the protein patterns as a single character rather than treating the seven to ten individual protein bands independently. On that basis two aspects of the character were visually evaluated: 1) The overall pattern of the protein bands and 2) The relative density of the bands within the pattern.

The patterns of the Catharus fuscescens sample are most similar to those of the mimids. In the plate containing the comparative samples, (figure 3.1B) the Catharus sample is next to Ramphocinclus. Without labels it would not be possible determine which is the mimid and which is the thrush. The samples are nearly identical in both position and density. The close match of Catharus fuscescens and Ramphocinclus brachyurus is remarkable.

The similarity of the other available turdine thrush samples to the mimids is less striking. In the Turdus specimen, the position of the bands is quite comparable to the mimids, although the density pattern is rather different. Hylocichla is intermediate, with a density pattern that is comparable to Catharus and the mimids and a position pattern of the bands that is only slightly shifted. The only saxicoline thrush available in this study was Myadestes ralioides. As can be seen in plate 1443, figure 3.2B, the egg white pattern of this species is quite different from the turdine thrushs and mimids

Since the egg white pattern shared by the Catharus species, and with minor variation, the two other turdine thrushes studied, plus all of the mimid species is different from any other pattern available, I consider it to be a shared derived condition. It is unlikely to be primitive because it is quite different from the egg white protein patterns of other members of the Old World insect eater assemblage that were available for comparison.

On the basis of the shared derived skeletal and egg white protein characters, the mimids are most closely related to and are the sister group of the turdine thrushes.

PHYLOGENETIC RELATIONSHIPS AMONG THE MINIDS

The condition of the temporal region in which the posterior strut of the suprameatic fossa is lost and the post tympanic shelf develops can be used to separate minid species into two basic groups. One group, consisting of most of the minid species, exhibit only the primitive organization of the temporal and tympanic region common to the supertribe Turdini. The other consisting of the genera Melanotis, Cinclocerthia, and Margarops shows differing degrees of development towards a condition that is structurally the same as that found in some genera of turdine thrushes. The condition of the region in Melanotis is variable. In some specimens, the region is quite like the typical, primitive turdine - minid condition (figure 6.6A). In others (figure 6.6B), the region is like that found in the infratribe Cinclocerthies. Other specimens are intermediate (figure 6.5C). Since the derived condition is never present in minid species other than those listed above, I consider Melanotis to be the primitive sister taxon of the infratribe Cinclocerthies.

The two species Margarops fuscus and M. fuscatus share the most extreme expression of the derived condition of the temporal - tympanic region. Except for minimal inflation of the exoccipital wing, these two minid species have temporal organizations that are quite like that of typical

turdine thrushes. The sister group relationship of these two species with regard to the third member of the group, Cinclocerthia is supported by the following shared derived characters: 1) Most extreme development of the derived condition of the temporal-tympanic region; 2) The angle made by the suprameatic ridge relative to the midline is different from that of all other mimids (skeletal variable 25 in table 5.2); 3) Scaly ventral plumage patterns.

The temporal characters were not useful in analyzing relationships among the rest of the mimid species since I was unable to discover additional derived conditions. Despite variation in the organization of the temporal region in response to shifts in the feeding mechanism, which were analyzed by Engels (1940) and which help separate clusters of species in the phenetic analysis of chapter five, most mimid species have the same organization of the exoccipital wing - zygomatic ridge junction. The strut illustrated and discussed above is present in all other species of mimid.

In analyzing sister group relationships among the mimid subgroups, patterns and other external characters become important. Two derived patterns serve to establish the relationship between Dumetella and the Mimus - Toxostoma complex. The first is a contrasting color pattern in the rectrices of this group. In its extreme

expression, it takes the form of the dramatic white and dark grey markings typical of Mimus species. In less dramatic form, it is present in most of the Toxostoma thrashers and Mimodes as contrasting shades of brown. The outer webs of the outer rectrices are lighter in shade (sometimes only slightly so) than the inner webs. This pattern is often accompanied by a comparable pattern in the tips of the rectrices. In Dumetella, the pattern is evident as contrasting shades of grey. The outer webs of the rectrices are much lighter than the inner webs. In Dumetella, the lighter grey of the outer web continues to the distal end of the feather. The inner web is dark nearly to the end where it is edged with the same lighter shade of grey as that of the outer web.

Coupled with the rectrix pattern is the contrasting cinnamon, rufous, chestnut, or as in some Mimus species, pinkish - buff color of the under tail coverts. This character is most striking in Dumetella and in the sickle - billed Toxostoma thrashers. In many species of the Mimus - Toxostoma complex, the distinctive coloring extends into the posterior parts of the flanks. These two pattern characters are derived conditions that link Dumetella and the rest of the complex.

Clark (1972) pointed out that among the minids a dichotomy exists with regard to the state of the scute at

the base of the two outer toes. It is only in one mimid subgroup among the entire Old World insect eater assemblage that the basal scute is single, forming a relatively large shield-shaped scute at the junction of the outer toes. In all of the other mimids, turdines, saxicolines, and other groups of Old World insect eaters, there are two scutes present, side by side (figure 4.10). Melanoptila, Toxostoma, Mimus and Mimodes share the unique single scute condition. Dumetella has the two scute condition and therefore must be considered to be the primitive sister group of the complex made up of these genera (figure 6.1).

MELANOPTILA

Clark (1972) states that Melanoptila has the divided scute condition. I reviewed the condition of this scute in fifty specimens from the collections of the United States National Museum and The American Museum of Natural History, including two live adults and two fledglings captured on Cozumel Island, Mexico. Seventy percent of these specimens had the single toe scute condition. In some cases, there was a ridge down the center of the scute but it was not in anyway divided. In only 15 of the cases was the scute actually split. In another 15, the scute was divided on one foot and single on the other. Therefore, I categorize this species as having, in the majority of cases, the single basal toe scute condition.

Since the derived condition of the basal toe scutes is the single, fused condition, Melanoptila, the Black Catbird, is the primitive sister taxon of the extensive Mimus - Toxostoma complex.

Melanoptila has two unique characteristics for a member of the mimid complex. First, it is the only member of the group to have developed iridescence in the feathers. Secondly, the songs of this species are quite unlike those of any other mimid. This aspect of the birds biology will be considered in a separate study. At this point, I will only comment on the most obvious differences. First, Melanoptila sings short phrases which are repeated over and over again, and could even be considered monotonous, an adjective hardly applicable to the song of any other mimid. There is no long rambling structure to the song as is found in so many mimid species. A typical feature of many mimid songs is the large number of harmonically structured syllables (Gulledge, 1970). In the songs of Melanoptila, there are few such syllables.

As discussed previously, I see no reason to consider the Black Catbird and Gray Catbird as being closely related. They are quite different in several respects and have only primitive generalized thrush - mimid features in common. These cannot be used to suggest a close phylogenetic relationship between them. In contrast, the

nature of the basal toe scute, a derived condition, indicates that Melanoptila is the primitive sister taxon of the Mimus - Toxostoma complex. Dumetella, having only the primitive two scute condition, must be placed as the primitive sister taxon of Melanoptila plus the Mimus - Toxostoma complex.

MIMUS - TOXOSTOMA

The large Mimus - Toxostoma complex contains two thirds of all mimid species. It includes Mimus (Oreoscoptes) montanus and Mimodes graysoni, species currently recognized as monotypic genera. In addition to the derived basal toe scute condition of this division of the mimids, the Mimus - Toxostoma complex is distinguishable by two other derived conditions. These are: 1) The presence in most species of central linear streaks in the flank feathers. These streaks extend into surrounding regions of some species (for example in Mimus thenca, M. gundlachii, and the M. (Nesomimus) trifasciatus complex the feathers of the abdomen and occasionally the posterior parts of the breast are streaked); 2) In contrast to all other mimids, the species of this complex have spotted eggs. The single exception is the Crissal Thrasher (Toxostoma dorsale) which has secondarily lost the spots. In conjunction with spots, there is a shift in the ground color of the eggs from the

rich blue - green shades of the West Indian endemics, Melanotis, and the two catbirds towards a much paler condition, typical of the eggs of Mimus species. Unfortunately, no information about the eggs of Mimodes is available.

The Mimus - Toxostoma complex is divisible into two distinct sections. One division, the traditional genus Toxostoma, is distinguished by two derived conditions. First, all members of this group have lost the primitive subterminal notch of the premaxillary tomium. All other mimids, thrushes and Old World insect eaters generally have such a notch, although in some species of Mimus, it is very weakly developed.

The second derived character which unites the Toxostoma thrashers as a monophyletic group is the distinctive nature of the egg white protein pattern. It was not possible to examine every species, but, as discussed in chapter 3, samples from the morphological extremes of the group, (T. rufum, T. redivivum) and an intermediate morphological form (T. curvirostre) were available. The Toxostoma egg white protein pattern is unique as a result of the heavy concentration of protein in the band preceding the 30 mm. reference band of the chapter three plates (figures 3.2 and 3.3).

MIMODES

Mimodes graysoni presents a special problem in an analysis of the Mimus - Toxostoma complex. It shares all of the derived characters used to link Mimus and Toxostoma. On the other hand, it has neither the unique characters of Toxostoma nor those of Mimus. Eggs and egg white protein samples were not available. These plus more knowledge about the natural history of the species will hopefully furnish characters which will make it possible to determine the phylogenetic relationships of Mimodes graysoni to the rest of the Mimus - Toxostoma complex. In the meantime it can only be placed as part of an unresolved trichotomy (see figure 6.3).

SUBDIVISIONS OF TOXOSTOMA

The traditional genus Toxostoma has been of interest to students of adaptive radiation for many years. The primary groups within the genus were analyzed in detail with regard to morphological shifts accompanying ecological adaptation by Engels (1940). Miller (1949) discussed some of the broader implications of the adaptive radiation of the group and some aspects of the overall Mimus - Toxostoma complex. Sheppard (1973) provides a detailed account of the ecology of the Le Conte's Thrasher and its sickle -

billed allies.

Engels divided the ten species into subgroups on the basis of the shape of the spots of the ventral plumage which are characteristic of most of the species. There are, however, three species in the group which exhibit the primitive lack of spots in the adult plumage. These three species have additionally lost all trace of spots in the juvenal plumage. Spotted adult plumages occur in various turdine and thrush lineages but within the mimids are absent outside of the Mimus - Toxostoma complex. More generally present in all of the turdine thrush - mimid complex are spotted juvenal plumages. Among thrushes, both dorsal and ventral spots are usually present. Among mimids, only ventral spots are evident. In the mimids, juvenal spots have been lost in Margarops fuscatus and M. fuscus, as well as in Melanotis and Melanoptila. Cinclocerthia shows traces of ventral spots. Spotted juvenal plumages are generally present in the Mimus - Toxostoma group and in Dumetella. Within this large complex, only the sickle - billed Toxostoma thrashers have lost all trace of spots in any plumage.

Sister group relationships among the remaining members of the Toxostoma group are clearly discernable on the basis of the shape of the ventral spots, the character used by Engels (1940) to establish subgroups within

Toxostoma (figure 6.3). I interpret the long lanceolate streaks discussed above as being present in the flank and occasionally the posterior breast feathers of both Mimus and Toxostoma as representing the primitive condition. On that basis, a transitional series can be discerned with the T. rufum group forming a primitive sister group to the other two spotted breasted groups within the Toxostoma complex, the T. curvirostre - T. ocellatum group and the T. cinereum - T. bendirei group. An additional derived character serves to distinguish the T. rufum group. Only these three species of Toxostoma exhibit the rich rufous color on the dorsal surfaces. I could determine no condition to suggest which two of these three species are most closely related. Similarly, it is not at present possible to propose, on the basis of shared derived characters, which of the three sickle - billed thrasher species is most closely related to either of the other two.

THE MIMUS COMPLEX

The birds of this complex, including Mimus (Oreoscoptes) montanus, exhibit two derived conditions which set them apart from other mimids: 1) Only in this group are the edges of the remiges and rectrices distinctly marked with white. 2) Only within this group of mimid species has streaked dorsal plumage developed. Margarops fuscatus (but not M. fuscus, its sister species) of the

West Indies has a superficially similar pattern but in that species the dorsal feathers are uniform centrally, with a light edging. This creates, in Ridgway's words (1907; 265): " - - an indistinctly spotted or scaled effect."

The species of Mimus and Nesomimus are very similar structurally. Only the Galapagos Island birds are distinguishable on the basis of shared derived structural characters relative to the rest of the Mimus species. It is necessary therefore to concentrate on patterns to discern phylogenetic lines within the Mimus complex. The only one that seems useful is the prominent dorsal streaking. I interpret the primitive condition to be the lack of such streaks in the adult plumage. Rarely in any line of thrushes, saxicoline or turdine are dorsal patterns present in the adult plumage. Among the mimids, the only species other than those in Mimus to have dorsal patterns is Margarops fuscatus, discussed above.

Considering the dorsal streaks as derived, two lines are discernable within the currently recognized genus Mimus. One consists of M. gundlachii, M. thenca, M. longicaudatus, M. (Nesomimus) trifasciatus, M. saturninus and M. patagonicus. The other branch consists of the other species (M. polyglottos, M. gilvus, M. dorsalis and M. triurus) which show only the primitive condition. Beyond this division, I can propose only one additional

subdivision. Mimus longicaudatus and the Galapagos mockingbirds both have a prominent white collar. On the basis of this shared derived condition, I consider Mimus longicaudatus to be the sister species of M. trifasciatus. The Galapagos birds are a monophyletic group unified by the constriction of the base of the bill and the lengthening of the tibiotarsus. These modifications are present in all of the island forms and were the basis upon which Ridgway (1890) erected the genus Nesomimus.

MIMUS (OREOSCOPTES) MONTANUS

Most ornithologists, (for example Mayr and Short (1970)), have preferred to think of Oreoscoptes, the Sage Thrasher, as being much closer to Toxostoma than to Mimus. Reasons for these views and evidence to support the suggested relationship have not been given. The species does have ventral spots and is terrestrial in nature. However, the bird has not lost the subterminal premaxillary tomial notch, a condition unique to Toxostoma. On the other hand, it does possess the white - grey derived condition of the wing and tail markings of Mimus and does have the prominent dorsal markings which within the Mimus - Toxostoma complex are unique to Mimus.

Another line of evidence also supports the view that Mimus montanus is not closely related to Toxostoma. In the

discriminant functional analysis of the skeletal characters of all the mimids and 14 thrushes (chapter 5), M. montanus shares none of the specialized combinations of structural characters which clearly separate the thrashers from the mockingbirds. Although the generalized mimid skeletal organization in which M. montanus is quite typical is not useful in suggesting relationships, it does suggest that there is little reason, other than the ventral spots, for placing the Sage Thrasher close to the Toxostoma thrashers.

The terrestrial nature of the Sage Thrasher is a necessity in a treeless, sagebrush plain habitat. In a group of birds such as the mockingbirds and thrashers which contains many members that are quite terrestrial, such a mode of life and superficial similarities provide no basis upon which to suggest phylogenetic relationships when shared derived characters to support them have not been discovered.

It is appropriate to ask in what manner Mimus montanus may be related to other Mimus species. The answer hinges upon interpretation of the nature of the dorsal streaks. If dorsal streaks are primitive, they cannot be used to suggest that the species is more closely related to Mimus than to Toxostoma. On the other hand, if dorsal streaks are a derived condition, as argued above, two possibilities exist: 1) M. montanus is actually the primitive sister

taxon of only the Mimus species having dorsal streaks, or;
2) The dorsal streaks evolved in the common Mimus ancestor and were lost again in one line of its descendents. This would imply a secondary loss of the derived condition. Although such is certainly possible, it is a much less parsimonious solution than to propose that dorsal streaks appeared in only one line of Mimus and that M. montanus is most closely related to that line. In view of the evidence as to primitive and derived conditions, the most parsimonious hypothesis is that M. montanus is the sister taxon, not of all of Mimus but of the group of species having the derived, dorsally streaked condition.

One is still faced with the problem of the ventral spots. If the most parsimonious solution to the dorsal streaking problem is accepted, then the ventral spots are a case of parallelism in a phylogenetic line that is not far removed from Toxostoma anyway.

With regard to ventral spots, it is of interest to note that among the dorsally streaked Mimus species, one, M. gundlachii of the Bahamas, consistently has ventral spots in the adult plumage. The spots are quite small and are not evident in some specimens, especially those with worn plumage, nevertheless they are clearly present in most specimens. The spots are not the large, light brownish-grey of the juvenals but are instead, quite intensely

colored and small. In addition to Mimus gundlachii, the Galapagos island mockingbirds often have a few spots in their breast plumage. Ventral spots are therefore not unique to Toxostoma and have developed in the adult plumage of both mockingbirds and thrashers.

In conclusion, Mimus montanus is nothing more than a ground dwelling mockingbird of the sagebrush plains of western North America. It shares none of the specialized derived conditions which characterize the Toxostoma thrashers. On the other hand, it does share derived characters with species of Mimus.

RAMPHOCINCLUS

Ramphocinclus possesses none of the derived conditions that have been used to establish sister group relationships among the various mimid taxa. Its temporal region is of the primitive mimid type, it has the primitive double basal toe scute condition, it shares no derived pattern characters and its egg white proteins are not particularly different from any of the other mimids.

In addition to having all of the primitive conditions shared throughout the turdine - mimid complex, it clearly has the derived mimid condition with regard to the ectethmoid plate and lacrimal. It is therefore not

at present possible to determine with which major division of the mimids this species should be associated. Nor can I eliminate the possibility that Ramphocinclus is actually the primitive sister taxon of all the mimids. The only course is to leave Ramphocinclus as a member of a trichotomy at the point of division between the Melanotis - Cinclocerthia group and the Dumetella - Mimus group. (See figure 6.1)

CLASSIFICATION

Current classifications of the mimids (Davis and Miller, 1960) and thrushes (Ripley, 1964), are the result of subjective evaluations of similarities and differences by experienced taxonomists. The philosophical foundations for these kinds of traditional classifications are discussed by Bock (1973). In the case of the mimids the phenetic analysis of external characters reported in chapter four of this study has demonstrated that the traditional groupings of species can be determined solely on the basis of purely phenetic associations. It is not at all necessary to include judgements of phylogenetic relationships.

It is evident that currently accepted supraspecific mimid taxa were constructed in a manner quite in keeping with the rationale so clearly stated by Mayr (1969) as to

the meaning of such supraspecific taxa. According to Mayr (1969: 92): "A genus is a taxonomic category containing a single species, or a monophyletic group of species, which is separated from other taxa of the same rank (other genera) by a decided gap."

I feel that creating taxonomic hierarchies in such a manner will distort any suggestion of phylogenetic relationships that the taxonomist proposing the classification may believe to exist. For readers not familiar with both the species of organisms included and the concepts that guided the taxonomist as to how different the taxonomic units must be to deserve certain ranks, traditional classifications are little more than lists of names.

In as much as I do not believe that it is possible for a classification to accurately express both phenetic and phyletic information, I have chosen to follow the school that argues that a classification should precisely express an hypothesis of phylogenetic relationships among the taxonomic units analyzed. The rationale for this approach to classifications is discussed at length in Crowson (1970) and Nelson (1973).

Such a strictly phylogenetic classification does not take into consideration evaluations of similarity and

difference. Similarities and differences among taxa are better expressed through the three dimensional graphs and phenograms that result from numerical taxonomic analyses such as those discussed in chapters 4 and 5 of this study.

Since the classification of the mimiids given in table 6.4 reflects only the hypotheses of intertaxa relationships proposed and discussed in this chapter, the nomenclatural ranks in the classification do not in anyway imply amounts of similarity and difference. For convenience and clarity, and for these reasons only, I have tried to make the classification as compatible with those currently followed as possible. However, a phylogenetic classification normally has no more than two taxa at any single level, with the exception of unresolved relationships. A number of intermediate taxonomic ranks were therefore necessary.

It must be emphasized that this classification and the phylogeny that is represented in figures 6.1 - 6.3 represent hypotheses of relationship. In that light, they are subject to continual testing and revision in the light of additional information. Testing of the hypotheses of phylogenetic relationships among mimiid and thrush taxa and the classification in table 6.4 can only be accomplished through further phylogenetic analysis. Analyses of similarities and differences among the taxa, whether intuitive or numerical cannot help answer questions of

phylogenetic relationship if they do not resolve systems of shared derived characters.

TABLE 6.4 CLASSIFICATIONS OF THE FOCKINGBIRDS, THRASHERS AND ALLIES

Family Mimidae ¹	Family Mimidae ²	Family Muscicapidae ³
Genus <u>Toxostoma</u>	Genus <u>Dumetella</u>	Subfamily Turdinae
Genus <u>Melanotis</u>	Genus <u>Melanoptila</u>	Supertribe Saxicolini
Genus <u>Melanoptila</u>	Genus <u>Melanotis</u>	Supertribe Turdini
Genus <u>Mimodes</u>	Genus <u>Mimus</u>	Tribe Turdini
Genus <u>Dumetella</u>	Genus <u>Nesomimus</u>	Tribe Mimini
Genus <u>Mimus</u>	Genus <u>Mimodes</u>	Subtribe Ramphocincliae
Genus <u>Nesomimus</u>	Genus <u>Oreoscoptes</u>	Genus <u>Ramphocinclus</u>
Genus <u>Oreoscoptes</u>	Genus <u>Toxostoma</u>	Subtribe Cinclocerthiae
Genus <u>Allenia</u>	Genus <u>Cinclocerthia</u>	Infratribe Melanotes
Genus <u>Margarops</u>	Genus <u>Ramphocinclus</u>	Genus <u>Melanotis</u>
Genus <u>Ramphocinclus</u>	Genus <u>Donacobius</u>	Infratribe Cinclocerthies
Genus <u>Cinclocerthia</u>	Genus <u>Allenia</u>	Genus <u>Cinclocerthia</u>
Genus <u>Donacobius</u>	Genus <u>Margarops</u>	Genus <u>Margarops</u>
		Subtribe Mimae
		Infratribe Dumetelles
		Genus <u>Dumetella</u>
		Infratribe Mimes
		Supergenous <u>Melanoptila</u>
		Genus <u>Melanoptila</u>
		Supergenous <u>Mimus</u>
		Genus <u>Toxostoma</u>
		Genus <u>Mimodes</u>
		Genus <u>Mimus</u>

¹Ridgway (1907) and Hellmayr (1934). Donacobius was not included in Ridgway's classification as the species is extralimital to his work.

²Davis and Miller (1960).

³Classification proposed as a result of the phylogenetic analysis carried out in this study. Donacobius is not included as its affinities to any subdivision of the Turdinae could not be demonstrated. The hierarchical categories used in this classification are not intended to estimate the size of phenetic gaps. They are used as convenient labels to indicate phylogenetic branching sequences.

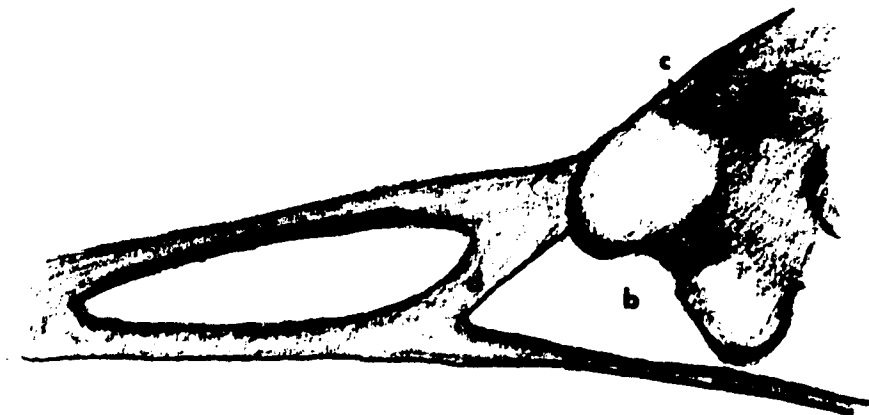
DONACOBIOUS ATRICAPILLUS

The monotypic genus Donacobius presents a special problem with regard to any discussion of relationships among the mimids. Every worker who has discussed the group has been compelled to take note of the many unique features of this species. Donacobius atricapillus was added by Baird (1864) to the mimids on the merest shred of evidence and has remained there, not because it belongs, or has any particularly mimid feature, but because no one has studied it and discovered where it actually should be placed relative to other possible groups.

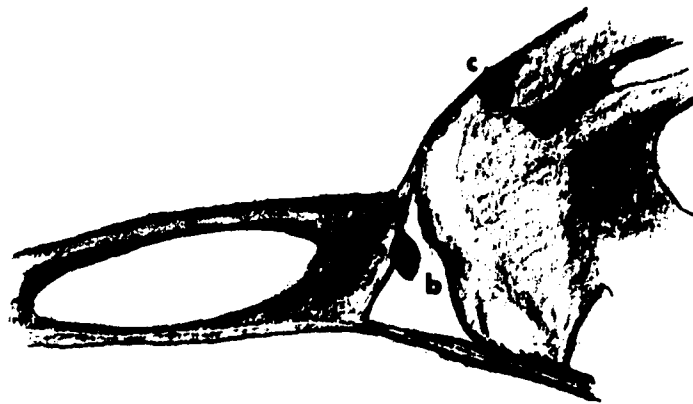
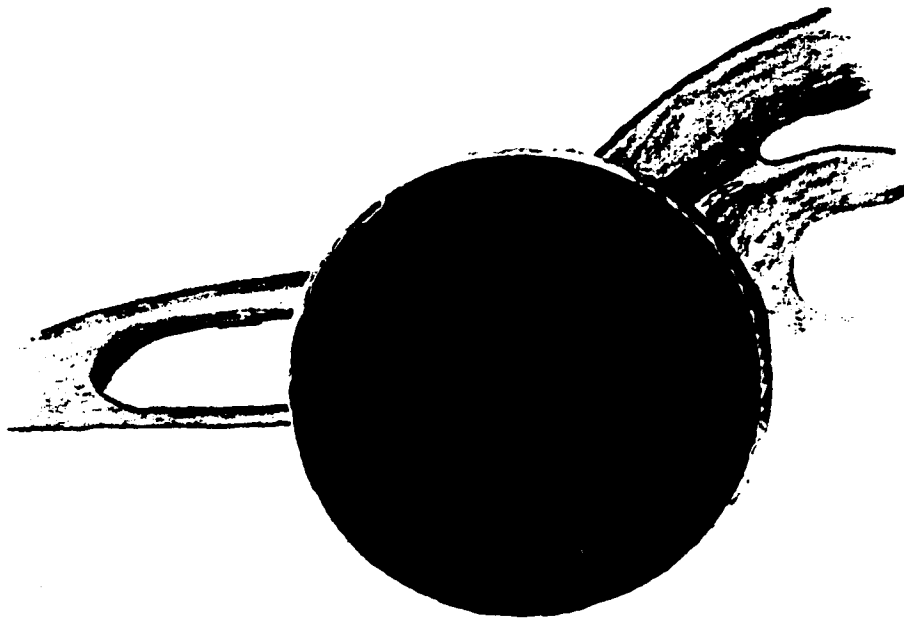
On the basis of the shared derived characters that I have used to differentiate the mimids from the turdines, Donacobius must be excluded. It has no trace of a lacrimal, much less the specific type of lacrimal characteristic of mimids (figure 7.1). It is always possible for a small bone such as the lacrimal to be lost. However, five specimens were available for this study, one collected quite recently and carefully prepared with this problem in mind. It shows no trace of a lacrimal.

Donacobius does have a deeply winged ectethmoid plate, a typically mimid feature (figure 7.2). However even a casual inspection of the plate shows that it is quite differently organized when compared to mimids (Dumetella in

FIGURE 7.1. LATERAL VIEW OF ANTERIOR SECTION OF SKULLS OF:
(A) DONACOBIOUS ATRICAPILLUS (MVZ 120755); (B) DUMETELLA
CAROLINENSIS (AMNH 5450); (C) CATHARUS USTULATA (AMNH
8077). (a) Lacrimal. (b) Ectethmoid plate. (c) Lateral
ectethmoid foramen. (d) Descending process of nasal.



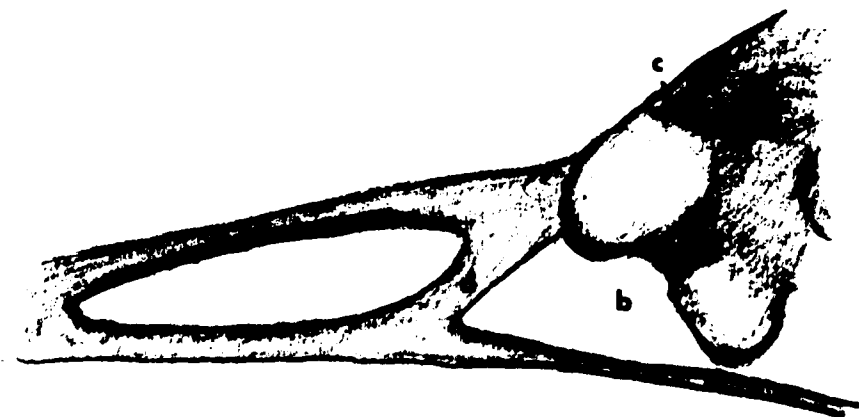
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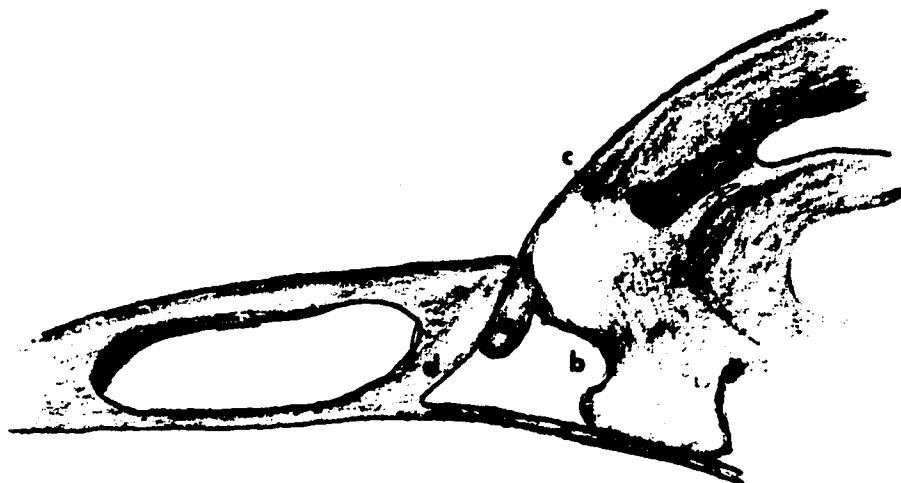
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figure 7.2 for example). The dorsal wing, instead of being flat on its posterior face, is bulbous and inflated. The anterior face is conversely quite recessed. The olfactory process on the dorsal anterior face of the ectethmoid (chapter 5) is totally lacking. The ventral wing of the ectethmoid plate is quite narrow and is completely within the jugal bars, a condition not found in any *siniid*, or *turdine* thrush. The ectethmoid foramen is divided however, with the outer foramen just ventral to the outer edge of the frontal where the bulbous dorsal ectethmoid wing wraps out and just slightly around the edge of the frontal.

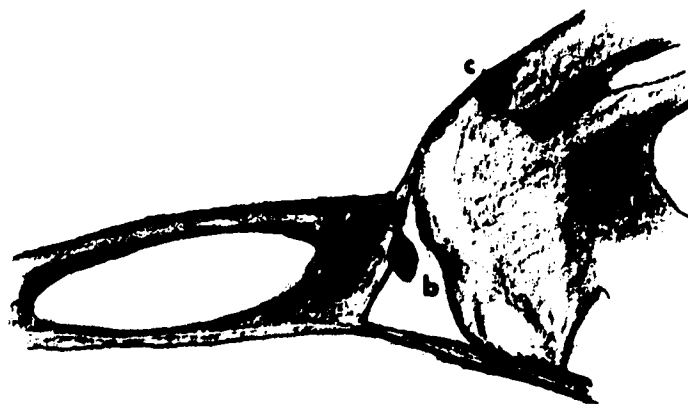
Moving to the sister group of the *siniids*, the *turdine* thrushes, *Donacobius* must again be excluded. The temporal complex which was used to establish the *turdine-siniid* relationship is organized in a completely different manner. This is evident in figure 7.3. There is no suprascenic fossa. The edge of the exoccipital wing sweeps around and is apparently continuous with the suprascenic ridge which seems to have rolled outward and upward. That is why in figures 7.3A1 and A2 no suprascenic fossa is evident. The ledge, or plate visible in figure 7.3A2 is the inner surface of the dorsal border of the tympanic cavity rolled out and is thus not visible in figure 7.3A1. A zygomatic ridge passing posteriorly above the tympanic cavity is absent. The maxillopalatines (figure 7.4) are not inflated as is true of all *siniids* and of all but a very few (for



A



B



C

figure 7.2 for example). The dorsal wing, instead of being flat on its posterior face, is bulbous and inflated. The anterior face is conversely quite recessed. The olfactory process on the dorsal anterior face of the ectethmoid (chapter 5) is totally lacking. The ventral wing of the ectethmoid plate is quite narrow and is completely within the jugal bars, a condition not found in any mimid, or turdine thrush. The ectethmoid foramen is divided however, with the outer foramen just ventral to the outer edge of the frontal where the bulbous dorsal ectethmoid wing wraps out and just slightly around the edge of the frontal.

Moving to the sister group of the mimids, the turdine thrushes, Donacobius must again be excluded. The temporal complex which was used to establish the turdine-mimid relationship is organized in a completely different manner. This is evident in figure 7.3. There is no suprameatic fossa. The edge of the exoccipital wing sweeps around and is apparently continuous with the suprameatic ridge which seems to have rolled outward and upward. That is why in figures 7.3A1 and A2 no suprameatic fossa is evident. The ledge, or plate visible in figure 7.3A2 is the inner surface of the dorsal border of the tympanic cavity rolled out and is thus not visible in figure 7.3A1. A zygomatic ridge passing posteriorly above the tympanic cavity is absent. The maxillopalatines (figure 7.4) are not inflated as is true of all mimids and of all but a very few (for

FIGURE 7.2. POSTERIOR OBLIQUE VIEWS OF ECTETHMOID PLATES
OF: (A) DONACOBIOUS ATRICAPILLUS (MVZ 120755); (B)
DUMETELLA CAROLINENSIS (AMNH 5450); (C) CATHARUS USTULATA
(AMNH 8077). (a) Ectethmoid plate. (b) Lateral ectethmoid
foramen



A



B



C

FIGURE 7.3. THREE VIEWS OF TYMPANIC TEMPORAL REGION OF
SKULL OF DONACOBIOUS ATRICAPILLUS (MVZ 120755). (A)
LATERAL; (B) ANTERIOR LATERAL OBLIQUE; (C) VENTRAL.



A



B

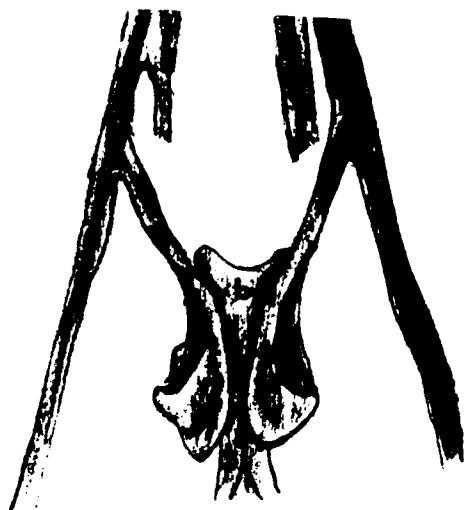


C

FIGURE 7.4. VENTRAL VIEWS OF THE MAXILLOPALATINE REGION OF THE SKULLS OF: (A) DONACOBIOUS ATRICAPILLUS (MVZ 120755); (B) DUMETELLA CAROLINENSIS (AMNH 5450); (C) CATHARUS USTULATA (AMNH 8077). (a) Right maxillopalatine. (b) Vomer



A



B



C

example Myadestes) thrushes. The postorbital process which Morioka (1967) noted is always smaller than the zygomatic process in turdine thrushes (and mimids) is quite large in Donacobius. All of this suggests that rather than being a modified turdine-mimid skull, the structural organization of the skull of Donacobius is fundamentally different and has little in common with any of the thrushes, much less the mimids.

Examining Donacobius in comparison to an even larger segment of the Old World insect eaters, it becomes clear that this species cannot be placed anywhere within the subfamily Turdinae of the Muscicapidae. Although no attempt was made to determine sister group relationships at the level of major subdivisions of the Muscicapidae, it is possible to discuss one aspect of the issue. Bock (1962) reviewed the nature of the double pneumatic fossa in the proximal end of the humerus and its occurrence in major divisions of the Passeriformes. He found that a fully developed double fossa was present in several distinct lines within the order. Based on the occurrence of the single fossa condition in widely diverse groups and in the most primitive oscines, he agreed with previous workers that a double fossa is a derived condition.

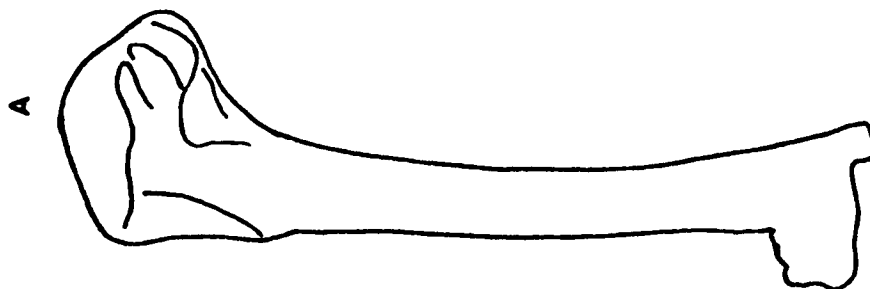
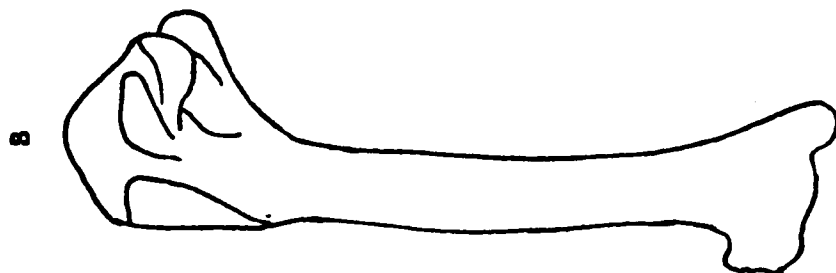
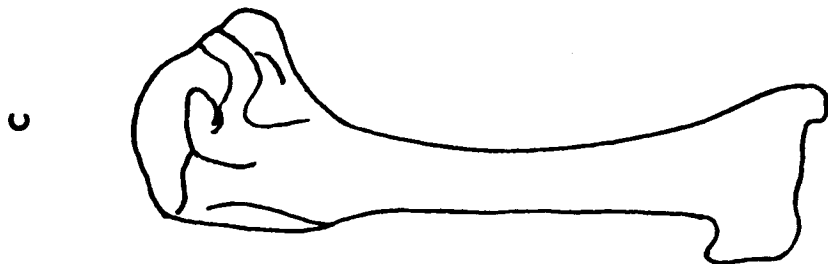
Although the double fossa was found to be developing in several different lines of passerines, Bock found

consistent patterns within the individual assemblages. In the Muscicapidae, a clear transitional series is present. In the Old World warblers, the Sylviinae, the Old World flycatchers, the Muscicapinae, and the babblers, the Timaliinae, the second fossa is in an early stage of development. Likewise, the second fossa is only "forming" in the wrens (Troglodytidae). In contrast to these groups, Bock found that the thrushes, the mimids, and the dippers (Cinclidae) all have a fully developed second fossa. Therefore, it would appear that the presence of a second humeral fossa is a derived character within the Old World insect eater complex. Figure 7.5 shows camera lucida tracings of the humerus of Donacobius, Dumetella and Catharus. As is evident, Donacobius lacks the developed second fossa characteristic, without exception, of the thrushes and mimids. For this reason, I believe that it is necessary to examine other groups outside the Turdinae in order to find the group to which Donacobius is most closely related. It was not possible within the framework of the present study to carry out such a greatly expanded survey.

ADDITIONAL PECULIARITIES OF DONACOBIOUS

Any aspect of the biology of Donacobius that is examined adds additional ways in which this bird stands apart from both mimids and thrushes. I will not attempt to analyze all of these in detail at this point but will

FIGURE 7.5. CAMERA LUCIDA TRACINGS OF THE HUMERUS OF: (A) DOMACOBIOUS ATRICAPILLUS; (B) DUMETELLA CAROLINENSIS; (C) CATHARUS USTULATA.



merely point out the more obvious differences, selecting them from as many aspects of the bird's biology as possible.

Plumage: In most turdines and mimids, the young are spotted, at least ventrally. Exceptions to this occur among the mimids as noted previously. Donacobius is also an exception. There is no sign of markings in the plumage of fledgling and juvenal individuals. In fact, the peculiar narrow transverse bars of the flank feathers of the adult birds is also lacking. This barring of the flanks is unknown in any other turdine thrush or mimid. In addition, I have not found the condition in any saxicoline thrush examined.

Bare neck patches: This most distinctive external character of Donacobius is unknown in mimids, or thrushes, turdine or saxicoline. The only other group of passerines in which I know of such a condition are a few species of babbler, for example Stachyris maculata of Southeast Asia.

Natural history: Skutch (1968) describes in detail many aspects of the natural history of Donacobius. Skutch said: "The book name "Black-capped Mockingthrush", widely applied to this species, is unfortunate. It is not a mimic; there is nothing thrushlike in its appearance, voice, or behavior----". Donacobius's choice of habitat,

marshes, reed beds and swamps, is unknown among turdine thrushes or mimids. The nest described by Skutch was made of fibrous vegetable materials, and narrow strips of grass blades. It was looped around three upright, dead grass stalks. Turdine thrushes and mimids, in contrast, build bulky platforms of substantial sticks and in the case of many turdines, mud. Although nest sites vary, I know of no reported case of such a relatively flimsy and precarious site being used by a mimid or thrush.

Eggs: The eggs of Donacobius are, according to Skutch (1968), densely mottled with slightly varying shades of reddish brown. In all turdine thrushes, and mimids, the eggs are in varying shades of blue or blue-green, in many cases with spots and broad mottled markings.

Young birds: As pointed out above, the young of Donacobius lack any trace of the typical thrush spotting. They differ from thrushes and mimids in an even more striking way. The interior of their mouths is initially a dark flesh color turning at about eight days of age to a purplish flesh color (Skutch, 1968). In thrushes the usual color is some shade of yellow or orange. This is always the case in the mimids. Even more unusual is that the tongue is marked with three conspicuous black spots, one anterior and two posterior. I know of no such markings among the Old World insect eaters.

Post cranial skeleton: In addition to the cranial features which made it impossible to include Donacobius in the turdine thrushes or mimids, the species has postcranial skeletal differences which emphasize its uniqueness. The lack of a turdine-mimid double humeral fossa was discussed above. In addition, the distal end of the humerus is organized differently (figure 7.5). The mimid and thrush humerus shows the same structural organization of the distal end, especially with regard to the epicondylar process.

The tibiotarsus also shows a different organization of toe articulation when compared to the mimids or thrushes (figure 7.6). In Donacobius, the unfused metatarsal against which the hallus articulates extends well past the other articulating surfaces. Thus any measure of tarsus-metatarsus length will be to the end of this bone rather than to the end of the central, fused metatarsal, which is always the longest part of the tibiotarsus. This suggests a fundamental difference in the functional organization of the foot when compared to thrushes or mimids.

The pelvis of Donacobius also shows a different structural organization. In all mimids and thrushes examined, the crests of the ilia are either essentially parallel (the most common case) or slightly concave so that

FIGURE 7.6. CAMERA LUCIDA TRACINGS OF THE DISTAL END OF
TIBIOTARSUS (TOP) AND POSTERIOR VIEW OF PYGOSTYLE (BOTTOM) OF:
(A) DONACOBIOUS ATRICAPILLUS; (B) DUMPETELLA CAROLINENSIS; (C)
CATHARUS USTULATA.



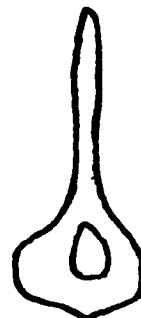
A



B



C



they resemble two very shallow parentheses back to back with a considerable gap between them at any point. In Donacobius the crests of the ilia form a "v", coming together very closely and sometimes fusing at the posterior end.

Finally, the posterior end of the axial skeleton exhibits another peculiarity. The centrum of the pygostyle of both thrushes and mimids is flared out into a basically cuboid plate (figure 7.6). In Donacobius, the centrum of the pygostyle is a narrow oval.

In summary, Donacobius differs fundamentally in its structural organization, its natural history, and its external characters when compared to thrushes and mimids. It lacks any of the derived characters of the broadest groups to which the mimids belong. It is therefore not possible to justify even a remote association between this species and any mimid. Donacobius must be considered incertae sedis until it is possible to determine its phylogenetic relationships to other passerine groups.

SUMMARY AND DISCUSSION

The analyses of relationships among the mimids, thrashers and their allies that are reported in this study were based on characters obtained from three sources: 1) Egg white proteins; 2) External morphology and natural history; 3) Skeletons. These sets of characters were examined with both phenetic and phylogenetic techniques and procedures. Shared derived characters were determined and used to develop an hypothesis of phylogenetic relationships.

Following procedures customary in studies of avian egg white proteins, it was not possible, with one notable exception, to determine the interspecific phenetic relationships of thirteen mimid taxa with any confidence. These difficulties were the result of the inability in this study to adequately quantify information derived from the electrophoretic separations. In three morphologically diverse Toxostoma species (T. rufum, T. curvirostre, and T. lecontei), however, one particular protein band was found to always be conspicuously more dense than the comparable band in samples of all the other available mimid species. This feature provides support for the hypothesis that the species grouped as the genus Toxostoma are a monophyletic assemblage. Careful quantification of the egg white protein data will permit a great improvement in the ability of these characters to clarify relationships among mimids at the species level.

At a higher taxonomic level, based on subjective evaluation of the egg white patterns of the thirteen species of mimids available plus examples of thrushes and wrens, the mimids have little or no resemblance to the wrens, a group to which they have been frequently allied. On the other hand, the pattern of positions (representing the isoelectric pH points) of the proteins in the electrophoretic gels is quite similar in both mimids and turdine thrushes. A sample of egg white from the turdine thrush Catharus fuscescens is not distinguishable from that of a number of mimid species, particularly Ramphocinclus brachyurus.

Phenetic relationships among thirty four mimid species (considering the four major Galapagos forms as species), using external morphological and other non skeletal characters, were analyzed with numerical taxonomic procedures. Three subsets of characters, color, pattern and a small group of miscellaneous, nonskeletal variables, were analyzed. Color information used alone produced only large groups that were consistent with traditional views of mimid relationships. Detailed associations were confused and inconsistent. These results indicate that color, alone, is not a very useful source of information for assembling clusters of mimid species. In some cases, color contributes a useful derived character. For example, the two species that comprise the genus Melanotis alone among

mimids, have blue plumage.

Associations of taxa, based on pattern characters, were much more consistent with traditionally accepted clusters of species. Three groups were suggested by the numerical procedures. These were: 1) Mimus species; 2) Spotted breasted Toxostoma species; 3) The West Indian endemic mimids, the two catbirds, and the blue mockingbirds. The three groups connect phenetically through the unspotted, sickle-billed Toxostoma thrashers. The pairing of taxa and the formation of small clusters of species was also generally consistent with traditionally accepted relationships.

When color and pattern characters were combined, the overall groupings changed little, compared to those suggested by pattern alone. There was, however, some "improvement" in the pairing of species and the formation of small clusters. The results were, with a few exceptions, comparable to traditional associations of mimid taxa.

When the mimid taxa were analyzed on the basis of thirteen miscellaneous nonskeletal characters, a number of which are either dichotomous or were coded in only a few states, only two distinct groups of taxa are suggested. One consists of the Mimus and Toxostoma species, plus

Mimodes. The other contains the West Indian endemics, the two catbirds and the blue mockingbirds. Donacobius atricapillus is separated sharply from the other species by the principal component analysis of these characters, a result which did not occur when the color and pattern characters were analyzed.

When all of the external characters were combined, the various phenetic analyses generated a picture of mimid relationships that is remarkably congruent with that suggested by currently accepted views of mimid relationships. The numerical procedures, in addition, were able to suggest larger associations of the taxa which are not normally expressed in taxonomic works treating the group. These include the close phenetic association of Mimus longicaudatus to the Galapagos mockingbirds; the connection of the genus Melanotis to Cinclocerthia; and the phenetic association of the two catbirds with Melanotis and the West Indian endemics on the one hand and with the unpatterned Toxostoma species on the other.

It is significant that a strictly phenetic analysis, with no a priori assumptions as to phylogenetic relationships, is able to so accurately duplicate associations of mimid taxa suggested by conventional classifications which were produced by subjective evaluation and interpretation of "decided gaps" among the

taxa. It demonstrates how purely phenetic current views of relationships among the minids are. Since so few avian groups have been subjected to a rigorous phylogenetic analysis (in the sense of Hennig), the results of this study further suggest that much of higher category avian systematics consists of little more than subjective evaluations of overall phenetic similarities and differences, despite philosophical assertions of phylogenetic insight.

The second major category of characters that were analyzed in this study consisted of skeletal variables. The primary analytical methods used to determine phenetic relationships using these characters were discriminant functions and cluster analysis and minimum spanning trees computed from generalized distances. Because of traditional associations of minids and thrushes and because of the suggestions of affinities between the two groups provided by the egg white protein study, fourteen thrush species, representing major groups, were included in the analysis.

Size differences among the species presented a major problem in the analysis. Two approaches were employed to reduce or eliminate these effects. First, regression coefficients for each variable were calculated on the basis of a reference variable chosen for its high correlation

with many variables in different parts of the skeletal system. These coefficients were used to scale the variables for each specimen. The second method, and the one chosen as the primary approach in the study, was to compute discriminant functions and generalized distances which remove most correlating factors, from whatever source, including size.

The first discriminant function derived from the skeletal variables of both thrushes and mimids was barely, if at all, able to separate a Copsychus thrush and four species of Cossypha thrushes from Dumetella, Margarops fuscus, Mimus polyglottos, M. gilvus, and M. montanus. The second and third functions were even less able, independently, to discriminate between thrush and mimid species. Only when the functions were examined together were clear separations evident. The cluster analysis of the generalized distance matrix demonstrated a similar inability to separate the Cossypha thrushes from clusters of mimid thrushes. The conclusion is that a number of mimid species are structurally very similar to at least the Cossypha thrushes. The turdine thrushes, on the other hand, were quite distinctly separated from the mimids both by the discriminant functions and the cluster analysis of the generalized distances.

The minimum spanning tree computed from the generalized distance matrix derived from the skeletal variables of the thirty two mimid and fourteen thrush species in no case connected a turdine thrush with a saxicoline thrush. The links were from Melanoptila to the saxicoline species via Cossypha humeralis and from Dumetella to the turdine species via Catharus ustulata.

The various numerical analyses demonstrate the generalized and intermediate nature of the structural organization of the skeletal systems of several mimid species. They further suggest that the structural organization shared by such diverse mimid and thrush taxa represents a shared primitive, generalized, mimid - thrush condition.

The discriminant function which best separated the thrushes and mimids strongly reflects the characters which have traditionally been used to characterise their skulls relative to one another. These include the narrow descending process of the nasal, the narrow angle between the process and the maxilla, and the sharp lateral indentation of the ectethmoid plate. In addition, several post cranial characters were found to be nearly as influential in establishing the function as were the traditional discriminatory variables. These include the minimum distance between the crests of the ilia, the depth

of the sternal keel and the length of the first phalanx of the third digit.

The graphic picture of phenetic relationships among mimid species, derived from skeletal variables, is of a central core of generalized species, such as Dumetella, Melanoptila, Mimus montanus, and several other Mimus species, from which three specialized groups radiate. One large group begins with Toxostoma rufum and extends to the most structurally derived Toxostoma species, T. redivivum. A second group consists of the two arboreal Margarops species and the third is made up of the Galapagos mockingbirds.

When considered in terms of natural history and the ecological niches occupied by the various mimid species, the correlations of the discriminant functions and the skeletal variables clearly suggests that the discriminant functions are reflecting structural adaptations to these niches. In the case of the Toxostoma thrashers, placement of the species relative to the other mimids by the discriminant functions results from the interactions of a combination of cranial and pelvic limb variables that in previous studies have been shown to be associated with modifications for terrestrial life, especially digging. The Galapagos mockingbirds are also terrestrial but the modifications characteristic of the terrestrial Toxostoma

thrashers are absent. Instead, the modifications are for elongated cranial structures and slender pelvic appendages. Ecologically, the Galapagos mockingbirds do not dig. Rather, they are terrestrial probers, quite appropriate for the broken, often porous substrate of volcanic rock characteristic of the Galapagos Islands. The two Margarops species are separated from all other mimids by their well developed, powerful flight mechanisms, necessary for the arboreal, largely fruit gathering life style (particularly M. fuscus) of these birds. As with the Toxostoma thrashers and the Galapagos mockingbirds, the skeletal structural adaptations accompanying these life styles are clearly reflected in the discriminant functions.

Since the elements of the discriminant functions suggest associations not only among pairs of variables but among groups of variables as well, they are superior to the usual ratios and indices as analytic tools with which to study interrelationships among the variables. They allow more penetrating analyses of relationships between structural modifications and ecological adaptations of skeletal systems among a group of related species. Although the analysis of skeletal structural modifications in terms of ecological adaptations was not a primary objective of this study, the preliminary results suggest that the use of discriminant functions in such studies has great promise. By so efficiently eliminating problems of

correlations, largely size, among the variables, relative shapes of structures can be more accurately evaluated. By working with species as the predetermined groups in the discriminant analysis, shared patterns of skeletal adaptations among taxa and groups of taxa become apparent.

Because the study of mimid phenetic relationships with discriminant functions derived from skeletal variables is so clearly a study of functional relationships among the variables and groups of variables, drawing phylogenetic conclusions directly from the phenetic analyses is unreliable. For example, phylogenetic analysis of the relationships of Margarops and Cinclocerthia relative to other mimids leaves little doubt that Margarops is most closely related to Cinclocerthia. Yet the very different ecological niches occupied by the two taxa and the structural modifications made to exploit these niches caused the discriminant functions to be quite insensitive to the phylogenetic relationship.

On the other hand, the sharing of a complex set of interrelationships among skeletal variables, as reflected by the discriminant functions, can support an hypothesis of phylogenetic relationships. This is true in the case of the Toxostoma thrashers which share the same kinds of adaptations and the same modifications of skeletal structures for digging. It is also true of the

terrestrial, but non digging Galapagos mockingbirds, and the modifications of the two Margarops species for a more aerial lifestyle.

The fact that a species does not share a complex set of interrelationships among a set of variables suggests that it is unlikely to be a member of a group that does exhibit them. This is the case with Mimus montanus relative to the Toxostoma thrashers and is a strong argument against associating the species with that genus. Such an association would have to be supported by strong phylogenetic evidence, as is available to support the association of the structurally quite different genera Cinclocerthia and Margarops.

The pictures of phenetic relationships among the mimids that are given by the external characters and by the skeletal characters are different in a number of details as well as in general associations of taxa. For example, the major groups of mimid taxa link, on the basis of the external character set, through the unspotted Toxostoma thrashers, making these species the focal point of the analysis. The skeletal character set emphasizes the extremely specialized nature of the skeletal structure of these same Toxostoma species and places them on the periphery of the system of taxa. Similarly, the skeletal characters suggest that the two catbirds and several

unspecialized Mimus species are at the phenetic "center" of the system of taxa whereas these same species are widely separated by the external characters.

These results suggest that the two sets of characters are reflecting quite different aspects of the biology of the species. In the case of the skeletal variables, structural adaptation to ecological niches seems to predominate. In the case of the external characters, markings such as spots, eye masks, scutellation, egg shell characters, and patterns of the edgings of tail and wing feathers are important. It is not known what function most of these nonskeletal characters have in the biology of the birds nor if any of them are functionally related.

The obvious incongruence of the external and skeletal character sets suggested that little would be gained by attempts to combine them and indeed might obscure important information clearly expressed by each. Despite these reservations, the Euclidean distance matrix derived from the external character set was combined with the generalized distance matrix derived from the skeletal character set. This method of combining the phenetic information of the two character sets allowed the skeletal information, with most of the obscuring correlations such as size removed, to be combined with the external information. Generalized distances could not be computed

among the species on the basis of the external characters due to the fact that the characters were coded from a subjective evaluation of species and not individuals. This prevented the formation of a pooled within group variance matrix with which to weight in the generation of discriminant functions.

The axes of the combined distance matrix were obtained by principal coordinate procedures. When plotted, the relationships among the taxa and the minimum spanning tree linking them were quite similar to those produced by the skeletal data alone. On the other hand, cluster analysis of the combined distance matrix showed an organization of the taxa not greatly different from that produced by cluster analysis of the taxonomic distance matrix derived from the external data. The different relative influences of the external and skeletal character sets on the two kinds of phenetic analysis were not analyzed.

As the examples discussed above so clearly demonstrate, it is not possible to reliably derive phylogenetic relationships from purely phenetic analyses. The phenetic associations of taxa can, however, be used to support phylogenetic hypotheses produced apart from the phenetic analysis. Hypotheses of relationship produced by phylogenetic analysis are, therefore, the criterion against which suggestions of relationship derived from phenetic

studies must be evaluated.

The phylogenetic analysis performed in this study was carried out following the principles and procedures of Hennig and Brundin. The classification that resulted from the study is a strictly cladistic one. As such it is a faithful and exact expression of the hypotheses of relationships among the taxa that were developed in this study. No attempt was made to reflect phenetic diversity in the classification. That aspect of evolutionary relationships is much better and more precisely given by the graphic summaries of the multivariate studies discussed above. As a result of this approach, the hierarchical ranks of the classification provide no measure of "gaps" and thus differ fundamentally from classical classifications.

For a character to be useful in a cladistic analysis, it is necessary to be able to determine whether it is present in a derived or primitive state. This fundamental requirement quickly eliminated many characters that were used in the phenetic analyses. Since, at any point in a cladistic network, characters used to establish sister group relationships must be derived, only a few were usually available. Large numbers of characters about which no decision could be made as to their primitive or derived state were not useful. Further study of some of these

characters may enable decisions to be made about their primitive - derived nature. At that point the hypotheses of relationship arrived at in this study can be tested against them and, if necessary, modified. Shared primitive characters cannot contribute any information about the relationships of taxa possessing them. The result is again to reduce the number of usable characters at a given point in the phylogenetic analysis.

On the basis of shared derived characters, the mimids are most closely related to the turdine thrushes. Two independent lines of evidence support this hypothesis. First are shared modifications of the temporal - tympanic cranial region which are not found in any other group of Old World insect eaters. Among members of the Old World insect eater family Muscicapidae that share possession of a fully developed double humeral fossa, inflated maxillopalatines, and that lack ossified nasal septa or alinasal turbinals, only the mimids and turdine thrushes share the shift of the posterior end of the supraneatic ridge to a position medial to the dorsal end of the exoccipital wing. The connection between these two structures, if one remains, consists of a broad raised strut.

The second line of evidence supporting the sister group relationship of mimids and turdine thrushes is

derived from egg white protein characters. Only the mimids and turdine thrushes share a closely similar pattern of protein isoelectric points. The pattern of relative densities of these proteins is also often quite similar. In the case of the turdine thrush Catharus fuscescens, it was not possible to distinguish it from mimid species simultaneously analyzed -- most notably Ramphocinclus brachyurus. No other available representatives of various groups of passerines, including wrens, with which the mimids have been associated, were found to share these patterns.

Within the tribe Mimini, a basic division is apparent with the subtribe Cinclocerthiae, which consists of Margarops (including Allenia), Cinclocerthia and Melanotis, forming a sister group to all other mimids except Ramphocinclus brachyurus. This species remains unresolved as to its phylogenetic affinities as it exhibits none of the derived characters used to establish subgroups within the tribe. The cladistic result is a trichotomy at this point in the network.

The subtribe Mimae comprises the majority of mimid species, including the genera Toxostoma, Mimus, Melanoptila, and Dumetella. The species making up the subtribe share (with an occasional secondarily derived exception) two plumage pattern and color characters. Only

in this complex of species among mimids, are found differential shadings of the outer edges of the rectrices. Likewise, only the species in this group exhibit contrastingly colored under tail coverts (cinnamon, rufous, or pinkish buff).

Melanoptila is hypothesized to be the primitive sister taxon of the supergenus Mimus. Only in this monotypic taxon and in the species rich supergenus Mimus are the two scutes at the base of the outer toes fused into a large shield shaped basal scute. This condition is not found in any other group within the Muscicapidae. It has been suggested that Melanoptila is congeneric with Dumetella (Paynter, 1954). The phylogenetic evidence does not support this. Although, diagrammatically, Melanoptila may be placed "next" to Dumetella in the cladistic network, it shares a common ancestor, not with Dumetella, but with the supergenus Mimus and therefore does not form a monophyletic cluster with Dumetella. The primary source of confusion is that both Dumetella and Melanoptila are generalized mimids and therefore are quite similar. Their shared similarities are, however, the result of shared primitive mimid - thrush characteristics and not of shared derived characters that must be discovered if they are to be linked as sister taxa.

The sister group relationship of Toxostoma and Mimus

is hypothesized on the basis of two shared derived egg shell characters (spotted eggs and decreased blue green egg shell color when compared to any other mimids) and the presence in the flank feathers of central, linear streaks. Toxostoma is a monophyletic group as evidenced by the derived pattern of density relationships of the egg white proteins and the loss of the subterminal tomial notch. The tomial notch is primitively characteristic of the Muscicapidae. A third derived condition supporting the hypothesis of shared relationship among Toxostoma species is the peculiar combination of structural adaptations reflected in the discriminant analysis of skeletal characters. No other group of mimid or thrush species studied shares this condition.

Subdivisions of Toxostoma are based largely on pattern characters and follow the groupings of Engels (1940). The primary improvement accomplished in this study was to impose directionality on the associations of Engels' groups. The Toxostoma rufum group, exhibiting the shared derived rust brown color character are considered primitive among the spotted breasted species in as much as the spots are of the primitive lanceolate shape. The progression through the genus is to the wedge-shaped spots of T. cinereum and T. bendirei and finally to the rounded spots of T. curvirostre and T. ocellatum.

The Toxostoma redivivum group, the sickle-billed thrashers are hypothesized to be the primitive sister group to all of the other Toxostoma thrashers, although they are structurally more specialized than any of the others. The sickle-billed thrashers have secondarily lost all spots in any plumage, including the juvenal. This is unusual among mimids or thrushes. These species retain more of the deeper blue egg shell coloration, a primitive trait with regard to the supergenus Mimus. One species, T. dorsale has secondarily lost all egg shell markings.

Sheppard (1973) proposed, in a traditional, subjective phenetic analysis, that the sickle-billed thrashers be recognized as the subgenus Harporhynchus. In this study I have not formally named the cladistic branching points below the "genus" level and therefore do not follow Sheppard.

The genus Mimus consists of the only mimid species to possess white edgings on the lateral borders of the lateral rectrices. The group can be divided into two sections on the basis of the streaked dorsal plumage found in seven of the species (including Mimus montanus). Such streaked dorsal plumage is not found in any other mimid or turdine thrush species that I examined. Among these dorsally streaked species, I was able, on the basis of shared derived characters to determine one further sister group.

This group consists of Mimus longicaudatus, the primitive taxon, and Mimus trifasciatus, the Galapagos mockingbird. M. longicaudatus and M. trifasciatus, alone among mimids, possess a white collar at the base of the neck. Mimus trifasciatus may in reality consist of more than one species. There are four phenetically distinct forms (Swarth, 1931). In as much as they are all allopatric, it is not possible to objectively evaluate the degree of specific separation they have achieved.

Mimus montanus is associated with the dorsally streaked species of Mimus. Based on both the phenetic analysis of skeletal variables and on the phylogenetic analysis of shared derived characters, I can find no justification for the commonly held view that this species is closely related to Toxostoma. It was placed in a nearly precisely intermediate position between Toxostoma and Mimus by the phenetic analysis of external characters. However, if its most Toxostoma like character, the ventral spots in the plumage are eliminated, it would have been shifted to a close association with Mimus. In analyzing the patterns of Mimus species it was discovered that M. gundlachii, another dorsally streaked Mimus species, also exhibits ventral spots in the adult plumage, although they are quite small.

Mimus montanus was found to possess none of the shared derived characters of Toxostoma, not the least of which are the structural modifications reflected by the discriminant function analysis of the skeletal variables and which are exhibited by even the most generalized Toxostoma thrasher, T. rufum. I therefore conclude that M. montanus is, in fact, a ground dwelling mockingbird of the western Sagebrush plains of North America.

Mimodes graysoni has been left as a member of a trichotomy with Toxostoma and Mimus. This course was necessary in as much as shared derived characters were not discovered with which to more precisely associate the species relative to the other two groups. A number of characters could not be evaluated because of lack of material. When such is available, this trichotomy will probably be resolved.

Donacobius atricapillus was found to possess none of the derived conditions that were used in this study to form even the broadest associations of thrush and mimid taxa. This species differs fundamentally in its cranial and postcranial skeletal organization, its natural history, and its juvenal characters. Within the context of this study, I was not able to determine with what ten primaries, insect eating passerine group to associate it. Donacobius atricapillus must therefore be considered incertae sedis

pending the discovery of evidence to positively link it, on the basis of shared derived characters, with some other group.

The phenetic and phylogenetic analyses carried out in this study are generally compatible. The gross structure of relationships suggested by the phenetic analyses and, frequently, specific relationships are similar to those developed in the cladistic analysis. Exceptions to these generalizations are not unusual, however. These exceptions include the position of the two catbirds relative to each other and to other mimids; the relationship of Margarops and Cinclocerthia; the linking of these two genera to continental taxa; and the position of Mimus montanus relative to Toxostoma and Mimus. The phenetic analysis of the skeletal variables also suggested that the mimids have close affinities to some saxicoline thrushes whereas the phylogenetic analysis demonstrated that the mimids are in reality more closely related to the turdine thrushes. In each of these cases, the cladistic analysis made it possible to clearly determine relationships that were otherwise submerged in and obscured by the general mass of phenetic information.

Phenetic and phylogenetic analysis in reality serve different purposes. Phenetic analyses, using multivariate statistical techniques, especially various ordination

procedures, are particularly useful in studies of relationships among the taxa in terms of the interactive effects of large numbers of variables. In the case of skeletal variables, these techniques would appear to be useful in studies of structural adaptation to different ecological niches. The ease with which large numbers of variables can be simultaneously examined for interrelationships is especially valuable here. Phylogenetic analysis, in contrast, by concentrating on a carefully chosen set of characters which are analyzed in a rigorously logical manner, allows the formulation of precise hypotheses of phylogenetic relationships. It is therefore possible to cut through the conflicting wealth of phenetic detail which, as in the instances mentioned above, prevent clear preception of phylogenetic relationships in the phenetic studies.

Points at which the results of the phenetic analyses and phylogenetic analyses differ are particularly interesting. They often suggest further studies to determine the shifts in the biology of the species involved that caused the phenetic characters to suggest relationships that contradict the results of the phylogenetic analysis. In the present study, for example, the phenetic analysis of skeletal variables suggests that T. ocellatum, a species whose natural history is poorly known, has structurally shifted towards the sickle-billed

thrashers, species with which it is no more than marginally sympatric. The phylogenetic analysis indicates that T. ocellatum is the sister species of T. curvirostre. It would be interesting indeed to study the ecology of T. ocellatum and learn if the species has shifted to exploit some aspects of the sickle-billed thrasher niche, as the structural shifts suggest.

In that phenetic and phylogenetic studies are complementary, both kinds of analysis are needed and must be carried out if a reasonably comprehensive understanding of evolutionary relationships among taxa and groups of taxa is to be achieved. The phenetic studies permit quantification, in terms of correlation and measures of distance, of the diversity of taxa. Phylogenetic studies provide the hypotheses of historical evolution which are essential references when evaluating the results of comparative studies of any aspect of the biology of taxa and groups of taxa.

APPENDIX

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APPENDIX TABLE 1

POSITION DATA FROM EGG WHITE PROTEINS FROM 13 SPECIES OF MIMIDAE

	POS 1	POS 2	POS 3	POS 4	POS 5	POS 6	POS 7	POS 8	POS 9	ADJ*
DUMETEL	18.0	24.5	30.5	38.0	48.0	57.5	65.0	71.5	74.5	+ .5
MELANOP	18.5	24.5	30.0	37.5	47.5	57.5	65.0	72.5	75.5	0
MELANOT	20.0	25.0	30.0	36.5	46.0	57.0	65.5	72.0	75.0	0
MIM POL	18.5	24.5	30.5	38.5	49.5	60.0	68.0	74.0	77.0	+ .5
MIM GIL	18.5	25.0	31.0	39.0	49.5	59.5	67.5	74.0	77.0	+ 1.0
MIM SAT	16.5	21.0	30.0	37.5	48.0	58.0	66.5	74.0	76.0	0
TOX RUF	18.0	23.5	30.5	37.5	46.5	56.5	65.5	71.5	76.0	+ .5
TOX CUR	17.5	23.0	30.0	37.5	47.0	57.5	65.0	71.5	76.0	0
TOX LEC	17.5	23.0	30.5	38.0	47.5	57.5	66.0	71.5	76.5	+ .5
RAMPHOC	20.0	27.5	32.0	40.0	51.0	61.0	69.0	74.5	78.0	+ 2.0
CINCLOC	18.0	24.5	31.0	39.0	49.5	60.0	68.0	74.0	77.0	+ 1.0
ALLENIA	20.0	24.5	30.5	39.0	49.5	59.5	67.5	73.5	76.5	+ .5
DONACOB	20.0	26.0	31.5	39.5	50.5	61.5	68.5	74.5	77.0	+ 1.5

DENSITY DATA FROM EGG WHITE PROTEINS FROM 13 SPECIES OF MIMIDAE

	DEN 1	DEN 2	DEN 3	DEN 4	DEN 5	DEN 6
DUMETEL	1	2	3	3	3	2
MELANOT	1	2	3	2	2	2
MELANOP	1	2	3	2	1	2
MIM POL	1	2	3	2	2	2
MIM GIL	1	2	3	2	2	1
MIM SAT	1	2	3	2	2	1
TOX RUF	1	3	3	2	2	1
TOX LEC	2	3	3	2	2	1
RAMPHOC	1	2	3	3	3	2
CINCLOC	1	2	3	3	3	2
ALLENIA	1	2	3	3	3	2
DONACOB	1	2	2	1	1	2

* Values used to adjust position measurements to reflect actual relative positions of the nominal 30 mm. reference band, POS 3, among the species.

APPENDIX TABLE 2

Color codes for 34 mimid species
(See table 4.1 for interpretation of characters and codes.)

	DUMETEL	MYLANOP	HEL CAP	HEL RYP	HIM POL	HIM GIL	HIM GUN	HIM THE	HIM LON	HIM SAT	HIM PAT	HIM TRI
CRN GRY1	6	6	6	6	5	5	5	5	5	5	5	5
CRN GRY2	0	0	3	4	0	3	4	4	3	4	4	4
CRN BKN	0	0	0	0	0	0	3	5	2	5	2	3
CRN BLU	0	0	3	3	0	0	0	0	0	0	0	0
CRN INT	0	0	3	3	0	0	1	2	1	1	1	1
PAK GRY1	5	6	5	5	5	4	5	5	5	5	5	5
PAK GRY2	0	0	0	0	0	0	4	4	3	4	4	0
PAK BRN	0	0	0	0	0	0	3	6	1	5	3	3
PAK BLU	0	0	3	3	0	0	0	0	0	0	0	0
PAK INT	0	0	2	2	0	0	1	1	1	1	1	1
PHP GRY1	5	6	5	5	5	3	5	5	5	5	4	4
PHP GRY2	0	0	0	0	0	0	4	4	3	4	0	0
PHP BRN	0	0	0	0	0	0	5	4	2	4	2	4
PHP BLU	0	0	3	3	0	0	0	0	0	0	0	0
PHP INT	0	0	2	2	0	0	1	1	1	1	2	2
THR GRY1	4	6	6	1	2	1	2	1	1	1	1	1
THR GRY2	0	0	2	0	0	0	0	0	0	0	0	0
THR BRN	0	0	0	0	0	0	0	0	0	2	0	0
THR BLU	0	0	3	0	0	0	0	0	0	0	0	0
THR INT	0	0	3	0	0	0	0	0	0	1	0	0
BRE GRY1	5	6	6	1	4	3	3	3	2	3	2	2
BRE GRY2	0	0	0	0	0	0	4	4	4	0	4	3
BRE BRN	0	0	0	0	0	0	2	3	0	2	3	3
BRE BLU	0	0	3	0	0	0	0	0	0	0	0	0
BRE INT	0	0	2	0	0	0	1	3	0	2	2	1
CPS GRY1	5	6	6	6	3	1	1	3	1	1	1	1
CPS GRY2	0	0	0	0	0	0	5	0	0	0	0	0
CPS BRN	4	0	0	0	1	2	1	2	0	2	2	2
CPS BLU	0	0	3	3	0	0	3	0	0	0	0	0
CPS INT	3	0	1	1	1	2	4	1	0	2	2	1
FLN GRY1	5	6	6	6	3	2	3	2	1	2	2	1
FLN GRY2	0	0	0	0	5	5	5	5	5	5	5	0
FLN BRN	0	0	0	0	1	1	3	3	2	2	3	3
FLN BLU	0	0	3	3	0	0	0	0	0	0	0	0
FLN INT	0	0	2	2	1	1	1	3	1	3	3	1
WNG GRY1	6	6	6	6	6	6	5	6	5	6	6	6
WNG GRY2	5	0	0	0	2	1	1	1	1	1	1	1
WNG BRN	0	0	0	0	3	0	3	3	2	3	3	3
WNG BLU	0	0	3	3	0	0	0	0	0	0	0	0
WNG INT	0	0	1	1	1	0	2	3	1	2	1	3
RFC GRY1	6	6	6	6	6	6	5	6	5	6	6	6
RFC GRY2	4	0	0	0	1	1	1	1	1	1	1	1
RFC BRN	0	0	0	0	0	0	3	3	2	3	0	0
RFC BLU	0	0	3	3	0	0	0	0	0	0	0	0
RFC INT	0	0	1	1	0	0	1	2	1	1	0	0

APPENDIX TABLE 2 CONTINUED

Color codes for 34 mimic species
(See table 4.1 for interpretation of characters and codes.)

	BIN DOR	NES TRI	NES HEL	NES PAR	NES PAC	MINODES	OREOSCO	TOX RUP	TOX LON	TOX GUT	TOX CIN	TOX BFW
CRW GRY1	5	6	5	6	5	5	5	5	5	5	5	4
CRW GRY2	4	1	3	3	3	4	4	4	4	4	4	3
CRW BRN	3	2	1	2	2	5	2	4	5	4	5	2
CRW BLD	0	0	0	0	0	0	0	0	0	0	0	0
CRW INT	2	1	1	1	1	2	1	2	1	2	2	1
DAK GRY1	5	6	5	5	5	5	5	4	5	5	5	4
DAK GRY2	0	4	3	4	4	0	4	0	0	0	0	0
DAK BRN	5	5	3	3	2	5	2	4	4	4	5	2
DAK BLD	0	0	0	0	0	0	0	0	0	0	0	0
DAK INT	2	1	1	1	1	2	1	3	1	3	2	1
RMP GRY1	3	5	5	5	5	5	4	4	4	5	5	3
RMP GRY2	0	3	3	3	3	0	0	0	0	0	0	0
RMP BRN	4	1	3	3	1	5	1	4	4	4	5	2
RMP BLD	0	0	0	0	0	0	0	0	0	0	0	0
RMP INT	2	1	2	1	1	2	1	3	1	3	2	1
THR GRY1	1	1	1	1	1	2	1	1	1	1	1	1
THR GRY2	0	0	0	0	0	0	0	0	0	0	0	0
THR BRN	2	0	0	0	0	0	0	2	0	0	0	2
THR BLD	0	0	0	0	0	0	0	0	0	0	0	0
THR INT	1	0	0	0	0	0	0	2	0	0	0	1
BRE GRY1	3	2	2	1	2	3	2	1	1	1	2	3
BRE GRY2	0	5	3	3	5	0	5	5	6	6	5	4
BRE BRN	2	0	3	0	2	3	2	2	2	2	2	2
BRE BLD	0	0	0	0	0	0	0	0	0	0	0	0
BRE INT	1	0	1	0	1	1	2	3	1	2	1	2
CPS GRY1	1	2	1	1	1	2	1	2	1	1	2	3
CPS GRY2	0	0	0	0	0	4	4	5	5	0	0	0
CPS BRN	1	0	0	0	0	3	2	2	1	2	2	2
CPS BLD	0	0	0	0	0	0	0	0	0	0	0	0
CPS INT	1	0	0	0	0	2	2	2	1	1	2	3
PLW GRY1	2	2	2	2	1	3	2	2	1	1	1	2
PLW GRY2	0	5	5	5	5	5	5	5	5	5	5	3
PLW BRN	3	1	3	1	2	3	2	2	2	1	2	2
PLW BLD	0	0	0	0	0	0	0	0	0	0	0	0
PLW INT	3	1	1	1	1	2	2	3	1	1	2	2
WNG GRY1	6	6	6	6	6	5	5	5	5	5	4	4
WNG GRY2	1	1	1	1	1	3	1	1	1	1	2	3
WNG BRN	3	3	2	3	2	5	2	4	4	4	3	2
WNG BLD	0	0	0	0	0	0	0	0	0	0	0	0
WNG INT	3	1	2	1	2	2	1	3	2	3	2	1
REC GRY1	6	6	6	6	6	5	5	4	4	5	6	5
REC GRY2	1	1	1	1	1	3	1	1	2	2	2	2
REC BRN	0	3	2	3	2	5	3	4	4	4	3	3
REC BLD	0	0	0	0	0	0	0	0	0	0	0	0
REC INT	0	1	1	1	1	3	1	3	1	3	2	1

APPENDIX TABLE 2 CONTINUED

Color codes for 34 mimid species
(See table 4.1 for interpretation of characters and codes.)

	TOX OCE	TOX CUR	TOX LEC	TOX RED	TOX DOR	CINCLOC	RANPHOC	MARGARO	ALLENIA	DONACOB
CRW GRY1	5	5	3	5	4	6	6	6	6	6
CRW GRY2	4	4	0	0	0	0	5	5	0	0
CRW BRN	3	3	2	5	2	5	6	6	6	0
CRW BLU	0	0	0	0	0	0	0	0	0	0
CRW INT	2	1	1	1	1	1	2	2	2	0
BAK GRY1	5	5	3	5	4	5	6	6	6	6
BAK GRY2	0	0	0	0	0	0	0	5	0	0
BAK BRN	5	2	2	5	2	4	6	5	6	6
BAK BLU	0	0	0	0	0	0	0	0	0	0
BAK INT	1	1	2	1	1	1	2	2	2	1
RMP GRY1	5	4	3	5	4	4	6	6	6	3
RMP GRY2	0	0	0	0	0	0	0	1	1	0
RMP BRN	5	3	2	5	1	4	6	6	6	3
RMP BLU	0	0	0	0	0	0	0	0	0	0
RMP INT	1	1	1	1	1	2	2	2	2	3
THR GRY1	1	1	1	1	1	3	1	5	5	1
THR GRY2	0	0	0	0	0	0	0	1	1	0
THR BRN	0	0	0	2	0	2	0	5	6	2
THR BLU	0	0	0	0	0	0	0	0	0	0
THR INT	0	0	0	2	0	1	0	2	2	3
BRE GRY1	1	3	4	4	4	4	1	4	5	1
BRE GRY2	6	4	0	2	2	0	0	1	2	0
BRE BRN	3	2	1	2	2	4	0	5	6	2
BRE BLU	0	0	0	0	0	0	0	0	0	0
BRE INT	1	1	1	2	1	1	0	2	2	4
CBS GRY1	2	2	2	3	3	3	1	5	5	1
CBS GRY2	6	0	0	0	0	0	6	1	1	0
CBS BRN	2	2	2	2	4	4	6	5	6	2
CBS BLU	0	0	0	0	0	0	0	0	0	0
CBS INT	1	2	3	4	3	1	1	2	2	3
PLN GRY1	1	3	3	4	4	4	6	5	5	1
PLN GRY2	5	4	0	0	0	0	0	1	1	5
PLN BRN	3	2	2	2	2	4	6	5	5	2
PLN BLU	0	0	0	0	0	0	0	0	0	0
PLN INT	2	1	2	3	1	2	2	2	2	3
UNG GRY1	5	4	3	6	6	6	6	6	6	6
UNG GRY2	1	1	2	1	0	2	0	1	0	1
UNG BRN	5	5	2	5	2	4	6	5	6	6
UNG BLU	0	0	0	0	0	0	0	0	0	0
UNG INT	2	1	2	2	2	2	1	2	1	1
REC GRY1	6	6	5	6	6	6	6	6	6	6
REC GRY2	1	1	2	3	3	0	0	1	1	1
REC BRN	5	5	3	4	4	4	6	5	6	6
REC BLU	0	0	0	0	0	0	0	0	0	0
REC INT	2	1	1	1	1	2	1	2	1	1

APPENDIX TABLE 3

Pattern codes for 34 mimid species
(See table 4.3 for interpretation of characters and codes.)

	DURETEL	NELANOP	NEL CAE	NEL HYP	NIN POL	NIN GIL	NIN GUN	NIN THE	NIN LOW	NIN SAT	NIN PAT	NIN TRI
CRO ST	0	0	2	2	1	2	3	2	3	3	2	2
CRO SC	0	0	0	0	0	0	0	0	0	0	0	0
BAK ST	0	0	0	0	0	0	2	1	0	0	1	0
BAK SC	0	0	0	0	0	0	0	0	1	3	0	0
RUMP ST	0	0	1	0	0	0	1	1	0	2	0	0
RUMP SC	0	0	0	0	0	0	0	0	3	0	0	0
BRES ST	0	0	1	0	0	0	0	0	0	0	0	0
BRES SC	0	0	0	0	0	0	1	1	2	1	1	1
BRES SP	0	0	0	0	0	0	0	0	0	0	0	0
CRISS ST	0	0	0	0	0	0	2	0	0	0	0	0
CRISS SC	0	0	0	0	0	0	0	0	0	0	0	0
PLANK ST	0	0	0	0	0	1	3	3	2	2	1	0
PLANK SC	0	0	0	0	0	0	0	0	0	0	0	0
PLANK SP	0	0	0	0	0	0	0	0	0	0	0	0
PLANK BR	0	0	0	0	0	0	0	0	0	0	0	0
SHAPE SP	0	0	0	0	0	0	1	0	0	0	0	0
SUPCILLN	1	0	0	0	1	2	2	3	3	3	3	3
MASK	0	0	3	3	1	2	2	3	3	3	3	3
AURIC ST	0	0	0	0	2	1	1	1	3	1	1	2
AURIC AR	0	0	3	3	1	1	2	2	2	1	1	2
WHISKER	0	0	0	0	0	0	3	3	3	1	0	1
BRES BWD	0	0	0	0	2	1	2	2	3	1	1	2
COLLAR	0	0	0	0	0	0	0	0	2	0	0	1
PORB STP	0	0	3	3	1	1	0	3	3	3	3	3
PRIM EDG	1	0	2	2	1	1	1	1	2	1	1	1
PRIM TIP	0	0	0	0	1	1	1	1	2	1	1	1
SEC EDG	2	0	3	3	2	2	1	1	1	2	1	1
SEC TIP	0	0	0	0	2	2	2	2	2	2	2	5
WNG BR1	0	0	0	0	3	3	3	2	3	3	3	2
WNG BR2	0	0	0	0	3	3	3	2	3	3	3	2
PRIM COV	0	0	0	0	6	2	1	2	4	2	3	6
IN RNG	0	0	0	0	3	2	1	1	2	1	2	3
REC1 EDG	3	0	0	0	4	3	1	1	2	2	1	4
REC1 TIP	0	0	0	0	0	4	2	3	3	3	3	5
REC2-4ED	1	0	0	0	5	1	1	0	1	1	1	5
REC2-4TP	2	0	0	0	3	3	2	2	3	3	2	5
REC4-6TP	0	0	0	0	1	1	1	1	2	2	1	1
RECEDCON	1	0	0	0	3	3	3	3	3	3	3	3
RECTPCON	0	0	0	0	3	3	3	3	3	3	3	3

APPENDIX TABLE 3 CONTINUED

Pattern codes for 34 mimid species
(See table 4.3 for interpretation of characters and codes.)

	MIM DOR	NES TRI	NES NEL	NES PAR	NES NAC	MIMODES	OREOSCO	TOX RUF	TOX LOW	TOX GUT	TOX CIN	TOX BEW
CRO ST	1	0	3	0	3	1	1	1	2	1	1	0
CRO SC	0	2	0	2	0	0	0	0	0	0	0	0
BAK ST	0	0	0	0	0	0	2	0	0	0	0	0
BAK SC	0	1	2	2	2	0	0	0	0	0	0	0
KOHP ST	0	0	2	2	0	0	0	0	0	0	0	0
KOHP SC	0	1	0	0	3	0	0	0	0	0	0	0
BRES ST	0	0	0	0	0	0	0	0	0	0	0	0
BRES SC	0	2	2	0	3	0	0	0	0	0	0	0
BRES SP	0	0	0	0	0	0	3	3	3	3	3	2
CRIS ST	0	0	0	0	0	2	0	1	0	0	0	0
CRIS SC	0	0	0	0	0	0	0	0	4	0	0	0
PLANK ST	0	3	3	3	3	3	3	3	3	3	3	1
PLANK SC	0	0	0	0	0	0	0	0	0	0	0	0
PLANK SP	0	0	0	0	0	0	0	0	0	0	0	0
PLANK BR	0	0	0	0	0	0	0	0	0	0	0	0
SHAPE SP	0	0	0	0	0	0	2	1	1	1	2	2
SUPCILLN	3	0	3	3	3	0	1	1	0	1	0	1
NASK	3	1	3	3	3	1	0	0	0	0	0	0
AURIC ST	1	0	1	1	2	1	2	2	2	1	2	2
AURIC AR	1	3	3	3	3	1	2	1	1	1	1	1
WHISKER	0	3	3	0	3	2	3	3	2	3	3	3
BRES BND	1	3	1	1	1	0	0	0	0	0	0	1
COLLAR	0	1	3	3	3	0	0	0	0	0	0	0
PORB STP	3	0	3	3	2	0	0	0	0	0	0	0
PRIP EDG	0	1	1	1	1	1	1	3	3	3	1	1
PRIP TIP	1	1	1	1	1	1	1	0	0	0	1	1
SEC EDG	2	1	1	1	2	1	1	3	3	3	0	1
SEC TIP	2	2	2	2	2	1	2	1	1	1	1	2
WNG BR1	2	3	3	3	3	2	3	3	3	3	1	2
WNG BR2	3	3	3	3	3	2	3	3	3	3	1	2
PRIP COV	5	1	2	2	1	1	1	0	0	0	0	1
IN WNG	3	1	1	1	1	0	0	1	0	1	0	0
REC1 EDG	4	1	1	1	1	1	1	0	0	0	3	3
REC1 TIP	5	2	3	3	2	2	2	2	1	1	2	2
REC2-NED	5	1	1	1	1	1	1	0	0	0	0	1
REC2-STP	5	2	2	2	1	1	2	1	1	1	1	2
REC4-6TP	1	1	1	1	1	1	1	0	0	0	0	0
PECTPCON	3	3	3	3	3	1	3	0	0	0	2	2
LECTPCON	3	3	3	3	3	1	3	2	2	2	3	3

APPENDIX TABLE 3 CONTINUED

Pattern codes for 34 mimid species
(See table 4.3 for interpretation of characters and codes.)

	TOX OCE	TOX CUB	TOX LEC	TOX RED	TOX DOR	CINCLOC	RANPHOC	MARGARO	ALLENIA	DONACOB
CRO ST	1	1	0	1	0	1	1	3	0	0
CRO SC	0	0	0	0	0	0	0	0	0	0
BAK ST	0	0	0	0	0	0	0	0	0	0
BAK SC	0	0	0	0	0	0	0	3	0	0
RUNP ST	0	0	0	0	0	0	0	0	0	0
RUNP SC	0	0	0	0	0	0	0	1	1	0
BRES ST	0	0	0	0	0	0	0	0	0	0
BRES SC	0	0	0	1	0	0	0	4	2	0
BRES SP	3	2	0	0	0	0	0	0	0	0
CRISS ST	0	0	0	0	0	0	0	0	0	0
CRISS SC	4	4	0	0	0	0	4	4	4	0
PLANK ST	0	0	0	0	0	0	0	0	0	0
PLANK SC	0	0	0	0	0	0	3	2	0	0
PLANK SP	3	1	0	0	0	0	0	0	0	0
PLANK BR	0	0	0	0	0	0	0	0	0	3
SHAPE SP	3	3	0	0	0	0	0	0	0	0
SUPCILLN	1	1	0	1	0	1	0	0	0	0
HASK	0	0	1	2	1	3	2	1	1	0
AURIC ST	1	1	1	2	2	0	0	0	0	0
AURIC AB	1	1	2	2	2	3	2	0	0	0
WHISKER	3	3	3	3	3	0	0	0	0	0
BRES BWD	0	2	1	2	1	1	0	0	0	0
COLLAR	0	0	0	0	0	0	0	0	0	0
PORB STP	0	0	2	2	1	3	2	0	0	0
PRIM EDG	1	1	1	1	0	2	0	0	0	0
PRIM TIP	0	0	1	0	0	0	0	0	0	0
SEC EDG	0	0	1	0	0	3	0	0	0	0
SEC TIP	0	1	1	1	0	1	0	2	1	0
WNG BR1	2	1	2	2	0	1	0	2	0	0
WNG BR2	2	1	1	1	0	0	0	1	0	0
PRIM COV	0	0	1	1	0	0	0	0	0	0
IN WNG	0	0	0	0	0	0	0	0	0	3
REC1 EDG	0	3	3	3	3	0	0	0	0	0
REC1 TIP	1	2	2	2	2	1	0	3	3	4
REC2-4ED	0	0	0	0	0	0	0	0	0	0
REC2-4TP	1	2	1	1	1	0	0	2	2	3
REC4-6TP	0	1	0	0	1	0	0	1	1	1
RECEDCOV	0	2	2	1	1	0	0	0	0	0
RECTPCOV	3	3	2	1	1	1	0	3	3	3

APPENDIX TABLE 4
Miscellaneous nonskeletal characters for 34 mimid species
(See chapter 4 for interpretation of characters and codes.)

	DURETEL	HELANOP	MEL CAE	MEL HYP	MIS POL	MIS GIL	MIS GUM	MIS THE	MIS LOW	MIS SAT	MIS PAT	MIS TRI
EYE COLR	1	1	2	2	3	3	3	3	3	3	3	3
B NOTCH	2	3	3	3	2	2	2	1	1	1	1	1
B CURV	1	1	1	1	2	2	2	2	2	2	2	2
TOE SCUT	2	1	2	2	1	1	1	1	1	1	1	1
TAR SCUT	1	1	2	2	3	3	3	3	3	3	3	3
WING SHP	2	1	2	1	2	2	2	2	2	2	2	2
TAIL SHP	2	1	3	3	2	2	2	3	3	3	3	3
RICT BRI	3	1	2	3	3	3	3	3	3	3	3	3
EGG COLR	4	3	3	3	1	1	1	1	1	1	1	1
EGG SPTS	0	0	0	0	1	1	1	1	1	1	1	1
WEST	2	2	2	2	2	2	2	2	2	2	2	2
YNG SPOT	2	0	0	1	2	2	2	2	2	2	2	2
GRND/ARB	2	2	1	1	1	1	1	1	1	1	1	1

	MIS DOR	MIS TRI	MIS MEL	MIS PAR	MIS HAC	MIS RODES	OREOSCO	TOX RUP	TOX LOW	TOX GUT	TOX CIN	TOX BEN
EYE COLR	3	3	3	3	3	1	3	3	3	3	3	3
B NOTCH	0	1	1	1	1	1	1	0	0	0	0	0
B CURV	2	2	2	2	2	2	2	1	2	3	3	2
TOE SCUT	1	1	1	1	1	1	1	1	1	1	1	1
TAR SCUT	3	3	3	3	3	3	2	2	2	2	3	2
WING SHP	2	2	2	2	2	1	3	1	1	1	2	2
TAIL SHP	3	3	3	3	3	3	1	3	3	3	3	3
RICT BRI	3	2	2	2	2	3	3	3	3	3	2	2
EGG COLR	1	1	1	1	1	9	2	1	1	1	1	1
EGG SPTS	1	1	1	1	1	9	1	1	1	1	1	1
WEST	2	2	2	2	2	9	2	2	2	2	2	2
YNG SPOT	2	2	2	2	2	9	2	2	2	2	2	2
GRND/ARB	1	1	1	1	1	1	1	1	1	1	1	1

	TOX OCE	TOX CUR	TOX LEC	TOX RED	TOX DOR	CINCLOC	RANPHOC	MARGARO	ALLENIA	DONACOB
EYE COLR	3	3	1	1	3	3	2	3	3	3
B NOTCH	0	0	0	0	0	3	3	3	3	2
B CURV	3	3	4	4	4	1	1	1	2	2
TOE SCUT	1	1	1	1	1	2	2	2	2	2
TAR SCUT	3	3	3	3	3	1	1	1	1	3
WING SHP	1	2	2	1	1	1	2	2	3	1
TAIL SHP	3	3	3	3	3	1	1	1	1	4
RICT BRI	1	2	2	2	2	1	3	3	1	3
EGG COLR	2	2	2	3	3	3	3	3	3	5
EGG SPTS	1	1	1	1	0	0	0	0	0	2
WEST	2	2	2	2	2	3	2	4	3	1
YNG SPOT	2	2	0	0	0	1	9	1	1	0
GRND/ARB	1	1	1	1	1	3	1	3	3	4

APPENDIX TABLE 5

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

STATISTICS FOR SETS MARKED *** HAVE BEEN UNWEIGHTED										- STATISTICAL SUMMARY -									
SET #	SET DESCRIPTION	SET N	V 55 N	TRUNK-L MEAN	S D	C V	V 8 N	CRAN-L1 MEAN	S D	C V	V 9 N	CRAN-H MEAN	S D	C V	V 10 N	CRAN-W1 MEAN	S D	C V	
1	DUMETELLA CAPOLINENSIS	25	23	17.61	0.48	2.7	24	10.42	0.21	2.0	24	13.67	0.33	2.4	23	16.36	0.30	1.8	
2	MELANOPTILA FLABRIROSTRIS	11	11	17.44	0.60	3.5	11	10.37	0.28	2.7	11	13.55	0.46	3.4	11	16.51	0.30	1.8	
34*	MELANOTOS	9	9	20.65	0.94	4.5	9	11.93	0.20	1.7	9	15.12	0.35	2.3	9	17.96	0.57	3.2	
35*	MIMUS	58	51	20.77	0.86	4.1	54	12.14	0.34	2.8	54	15.15	0.37	2.4	55	18.42	0.46	2.5	
36*	NESOMIMUS	16	15	20.05	0.56	2.8	16	12.19	0.40	3.3	16	14.73	0.39	2.6	15	18.44	0.52	2.8	
17	MIMODES GRAYSONI	1	1	21.60	0.0	0.0	1	12.80	0.0	0.0	1	14.80	0.0	0.0	1	19.50	0.0	0.0	
18	OREOSCOPTES MONTANUS	10	9	18.90	0.55	2.9	10	11.71	0.26	2.4	10	14.69	0.42	2.9	9	18.28	0.33	1.8	
37*	TOXOSTOMA	66	63	20.89	0.79	3.8	66	13.18	0.36	2.7	65	16.14	0.42	2.6	66	19.50	0.52	2.7	
29	CINCLORHYNCHUS RUFICAUDA	17	16	20.82	0.93	4.5	16	13.27	0.42	3.2	16	12.96	0.35	2.7	17	18.58	0.54	2.9	
30	RAMPHOCINCLUS BRACHYRUS	2	2	19.45	0.92	4.7	2	11.90	0.42	3.6	2	14.95	0.07	0.5	2	17.55	0.07	0.4	
31	CONACCIUS ATRICAPILLUS	8	8	20.09	1.08	5.4	7	10.94	0.63	5.8	8	13.36	0.41	3.1	7	16.76	0.96	5.7	
32	ALLHIA FUSCA	18	16	21.25	0.69	3.2	18	11.87	0.28	2.3	17	14.39	0.24	1.7	18	18.00	0.32	1.8	
33	MARGAROPS FUSCATUS	12	12	25.04	0.84	3.4	12	13.67	0.44	3.2	12	16.67	0.46	2.7	12	21.56	1.30	6.0	
3	MELANOTIS CAFFULI SCENS	5	5	20.48	1.13	5.5	5	11.92	0.24	2.0	5	15.24	0.27	1.8	5	17.92	0.72	4.0	
4	MELANOTIS HYPOLEUCUS	4	4	20.82	0.59	2.8	4	11.95	0.13	1.1	4	15.00	0.44	2.9	4	18.00	0.27	1.5	
5	MIMUS POLYGLOTTOS	22	19	19.79	0.84	4.3	21	11.41	0.38	3.4	21	14.27	0.37	2.6	21	17.29	0.44	2.5	
6	MIMUS GILVUS	4	9	20.23	0.81	4.0	8	11.70	0.35	3.0	9	14.59	0.40	2.7	9	17.69	0.64	3.6	
7	MIMUS GUNLACHII	5	3	22.30	1.50	6.7	4	12.32	0.19	1.5	4	15.45	0.37	2.4	4	19.17	0.17	0.9	
8	MIMUS THENEA	4	3	21.67	0.75	3.5	4	12.45	0.31	2.5	4	15.45	0.26	1.7	4	19.10	0.14	0.7	
9	MIMUS LEUCICAUDATUS	7	7	21.71	0.96	4.4	7	12.63	0.28	2.2	7	15.84	0.43	2.7	7	19.20	0.56	2.9	
10	MIMUS SATURNINUS	4	3	21.77	0.40	1.9	3	12.40	0.44	3.5	3	15.93	0.40	2.5	3	19.17	0.23	1.2	
11	MIMUS PATAGONICUS	4	4	19.62	0.65	3.3	4	12.25	0.17	1.4	3	15.30	0.00	0.0	4	18.47	0.46	2.5	
12	MIMUS TRIURUS	3	3	19.03	0.57	3.0	3	11.97	0.21	1.7	3	14.40	0.26	1.8	3	17.27	0.21	1.2	
13	MIMUS DOFFALIS							THERE ARE NO SPECIMENS IN THIS SET											
14	NESOMIMUS TRIFASCIATUS	3	3	20.00	0.36	1.8	3	12.50	0.46	3.7	3	15.47	0.38	2.4	3	19.10	0.36	1.9	
15	NESOMIMUS MACDONALDI	5	5	20.98	0.68	3.2	5	12.44	0.23	1.9	5	15.06	0.34	2.2	5	18.70	0.46	2.5	
16	NESOMIMUS PARVULUS	8	7	19.17	0.53	2.7	8	11.62	0.45	3.9	8	13.65	0.41	3.0	7	17.53	0.60	3.5	
19	TOXOSTOMA RUFUM	14	13	21.68	0.75	3.5	14	12.56	0.35	2.8	14	15.65	0.46	2.9	14	18.86	0.51	2.7	
20	TOXOSTOMA LONGIROSTRE	4	4	21.62	0.31	1.4	4	12.97	0.22	1.7	4	15.72	0.35	2.2	4	19.12	0.33	1.7	
21	TOXOSTOMA GUTTATUM	6	6	18.85	0.54	2.8	6	12.05	0.45	4.0	6	14.75	0.27	1.8	6	17.67	0.31	1.8	
22	TOXOSTOMA CINEREUM	1	1	19.70	0.0	0.0	1	12.80	0.0	0.0	1	15.70	0.0	0.0	1	19.80	0.0	0.0	
23	TOXOSTOMA FENNIPPEI	3	3	20.40	0.35	1.7	3	13.13	0.29	2.2	3	15.73	0.21	1.3	3	20.43	0.47	2.3	
24	TOXOSTOMA OCELLATUM	2	2	22.45	0.49	2.2	2	13.60	0.00	0.0	2	17.40	0.42	2.4	2	20.95	0.07	0.3	
25	TOXOSTOMA CURVIROSTRE	20	18	22.19	1.03	4.7	20	13.89	0.34	2.8	19	16.53	0.49	3.0	20	20.71	0.68	3.3	
26	TOXOSTOMA LEONTEI	4	4	19.75	0.53	2.7	4	13.05	0.17	1.3	4	16.30	0.24	1.5	4	18.87	0.35	1.9	
27	TOXOSTOMA RECIVIVUM	7	7	23.39	0.87	3.7	7	14.27	0.34	2.4	7	17.46	0.40	2.3	7	20.34	0.40	2.0	
28	TOXOSTOMA DOPSALF	5	5	19.96	0.32	1.6	5	13.46	0.35	2.6	5	16.14	0.30	1.9	5	18.28	0.33	1.8	
	GRAND VALUES	253	236	20.58			246	12.38			245	15.19			245	18.65			

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 11 N	CRAN-W2 MEAN	S D	C V	V 12 N	CRAN-W3 MEAN	S D	C V	V 13 N	CRAN-L2 MEAN	S D	C V	V 14 N	PMAX-L1 MEAN	S D	C V
1	DUMETELLA CAROLINENSIS	25	23	15.96	0.29	1.8	23	16.32	0.27	1.7	24	22.34	0.40	1.8	24	18.62	0.71	3.8
2	MELANOPTILA GLABRIPSTRIS	11	11	16.74	0.37	2.3	11	16.69	0.39	2.3	11	22.55	0.59	2.6	11	20.79	0.70	3.4
34*	MELANOTOS	9	9	17.39	0.46	2.6	9	18.31	0.42	2.3	9	25.39	0.79	3.1	9	26.14	1.08	4.1
35*	MIMUS	58	54	17.65	0.47	2.7	55	18.90	0.49	2.6	57	25.09	0.53	2.1	55	21.63	0.79	3.6
36*	NESOMIMUS	16	15	17.94	0.48	2.7	15	18.88	0.53	2.8	16	25.12	0.54	2.2	16	29.55	1.17	4.0
17	MIMODES GRAYSONI	1	1	19.00	0.0	0.0	1	19.60	0.0	0.0	1	26.20	0.0	0.0	1	23.20	0.0	0.0
18	DRESCOPTES MONTANUS	10	8	17.66	0.36	2.0	8	17.65	0.37	2.1	10	23.59	0.50	2.1	10	19.20	0.36	1.9
37*	TOXOSTOMA	66	66	19.15	0.48	2.5	65	19.82	0.50	2.5	65	26.20	0.59	2.3	65	28.61	1.12	3.9
29	CINCLOCERTHIA FUFICAUDA	17	16	18.65	0.51	2.7	16	19.00	0.37	1.9	17	26.12	0.77	2.9	16	35.71	4.19	11.7
30	RAMPHOCINCLUS BRACHYURUS	2	2	17.15	0.07	0.4	2	18.50	0.71	3.8	2	24.75	0.21	0.9	2	26.65	0.07	0.3
31	OMNACORIUS ATRICAPILLUS	8	7	16.41	0.95	5.8	8	17.36	0.53	3.0	8	23.24	0.78	3.3	8	25.75	1.35	5.2
32	ALLENIA FUSCA	18	18	17.60	0.38	2.2	18	18.19	0.27	1.5	18	24.79	0.46	1.9	18	21.08	0.75	3.6
33	MARGAROPS FUSCATUS	12	12	20.37	1.08	5.3	12	21.49	0.69	3.2	12	29.42	1.16	4.0	12	29.54	1.74	5.9
3	MELANOTIS CAERULESCENS	5	5	17.30	0.60	3.4	5	18.12	0.54	3.0	5	25.24	1.01	4.0	5	25.66	0.84	3.3
4	MELANOTIS HYPOLEUCUS	4	4	17.47	0.13	0.7	4	18.50	0.14	0.8	4	25.55	0.30	1.2	4	26.62	1.32	5.0
5	MIMUS POLYGLOTTOS	22	20	16.71	0.56	3.4	21	17.62	0.63	3.6	22	23.75	0.60	2.5	22	19.32	0.79	4.1
6	MIMUS GILVUS	9	9	16.94	0.52	3.1	9	16.08	0.38	2.1	9	24.32	0.58	2.4	8	20.67	0.82	4.0
7	MIMUS GUNDLACHII	5	4	18.75	0.25	1.3	4	19.75	0.13	0.7	4	25.67	0.57	2.2	4	24.15	0.33	1.4
8	MIMUS THENEA	4	4	18.40	0.36	1.9	4	19.42	0.36	1.9	4	26.07	0.31	1.2	4	21.85	0.30	1.4
9	MIMUS LONGICAUDATUS	7	7	18.14	0.35	1.9	7	19.94	0.41	2.1	7	26.29	0.50	1.9	7	24.91	0.82	3.3
10	MIMUS SATURNINUS	4	3	17.93	0.35	2.0	3	19.47	0.40	2.1	4	25.45	0.29	1.1	3	22.57	1.69	7.5
11	MIMUS PATAGONICUS	4	4	17.85	0.29	1.6	4	18.92	0.13	0.7	4	24.85	0.25	1.0	4	20.22	0.42	2.1
12	MIMUS TRIURUS	3	3	16.47	0.32	2.0	3	18.00	0.40	2.2	3	23.83	0.38	1.6	3	19.30	0.50	2.6
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NESOMIMUS TRIFASCIATUS	3	3	18.53	0.35	1.9	3	19.57	0.06	0.3	3	25.83	0.64	2.5	3	29.43	0.35	1.2
15	NESOMIMUS MACDONALDI	5	5	18.02	0.40	2.2	5	18.84	0.34	1.8	5	25.34	0.41	1.6	5	31.84	0.71	2.2
16	NESOMIMUS PARVULUS	8	7	17.26	0.56	3.2	7	18.23	0.70	3.8	8	24.19	0.58	2.4	8	27.39	1.49	5.4
19	TOXOSTOMA RUFUM	14	14	18.11	0.52	2.9	14	19.35	0.43	2.2	14	26.36	0.63	2.4	13	26.18	0.93	3.6
20	TOXOSTOMA LONGIROSTRE	4	4	18.45	0.44	2.4	4	19.37	0.55	2.8	4	26.42	0.26	1.0	4	28.32	0.67	2.4
21	TOXOSTOMA GUTTATUM	6	6	17.12	0.25	1.5	6	18.07	0.27	1.5	6	24.30	0.69	2.9	6	29.53	0.71	2.4
22	TOXOSTOMA CINEREFUM	1	1	19.30	0.0	0.0	1	19.60	0.0	0.0	1	25.00	0.0	0.0	1	25.30	0.0	0.0
23	TOXOSTOMA PENICILLI	3	3	19.40	0.26	1.4	3	19.67	0.06	0.3	3	26.17	0.45	1.7	3	25.43	0.85	3.3
24	TOXOSTOMA OCELLATUM	2	2	20.80	0.14	0.7	2	21.14	0.35	1.7	2	27.65	0.07	0.3	2	32.50	0.97	1.7
25	TOXOSTOMA CURVIROSTRE	20	20	20.17	0.53	2.6	20	20.79	0.62	3.0	20	27.46	0.55	2.0	20	29.35	1.13	3.9
26	TOXOSTOMA LECONTEI	4	4	18.95	0.37	2.0	4	19.45	0.29	1.5	4	25.07	0.64	2.6	4	26.90	1.22	4.5
27	TOXOSTOMA REDIVIVUM	7	7	20.57	0.56	2.7	6	21.38	0.62	2.9	7	27.67	0.68	2.5	7	31.69	1.09	3.4
28	TOXOSTOMA DORSALE	5	5	18.66	0.38	2.0	5	19.14	0.27	1.4	4	25.87	0.68	2.6	5	30.92	2.06	6.7
	GRAND VALUES	253	242	18.14			243	18.99			250	25.37			247	25.64		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 56 N	PMAX-L2 MEAN	S D	C V	V 15 N	INTORB-W MEAN	S D	C V	V 16 N	BILL-W1 MEAN	S D	C V	V 17 N	BILL-W2 MEAN	S D	C V
1	DIMETELLA CAROLINENSIS	25	25	8.39	0.51	6.1	25	4.58	0.35	7.6	25	3.55	0.17	4.7	23	6.73	0.30	4.5
2	MELANOPTILA GLAFKIROSTRIS	11	11	9.75	0.48	4.9	11	4.20	0.26	6.2	11	3.85	0.16	4.1	11	7.25	0.32	4.4
34*	MELANOTOS	9	9	12.63	0.76	6.0	9	6.37	0.27	4.2	9	4.25	0.35	8.1	9	7.96	0.15	1.9
35*	MIMUS	58	55	10.25	0.61	5.9	57	4.67	0.39	6.0	57	4.27	0.25	5.8	57	8.04	0.40	5.0
36*	MESCHIMUS	16	15	15.33	0.78	5.1	16	4.14	0.30	7.1	16	4.25	0.15	3.4	16	7.84	0.32	4.0
17	MIMODES GRAYSONI	1	1	10.90	0.0	0.0	1	4.80	0.0	0.0	1	4.90	0.0	0.0	1	9.10	0.0	0.0
18	PROSCOPTES MONTANUS	10	10	8.63	0.41	4.8	9	4.32	0.45	10.4	10	3.68	0.13	3.6	9	7.30	0.42	5.8
37*	TOXOSTOMA	66	65	16.44	1.17	7.1	66	5.48	0.40	7.2	66	4.92	0.26	5.3	66	8.10	0.44	5.4
29	CINCLERCERTHIA RUFICAUDA	17	16	21.12	3.07	14.5	17	4.54	0.40	8.8	17	4.41	0.26	6.0	17	8.02	0.40	5.0
30	RAMPHOCINCLUS FRACHYURUS	2	2	14.60	0.42	2.9	2	4.55	0.07	1.6	2	4.45	0.49	11.1	2	7.55	0.21	2.8
31	ONACERUS ATRICAPILLUS	8	8	12.60	1.03	8.2	8	4.42	0.44	10.9	8	4.40	0.39	8.9	8	7.70	0.56	7.3
32	ALLENIA FUSCA	18	18	9.48	0.42	4.4	18	5.13	0.47	9.1	18	4.53	0.26	5.7	18	8.96	0.33	3.7
33	MARGAROPS FUSCATUS	12	12	14.32	1.16	8.1	12	6.64	0.62	9.3	12	5.30	0.47	8.8	11	10.25	0.66	6.5
3	MELANOTIS CAFFINLESCENS	5	5	12.12	0.66	5.5	5	6.10	0.34	5.6	5	4.18	0.40	9.6	5	8.04	0.15	1.9
4	MELANOTIS HYPOLEUCUS	4	4	13.15	0.87	6.6	4	6.65	0.13	1.9	4	4.32	0.25	5.8	4	7.87	0.15	1.9
5	MIMUS POLYGLOTTOS	22	22	8.95	0.57	6.3	22	4.83	0.46	5.5	22	3.86	0.25	6.5	22	7.52	0.44	5.9
6	MIMUS GILVUS	9	8	9.71	0.48	4.9	9	4.86	0.26	5.3	9	4.14	0.26	6.3	9	7.89	0.38	4.8
7	MIMUS GUNDELACHII	5	4	12.12	0.29	2.4	4	5.20	0.45	6.7	4	4.30	0.18	4.2	4	8.37	0.30	3.6
8	MIMUS THENCA	4	4	10.02	0.69	6.9	4	4.40	0.29	6.7	4	4.32	0.17	3.9	4	7.72	0.32	4.1
9	MIMUS LONGICAUDATUS	7	7	12.03	0.83	6.9	7	5.04	0.38	7.5	7	4.59	0.30	6.6	7	8.64	0.46	5.3
10	MIMUS SATURNINUS	4	3	11.17	1.07	9.6	4	4.97	0.10	1.9	4	4.80	0.23	4.8	4	8.70	0.29	3.4
11	MIMUS PATAGONICUS	4	4	9.45	0.25	2.7	4	4.75	0.31	6.5	4	4.15	0.24	5.7	4	7.55	0.31	4.1
12	MIMUS TPIURUS	3	3	8.50	0.56	6.6	3	4.90	0.40	8.2	3	4.00	0.20	5.0	3	7.93	0.32	4.1
13	MIMUS DORSALIS							THREE	MAKE NO SPECIMENS	IN THIS SET								
14	MESCHIMUS TRIFASCIATUS	3	3	15.43	0.25	1.6	3	4.17	0.23	5.5	3	4.23	0.06	1.4	3	7.80	0.26	3.4
15	MESCHIMUS MACINALEI	5	5	16.34	0.81	5.0	5	4.44	0.18	4.1	5	4.56	0.17	3.7	5	8.34	0.21	2.5
16	MESCHIMUS PARVULUS	8	7	14.23	0.88	6.1	8	3.95	0.36	9.2	8	3.96	0.15	3.8	8	7.37	0.38	5.1
19	TOXOSTOMA RUFUM	14	13	13.55	0.86	6.4	14	5.64	0.33	5.9	14	4.81	0.22	4.7	14	7.63	0.54	7.1
20	TOXOSTOMA LONGIROSTRE	4	4	15.15	0.85	5.6	4	5.37	0.54	10.1	4	4.40	0.14	2.9	4	8.20	0.22	2.6
21	TOXOSTOMA CUTTATUM	6	6	16.37	1.07	6.5	6	4.73	0.33	7.0	6	4.88	0.29	6.0	6	7.65	0.32	4.2
22	TOXOSTOMA CINEREUM	1	1	14.50	0.0	0.0	1	6.10	0.0	0.0	1	5.00	0.0	0.0	1	8.60	0.0	0.0
23	TOXOSTOMA FENDLERI	3	3	14.63	0.06	0.4	3	5.47	0.15	2.8	3	4.93	0.29	5.9	3	8.57	0.12	1.3
24	TOXOSTOMA OCELLATUM	2	2	18.30	0.71	3.9	2	5.70	0.14	2.5	2	5.45	0.21	3.9	2	8.70	0.14	1.6
25	TOXOSTOMA CURVIROSTRE	20	20	16.84	1.01	6.0	20	5.97	0.44	7.4	20	5.23	0.26	5.0	20	8.63	0.42	4.9
26	TOXOSTOMA LECONTEI	4	4	16.47	1.35	8.2	4	4.65	0.38	8.1	4	4.32	0.36	8.3	4	7.55	0.31	4.1
27	TOXOSTOMA REDIVIVUM	7	7	18.94	1.00	5.3	7	5.80	0.26	4.6	7	5.31	0.35	6.6	7	8.34	0.61	7.3
28	TOXOSTOMA DORSALIS	5	5	19.66	2.57	13.1	5	5.34	0.55	10.3	5	4.34	0.15	3.4	5	7.16	0.23	3.2
	GRAND VALUES	253	247	13.36			251	5.07			252	4.49			246	8.05		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SFT DESCRIPTION	SFT N	V 18 N	WILL-H MEAN	S D	C V	V 21 N	PEDGRIG MEAN	S D	C V	V 20 N	NARES-W MEAN	S D	C V	V 19 N	NAREL-L MEAN	S D	C V			
1	DUMETELLA CAROLINENSIS	25	25	2.41	0.13	5.4	25	6.41	0.29	4.5	23	2.84	0.20	7.0	24	7.41	0.22	3.0			
2	MELANOPTILA GLAPPIROSTRIS	11	11	2.57	0.15	5.8	11	6.44	0.31	4.8	11	2.85	0.21	7.2	11	7.95	0.40	5.0			
34*	MELANOTOS	9	9	2.90	0.09	3.1	9	7.80	0.42	5.4	9	3.20	0.22	6.9	9	9.64	0.49	5.1			
35*	MIMUS	58	58	2.84	0.13	4.5	58	5.83	0.36	6.2	58	3.10	0.22	7.0	58	8.06	0.48	6.0			
36*	NESCHIMUS	16	16	2.81	0.12	4.4	16	7.09	0.19	2.7	16	2.85	0.16	5.6	16	10.46	0.34	3.2			
17	MIMODES GRAYSONI	1	1	2.90	0.0	0.0	1	6.40	0.0	0.0	1	3.10	0.0	0.0	1	8.70	0.0	0.0			
18	OPHSCOPHUS MONTANUS	10	10	2.39	0.09	3.9	10	5.73	0.29	5.1	10	2.41	0.19	6.8	10	7.73	0.22	2.9			
37*	TOXOSTOMA	66	66	2.94	0.16	5.5	66	5.98	0.43	7.2	66	3.06	0.16	5.3	66	8.01	0.44	5.5			
29	CINCLOCERTHIA RUFICAUDA	17	17	2.95	0.20	6.7	17	6.75	0.56	8.3	17	2.68	0.12	4.4	17	10.06	0.72	7.2			
30	RAMPHOCEINUS BRACHYURUS	2	2	2.88	0.07	2.4	2	6.50	0.57	6.7	2	2.60	0.0	0.0	2	8.80	0.71	8.0			
31	ONACORHUS ATRICAPILLUS	8	8	2.40	0.21	8.6	8	8.24	0.89	10.4	8	2.62	0.18	7.0	8	9.15	0.77	8.4			
32	ALLIPIA FUSCA	18	18	2.88	0.13	4.6	18	6.18	0.48	7.7	18	3.17	0.11	3.4	18	8.44	0.51	6.0			
33	MARGAROPS FUSCATUS	12	12	3.95	0.22	5.7	12	7.58	0.39	5.1	12	3.63	0.16	4.4	12	10.67	0.48	4.5			
3	MELANOTIS CAERULESCENS	4	5	2.78	0.08	3.0	5	7.60	0.14	1.8	5	3.16	0.11	3.6	5	9.50	0.19	2.0			
4	MELANOTIS HYPOLEUCUS	4	4	3.02	0.10	3.2	4	7.80	0.62	7.9	4	3.25	0.31	9.6	4	9.77	0.72	7.3			
5	MIMUS POLYCHLOTTUS	22	22	2.55	0.09	3.6	22	5.30	0.39	7.3	22	2.88	0.27	9.3	22	7.32	0.51	7.0			
6	MIMUS GILVUS	4	9	2.74	0.19	6.8	9	5.23	0.39	7.5	9	2.96	0.22	7.6	9	7.59	0.64	8.4			
7	MIMUS GUNDELACHII	5	4	3.10	0.14	4.6	4	5.62	0.45	8.0	4	3.12	0.13	4.0	4	8.40	0.27	3.2			
8	MIMUS THINCA	4	4	2.60	0.08	3.1	4	6.32	0.34	5.4	4	3.00	0.18	6.1	4	8.40	0.76	9.1			
9	MIMUS LONGICAUDATUS	7	7	3.03	0.13	4.1	7	6.49	0.33	5.1	7	3.43	0.15	4.4	7	9.30	0.13	1.4			
10	MIMUS SATURNINUS	4	3	3.43	0.12	3.4	3	6.23	0.15	2.5	3	3.47	0.06	1.7	3	8.50	0.26	3.1			
11	MIMUS PATAGONICUS	4	4	2.65	0.19	7.2	4	6.15	0.24	3.9	4	3.02	0.10	3.2	4	7.70	0.14	1.8			
12	MIMUS TRIURUS	3	3	2.60	0.10	3.8	3	5.27	0.12	2.2	3	2.93	0.15	5.2	3	7.23	0.12	1.6			
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SFT													
14	NESCHIMUS TRIFASCIATUS	3	3	2.90	0.10	3.4	3	7.23	0.25	3.5	3	2.90	0.10	3.4	3	10.03	0.06	0.6			
15	NESCHIMUS MACDONALDI	5	5	2.92	0.15	5.1	5	7.36	0.09	1.2	5	2.94	0.19	6.6	5	11.80	0.32	2.7			
16	NESCHIMUS PARVULUS	8	8	2.62	0.12	4.4	8	6.67	0.22	3.3	8	2.72	0.15	5.5	8	9.54	0.39	4.1			
19	TOXOSTOMA RUFUM	14	14	2.95	0.13	4.4	13	6.19	0.42	6.7	14	2.96	0.25	8.4	14	8.26	0.41	5.0			
20	TOXOSTOMA LONGIROSTRE	4	4	3.00	0.14	4.7	4	6.75	0.50	7.4	4	3.15	0.13	4.1	4	9.50	0.39	4.1			
21	TOXOSTOMA CUTTATUM	6	6	2.77	0.15	5.4	6	6.50	0.53	8.1	6	2.92	0.15	5.0	6	8.73	0.54	6.2			
22	TOXOSTOMA CINEREUM	1	1	2.80	0.0	0.0	1	5.60	0.0	0.0	1	3.00	0.0	0.0	1	7.60	0.0	0.0			
23	TOXOSTOMA BENDIREI	3	3	3.03	0.06	1.9	3	4.93	0.51	10.4	3	3.10	0.10	3.2	3	6.53	0.15	2.3			
24	TOXOSTOMA SCOLLATUM	2	2	3.15	0.07	2.2	2	6.25	0.21	3.4	2	3.00	0.14	4.7	2	8.80	0.28	3.2			
25	TOXOSTOMA CURVIROSTRE	20	20	3.10	0.19	6.3	19	6.02	0.39	6.5	20	3.18	0.12	3.8	20	8.32	0.52	6.2			
26	TOXOSTOMA LEONTEI	4	4	2.57	0.10	3.7	4	5.62	0.41	7.3	4	2.97	0.13	4.2	4	7.37	0.26	3.6			
27	TOXOSTOMA PERIVIVUM	7	7	3.16	0.14	4.4	7	6.21	0.41	6.7	7	3.33	0.16	4.8	7	7.83	0.44	5.6			
28	TOXOSTOMA DORSALE	5	5	2.84	0.21	7.3	5	5.70	0.51	8.9	5	2.94	0.05	1.9	5	7.18	0.26	3.6			
	GRAND VALUES	253	251	2.87			249	6.36			249	3.03			250	8.57					

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 22 N	ECTH-W1			V 23 N	ECTH-W2			V 24 N	ECTH-W3			V 25 N	DPN-W				
				MEAN	S D	C V		MEAN	S D	C V		MEAN	S D	C V		MEAN	S D	C V		
1	DUMETELLA CAROLINENSIS	25	25	9.38	0.43	4.5	25	7.49	0.34	4.6	25	9.59	0.33	3.5	25	1.09	0.15	14.0		
2	MELANOPTILA GLABRIROSTRIS	11	11	9.55	0.33	3.4	11	7.89	0.21	2.7	11	9.66	0.29	3.0	11	1.18	0.13	10.6		
34*	MELANOTOS	9	9	11.56	0.35	3.1	9	9.17	0.17	1.8	9	11.27	0.37	3.3	9	1.39	0.30	21.7		
35*	MIMUS	56	56	10.57	0.35	3.3	56	8.37	0.32	3.8	55	10.50	0.34	3.2	57	1.03	0.15	15.0		
36*	NEOSOMINUS	16	16	9.20	0.49	5.3	16	7.28	0.32	4.4	16	9.05	0.50	5.5	16	1.02	0.09	9.2		
17	MIMODES GRAYSONI	1	1	10.50	0.0	0.0	1	8.20	0.0	0.0	1	10.20	0.0	0.0	1	1.40	0.0	0.0		
16	DRESCOPTES MONTANUS	10	10	10.08	0.35	3.5	9	8.39	0.41	4.9	9	9.97	0.48	4.8	10	1.11	0.17	15.6		
37*	TOXOSTOMA	66	65	11.45	0.54	4.7	65	8.78	0.32	3.6	63	10.25	0.37	3.6	66	1.19	0.20	17.0		
29	CINCLUCETTA RUFICAUDA	17	17	9.64	0.59	6.2	17	7.55	0.47	6.2	17	10.30	0.46	4.4	17	0.92	0.08	9.0		
30	RAMPHOCINCLUS BRACHYURUS	2	2	9.65	0.07	0.7	2	7.85	0.35	4.5	2	9.75	0.35	3.6	2	1.00	0.0	0.0		
31	ONACCEIUS ATRICAPILLUS	8	8	8.31	0.70	8.4	8	6.40	0.45	7.0	8	8.41	0.67	8.0	8	0.90	0.13	14.5		
32	ALLENIA FUSCA	18	18	11.29	0.34	3.0	18	9.46	0.35	3.7	18	12.07	0.37	3.1	18	1.07	0.16	15.3		
33	MARCACOPS FUSCATUS	12	12	13.69	1.06	7.7	12	10.52	0.64	6.1	12	14.25	0.71	5.0	12	1.21	0.14	11.4		
3	MELANCTIS CATRULESCENS	5	5	11.38	0.44	3.9	5	9.06	0.17	1.8	5	11.16	0.23	2.1	5	1.36	0.11	8.4		
4	MELANCTIS HYPOLEUCUS	4	4	11.75	0.17	1.5	4	9.27	0.17	1.8	4	11.37	0.51	4.4	4	1.42	0.44	31.1		
5	MIMUS POLYLOTTOS	22	21	10.26	0.33	3.2	21	7.95	0.31	3.9	21	10.02	0.29	2.9	22	0.95	0.17	17.8		
6	MIMUS GILVUS	9	9	10.61	0.27	2.5	9	8.56	0.27	3.2	9	10.39	0.40	3.9	9	1.07	0.14	13.3		
7	MIMUS GUNDLACHII	5	4	10.85	0.61	5.7	4	8.52	0.43	5.1	4	10.70	0.28	2.6	4	1.15	0.19	16.7		
8	MIMUS THENEA	4	4	10.02	0.36	3.6	4	8.17	0.15	1.8	4	10.42	0.26	2.5	4	0.92	0.05	5.4		
9	MIMUS LONGICAUDATUS	7	7	11.21	0.27	2.4	7	8.76	0.44	5.1	7	11.33	0.37	3.3	7	1.09	0.13	12.4		
10	MIMUS SATURNINUS	4	4	11.05	0.35	3.2	4	8.62	0.21	2.4	3	10.60	0.20	1.9	4	1.10	0.18	16.6		
11	MIMUS PATAGONICUS	4	4	10.00	0.36	3.6	4	8.15	0.37	4.5	4	10.05	0.42	4.2	4	0.97	0.10	9.8		
12	MIMUS TRIURUS	3	3	10.53	0.35	3.3	3	8.23	0.12	1.4	3	10.47	0.47	4.5	3	0.97	0.15	15.8		
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET												
14	NEOSOMINUS TRIFASCIATUS	3	3	9.17	0.35	3.8	3	7.50	0.40	5.3	3	8.77	0.61	7.0	3	1.13	0.06	5.1		
15	NEOSOMINUS MACDONALDI	5	5	9.42	0.36	3.9	5	7.44	0.28	3.8	5	9.76	0.26	2.7	5	0.98	0.11	11.2		
16	NEOSOMINUS PARVULUS	8	8	9.01	0.58	6.4	8	6.90	0.32	4.6	8	8.64	0.56	6.5	8	0.95	0.09	9.7		
19	TOXOSTOMA RUFUM	14	14	11.91	0.65	5.4	14	9.52	0.35	3.6	13	10.65	0.38	3.6	14	1.09	0.13	13.4		
20	TOXOSTOMA LONGIROSTRE	4	4	11.20	0.24	2.5	4	8.70	0.16	1.9	4	10.27	0.46	4.5	4	1.02	0.13	12.3		
21	TOXOSTOMA CUTTATUM	6	6	10.12	0.31	3.0	6	8.38	0.32	3.8	6	9.67	0.40	4.2	6	1.10	0.11	10.0		
22	TOXOSTOMA CINEREUM	1	1	11.60	0.0	0.0	1	9.30	0.0	0.0	1	10.70	0.0	0.0	1	1.00	0.0	0.0		
23	TOXOSTOMA FENDIREI	3	3	11.67	0.32	2.8	3	8.87	0.50	5.7	3	10.63	0.21	2.0	3	1.27	0.25	19.9		
24	TOXOSTOMA OCELLATUM	2	2	11.60	0.57	4.9	2	8.70	0.28	3.3	2	10.85	0.35	3.3	2	1.25	0.21	17.0		
25	TOXOSTOMA CURVIRESTRE	20	20	11.95	0.47	3.9	20	8.74	0.31	3.5	19	10.59	0.34	3.2	20	1.16	0.28	24.2		
26	TOXOSTOMA LEOCOTTEI	4	4	11.10	0.47	4.2	4	8.22	0.25	3.0	4	9.42	0.50	5.3	4	1.10	0.14	12.9		
27	TOXOSTOMA RELIQUIUM	7	7	12.34	0.64	5.2	7	9.33	0.34	3.6	7	10.57	0.27	2.5	7	1.54	0.05	3.5		
28	TOXOSTOMA DORSALE	5	4	10.97	0.79	7.2	4	8.02	0.29	3.6	4	9.17	0.38	4.1	5	1.32	0.19	14.6		
	GRAND VALUES	253	250	10.68			249	8.40			246	10.33			252	1.12				

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 26 N	SF-W MEAN	S D	C V	V 27 N	SF-L MEAN	S D	C V	V 28 N	INTPTG-W MEAN	S D	C V	V 30 N	JUGAL-L MEAN	S D	C V
1	DIMETELLA CAROLINENSIS	25	25	1.26	0.14	10.9	25	2.48	0.06	2.2	19	6.53	0.35	5.4	24	15.95	0.49	3.1
2	MELANOPTILA GLAUCIROSTRIS	11	11	1.28	0.13	9.8	11	2.61	0.16	6.3	9	6.56	0.54	8.2	10	16.68	0.78	4.7
340	MELANOTOS	9	9	1.50	0.11	7.1	9	2.83	0.18	6.5	9	7.76	0.44	5.7	9	18.92	0.63	3.3
350	MIMUS	58	56	1.53	0.16	10.6	56	2.53	0.19	7.7	47	7.43	0.49	6.6	57	18.89	0.57	3.0
360	NEOMIMUS	16	16	1.44	0.09	6.3	16	2.58	0.21	8.3	15	6.86	0.45	6.5	16	20.04	0.79	3.9
17	MIMODES GRAYSONI	1	1	1.60	0.0	0.0	1	3.10	0.0	0.0	1	8.60	0.0	0.0	1	19.50	0.0	0.0
18	CREOSCEPTELES MONTANUS	10	10	1.24	0.16	13.3	10	2.94	0.17	5.6	7	6.79	0.31	4.5	9	16.46	0.56	3.4
370	TOXOSTOMA	66	66	1.98	0.18	9.1	66	3.26	0.21	6.3	61	8.30	0.40	6.0	66	20.23	0.57	2.8
29	CINCLOCERTHIA RUFICAUDA	17	17	1.45	0.12	8.1	17	2.52	0.31	12.3	13	7.47	0.40	5.4	17	21.62	1.01	4.7
30	RAMPHOCINCLUS ERACHYRUS	2	2	1.10	0.14	12.9	2	3.15	0.35	11.2	2	7.30	0.42	5.8	2	20.10	0.14	0.7
31	ONCHOCORPUS ATRICAPILLUS	8	8	0.10	0.0	0.0	8	1.80	0.18	9.8	5	6.90	0.63	9.1	7	17.96	0.83	4.6
32	ALLFATA FUSCA	18	18	1.52	0.20	13.2	18	2.18	0.27	12.2	15	7.84	0.48	6.1	18	19.14	0.56	2.9
33	MARGAROPS FUSCATUS	12	12	1.58	0.29	18.6	12	2.18	0.21	9.7	11	9.53	0.80	8.4	12	24.64	1.21	4.9
3	MELANOTIS CARPULSCENS	5	5	1.50	0.12	8.2	5	2.98	0.15	5.0	5	7.44	0.42	5.6	5	18.86	0.67	3.5
4	MELANOTIS HYPOLEUCUS	4	4	1.50	0.08	5.4	4	2.67	0.22	8.3	4	8.07	0.47	5.8	4	18.97	0.57	3.0
5	MIMUS POLYGLOTOS	22	21	1.30	0.15	11.2	21	2.34	0.15	6.2	18	6.82	0.40	7.3	22	17.28	0.49	2.8
6	MIMUS GILVUS	9	9	1.32	0.19	14.0	9	2.77	0.19	8.5	7	7.03	0.39	5.6	9	18.08	0.84	4.6
7	MIMUS GUNDLACHII	5	4	1.75	0.19	10.9	4	2.47	0.34	13.8	2	7.60	0.57	7.4	4	20.05	0.10	0.5
8	MIMUS THENCA	4	4	1.70	0.16	9.6	4	2.90	0.18	6.3	4	7.80	0.43	5.5	4	19.45	0.48	2.5
9	MIMUS LONGICAUDATUS	7	7	1.37	0.20	14.4	7	2.44	0.27	10.8	6	7.65	0.67	8.8	7	20.77	0.73	3.5
10	MIMUS SATURNINUS	4	4	1.57	0.15	9.5	4	2.60	0.14	5.4	3	7.70	0.10	1.3	4	19.92	0.62	3.1
11	MIMUS PATACONICUS	4	4	1.65	0.13	7.8	4	2.75	0.17	6.3	4	7.60	0.54	7.0	4	18.15	0.34	1.9
12	MIMUS TRIURUS	3	3	1.60	0.10	6.2	3	2.40	0.17	7.2	3	7.20	0.20	2.8	3	17.40	0.26	1.5
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NEOMIMUS TRIFASCIATUS	3	3	1.40	0.10	7.1	3	2.67	0.15	5.7	3	7.33	0.49	6.7	3	20.37	0.51	2.5
15	NEOMIMUS MACDONALDI	5	5	1.44	0.09	6.2	5	2.54	0.05	2.2	4	6.82	0.69	10.2	5	20.70	0.77	3.7
16	NEOMIMUS PARVULUS	8	8	1.47	0.09	6.0	8	2.54	0.28	10.9	8	6.42	0.26	4.1	8	19.05	0.86	4.5
19	TOXOSTOMA RUFUM	14	14	1.65	0.17	10.0	14	3.09	0.20	6.5	14	8.51	0.55	6.4	14	19.88	0.59	2.9
20	TOXOSTOMA LONGIROSTRE	4	4	1.50	0.33	21.8	4	2.88	0.25	8.7	4	8.20	0.18	2.2	4	20.62	0.53	2.5
21	TOXOSTOMA GUTTATUM	6	6	1.38	0.10	7.1	6	2.72	0.21	7.9	6	7.40	0.53	7.2	6	18.90	0.28	1.5
22	TOXOSTOMA CINEREUM	1	1	2.10	0.0	0.0	1	3.40	0.0	0.0	0	999.99	0.0	0.0	1	21.20	0.0	0.0
23	TOXOSTOMA BENDIREI	3	3	2.27	0.12	5.1	3	3.27	0.31	9.4	3	8.53	0.31	3.6	3	19.87	0.21	1.0
24	TOXOSTOMA OCELLATUM	2	2	2.15	0.21	9.9	2	3.00	0.14	4.7	2	9.05	0.21	2.3	2	22.10	0.71	3.2
25	TOXOSTOMA CURVIROSTRE	20	20	2.28	0.19	8.2	20	3.10	0.17	5.6	18	8.88	0.56	6.4	20	20.95	0.72	3.4
26	TOXOSTOMA LICENTEI	4	4	1.70	0.08	4.8	4	3.65	0.19	5.0	4	8.10	0.54	6.6	4	18.65	0.33	1.8
27	TOXOSTOMA REDIVIVUM	7	7	2.63	0.21	8.1	7	3.99	0.27	6.7	6	8.70	0.74	2.8	7	21.39	0.40	1.9
28	TOXOSTOMA CORSALE	5	5	2.18	0.13	6.0	5	3.36	0.17	5.0	4	7.27	0.53	7.3	5	18.74	0.51	2.7
	GRAND VALUES	253	251	1.58			251	2.79			214	7.43			248	19.48		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 31 N	PFLV-L1 MEAN	S D	C V	V 32 N	PFLV-L2 MEAN	S D	C V	V 33 N	PFLV-W1 MEAN	S D	C V	V 35 N	PFLV-W3 MEAN	S D	C V
1	DUMETELLA CAROLINENSIS	25	23	21.43	0.46	2.1	23	13.87	0.32	2.3	21	14.99	0.43	2.8	20	8.01	0.36	4.5
2	MELANOPTILA GLAUCIRESTRIS	11	11	20.94	0.68	3.3	11	13.47	0.47	3.5	11	14.75	0.40	2.7	11	7.90	0.24	3.1
34*	MELANCTOS	9	9	25.91	0.73	2.8	9	17.04	0.63	3.7	9	17.66	1.03	5.8	9	9.49	0.50	5.2
35*	MIMUS	58	55	25.64	0.81	3.2	56	16.42	0.60	3.6	53	17.14	0.79	4.6	56	8.61	0.40	4.7
36*	NESOMIMUS	16	14	25.10	0.98	3.9	14	16.39	0.64	3.9	15	16.31	0.71	4.4	14	8.15	0.34	4.2
17	MIMOCLES GRAYSONI	1	1	26.90	0.0	0.0	1	17.80	0.0	0.0	1	17.50	0.0	0.0	1	9.00	0.0	0.0
18	OPHOSCOPTES MONTANUS	10	10	22.69	0.58	2.5	10	14.77	0.42	3.5	10	15.90	0.42	2.7	10	7.82	0.51	6.5
37*	TOXOSTOMA	66	65	26.82	0.79	2.9	65	16.93	0.58	3.5	64	17.29	0.55	3.2	65	8.19	0.42	5.2
29	CINCLOCEPHALIA RUFICAUDA	17	17	26.13	1.24	4.7	17	16.46	0.90	5.5	17	15.98	0.58	3.6	17	7.45	0.27	3.6
30	RAMPHOCINCLUS BRACHYURUS	2	2	26.15	0.49	1.9	2	16.95	0.64	3.8	2	16.70	0.57	3.4	2	8.40	0.00	0.0
31	ORNACORHUS ATRICAPILLUS	8	7	21.34	0.90	4.2	7	13.87	0.78	5.7	7	12.09	0.51	4.3	7	5.34	0.24	4.8
32	ALLERIA FUSCA	18	18	25.97	0.50	1.9	18	16.87	0.45	2.7	18	17.46	0.54	3.1	18	9.38	0.63	6.7
33	MARGAROPUS FUSCATUS	12	12	32.33	1.79	5.5	12	20.42	1.32	6.5	12	20.35	1.09	5.4	11	10.65	0.69	6.4
3	MELANCTIS CAERULESCENS	5	5	25.68	0.94	3.7	5	16.96	0.82	4.8	5	17.32	1.30	7.5	5	9.24	0.57	6.2
4	MELANCTIS HYPERLEUCUS	4	4	26.15	0.25	1.0	4	17.12	0.19	1.1	4	18.00	0.47	2.6	4	9.75	0.38	3.9
5	MIMUS POLYCLOTOS	22	19	23.29	0.85	3.6	20	14.65	0.59	4.0	19	15.75	0.41	2.6	20	7.77	0.25	3.2
6	MIMUS GILVUS	9	9	24.16	0.91	3.8	9	15.23	0.83	5.4	9	16.19	0.82	5.1	9	7.90	0.51	6.4
7	MIMUS GUNDLACHI	5	5	27.76	0.85	3.1	5	17.38	0.38	2.2	4	17.95	0.34	1.9	5	8.52	0.59	6.9
8	MIMUS THENCA	4	4	26.90	0.73	2.7	4	17.85	0.47	2.6	4	17.62	0.47	5.5	4	9.45	0.25	2.7
9	MIMUS LONGICAUDATUS	7	7	26.73	0.74	2.8	7	17.03	0.58	3.4	6	18.62	1.67	9.0	7	8.81	0.35	4.0
10	MIMUS SATURNINUS	4	4	27.70	0.34	1.2	4	18.02	0.38	2.1	4	18.50	0.88	4.8	4	9.45	0.76	8.0
11	MIMUS PATACENICUS	4	4	24.82	0.59	2.4	4	15.97	0.40	2.5	4	16.87	0.72	1.3	4	9.10	0.18	2.0
12	MIMUS TRIUMPH	3	3	23.73	1.04	4.4	3	15.20	0.62	4.1	3	15.63	0.32	2.1	3	7.87	0.42	5.3
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NESOMIMUS TRIFASCIATUS	3	3	25.17	0.78	3.1	3	16.83	0.50	3.0	3	16.70	0.56	3.3	3	8.50	0.35	4.1
15	NESOMIMUS MACDONALDI	5	4	27.02	1.24	4.6	4	17.42	0.67	3.8	5	16.80	0.46	2.8	4	8.57	0.46	5.4
16	NESOMIMUS PARVULUS	8	7	23.11	0.89	3.8	7	14.81	0.66	4.4	7	15.43	0.88	5.7	7	7.37	0.25	3.4
19	TOXOSTOMA RUFUM	14	13	26.78	0.84	3.2	13	17.28	0.44	2.6	12	17.57	0.45	2.6	13	8.82	0.40	4.5
20	TOXOSTOMA LONGIROSTRE	4	4	27.52	0.37	1.3	4	17.62	0.22	1.3	4	17.25	0.47	2.7	4	8.55	0.53	6.2
21	TOXOSTOMA GUTTATUM	6	6	24.22	0.38	1.6	6	15.47	0.33	2.2	6	15.88	0.33	2.1	6	8.05	0.21	2.6
22	TOXOSTOMA CINEREUM	1	1	24.90	0.0	0.0	1	15.80	0.0	0.0	1	16.10	0.0	0.0	1	7.60	0.0	0.0
23	TOXOSTOMA FENDIFFI	3	3	25.97	0.25	1.0	3	16.07	0.60	3.8	3	16.20	0.17	1.1	3	8.10	0.10	1.2
24	TOXOSTOMA OCELLATUM	2	2	29.15	0.07	0.2	2	18.25	0.35	1.9	2	18.20	0.28	1.6	2	8.30	0.28	3.4
25	TOXOSTOMA CURVIRESTRE	20	20	28.98	0.86	3.0	20	18.50	0.72	3.9	20	18.58	0.75	4.0	20	9.01	0.52	5.7
26	TOXOSTOMA LECCHEI	4	4	25.40	0.81	3.2	4	15.67	0.74	4.7	4	16.75	0.21	1.2	4	7.22	0.22	3.1
27	TOXOSTOMA REFLIVUM	7	7	29.30	0.99	3.4	7	18.27	0.59	3.2	7	19.36	0.46	2.4	7	8.57	0.45	5.2
28	TOXOSTOMA DORSALIS	5	5	25.94	0.79	3.1	5	16.34	0.58	3.5	5	17.00	0.35	2.0	5	7.64	0.30	4.0
	GRAND VALUES	253	244	25.76			245	16.51			240	16.89			241	8.38		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 72 N	PELV-M4 MEAN S D C V	V 73 N	PELV-M5 MEAN S D C V	V 36 N	STERN-L MEAN S D C V	V 39 N	STERN-KL MEAN S D C V
1	DIMETELLA CAROLINENSIS	25	23	3.09 0.22 7.2	23	3.78 0.23 6.0	23	23.54 0.77 3.3	23	21.30 0.91 4.3
2	MELANOPTILA CLABRIROSTRIS	11	11	3.16 0.24 7.5	11	3.75 0.28 7.4	10	22.02 0.85 3.9	9	20.20 1.03 5.1
34*	MELANOTOS	9	9	3.26 0.30 9.3	9	4.38 0.33 7.5	9	28.66 0.99 3.5	9	26.80 1.30 4.9
35*	MIMUS	58	55	3.52 0.32 9.0	55	4.31 0.36 8.3	53	26.44 1.45 5.5	54	24.43 1.48 4.1
36*	NEOSCHIMUS	16	14	3.41 0.28 8.2	14	4.24 0.27 6.4	14	23.10 1.38 6.0	14	20.26 1.20 5.9
17	MIMODES GRAYSONI	1	0	999.99 0.0 0.0	1	5.50 0.0 0.0	1	23.20 0.0 0.0	1	21.20 0.0 0.0
18	CREOPECTES MONTANUS	10	10	3.20 0.25 7.8	10	3.93 0.42 10.7	10	24.86 0.57 2.3	10	24.00 0.66 2.8
37*	TOXOSTOMA	66	62	3.43 0.35 10.3	62	4.64 0.45 9.7	60	26.70 0.90 3.4	60	24.69 0.90 3.6
29	CINCLERCETIA RUFICAUDA	17	17	2.66 0.31 11.5	17	3.92 0.39 9.9	17	22.26 1.39 6.3	17	19.21 1.32 6.9
30	RAMPHOCINCLUS BRACHYURUS	2	2	3.10 0.28 9.1	2	3.95 0.35 9.0	2	23.15 0.07 0.3	2	20.60 0.28 1.4
31	ONACORHUS ATRICAPILLUS	8	6	0.62 0.36 58.4	6	2.90 0.23 7.4	8	21.45 1.29 6.0	8	18.94 1.79 9.4
32	ALLIPHIA FUSCA	18	18	3.56 0.30 8.5	17	4.46 0.30 6.7	18	26.16 0.85 3.2	18	23.59 1.23 5.2
33	MARGAROPS FUSCATUS	12	11	3.50 0.25 7.1	11	4.98 0.30 6.0	12	31.59 1.84 5.8	12	28.38 1.45 5.1
3	MELANCTIS CAERULESCENS	5	5	3.42 0.36 10.4	5	4.36 0.38 8.7	5	28.74 1.15 4.0	5	26.72 1.61 6.0
4	MELANCTIS HYPOLEUCUS	4	4	3.10 0.22 7.0	4	4.40 0.24 5.6	4	28.57 0.71 2.5	4	26.87 0.69 2.6
5	MIMUS POLYGLOTTOS	22	20	3.38 0.32 9.4	20	4.01 0.41 10.3	20	25.67 1.40 5.4	20	24.03 1.55 6.4
6	MIMUS GILVUS	9	8	3.49 0.38 11.0	8	4.19 0.23 5.5	8	25.76 1.89 7.4	9	24.28 1.97 8.1
7	MIMUS GUNDLACHII	5	5	3.82 0.25 6.5	5	4.94 0.59 11.9	5	26.48 1.63 6.1	5	24.74 0.88 3.6
8	MIMUS THYENCA	4	4	3.55 0.34 9.6	4	4.35 0.06 1.3	4	28.00 1.88 6.7	4	24.85 1.60 6.4
9	MIMUS LONGICAUDATUS	7	7	3.54 0.28 8.0	7	4.33 0.37 8.5	5	27.02 1.16 4.3	5	25.22 1.50 6.0
10	MIMUS SATURNINUS	4	4	3.72 0.42 11.3	4	4.70 0.08 1.7	4	28.17 0.97 3.5	4	25.92 0.77 3.0
11	MIMUS PATAGONICUS	4	4	3.50 0.22 6.2	4	4.22 0.22 5.2	4	25.15 0.86 3.4	4	23.00 0.92 4.0
12	MIMUS TRIPIUS	3	3	3.17 0.06 1.8	3	3.77 0.15 4.1	3	25.23 0.50 2.0	3	23.37 0.35 1.5
13	MIMUS DORSALIS					THERE ARE NO SPECIMENS IN THIS SET				
14	NEOSCHIMUS TRIFASCIATUS	3	3	3.17 0.06 1.8	3	4.17 0.15 3.7	3	23.90 1.06 4.4	3	20.27 1.07 5.3
15	NEOSCHIMUS MACDONALDI	5	4	3.72 0.41 11.0	4	4.47 0.13 2.8	4	23.52 1.36 5.8	5	21.54 1.21 5.6
16	NEOSCHIMUS PARVULUS	8	7	3.34 0.24 7.1	7	4.07 0.35 8.5	7	21.89 1.48 6.7	6	18.97 1.25 6.6
19	TOXOSTOMA RUFUM	14	13	3.79 0.35 9.2	13	4.48 0.34 7.6	13	29.00 0.66 2.3	13	27.35 0.74 2.7
20	TOXOSTOMA LONGIROSTRIS	4	4	3.85 0.44 11.3	4	4.90 0.47 9.6	4	27.92 0.87 3.1	4	25.90 0.64 2.5
21	TOXOSTOMA GUTTATUM	6	6	3.43 0.20 5.7	6	4.32 0.26 6.1	6	24.37 0.76 3.1	6	22.60 1.15 5.1
22	TOXOSTOMA CINEREUM	1	1	3.70 0.0 0.0	1	4.70 0.0 0.0	1	23.30 0.0 0.0	1	21.50 0.0 0.0
23	TOXOSTOMA PNEIPEI	3	3	2.97 0.29 9.7	3	4.67 0.47 10.1	3	26.23 0.45 1.7	3	25.07 0.60 2.4
24	TOXOSTOMA OCELLATUM	2	2	3.40 0.42 12.5	2	4.75 0.21 4.5	2	27.05 0.64 2.4	2	25.00 0.28 1.1
25	TOXOSTOMA FUSCIVIRESCENS	20	18	3.54 0.41 11.6	18	4.69 0.55 11.6	16	28.50 1.20 4.2	17	26.39 1.07 4.0
26	TOXOSTOMA LECOTHEI	4	3	2.83 0.32 11.3	3	4.30 0.30 7.0	4	25.62 0.81 3.1	3	23.33 0.81 3.5
27	TOXOSTOMA REIDIVIVUM	7	7	3.67 0.35 9.5	7	5.36 0.63 11.7	6	29.43 0.71 2.4	6	26.70 0.68 2.6
28	TOXOSTOMA FORSALE	5	5	3.10 0.16 5.1	5	4.26 0.21 4.9	5	25.56 0.88 3.5	5	23.04 0.87 3.8
	GRAND VALUES	253	238	3.19	238	4.36	237	25.73	237	23.57

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 37 N	STFRN-D MEAN S D C V	V 38 N	STFRN-W MEAN S D C V	V 40 N	FEMUR-L MEAN S D C V	V 41 N	FEMUR-HW MEAN S D C V
1	DUMETELLA CAROLINENSIS	25	25	6.82 0.29 4.2	23	10.84 0.45 4.1	25	22.09 0.59 2.7	25	3.95 0.14 3.4
2	MELANOPTILA GLABRIROSTRIS	11	11	6.21 0.44 7.0	11	10.36 0.41 4.0	11	21.74 0.58 2.7	11	3.84 0.15 3.9
34*	MELANOTOS	9	9	8.01 0.19 2.4	9	12.80 0.31 2.4	9	27.12 0.57 2.1	9	4.98 0.17 3.4
35*	MIMUS	58	54	7.53 0.47 6.2	53	12.11 0.60 5.0	55	26.41 0.88 3.3	56	4.80 0.24 5.3
36*	NESCHIMUS	16	14	6.05 0.39 6.5	14	11.60 0.65 5.6	15	25.70 0.92 3.6	15	4.72 0.27 5.7
17	MIMODES GRAYSONI	1	1	5.80 0.0 0.0	1	12.20 0.0 0.0	0	999.99 0.0 0.0	1	5.00 0.0 0.0
18	OREOSCOPTES MONTANUS	10	10	8.00 0.53 6.6	10	10.74 0.25 2.3	10	23.59 0.56 2.4	10	4.02 0.12 3.1
37*	TOXOSTOMA	66	62	7.21 0.42 5.8	59	12.11 0.54 4.4	62	27.91 0.79 2.8	65	5.25 0.21 3.9
2*	CINCLOCERYTHIA RUFICAUDA	17	17	5.48 0.31 5.6	17	11.31 0.44 3.9	17	25.56 1.18 4.6	17	4.88 0.20 4.1
30	RAMPHOCINCLUS BRACHYURUS	2	2	6.55 0.64 9.7	2	12.40 0.57 4.6	2	25.30 0.85 3.4	2	4.90 0.28 5.8
31	ONACORHUS ATRICAPILLUS	8	8	5.25 0.42 8.1	8	10.20 0.64 6.3	8	25.71 1.72 6.7	8	4.40 0.33 7.5
32	ALLENIA FUSCA	18	18	7.67 0.50 6.5	18	12.69 0.66 5.2	18	25.87 0.42 1.6	18	4.77 0.15 3.1
33	MACGARGPS FUSCATUS	12	12	9.27 0.54 5.9	12	14.57 0.83 5.7	12	31.12 1.60 5.1	12	6.06 0.31 5.1
3	MELANCTIS CAERULESCENS	5	5	8.04 0.21 2.6	5	12.72 0.23 1.8	5	26.74 0.43 1.6	5	4.98 0.19 3.9
4	MELANCTIS HYPOLEUCUS	4	4	7.97 0.17 2.1	4	12.87 0.39 3.1	4	27.50 0.72 2.6	4	4.97 0.13 2.5
5	MIMUS POLYGLOTTOS	22	20	7.54 0.55 7.2	19	11.41 0.70 6.2	19	23.61 0.57 2.4	20	4.16 0.22 5.2
6	MIMUS GILVUS	9	9	7.56 0.43 5.7	9	11.27 0.56 5.0	9	24.47 1.21 4.9	9	4.34 0.27 6.1
7	MIMUS GUNDLACHII	5	5	7.10 0.21 3.0	5	12.90 0.26 2.1	5	26.02 1.17 4.2	5	5.34 0.32 6.0
8	MIMUS THENCA	4	4	7.52 0.26 3.5	4	13.05 0.70 5.4	4	27.95 1.27 4.5	4	5.12 0.30 5.8
9	MIMUS LONGICAUDATUS	7	5	7.50 0.47 6.3	5	12.20 0.66 5.4	7	28.01 1.01 3.6	7	5.10 0.26 5.2
10	MIMUS SATURNINUS	4	4	7.97 0.26 3.3	4	12.62 0.61 4.8	4	28.87 0.32 1.1	4	5.27 0.10 1.8
11	MIMUS PATACONICUS	4	4	7.37 0.43 5.9	4	11.57 0.22 1.9	4	25.92 0.38 1.5	4	4.62 0.39 8.4
12	MIMUS TRIURUS	3	3	7.67 0.61 8.0	3	11.67 0.21 1.8	3	24.40 0.87 3.6	3	4.43 0.23 5.2
13	MIMUS DORSALIS									
14	NESCHIMUS TRIFASCIATUS	3	3	6.07 0.49 8.1	3	12.40 1.08 8.7	3	27.10 0.40 1.5	3	4.90 0.26 5.4
15	NESCHIMUS MACDONALDI	5	5	6.22 0.35 5.6	5	11.58 0.48 4.1	5	26.06 0.69 2.6	5	4.86 0.31 6.4
16	NESCHIMUS PARVULUS	8	6	5.87 0.38 6.4	6	10.83 0.53 4.9	7	23.94 1.15 4.8	7	4.40 0.24 5.4
19	TOXOSTOMA RUFUM	14	13	8.42 0.45 5.4	12	12.76 0.57 4.5	13	28.05 0.80 2.9	13	5.20 0.20 3.9
20	TOXOSTOMA LONGIROSTRE	4	4	7.57 0.25 3.3	4	12.60 0.24 1.9	3	28.63 0.57 2.0	4	5.37 0.13 2.3
21	TOXOSTOMA GUTTATUM	6	6	6.55 0.26 4.0	6	11.68 0.38 3.3	6	24.50 0.47 1.9	6	4.62 0.20 4.4
22	TOXOSTOMA CINEREUM	1	1	6.70 0.0 0.0	1	11.40 0.0 0.0	1	25.70 0.0 0.0	1	4.80 0.0 0.0
23	TOXOSTOMA RENDIRFI	3	3	7.73 0.06 0.7	3	11.67 0.97 8.3	3	26.67 0.25 0.9	3	4.80 0.30 6.2
24	TOXOSTOMA OCCIDENTALE	2	2	6.55 0.07 1.1	2	12.30 0.00 0.0	2	31.20 0.28 0.9	2	5.80 0.14 2.4
25	TOXOSTOMA CURVIROSTRE	20	17	8.03 0.46 5.7	16	13.09 0.62 4.7	18	29.13 0.92 3.2	20	5.53 0.24 4.3
26	TOXOSTOMA LECOICE	4	4	6.52 0.39 6.0	4	11.15 0.10 0.9	4	26.40 0.59 2.3	4	5.10 0.14 2.8
27	TOXOSTOMA REICIVIVUM	7	7	7.26 0.49 6.8	6	13.10 0.57 4.3	7	31.64 1.04 3.3	7	6.10 0.19 3.1
28	TOXOSTOMA DORSALE	5	5	6.72 0.45 6.7	5	11.32 0.33 2.9	5	27.18 0.44 2.0	5	5.14 0.09 1.7
	GRAND VALUES	253	243	7.11	237	11.99	244	25.71	249	4.90

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 59 N	FEMUR-SW MEAN	S D	C V	V 42 N	TIBIA-L MEAN	S D	C V	V 60 N	TIBIA-SW MEAN	S D	C V	V 57 N	TARNET-L MEAN	S D	C V
1	DUMETELLA CAROLINENSIS	25	25	1.71	0.08	4.6	25	38.79	1.00	2.6	25	1.44	0.08	5.6	24	27.75	0.69	2.5
2	MELANOPTILA GLAFRIROSTRIS	11	11	1.62	0.06	3.7	11	38.66	1.33	3.4	11	1.45	0.05	3.6	11	28.04	1.18	4.2
34*	MELANOTOS	9	9	2.26	0.10	4.4	9	45.67	0.78	1.7	9	1.84	0.11	6.1	9	32.45	0.56	1.7
35*	MIMUS	58	56	2.07	0.09	4.2	51	48.08	1.35	2.8	54	1.87	0.09	5.0	54	35.96	1.82	5.1
36*	NESOMIMUS	16	15	1.92	0.09	4.6	15	49.26	1.84	3.7	15	1.78	0.09	4.9	15	37.72	1.46	3.9
17	MIMODES GRAYSONI	1	1	2.20	0.0	0.0	0	999.99	0.0	0.0	1	2.00	0.0	0.0	1	36.20	0.0	0.0
18	OREOSCOPTES MONTANUS	10	10	1.80	0.09	5.2	9	42.30	0.96	2.3	10	1.69	0.06	3.4	9	30.76	0.67	2.2
37*	TOXOSTOMA	66	63	2.27	0.11	4.8	57	47.66	1.32	2.8	62	1.99	0.12	6.0	63	34.19	1.12	3.3
29	CINCLODERCETHIA RUFICAUDA	17	17	2.12	0.10	4.5	16	42.33	1.51	3.6	17	1.93	0.10	5.4	17	29.48	0.99	3.4
30	FAHNECINCLUS PRACHYURUS	2	2	2.10	0.14	6.7	2	43.70	1.27	2.9	2	1.75	0.07	4.0	2	31.75	0.92	2.9
31	ONACORIS ATRICAPILLUS	8	8	1.84	0.14	7.7	8	44.70	1.89	4.2	8	1.77	0.13	7.4	8	32.95	1.56	4.7
32	ALLENIA FUSCA	18	18	2.04	0.10	4.8	18	42.85	1.11	2.6	18	1.84	0.11	5.9	17	28.98	0.64	2.2
33	MARGAROPUS FUSCATUS	12	12	2.60	0.15	5.9	12	53.62	2.85	5.3	12	2.29	0.16	7.1	12	37.67	2.50	6.6
3	MELANOTIS CAPRULFESCENS	5	5	2.22	0.04	2.0	5	44.44	0.78	1.8	5	1.80	0.07	3.9	5	30.90	0.52	1.7
4	MELANOTIS MYDOLUCUS	4	4	2.30	0.14	6.1	4	46.90	0.79	1.7	4	1.87	0.15	8.0	4	34.00	0.59	1.7
5	MIMUS POLYGLOTTOS	22	20	1.80	0.09	4.8	19	43.24	1.08	2.5	20	1.70	0.09	5.5	19	31.76	1.06	3.3
6	MIMUS GILVUS	9	9	1.86	0.10	5.5	8	44.00	0.73	1.7	9	1.71	0.09	5.4	9	33.09	1.46	4.4
7	MIMUS GUNDLACHII	5	5	2.32	0.04	1.9	4	51.47	1.44	2.8	4	2.15	0.06	2.7	4	39.07	1.79	4.6
8	MIMUS TRENCA	4	4	2.20	0.12	5.2	4	50.82	1.67	3.7	4	2.02	0.10	4.7	4	38.75	1.73	4.5
9	MIMUS LONGICAUDATUS	7	7	2.13	0.08	3.6	6	51.25	2.25	4.4	6	1.88	0.13	7.1	7	37.60	3.74	9.9
10	MIMUS SATURNINUS	4	4	2.27	0.10	4.2	4	51.30	1.17	2.3	4	1.97	0.10	4.8	4	37.80	1.59	4.2
11	MIMUS PATAONICUS	4	4	2.05	0.06	2.8	3	47.63	0.84	1.8	4	1.85	0.06	3.1	4	36.07	0.49	1.4
12	MIMUS TRIUPUS	3	3	1.90	0.10	5.3	3	44.90	1.71	3.8	3	1.70	0.0	0.0	3	33.53	1.46	4.4
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NESOMIMUS TRIFASCIATUS	3	3	1.97	0.06	2.9	3	53.60	0.62	1.2	3	1.87	0.06	3.1	3	40.80	0.69	1.7
15	NESOMIMUS MACDONALDI	5	5	2.06	0.11	5.5	5	49.18	1.48	3.0	5	1.84	0.09	4.9	5	37.86	1.39	3.7
16	NESOMIMUS PARVULUS	8	7	1.73	0.08	4.4	7	44.99	2.28	5.1	7	1.63	0.10	5.8	7	34.49	1.67	4.9
19	TOXOSTOMA	14	13	2.28	0.11	4.7	13	48.48	1.24	2.6	13	1.96	0.09	4.4	13	34.48	1.08	3.1
20	TOXOSTOMA LONGIROSTRE	4	4	2.25	0.10	4.4	3	49.27	1.01	2.1	3	1.97	0.15	7.8	4	36.10	0.91	2.5
21	TOXOSTOMA GUTTATUM	6	6	2.07	0.10	5.0	6	42.28	1.15	2.7	6	1.68	0.08	4.5	6	31.35	1.14	3.6
22	TOXOSTOMA CINEREUM	1	1	2.00	0.0	0.0	1	43.30	0.0	0.0	1	1.80	0.0	0.0	1	32.20	0.0	0.0
23	TOXOSTOMA PENDIRELI	3	3	2.17	0.06	2.7	3	46.30	0.85	1.8	3	1.90	0.10	5.3	3	34.47	0.85	2.5
24	TOXOSTOMA OCELLATUM	2	2	2.55	0.07	2.8	2	53.35	0.78	1.5	2	2.20	0.0	0.0	2	37.60	0.28	0.8
25	TOXOSTOMA CURVIROSTRE	20	18	2.30	0.12	5.1	15	48.36	1.42	2.9	18	2.05	0.12	5.6	19	33.69	1.25	3.7
26	TOXOSTOMA LECENTEI	4	4	2.10	0.12	5.5	4	45.05	1.02	2.3	4	1.90	0.08	4.3	4	30.62	0.98	3.2
27	TOXOSTOMA REFINIVUM	7	7	2.64	0.11	4.3	5	54.22	2.04	3.8	7	2.47	0.22	9.0	6	38.50	1.17	3.0
28	TOXOSTOMA DORSALE	5	5	2.20	0.07	3.2	5	45.94	1.06	2.3	5	1.94	0.05	2.8	5	32.88	0.96	2.9
	CRANIUM VALUES	253	247	2.11			233	45.23			244	1.88			242	34.10		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 58 N	TARGET-W MEAN	S D	C V	V 43 N	MUM-L MEAN	S D	C V	V 44 N	MUM-MW MEAN	S D	C V	V 45 N	MUM-OCL MEAN	S D	C V
1	DUMETELLA CAROLINENSIS	25	24	1.20	0.09	7.2	24	21.91	0.55	2.5	24	6.42	0.23	3.5	23	6.55	0.25	3.9
2	MELANOPTILA CLAFRISTROSTRIS	11	11	1.22	0.06	5.0	11	21.95	0.66	3.0	11	6.52	0.24	3.6	11	6.72	0.29	4.3
34*	MELANOTOS	9	9	1.56	0.10	6.3	9	27.29	0.56	2.0	9	8.18	0.34	4.1	9	8.20	0.29	3.6
35*	MIMUS	58	55	1.54	0.08	5.3	52	27.61	1.00	3.6	54	7.52	0.31	4.2	54	8.56	0.41	4.7
36*	NESOMIMUS	16	15	1.46	0.08	5.5	15	27.56	1.08	3.9	15	7.07	0.41	5.8	15	8.34	0.54	6.4
17	MIMODES GRAYSONI	1	1	1.60	0.0	0.0	0	999.99	0.0	0.0	1	6.80	0.0	0.0	1	7.50	0.0	0.0
18	OPEUCOPTES MONTANUS	10	10	1.27	0.07	5.3	10	23.77	0.73	3.1	10	6.81	0.21	3.1	10	6.75	0.33	4.9
37*	TOXOSTOMA	66	65	1.67	0.12	7.1	63	26.68	0.78	2.9	65	7.52	0.34	4.5	65	7.88	0.38	5.0
29	CINCLODACTYLUS RUFICAUDA	17	17	1.73	0.14	8.1	17	24.75	1.36	5.5	17	7.09	0.32	4.4	17	8.04	0.45	5.6
30	RAMPHOCINCLUS BRACHYURUS	2	2	1.60	0.14	8.8	2	25.40	0.42	1.7	2	7.00	0.14	2.0	2	7.70	0.42	5.5
31	ONACCEPIUS ATRICAPILLUS	8	8	1.55	0.09	6.0	8	22.94	1.31	5.7	8	6.09	0.46	7.6	8	6.69	0.50	7.5
32	ALLENIA FUSCA	18	17	1.55	0.07	4.6	18	27.14	0.39	1.5	18	8.01	0.29	3.6	18	8.98	0.48	4.5
33	MARGAROPS FUSCATUS	12	12	2.01	0.15	7.5	12	33.19	1.67	5.0	12	10.00	0.61	6.1	12	10.65	0.45	4.2
3	MELANOTIS CAERULESCENS	5	5	1.52	0.08	5.5	5	27.48	0.42	1.5	5	8.26	0.23	2.8	5	8.16	0.28	3.4
4	MELANOTIS HYPOLEUCUS	4	4	1.60	0.12	7.2	4	27.10	0.70	2.6	4	8.07	0.44	5.5	4	8.25	0.31	3.8
5	MIMUS POLYGLOTTOS	22	20	1.40	0.10	7.0	19	26.08	0.85	3.3	20	7.25	0.38	5.2	20	8.08	0.41	5.1
6	MIMUS GILVUS	9	9	1.41	0.08	5.5	9	26.16	1.09	4.2	9	7.19	0.37	4.4	9	7.99	0.46	5.8
7	MIMUS GUNDLACHI	5	4	1.67	0.05	3.0	4	28.42	0.84	3.0	4	7.97	0.39	4.9	4	8.90	0.48	5.4
8	MIMUS THENEA	4	4	1.62	0.05	3.1	4	28.90	1.07	3.7	4	7.65	0.17	2.2	4	9.05	0.10	1.1
9	MIMUS LONGICAUDATUS	7	7	1.57	0.08	4.8	7	29.04	1.43	4.9	7	7.57	0.17	2.3	7	8.67	0.46	5.4
10	MIMUS SATURNINUS	4	4	1.75	0.06	3.3	3	29.97	0.21	0.7	3	8.33	0.31	3.7	3	10.03	0.15	1.5
11	MIMUS PATAGONICUS	4	4	1.50	0.08	5.4	3	26.70	0.56	2.1	4	7.05	0.13	1.8	4	8.02	0.36	4.5
12	MIMUS TRIURUS	3	3	1.40	0.0	0.0	3	25.60	1.22	4.8	3	6.97	0.21	3.0	3	7.77	0.25	3.2
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NESOMIMUS TRIFASCIATUS	3	3	1.40	0.10	6.7	3	29.17	0.76	2.6	3	7.30	0.30	4.1	3	9.03	0.25	2.8
15	NESOMIMUS MACDONALDI	5	5	1.48	0.04	3.0	5	27.66	0.82	3.0	5	7.16	0.38	5.3	5	8.10	0.39	4.9
16	NESOMIMUS PARVULUS	8	7	1.39	0.09	6.5	7	25.86	1.31	5.1	7	6.76	0.45	6.7	7	7.89	0.67	8.5
19	TOXOSTOMA RUFUM	14	13	1.62	0.10	6.1	13	27.52	0.86	3.1	13	7.99	0.27	3.3	13	8.05	0.31	3.9
20	TOXOSTOMA LONGIROSTRE	4	4	1.52	0.13	8.3	4	26.95	0.31	1.2	4	7.77	0.22	2.9	4	7.80	0.24	3.1
21	TOXOSTOMA GUTTATUM	6	6	1.50	0.06	4.2	5	23.38	0.39	1.7	6	6.78	0.15	2.2	6	6.52	0.23	3.6
22	TOXOSTOMA CINEREUM	1	1	1.60	0.0	0.0	1	25.40	0.0	0.0	1	7.00	0.0	0.0	1	6.70	0.0	0.0
23	TOXOSTOMA PENNIPES	3	3	1.63	0.06	3.5	3	27.63	0.64	2.3	3	7.67	0.29	3.8	3	7.87	0.31	3.9
24	TOXOSTOMA OCELLATUM	2	2	1.80	0.14	7.9	2	27.40	0.57	2.1	2	7.60	0.14	1.9	2	8.00	0.28	3.5
25	TOXOSTOMA CURVIROSTRE	20	20	1.80	0.16	8.7	19	29.37	0.97	3.3	20	8.31	0.45	5.4	20	8.70	0.48	5.5
26	TOXOSTOMA LEUCOTI	4	4	1.67	0.05	3.0	4	25.12	0.67	2.6	4	7.12	0.24	3.3	4	6.90	0.22	3.1
27	TOXOSTOMA PERIVIVUM	7	7	1.91	0.11	5.6	7	28.07	0.66	2.3	7	7.93	0.38	4.8	7	8.09	0.29	3.6
28	TOXOSTOMA DORSALIS	5	5	1.68	0.08	5.0	5	25.98	0.40	1.5	5	7.04	0.25	3.6	5	7.16	0.50	7.0
	GRAND VALUES	253	246	1.57			241	25.81			246	7.43			245	7.98		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 46 N	HUM-HD MEAN	S D	C V	V 62 N	HUM-SW MEAN	S D	C V	V 47 N	ULNA-L MEAN	S D	C V	V 61 N	ULNA-SW MEAN	S D	C V
1	DUMETELLA CAROLINENSIS	25	24	4.24	0.19	4.5	24	1.92	0.08	4.1	23	25.41	0.69	2.7	25	1.64	0.08	5.0
2	MELANOPTILA GLABRIROSTRIS	11	11	4.05	0.29	7.1	11	1.89	0.09	5.0	11	26.55	1.03	3.9	11	1.66	0.08	4.9
34*	MELANOTOS	9	9	4.91	0.33	6.7	9	2.31	0.11	4.8	9	31.55	1.22	3.9	9	2.07	0.08	4.1
35*	MIMUS	58	54	4.67	0.29	6.1	54	2.25	0.09	4.1	53	32.19	1.27	3.9	54	2.00	0.09	4.3
36*	NEOSCHIMUS	16	15	4.26	0.32	7.5	15	2.09	0.10	4.6	15	31.44	1.59	5.0	15	1.92	0.08	4.1
17	MIMODES GRAYSONI	1	1	3.90	0.0	0.0	1	2.10	0.0	0.0	1	29.90	0.0	0.0	1	2.00	0.0	0.0
18	CREOSCOPTES MONTANUS	10	10	4.28	0.15	3.4	10	1.98	0.09	4.6	10	28.16	0.83	2.9	10	1.76	0.11	6.1
37*	TOXOSTOMA	66	65	4.47	0.29	6.4	64	2.23	0.10	4.6	63	29.24	0.90	3.1	64	1.95	0.11	5.5
29	CINCLOCERTHIA RUFICAUDA	17	17	4.22	0.24	5.7	17	2.17	0.11	5.1	17	28.69	1.37	4.8	17	1.94	0.12	6.3
30	RAMPHOCINCLUS PRACHYURUS	2	2	4.20	0.57	13.5	2	2.00	0.14	7.1	2	28.55	0.64	2.2	2	1.80	0.0	0.0
31	ONACORPUS ATRICAPILLUS	8	8	3.51	0.32	9.1	8	1.82	0.12	6.4	8	23.50	1.51	6.4	8	1.59	0.11	7.1
32	ALLENIA FUSCA	18	18	4.73	0.24	5.2	18	2.42	0.08	3.3	18	33.67	0.73	2.2	18	2.21	0.07	3.1
33	MARGAROPUS FUSCATUS	12	12	5.97	0.37	6.2	12	3.01	0.17	5.8	11	41.55	2.31	5.6	12	2.76	0.17	6.3
3	MELANOTIS CAFFULESCENS	5	5	4.90	0.72	4.6	5	2.30	0.0	0.0	5	31.50	1.34	4.2	5	2.10	0.07	3.4
4	MELANOTIS HYPOLEUCUS	4	4	4.92	0.43	8.8	4	2.32	0.17	7.3	4	31.60	1.04	3.3	4	2.05	0.10	4.9
5	MIMUS POLYGLOTTOS	22	20	4.49	0.32	7.2	19	2.15	0.10	4.8	20	31.55	1.22	3.9	20	1.92	0.08	4.3
6	MIMUS GILVUS	9	9	4.46	0.32	7.3	9	2.16	0.09	4.1	8	31.39	1.01	3.2	9	1.89	0.06	3.2
7	MIMUS CUNDLACHI	5	4	4.90	0.36	7.3	5	2.42	0.08	3.5	4	33.50	1.60	4.8	4	2.12	0.05	2.4
8	MIMUS THENCA	4	4	4.87	0.10	2.0	4	2.37	0.13	5.3	4	32.42	1.68	5.2	4	2.07	0.10	4.6
9	MIMUS LONGICAUDATUS	7	7	4.59	0.25	5.5	7	2.24	0.08	3.5	7	33.23	1.57	4.7	7	2.04	0.11	5.6
10	MIMUS SATURNINUS	4	3	5.53	0.15	2.8	4	2.32	0.05	2.2	4	34.10	0.98	2.9	4	2.17	0.10	4.4
11	MIMUS PATAGONICUS	4	4	4.37	0.10	2.2	3	2.17	0.06	2.7	3	30.97	0.32	1.0	3	1.90	0.10	5.3
12	MIMUS TRIURUS	3	3	4.13	0.15	3.7	3	2.13	0.06	2.7	3	30.37	1.15	3.8	3	1.90	0.10	5.3
13	MIMUS DOSSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NEOSCHIMUS TRIFASCIATUS	3	3	4.47	0.15	3.4	3	2.13	0.12	5.4	3	33.30	1.13	3.4	3	1.97	0.06	2.9
15	NEOSCHIMUS MACDONALDI	5	5	4.28	0.31	7.3	5	2.18	0.08	3.8	5	31.74	1.14	3.6	5	2.04	0.05	2.7
16	NEOSCHIMUS PARVULUS	8	7	4.03	0.36	9.0	7	1.96	0.10	5.0	7	29.44	1.93	6.6	7	1.74	0.10	5.6
19	TOXOSTOMA RUFUM	14	13	4.99	0.27	5.4	13	2.38	0.10	4.3	13	30.46	0.82	2.7	13	2.10	0.14	6.4
20	TOXOSTOMA LONGIROSTRE	4	4	4.40	0.14	3.2	4	2.32	0.15	6.5	4	30.07	0.54	1.8	4	1.95	0.06	3.0
21	TOXOSTOMA GUTTATUM	6	6	4.07	0.22	5.3	5	2.06	0.09	4.3	5	26.12	0.53	2.0	5	1.80	0.12	6.8
22	TOXOSTOMA CINEREUM	1	1	4.00	0.0	0.0	1	2.10	0.0	0.0	1	28.30	0.0	0.0	1	1.80	0.0	0.0
23	TOXOSTOMA FENDIRPI	3	3	4.73	0.35	7.4	3	2.20	0.10	4.5	3	30.73	1.15	3.8	3	1.93	0.12	6.0
24	TOXOSTOMA OCELLATUM	2	2	4.25	0.07	1.7	2	2.20	0.0	0.0	2	28.30	0.42	1.5	2	2.00	0.14	7.1
25	TOXOSTOMA CUKVIROSTRE	20	20	5.01	0.36	7.1	20	2.45	0.11	4.5	19	32.92	1.15	3.5	20	2.13	0.10	4.8
26	TOXOSTOMA LECOITEI	4	4	4.07	0.17	4.2	4	2.02	0.05	2.5	4	27.22	0.75	2.7	4	1.90	0.08	4.3
27	TOXOSTOMA REDIVIVUM	7	7	4.64	0.24	5.3	7	2.49	0.09	3.6	7	30.31	0.73	2.4	7	2.03	0.08	3.7
28	TOXOSTOMA DOSSALE	5	5	4.48	0.26	5.8	5	2.10	0.10	4.8	5	27.92	0.62	2.2	5	1.90	0.10	5.3
	GRAND VALUES	253	246	4.49			245	2.20			241	30.42			246	1.96		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SFT #	SFT DESCRIPTION	SET N	V 63 N	CARMET-L MEAN	S D	C V	V 64 N	PHALNX-L MEAN	S D	C V	V 65 N	POLLEX-L MEAN	S D	C V	V 66 N	CORAC-L MEAN	S D	C V			
1	DUMETELLA CAROLINENSIS	25	25	14.30	0.34	2.4	24	6.32	0.19	3.1	19	3.43	0.17	4.9	25	19.74	0.51	2.6			
2	MELANOPTILA GLABRIROSTRIS	11	10	14.25	0.52	3.6	10	6.15	0.25	4.1	8	3.60	0.37	10.4	10	18.97	0.48	2.5			
34*	MELANOTOS	9	9	17.01	0.53	3.1	9	7.09	0.41	5.8	8	4.35	0.19	4.4	9	24.03	0.72	3.0			
35*	MIMUS	58	52	18.22	0.73	4.0	53	8.13	0.39	4.8	46	4.55	0.36	7.8	57	22.58	0.81	3.6			
36*	NESOMIMUS	16	15	18.07	0.86	4.8	15	7.92	0.50	6.3	14	4.48	0.27	6.1	14	21.60	1.01	4.7			
17	MIMODES GRAYSONI	1	1	16.60	0.0	0.0	1	7.20	0.0	0.0	1	4.30	0.0	0.0	1	21.00	0.0	0.0			
18	ORESCOPTES MONTANUS	10	10	16.29	0.48	2.9	10	7.28	0.42	5.7	10	3.87	0.29	7.4	10	21.13	0.65	3.1			
37*	TOXOSTOMA	66	63	16.42	0.60	3.6	64	6.94	0.30	4.4	56	4.04	0.40	9.9	64	23.23	0.63	2.7			
29	CINCLORHIZA RUFIGAUDA	17	17	16.26	0.77	4.7	17	6.75	0.41	6.1	16	3.91	0.32	8.1	16	22.37	0.82	3.7			
30	RAMPHOCINCLUS FRACHYURUS	2	2	16.15	0.78	4.8	2	7.00	0.42	6.1	2	3.80	0.57	14.9	2	21.80	0.57	2.6			
31	ONACORPUS ATRICAPILLUS	8	8	13.29	0.82	6.2	8	5.35	0.61	11.4	7	3.69	0.44	11.9	8	20.22	1.23	6.1			
32	ALLENTIA FUSCA	18	18	19.23	0.60	3.1	16	8.15	0.28	3.4	17	4.34	0.25	5.8	18	23.22	0.51	2.2			
33	MARGAROPUS FUSCATUS	12	11	23.52	1.28	5.5	12	9.77	0.40	4.1	9	5.34	0.36	6.8	12	28.27	1.41	5.0			
3	MELANOTIS CAPRULIFENS	5	5	16.98	0.36	2.1	5	7.24	0.50	6.9	5	4.30	0.14	3.3	5	24.02	0.69	2.9			
4	MELANOTIS HYPOLEUCUS	4	4	17.05	0.70	4.1	4	6.95	0.24	3.4	3	4.40	0.26	6.0	4	24.05	0.75	3.1			
5	MIMUS POLYLOCTES	22	19	17.35	0.63	3.6	19	7.64	0.32	4.2	18	4.25	0.31	7.4	21	21.58	0.80	3.7			
6	MIMUS GILVUS	9	9	17.42	0.85	4.9	9	7.61	0.45	5.9	6	4.23	0.52	12.3	9	21.77	0.96	4.4			
7	MIMUS GUNLACHI	5	4	18.92	0.79	4.2	4	8.60	0.63	7.3	4	4.57	0.44	9.7	5	23.38	0.86	3.7			
8	MIMUS TENICA	4	4	18.72	0.74	3.9	4	8.45	0.39	4.6	4	4.65	0.31	6.7	4	22.82	0.90	3.9			
9	MIMUS LONGICAUDATUS	7	6	19.10	0.90	5.2	6	8.65	0.34	4.0	5	4.90	0.16	3.2	7	23.47	0.98	4.2			
10	MIMUS SATURNINUS	4	4	19.60	0.50	2.6	4	8.63	0.48	5.6	3	5.13	0.15	3.0	4	24.97	0.25	1.0			
11	MIMUS PATAGONICUS	4	4	17.70	0.22	1.2	4	7.72	0.19	2.5	3	4.30	0.0	0.0	4	21.50	0.32	1.5			
12	MIMUS TRIURUS	3	2	16.95	0.92	5.4	3	7.73	0.40	5.2	3	4.33	0.60	13.9	3	21.13	0.40	1.9			
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET													
14	NESOMIMUS TRIFASCIATUS	3	3	18.87	0.76	4.0	3	8.07	0.32	4.0	2	4.70	0.28	6.0	3	22.47	0.84	3.7			
15	NESOMIMUS MACDONALDI	5	5	18.66	0.64	3.4	5	8.24	0.54	6.6	5	4.58	0.33	7.1	4	22.57	0.88	3.9			
16	NESOMIMUS PARVULUS	8	7	16.67	1.01	6.1	7	7.46	0.52	7.0	7	4.16	0.23	5.5	7	19.77	1.12	5.7			
19	TOXOSTOMA RUFUM	14	13	17.28	0.89	5.2	13	7.28	0.40	5.4	12	4.33	0.62	14.2	13	24.26	0.70	2.9			
20	TOXOSTOMA LONGIROSTRE	4	4	16.40	0.14	0.9	4	6.85	0.17	2.5	4	3.95	0.19	4.8	4	24.32	0.41	1.7			
21	TOXOSTOMA CUTIATUM	6	5	14.52	0.29	2.0	6	6.28	0.10	1.6	4	3.50	0.12	3.3	5	20.66	0.39	1.9			
22	TOXOSTOMA CINKEUM	1	1	16.10	0.0	0.0	1	7.00	0.0	0.0	1	4.00	0.0	0.0	1	21.70	0.0	0.0			
23	TOXOSTOMA FENDIRFI	3	3	17.57	0.45	2.6	3	7.83	0.23	2.9	3	4.30	0.26	6.2	3	22.90	0.36	1.6			
24	TOXOSTOMA OCELLATUM	2	2	16.10	0.28	1.8	2	6.85	0.07	1.0	2	3.85	0.07	1.8	2	23.90	0.42	1.8			
25	TOXOSTOMA CURVIROSTRE	20	19	18.46	0.63	3.4	19	7.77	0.34	4.4	17	4.56	0.37	8.1	20	25.06	0.77	3.1			
26	TOXOSTOMA LEOCOTTEI	4	4	15.57	0.34	2.2	4	6.37	0.13	2.0	3	3.93	0.12	2.9	4	22.12	0.57	2.6			
27	TOXOSTOMA EFFIVIVUM	7	7	16.67	0.39	2.4	7	6.66	0.30	4.5	7	4.06	0.32	7.9	7	24.84	0.38	1.5			
28	TOXOSTOMA DORSALE	5	5	15.56	0.19	1.3	5	6.46	0.18	2.8	3	3.93	0.12	2.9	5	22.50	0.42	1.9			
	GRAND VALUES	253	241	17.12			243	7.39			213	4.23			246	22.58					

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 67 N	CCRAC-MW MEAN	S D	C V	V 68 N	CCRAC-SW MEAN	S D	C V	V 69 N	CORA-CPL MEAN	S D	C V	V 70 N	PYGO-MH MEAN	S D	C V			
1	DMETELLA CARLINFENSIS	25	25	3.54	0.17	4.7	25	1.05	0.06	5.6	23	8.37	0.40	4.8	19	8.98	0.41	4.6			
2	MELANOPTILA GLAPPIROSTRIS	11	11	3.26	0.28	8.7	11	1.11	0.07	6.3	10	7.76	0.27	3.5	6	8.58	0.40	4.6			
34*	MELANOTOS	9	9	4.32	0.25	5.7	9	1.37	0.11	8.2	9	9.61	0.42	4.3	7	11.02	0.59	5.4			
35*	MIMUS	58	57	4.06	0.26	6.3	57	1.30	0.11	8.3	57	9.25	0.56	6.0	46	10.58	0.78	7.4			
36*	NESCHIMUS	16	15	3.75	0.21	5.7	15	1.15	0.07	6.2	15	8.72	0.71	8.1	15	10.21	0.63	6.1			
17	MIMODES GRAYSONI	1	1	4.00	0.0	0.0	1	1.30	0.0	0.0	1	8.00	0.0	0.0	1	8.40	0.0	0.0			
18	OEESECEPTES MONTANUS	10	10	3.71	0.21	5.7	10	1.17	0.11	9.1	10	8.48	0.42	5.0	8	8.59	0.55	6.4			
37*	TOXOSTOMA	66	65	3.82	0.24	6.3	65	1.33	0.09	6.9	65	9.38	0.45	4.8	55	10.47	0.58	5.4			
29	CINCLOCERTHIA RUFIGAUCHA	17	17	3.72	0.28	7.6	17	1.26	0.09	6.8	16	9.50	0.52	5.4	17	9.16	0.60	6.5			
30	RAMPHOCINCLUS BRACHYURUS	2	2	3.80	0.14	3.7	2	1.30	0.0	0.0	2	8.50	0.71	8.3	1	9.20	0.0	0.0			
31	ONNACORIUS ATRICAPILLUS	8	8	3.09	0.18	5.9	8	1.02	0.07	6.9	8	8.46	0.43	5.1	7	8.80	0.40	4.9			
32	ALLENIA FUSCA	10	18	4.38	0.25	5.7	18	1.43	0.08	5.8	18	9.43	0.39	4.1	13	9.80	0.44	4.5			
33	MARGAROPS FUSCATUS	12	12	5.30	0.36	6.8	12	1.73	0.11	6.2	12	11.07	1.10	9.9	9	12.20	0.70	5.8			
3	MELANOTIS CAERULESCENS	5	5	4.30	0.19	4.4	5	1.40	0.12	8.7	5	9.64	0.47	4.9	4	11.05	0.68	4.2			
4	MELANOTIS HYPOLEUCUS	4	4	4.35	0.31	7.1	4	1.35	0.10	7.4	4	9.57	0.33	3.5	3	11.00	0.44	4.0			
5	MIMUS POLYGLOTOS	22	21	4.03	0.31	7.7	21	1.23	0.09	7.4	21	8.71	0.58	6.7	18	10.03	0.60	6.0			
6	MIMUS GILVUS	9	9	4.03	0.21	5.3	9	1.23	0.11	9.1	9	8.78	0.56	6.4	6	10.33	0.74	7.1			
7	MIMUS CINCLACHII	5	5	4.28	0.28	6.5	5	1.50	0.22	14.9	5	9.40	0.55	5.8	2	11.15	0.49	4.4			
8	MIMUS THENCA	4	4	4.15	0.21	5.0	4	1.27	0.10	7.5	4	9.38	0.48	5.1	4	10.77	1.21	11.2			
9	MIMUS LONGICAUDATUS	7	7	4.07	0.11	2.7	7	1.27	0.08	5.9	7	9.80	0.58	5.9	7	10.79	0.93	8.6			
10	MIMUS SATURNINUS	4	4	4.52	0.10	2.1	4	1.47	0.05	3.4	4	10.00	0.0	0.0	4	11.52	1.08	9.4			
11	MIMUS PATACONICUS	4	4	3.62	0.33	9.1	4	1.17	0.05	4.3	4	8.45	0.42	4.7	2	9.90	0.00	0.0			
12	MIMUS TRIUSUS	3	3	3.80	0.17	4.6	3	1.20	0.10	8.3	3	9.00	0.87	9.6	3	10.17	0.67	6.5			
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET													
14	NESCHIMUS TRIFASCIATUS	3	3	3.67	0.25	6.9	3	1.30	0.10	7.7	3	8.77	0.46	5.3	3	10.80	0.53	4.9			
15	NESCHIMUS MACDONALDI	5	5	4.02	0.19	4.8	5	1.14	0.09	7.8	5	9.20	0.27	3.0	5	10.18	0.68	6.6			
16	NESCHIMUS PARVULUS	8	7	3.56	0.21	6.0	7	1.01	0.04	3.7	7	8.20	0.94	11.5	7	9.66	0.62	6.5			
19	TOXOSTOMA RUFUM	14	13	4.10	0.33	8.0	13	1.38	0.12	8.5	13	9.81	0.38	3.9	12	11.45	0.48	4.2			
20	TOXOSTOMA LONGIROSTRE	4	4	3.92	0.19	4.8	4	1.22	0.15	12.2	4	9.57	0.43	4.5	4	10.65	0.72	6.7			
21	TOXOSTOMA GUTTATUM	6	6	3.33	0.16	4.9	6	1.25	0.05	4.4	6	8.63	0.68	7.8	5	9.22	0.40	4.4			
22	TOXOSTOMA CINEREFUM	1	1	3.30	0.0	0.0	1	1.30	0.0	0.0	1	9.00	0.0	0.0	1	9.30	0.0	0.0			
23	TOXOSTOMA BENDIRPEI	3	3	4.07	0.12	2.8	3	1.40	0.10	7.1	3	9.27	0.25	2.7	3	10.13	0.99	9.7			
24	TOXOSTOMA OCELLATUM	2	2	3.55	0.07	2.0	2	1.30	0.0	0.0	2	9.25	0.35	3.8	1	11.10	0.0	0.0			
25	TOXOSTOMA CUVIEROSTRE	20	20	4.39	0.24	5.4	20	1.47	0.07	4.5	20	9.90	0.52	5.2	16	11.44	0.67	5.9			
26	TOXOSTOMA LECONTEI	4	4	3.75	0.13	3.4	4	1.15	0.06	5.0	4	8.95	0.10	1.1	3	9.57	0.55	5.8			
27	TOXOSTOMA PEDIVIVUM	7	7	4.03	0.21	5.3	7	1.44	0.11	7.9	7	10.14	0.38	3.7	5	12.46	0.18	1.5			
28	TOXOSTOMA DORSALE	5	5	3.78	0.24	6.3	5	1.36	0.09	6.6	5	9.30	0.27	2.9	5	11.36	0.42	3.7			
	GRAND VALUES	253	250	3.92			250	1.29			246	9.15			204	10.24					

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 71 N	PYGO-W MEAN	S D	C V	V 49 N	KEOW-SF MEAN	S D	C V	V 50 N	CDPN MEAN	S D	C V	V 51 N	CSF-MID MEAN	S D	C V
1	MIMETILLA CAROLINENSIS	25	19	3.83	0.20	5.1	25	56.68	3.34	5.7	25	50.80	5.63	11.1	25	22.16	3.65	16.5
2	MELANOPTILA CLAPRIROSTRIS	11	6	3.53	0.19	5.3	11	48.27	5.08	10.5	11	45.91	4.61	10.1	11	17.64	3.04	17.2
34*	MELANOTOS	9	7	4.92	0.50	10.2	9	53.88	6.29	11.7	9	43.27	4.80	11.1	9	18.77	3.73	19.9
35*	MIMUS	58	47	4.39	0.37	8.5	55	57.37	6.54	11.4	57	39.28	4.44	11.3	55	24.07	4.05	16.8
36*	NESCHIMUS	16	15	4.08	0.40	9.8	16	49.74	4.45	9.0	16	29.40	2.62	8.9	16	30.81	3.74	12.1
17	MIMODES GRAYSONI	1	1	4.80	0.0	0.0	1	55.00	0.0	0.0	1	40.00	0.0	0.0	1	20.00	0.0	0.0
18	OREOSCOPTES MONTANUS	10	8	3.85	0.27	6.9	10	48.50	5.30	10.9	10	45.00	6.02	13.4	10	25.00	3.09	12.4
37*	TOXOSTOMA	66	55	4.57	0.35	7.7	65	52.41	4.26	8.1	66	33.62	3.60	10.7	66	21.62	3.71	17.1
29	CINCLERCETIA RUFICAUDA	17	17	3.63	0.35	9.7	17	62.82	4.88	7.8	16	28.25	3.32	11.7	17	3.00	5.94	197.9
30	RAMPHOCINCLUS BRACHYURUS	2	1	3.40	0.0	0.0	2	51.50	2.12	4.1	2	36.50	4.95	13.6	2	18.00	4.24	23.6
31	ONACORPUS ATRICAPILLUS	8	7	3.60	0.26	7.2	8	61.63	5.45	8.8	8	34.13	2.42	7.1	8	35.63	6.78	19.0
32	ALLENTIA FUSCA	18	15	3.79	0.29	7.5	18	79.50	5.53	7.0	18	42.06	4.26	10.1	18	-8.33	6.07	72.8
33	MARGAROPS FUSCATUS	12	10	4.79	0.47	9.9	12	80.58	6.07	7.5	12	36.00	3.07	8.5	12	-6.75	9.32	*****
3	MELANOTIS CAIRULESCENS	5	4	4.90	0.57	11.7	5	52.00	6.71	12.9	5	43.80	2.68	6.1	5	18.80	3.90	20.7
4	MELANOTIS HYPOLEUCUS	4	3	4.93	0.38	7.7	4	55.75	5.68	10.2	4	42.75	6.65	15.6	4	18.75	3.50	18.7
5	MIMUS POLYGLOTOS	22	18	4.17	0.45	10.8	21	59.52	6.34	10.6	22	43.23	4.87	11.3	21	22.43	3.97	17.7
6	MIMUS GILVUS	9	7	4.16	0.43	10.3	8	61.88	6.51	10.5	9	42.78	3.77	8.8	9	21.89	4.83	22.1
7	MIMUS GUNDLACHII	5	2	4.25	0.21	5.0	4	58.75	2.50	4.3	4	38.00	1.41	3.7	4	25.00	1.63	6.5
8	MIMUS THENCA	4	4	4.35	0.31	7.1	4	53.25	6.24	11.7	4	39.50	3.70	9.4	4	27.25	4.03	14.8
9	MIMUS LONGICAUDATUS	7	7	4.43	0.24	5.3	7	53.57	6.63	12.4	7	37.00	5.20	14.0	7	24.14	4.88	20.2
10	MIMUS SATURNINUS	4	4	5.05	0.10	2.0	4	60.00	7.07	11.8	4	40.25	3.59	8.9	3	21.67	1.53	7.1
11	MIMUS PATAGONICUS	4	2	4.40	0.28	6.4	4	55.00	10.80	19.6	4	37.50	4.20	11.2	4	26.50	4.20	15.9
12	MIMUS TRIURUS	3	3	4.33	0.29	6.7	3	57.00	2.65	4.6	3	36.00	5.20	14.4	3	23.67	2.31	9.8
13	MIMUS DORSALIS							THERE ARE NO SPECIMENS IN THIS SET										
14	NESCHIMUS TRIFASCIATUS	3	3	4.20	0.10	2.4	3	49.33	4.04	8.2	3	33.33	2.89	8.7	3	28.67	1.53	5.3
15	NESCHIMUS MACDONALDI	5	5	4.24	0.47	11.1	5	47.40	4.34	9.1	5	27.00	2.74	10.1	5	31.40	4.88	15.5
16	NESCHIMUS PARVULUS	8	7	3.81	0.41	10.9	8	52.50	4.63	8.8	8	27.88	2.47	8.9	8	32.38	3.42	10.6
19	TOXOSTOMA RUFUM	14	11	4.85	0.77	4.5	13	59.69	3.25	5.4	14	34.50	4.83	14.0	14	20.93	2.95	14.1
20	TOXOSTOMA LONGIROSTRIS	4	4	4.40	0.43	9.8	4	61.75	3.95	6.4	4	31.75	4.27	13.5	4	21.75	2.87	13.2
21	TOXOSTOMA GUTTATUM	6	5	3.82	0.26	6.8	6	56.17	5.12	9.1	6	34.50	2.35	6.8	6	26.33	2.50	9.5
22	TOXOSTOMA CINEREUM	1	1	4.30	0.0	0.0	1	45.00	0.0	0.0	1	30.00	0.0	0.0	1	20.00	0.0	0.0
23	TOXOSTOMA BENDIRI	3	3	4.57	0.15	3.3	3	56.67	2.89	5.1	3	39.00	1.73	4.4	3	20.33	2.52	12.4
24	TOXOSTOMA CELLATUM	2	1	4.40	0.0	0.0	2	47.50	3.54	7.4	2	30.00	0.0	0.0	2	24.00	1.41	5.9
25	TOXOSTOMA CUKVIKOSTRE	20	16	4.46	0.30	6.8	20	51.60	5.01	9.7	20	33.30	3.25	9.7	20	22.30	4.67	20.9
26	TOXOSTOMA LEONTEI	4	3	4.60	0.10	2.2	4	48.00	2.45	5.1	4	31.75	2.87	9.0	4	21.75	4.27	19.6
27	TOXOSTOMA REDIVIVUM	7	6	5.45	0.70	12.8	7	52.14	4.88	9.4	7	37.00	2.24	6.0	7	18.57	2.99	16.1
28	TOXOSTOMA DORSALIS	5	5	4.84	0.30	6.3	5	45.60	2.61	5.7	5	34.40	4.39	12.8	5	20.20	3.96	19.6
	GRAND VALUES	253	208	4.32			249	51.83			251	37.00			250	20.78		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 52 N	CMXP-MTD MEAN S D C V	V 53 N	CLZY-POP MEAN S D C V	V 54 N	CLSF-POP MEAN S D C V	V 75 N	OLF PRO MEAN S D C V
1	DUMFELLA CAROLINENSIS	25	22	26.14 4.54 17.4	24	42.54 3.62 8.5	24	53.71 3.72 6.9	25	2.56 0.65 25.4
2	MELANOPTILA GLABRISTRIS	11	9	26.33 3.08 11.7	11	45.27 5.16 11.4	11	52.91 4.50 8.5	10	2.90 0.32 10.9
34*	MELANOTOS	9	9	21.50 4.31 20.0	9	42.20 4.09 9.7	9	48.82 3.93 8.0	8	1.63 0.35 21.8
35*	MIMUS	58	53	13.54 2.99 22.1	53	41.06 5.06 12.3	53	48.94 5.93 12.1	55	1.33 0.65 48.8
36*	NESCHIMUS	16	16	10.78 1.85 17.2	16	40.56 3.80 9.4	16	45.95 4.56 9.9	16	1.69 0.82 48.6
17	MIMODES GRAYSONI	1	1	15.00 0.0 0.0	1	40.00 0.0 0.0	1	45.00 0.0 0.0	1	1.00 0.0 0.0
18	OREOSCOPTES MONTANUS	10	7	17.57 2.23 12.7	10	35.90 2.92 8.1	10	47.60 3.69 7.7	10	1.50 0.53 35.1
37*	TOXOSTOMA	66	63	15.55 2.96 19.0	66	31.27 4.47 14.3	66	49.47 4.48 9.1	65	1.75 0.67 38.2
29	CINCLORHIZA PUFICAUDA	17	16	15.94 1.65 10.4	16	49.19 5.47 11.1	16	61.94 3.68 5.9	17	2.71 0.59 21.7
30	RAMPHOCINCLUS BRACHYURUS	2	2	17.50 3.54 20.2	2	51.00 1.41 2.8	2	55.00 7.07 12.9	2	3.00 0.0 0.0
31	COMPTONOTUS ATRICAPILLUS	8	7	32.43 4.43 13.7	7	46.43 2.44 5.3	7	48.57 2.44 5.0	6	4.00 0.0 0.0
32	ALLENTA FUSCA	18	18	25.50 1.98 7.8	18	47.61 4.58 9.6	18	63.22 3.81 6.0	18	1.44 0.62 42.6
33	MARGAROPUS FUSCATUS	12	12	20.33 3.03 14.9	12	56.00 6.55 11.7	12	64.67 10.25 15.9	12	2.67 0.49 18.5
3	MELANOTIS CAERULESCENS	5	5	23.00 5.70 24.8	5	41.40 4.98 12.0	5	48.40 5.03 10.4	4	1.25 0.50 40.0
4	MELANOTIS MYIOLEUCUS	4	4	20.00 0.0 0.0	4	43.00 2.45 5.7	4	49.25 1.50 3.0	4	2.00 0.0 0.0
5	MIMUS POLYGLOTTOS	22	21	13.62 3.40 25.0	18	41.61 4.57 11.0	18	49.50 5.90 11.9	20	1.40 0.68 48.6
6	MIMUS GILVUS	9	8	14.25 3.37 23.6	9	42.44 4.48 10.5	9	52.00 5.45 10.5	9	1.56 0.73 46.7
7	MIMUS GUNDLACHII	5	3	14.33 1.15 8.1	4	38.75 4.79 12.4	4	48.75 4.79 9.8	4	1.25 0.50 40.0
8	MIMUS THENEA	4	3	8.33 1.53 18.3	4	36.50 5.74 15.7	4	42.50 5.26 12.4	4	1.00 0.0 0.0
9	MIMUS LONGICAUDATUS	7	7	12.86 1.68 13.0	7	40.43 4.61 11.4	7	47.71 5.41 11.3	7	1.57 0.79 50.1
10	MIMUS SATURNINUS	4	4	18.50 3.11 16.8	4	47.50 5.00 10.5	4	49.25 6.50 13.2	4	1.25 0.50 40.0
11	MIMUS PATACNICUS	4	4	14.75 2.50 16.9	4	41.25 4.79 11.6	4	52.50 6.45 12.3	4	1.25 0.50 40.0
12	MIMUS TRIURUS	3	3	11.67 3.06 26.2	3	40.00 10.00 25.0	3	49.33 9.29 18.8	3	1.33 0.58 43.3
13	MIMUS DORSALIS					THERE ARE NO SPECIMENS IN THIS SET				
14	NESCHIMUS TRIFASCIATUS	3	3	11.33 0.58 5.1	3	45.33 2.52 5.6	3	47.00 7.94 16.9	3	1.33 0.58 43.3
15	NESCHIMUS MACDONALDI	5	5	10.00 1.41 14.1	5	41.60 2.30 5.5	5	44.60 2.70 6.1	5	1.60 0.55 34.2
16	NESCHIMUS PARVILUS	8	8	11.00 2.27 20.6	8	34.75 4.68 13.5	8	46.25 4.06 8.8	8	2.13 0.99 46.6
19	TOXOSTOMA RUFUM	14	14	13.93 2.46 17.7	14	37.93 2.27 6.0	14	54.50 3.20 5.9	14	2.64 0.50 18.8
20	TOXOSTOMA LONGIROSTRE	4	4	14.50 1.00 6.9	4	33.75 4.79 14.2	4	48.75 4.79 9.8	4	2.75 0.50 18.2
21	TOXOSTOMA GUTTATUM	6	6	18.17 4.31 23.7	6	35.00 3.16 9.0	6	50.83 4.92 9.7	6	2.00 0.0 0.0
22	TOXOSTOMA CINEREUM	1	1	18.00 0.0 0.0	1	35.00 0.0 0.0	1	45.00 0.0 0.0	1	1.00 0.0 0.0
23	TOXOSTOMA FENDIREI	3	3	12.33 2.52 20.4	3	33.33 2.89 8.7	3	52.33 4.04 7.7	3	1.00 0.0 0.0
24	TOXOSTOMA OCELLATUM	2	2	13.00 1.41 10.9	2	30.00 0.0 0.0	2	42.50 3.54 8.3	2	1.50 0.71 47.1
25	TOXOSTOMA CURVIOSTRE	20	18	13.89 2.45 17.6	20	32.65 5.71 17.5	20	48.30 4.24 8.8	20	1.10 0.31 28.0
26	TOXOSTOMA LEONTEI	4	4	15.25 3.40 22.3	4	27.00 2.45 9.1	4	54.50 1.00 1.8	3	2.00 1.73 86.6
27	TOXOSTOMA FEDIVIVUM	7	6	20.67 3.33 16.1	7	20.00 5.00 25.0	7	48.57 8.02 16.5	7	1.29 0.49 38.0
28	TOXOSTOMA FOREALE	5	5	15.80 4.55 28.8	5	28.00 5.70 20.4	5	49.40 2.61 5.3	5	2.20 1.64 74.7
	GRAND VALUES	253	235	16.75	245	39.41	245	50.45	245	1.82

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 76 N	ECTH FOR MEAN	S D	C V	V
1	DUMETELLA CAROLINENSIS	25	25	2.16	0.69	31.9	
2	MELANOPTILA GLAERIGSTRIS	11	11	2.91	0.30	10.4	
34*	MELANOTES	9	9	1.80	0.86	47.9	
35*	MIMUS	58	56	1.40	0.58	40.9	
36*	NEOSCHIMUS	16	16	1.63	0.50	30.4	
17	MIMODES GRAYSONI	1	1	1.00	0.0	0.0	
18	CREOSCOPTES MONTANUS	10	10	1.60	0.84	52.7	
37*	TOXOSTOMA	66	66	1.46	0.59	40.8	
2*	CINCLORHYTHIA PUFICAUDA	17	17	1.88	0.70	37.0	
30	RAMPHOCEINUS BRACHYURUS	2	2	1.50	0.71	47.1	
31	CONACOFIUS ATICAPILLUS	8	8	1.25	0.71	56.6	
32	ALLENIA RUCCA	18	18	2.67	0.59	22.3	
33	MARGAROPS FUSCATUS	12	12	2.00	0.43	21.3	
3	MELANOTIS CAERULESCENS	5	5	1.60	0.89	55.9	
4	MELANOTIS HYPOLEUCUS	4	4	2.00	0.82	40.8	
5	MIMUS POLYCHLOTTOS	22	21	1.29	0.46	36.0	
6	MIMUS GILVUS	9	9	1.33	0.50	37.5	
7	MIMUS GUNDELACHI	5	4	1.75	0.96	54.7	
8	MIMUS TENICA	4	4	1.50	1.00	66.7	
9	MIMUS LONGICAUDATUS	7	7	1.29	0.49	38.0	
10	MIMUS SATURNINUS	4	4	1.50	0.58	38.5	
11	MIMUS PATAGONICUS	4	4	1.25	0.50	40.0	
12	MIMUS TRIUPUS	3	3	1.33	0.58	43.3	
13	MIMUS COXSALIS						
14	NEOSCHIMUS TRIFASCIATUS	3	3	2.00	0.0	0.0	
15	NEOSCHIMUS MACDONALDI	5	5	1.40	0.55	39.1	
16	NEOSCHIMUS PARVULUS	8	8	1.50	0.53	35.6	
19	TOXOSTOMA RUFUM	14	14	1.50	0.76	50.6	
20	TOXOSTOMA LONGIROSTRE	4	4	2.00	0.82	40.8	
21	TOXOSTOMA GUTTATUM	6	6	1.00	0.0	0.0	
22	TOXOSTOMA CIPERUM	1	1	1.00	0.0	0.0	
23	TOXOSTOMA PENDREI	3	3	1.67	0.58	34.6	
24	TOXOSTOMA COLLATUM	2	2	1.00	0.0	0.0	
25	TOXOSTOMA CURVIROSTRE	20	20	1.20	0.52	43.6	
26	TOXOSTOMA LEONETTI	4	4	1.25	0.50	40.0	
27	TOXOSTOMA PEDIVIVUM	7	7	2.14	0.69	32.2	
28	TOXOSTOMA FLASALE	5	5	1.80	0.45	24.8	
	GRAND VALUES	253	251	1.60			

THERE ARE NO SPECIMENS IN THIS SET

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 55 N	TRUNK-L MEAN	S D	C V	V 8 N	CRAN-L1 MEAN	S D	C V	V 9 N	CRAN-H MEAN	S D	C V	V 10 N	CRAN-W1 MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	15.80	0.85	5.4	2	9.65	0.07	0.7	2	12.75	0.07	0.6	1	15.90	0.0	0.0
2	COSSYPHA CAFFER	2	2	15.50	0.28	1.8	2	10.05	0.07	0.7	2	12.50	0.28	2.3	2	15.80	0.14	0.9
3	COSSYPHA HUMERALIS	2	2	14.05	0.21	1.5	2	9.45	0.07	0.7	2	12.40	0.00	0.0	2	15.05	0.07	0.5
4	COSSYPHA NIVEICAPILLA	3	3	14.07	0.55	3.9	3	9.43	0.21	2.2	3	12.37	0.35	2.8	3	15.20	0.44	2.9
5	ALETHE CASTANIA	1	1	17.10	0.0	0.0	1	9.40	0.0	0.0	1	13.50	0.0	0.0	1	15.40	0.0	0.0
6	ALETHE PELIOCEPHALA	1	1	16.30	0.0	0.0	1	10.00	0.0	0.0	1	13.30	0.0	0.0	1	15.80	0.0	0.0
7	COPSYCHUS SULARIS	1	1	16.80	0.0	0.0	1	10.80	0.0	0.0	1	13.40	0.0	0.0	1	17.20	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	15.52	0.29	1.9	5	9.70	0.29	3.0	5	13.00	0.21	1.6	5	15.88	0.26	1.6
9	MYADestes CENIPARIS	3	3	15.37	0.32	2.1	3	9.13	0.23	2.5	3	12.83	0.06	0.4	3	15.93	0.32	2.0
10	MONTICOLA CINCLORHYNCHUS	1	1	17.00	0.0	0.0	1	9.80	0.0	0.0	1	13.40	0.0	0.0	1	16.20	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	19.30	0.50	2.6	3	11.20	0.26	2.4	3	14.50	0.36	2.5	2	18.90	0.0	0.0
12	CATHARUS FUSCESCENS	4	4	17.15	0.77	4.5	4	9.52	0.26	2.8	4	12.77	0.13	1.0	4	15.47	0.43	2.8
13	CATHARUS USTULATA	9	8	17.16	0.40	2.3	9	9.46	0.14	2.1	9	12.66	0.26	2.1	9	15.77	0.31	2.0
14	MYLOCICHLA MUSTELINA	7	7	19.39	0.57	3.0	7	10.57	0.30	2.9	7	14.43	0.29	2.0	7	17.63	0.49	2.8
15	TURDUS PHILOMELUS	6	4	21.05	0.53	2.5	6	11.70	0.15	1.3	6	15.32	0.19	1.3	6	19.52	0.35	1.8
16	TURDUS MIGRATORIUS	5	5	23.08	0.97	4.2	5	12.24	0.22	1.8	5	15.80	0.42	2.7	5	19.72	0.45	2.3
17*	COSSYPHA	9	9	14.85	0.54	3.6	9	9.65	0.14	1.5	9	12.50	0.26	2.1	8	15.49	0.32	2.1
18*	COPSYCHUS	6	6	16.16	0.29	1.8	6	10.25	0.29	2.8	6	13.45	0.21	1.6	6	16.54	0.26	1.6
19*	MONTICOLA	4	4	18.15	0.50	2.8	4	10.50	0.26	2.5	4	13.95	0.36	2.6	3	17.55	0.0	0.0
20*	CATHARUS	13	12	17.16	0.54	3.1	13	9.49	0.22	2.3	13	12.72	0.23	1.8	13	15.62	0.35	2.2
21*	TURDUS	11	9	22.06	0.81	3.7	11	11.97	0.19	1.6	11	15.46	0.32	2.0	11	19.62	0.40	2.0
	GRAND VALUES	55	52	17.16			55	10.12			55	13.46			53	16.59		

SET #	SET DESCRIPTION	SET N	V 11 N	CRAN-W2 MEAN	S D	C V	V 12 N	CRAN-W3 MEAN	S D	C V	V 13 N	CRAN-L2 MEAN	S D	C V	V 14 N	PHAX-L1 MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	1	16.10	0.0	0.0	1	16.10	0.0	0.0	2	22.20	0.71	3.2	2	18.10	0.28	1.6
2	COSSYPHA CAFFER	2	2	15.85	0.35	2.2	2	15.95	0.21	1.3	2	21.70	0.85	3.9	2	17.50	0.85	4.8
3	COSSYPHA HUMERALIS	2	2	14.75	0.07	0.5	2	14.75	0.21	1.4	2	20.05	0.35	1.8	2	16.55	0.07	0.4
4	COSSYPHA NIVEICAPILLA	3	3	15.37	0.51	3.3	3	15.83	0.21	1.3	3	20.23	0.51	2.5	3	16.37	0.51	3.1
5	ALETHE CASTANIA	1	1	15.70	0.0	0.0	1	16.20	0.0	0.0	1	22.30	0.0	0.0	1	18.70	0.0	0.0
6	ALETHE PELIOCEPHALA	1	1	15.60	0.0	0.0	1	16.20	0.0	0.0	1	23.20	0.0	0.0	1	17.90	0.0	0.0
7	COPSYCHUS SULARIS	1	1	16.90	0.0	0.0	1	17.60	0.0	0.0	1	22.40	0.0	0.0	1	21.50	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	15.28	0.19	1.3	5	16.06	0.29	1.8	5	22.22	0.24	1.1	5	17.56	0.80	4.6
9	MYADestes CENIPARIS	3	3	15.37	0.42	2.7	3	15.80	0.56	3.5	3	21.27	0.64	3.0	3	15.03	0.67	4.4
10	MONTICOLA CINCLORHYNCHUS	1	1	15.60	0.0	0.0	1	16.70	0.0	0.0	1	22.80	0.0	0.0	1	20.40	0.0	0.0
11	MONTICOLA SOLITARIUS	3	2	19.55	0.07	0.4	3	19.00	0.26	1.4	3	24.47	0.42	1.7	3	24.47	1.07	4.4
12	CATHARUS FUSCESCENS	4	4	14.97	0.32	2.1	4	15.60	0.18	1.2	4	20.50	0.26	1.3	4	16.10	0.83	5.1
13	CATHARUS USTULATA	9	9	15.29	0.18	1.2	9	15.69	0.27	1.7	9	21.24	0.43	2.0	9	15.42	1.10	7.1
14	MYLOCICHLA MUSTELINA	7	7	15.74	0.38	2.4	7	17.04	0.35	2.1	7	24.27	0.48	2.0	7	18.43	0.92	5.0
15	TURDUS PHILOMELUS	6	6	17.48	0.40	2.3	6	18.52	0.10	0.5	6	25.18	0.36	1.4	6	20.35	0.57	2.8
16	TURDUS MIGRATORIUS	5	5	17.32	0.41	2.4	5	19.14	0.30	1.5	5	25.98	0.67	2.6	5	20.60	0.85	4.1
17*	COSSYPHA	9	8	15.52	0.41	2.6	8	15.66	0.21	1.3	9	21.05	0.61	2.9	9	17.13	0.52	3.0
18*	COPSYCHUS	6	6	16.09	0.19	1.2	6	16.83	0.29	1.7	6	22.31	0.24	1.1	6	19.53	0.80	4.1
19*	MONTICOLA	4	3	17.07	0.07	0.4	4	17.85	0.26	1.5	4	23.63	0.47	1.8	4	22.43	1.07	4.8
20*	CATHARUS	13	13	15.13	0.23	1.5	13	15.44	0.25	1.6	13	20.87	0.39	1.9	13	15.76	1.03	6.6
21*	TURDUS	11	11	17.40	0.41	2.3	11	15.43	0.21	1.1	11	25.48	0.52	2.0	11	20.47	0.71	3.5
	GRAND VALUES	55	53	15.99			54	16.64			55	22.50			55	18.44		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 56 N	PMAX-L2 MEAN	S D	C V	V 15 N	INTORB-W MEAN	S D	C V	V 16 N	BILL-W1 MEAN	S D	C V	V 17 N	BILL-W2 MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	9.10	0.14	1.6	1	4.50	0.0	0.0	2	4.20	0.14	3.4	2	7.70	0.14	1.8
2	COSSYPHA CAFFER	2	2	7.65	0.64	8.3	2	3.30	0.27	8.6	2	3.40	0.0	0.0	1	7.20	0.0	0.0
3	COSSYPHA HUMERALIS	2	2	7.40	0.42	5.7	2	3.30	0.14	4.3	2	3.30	0.0	0.0	2	6.45	0.07	1.1
4	COSSYPHA NIVICAPILLA	3	3	7.27	0.15	2.1	3	3.43	0.23	6.7	3	4.03	0.12	2.9	3	7.13	0.06	0.8
5	ALETHE CASTANEA	1	1	9.20	0.0	0.0	1	4.90	0.0	0.0	1	4.40	0.0	0.0	1	7.40	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	8.70	0.0	0.0	1	4.70	0.0	0.0	1	3.60	0.0	0.0	1	7.50	0.0	0.0
7	CEPSYCHUS SULARIS	1	1	11.10	0.0	0.0	1	4.80	0.0	0.0	1	4.90	0.0	0.0	1	8.90	0.0	0.0
8	CEPSYCHUS MALABARICUS	5	5	8.30	0.63	7.6	5	4.66	0.62	13.4	5	3.74	0.15	4.1	5	7.34	0.27	3.7
9	MYAESTES GENIEARRIS	3	3	5.67	0.42	7.3	3	3.40	0.20	5.9	3	4.40	0.30	6.8	3	8.43	0.25	3.0
10	MONTICOLA CINCLORHYNCHUS	1	1	9.60	0.0	0.0	1	4.70	0.0	0.0	1	4.70	0.0	0.0	1	8.30	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	11.03	0.49	4.5	3	4.90	0.35	7.1	3	4.57	0.06	1.3	3	9.27	0.61	6.6
12	CATHARUS FUSCESCENS	4	4	7.12	0.54	7.6	4	3.70	0.42	11.5	4	3.92	0.10	2.4	4	7.02	0.13	1.8
13	CATHARUS USTULATA	9	9	6.78	0.46	6.8	9	3.59	0.31	8.6	9	3.84	0.28	7.3	8	6.95	0.32	4.6
14	HYLOCICHLA MUSTELINA	7	7	8.84	0.67	7.6	7	4.51	0.44	9.7	7	4.51	0.30	6.7	7	7.94	0.32	4.0
15	TURDUS PHILOMELUS	6	6	9.00	0.43	4.8	6	4.45	0.26	5.8	6	4.25	0.23	5.3	6	8.28	0.15	1.8
16	TURDUS MIGRATORIUS	5	5	9.98	0.49	4.9	5	5.32	0.39	7.3	5	4.62	0.28	6.0	5	8.46	0.48	5.7
17*	COSSYPHA	9	9	7.85	0.36	4.6	8	3.63	0.23	6.3	9	3.73	0.10	2.6	8	7.12	0.09	1.2
18*	CEPSYCHUS	6	6	9.70	0.63	6.5	6	4.73	0.62	13.7	6	4.32	0.15	3.5	6	8.12	0.27	3.3
19*	MONTICOLA	4	4	10.32	0.49	4.8	4	4.80	0.35	7.2	4	4.63	0.06	1.2	4	8.78	0.61	7.0
20*	CATHARUS	13	13	6.95	0.48	7.0	13	3.64	0.34	9.5	13	3.88	0.24	6.3	12	6.99	0.27	3.9
21*	TURDUS	11	11	9.49	0.46	4.8	11	4.86	0.32	6.6	11	4.43	0.25	5.6	11	8.37	0.34	4.1
	GRAND VALUES	55	55	8.55			54	4.26			55	4.15			53	7.77		
SET #	SET DESCRIPTION	SET N	V 18 N	BILL-W MEAN	S D	C V	V 21 N	PEDORIG MEAN	S D	C V	V 20 N	NARES-W MEAN	S D	C V	V 19 N	NARES-L MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	2.45	0.07	2.9	2	5.90	0.28	4.8	2	2.75	0.07	2.6	2	7.10	0.57	8.0
2	COSSYPHA CAFFER	2	2	2.00	0.14	7.1	2	5.60	0.28	5.1	2	2.50	0.28	11.3	1	7.50	0.0	0.0
3	COSSYPHA HUMERALIS	2	2	2.05	0.07	3.4	2	6.10	0.42	7.0	2	2.60	0.0	0.0	2	6.70	0.42	6.3
4	COSSYPHA NIVICAPILLA	3	3	2.27	0.06	2.5	3	5.90	0.10	1.7	3	2.80	0.10	3.6	3	6.57	0.15	2.3
5	ALETHE CASTANEA	1	1	2.70	0.0	0.0	1	4.90	0.0	0.0	1	2.60	0.0	0.0	1	7.20	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	2.80	0.0	0.0	1	5.40	0.0	0.0	1	2.40	0.0	0.0	1	7.10	0.0	0.0
7	CEPSYCHUS SULARIS	1	1	2.70	0.0	0.0	1	5.30	0.0	0.0	1	3.10	0.0	0.0	1	6.80	0.0	0.0
8	CEPSYCHUS MALABARICUS	5	5	2.42	0.13	5.4	5	5.96	0.18	3.0	5	2.56	0.09	3.5	5	6.70	0.10	1.5
9	MYAESTES GENIEARRIS	3	3	2.00	0.0	0.0	3	7.03	0.25	3.6	3	3.23	0.12	3.6	3	7.37	0.29	3.9
10	MONTICOLA CINCLORHYNCHUS	1	1	2.60	0.0	0.0	1	6.10	0.0	0.0	1	2.80	0.0	0.0	1	8.40	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	2.90	0.10	3.4	3	8.20	0.44	5.3	3	3.37	0.15	4.5	3	10.10	0.53	5.2
12	CATHARUS FUSCESCENS	4	4	2.30	0.20	8.7	4	6.52	0.38	4.8	4	3.05	0.06	1.9	4	6.60	0.45	6.9
13	CATHARUS USTULATA	9	9	2.09	0.06	2.9	9	6.86	1.27	18.5	9	2.91	0.11	3.6	9	6.62	0.49	7.4
14	HYLOCICHLA MUSTELINA	7	7	2.67	0.21	7.7	7	7.00	0.29	4.1	7	3.31	0.12	3.7	7	7.01	0.30	4.3
15	TURDUS PHILOMELUS	6	6	2.75	0.16	6.0	6	8.05	0.27	3.4	6	3.70	0.06	1.7	6	8.35	0.21	2.5
16	TURDUS MIGRATORIUS	5	5	3.06	0.15	5.0	5	7.40	0.19	2.5	5	3.66	0.18	5.0	5	7.82	0.31	4.0
17*	COSSYPHA	9	9	2.19	0.09	3.9	9	5.87	0.27	4.6	9	2.66	0.14	5.4	8	6.97	0.37	5.3
18*	CEPSYCHUS	6	6	2.56	0.13	5.1	6	5.63	0.18	3.2	6	2.83	0.09	3.2	6	6.75	0.10	1.5
19*	MONTICOLA	4	4	2.75	0.10	3.6	4	7.15	0.44	6.1	4	3.08	0.15	5.0	4	9.25	0.53	5.7
20*	CATHARUS	13	13	2.19	0.12	5.3	13	6.69	1.10	16.4	13	2.98	0.09	3.2	13	6.61	0.48	7.3
21*	TURDUS	11	11	2.90	0.16	5.5	11	7.72	0.24	3.1	11	3.68	0.13	3.5	11	8.08	0.26	3.2
	GRAND VALUES	55	55	2.48			55	6.39			55	2.96			54	7.37		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SFT DESCRIPTION	SET N	V 22 N	ECTH-W1 MEAN	S D	C V	V 23 N	ECTH-W2 MEAN	S D	C V	V 24 N	ECTH-W3 MEAN	S D	C V	V 25 N	DPH-W MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	8.60	0.57	6.4	1	7.60	0.0	0.0	1	9.70	0.0	0.0	2	1.15	0.35	30.7
2	COSSYPHA CAFFER	2	2	8.40	0.57	6.7	2	7.05	0.49	7.0	2	7.95	0.07	0.4	2	1.10	0.14	12.9
3	COSSYPHA HUMERALIS	2	2	7.85	0.21	2.7	2	6.90	0.14	2.0	2	8.15	0.07	0.9	2	1.30	0.14	10.9
4	COSSYPHA NIVIFCAPILLA	3	3	7.97	0.12	1.4	3	7.17	0.15	2.1	3	8.73	0.29	3.3	3	1.40	0.10	7.1
5	ALETHE CASTANEA	1	1	10.00	0.0	0.0	1	9.30	0.0	0.0	1	10.80	0.0	0.0	1	0.80	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	10.70	0.0	0.0	1	9.00	0.0	0.0	1	10.70	0.0	0.0	1	1.10	0.0	0.0
7	COPSYCHUS SULARIS	1	1	10.30	0.0	0.0	1	9.20	0.0	0.0	1	10.40	0.0	0.0	1	1.20	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	9.59	0.61	6.3	5	8.39	0.29	3.4	5	9.68	0.61	6.3	5	1.16	0.09	7.7
9	MYADestes GENIBARIS	3	3	9.67	0.38	3.9	3	8.43	0.12	1.4	3	10.80	0.50	4.6	3	1.13	0.06	5.1
10	MONTICOLA CINCLOPHYCHUS	1	1	11.70	0.0	0.0	1	9.80	0.0	0.0	1	11.70	0.0	0.0	1	0.90	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	11.30	0.20	1.8	3	9.50	0.26	2.8	3	12.30	0.66	5.3	3	1.37	0.31	22.4
12	CATHARIS FUSCESCENS	4	4	9.45	0.37	3.9	4	8.12	0.33	4.1	4	9.42	0.50	5.3	4	1.82	0.10	5.2
13	CATHARIS USTULATA	9	9	9.19	0.38	4.1	9	8.04	0.41	5.1	9	9.30	0.36	3.9	9	1.69	0.20	12.0
14	MYLOCECHLA MUSTELINA	7	7	11.01	0.57	5.1	7	9.80	0.43	4.4	7	11.24	0.33	2.9	7	2.29	0.18	7.8
15	TURDUS PHLOMELOS	6	6	11.88	0.26	2.3	6	9.76	0.20	2.1	6	11.10	0.29	2.6	6	2.15	0.10	4.9
16	TURDUS MIGRATORIUS	5	5	12.48	0.24	2.2	5	10.36	0.50	4.8	5	12.14	0.44	3.6	5	2.30	0.20	8.7
17	COSSYPHA	9	9	8.25	0.38	4.6	8	7.18	0.28	3.9	8	8.63	0.21	2.4	9	1.24	0.19	15.5
18	COPSYCHUS	6	6	9.94	0.61	6.1	6	8.79	0.29	3.3	6	10.04	0.61	6.1	6	1.18	0.09	7.6
19	MONTICOLA	4	4	11.50	0.20	1.7	4	9.65	0.26	2.7	4	12.00	0.66	5.5	4	1.13	0.31	27.0
20	CATHARIS	13	13	9.32	0.38	4.0	13	8.08	0.39	4.8	13	9.36	0.41	4.3	13	1.76	0.18	10.2
21	TURDUS	11	11	12.03	0.27	2.2	11	10.07	0.37	3.6	11	11.62	0.36	3.1	11	2.22	0.15	6.9
	GRAND VALUES	55	55	10.00			54	8.65			54	10.26			55	1.43		
SET #	SFT DESCRIPTION	SET N	V 26 N	SF-W MEAN	S D	C V	V 27 N	SF-L MEAN	S D	C V	V 28 N	INTPTG-W MEAN	S D	C V	V 30 N	JUGAL-L MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	1.00	0.0	0.0	2	2.00	0.0	0.0	2	6.65	0.21	3.2	2	15.10	0.28	1.9
2	COSSYPHA CAFFER	2	2	1.00	0.14	14.1	2	1.90	0.14	7.4	2	6.25	0.07	1.1	2	15.25	0.21	1.4
3	COSSYPHA HUMERALIS	2	2	1.25	0.07	5.7	2	2.20	0.0	0.0	2	5.75	0.07	1.2	2	13.15	0.21	1.6
4	COSSYPHA NIVIFCAPILLA	3	3	0.87	0.06	6.7	3	1.77	0.12	6.5	3	6.10	0.00	0.0	3	13.57	0.46	3.4
5	ALETHE CASTANEA	1	1	0.50	0.0	0.0	1	1.80	0.0	0.0	0	999.99	0.0	0.0	1	15.30	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	0.80	0.0	0.0	1	2.40	0.0	0.0	1	7.50	0.0	0.0	1	15.20	0.0	0.0
7	COPSYCHUS SULARIS	1	1	0.90	0.0	0.0	1	1.50	0.0	0.0	1	6.80	0.0	0.0	1	16.70	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	0.98	0.08	8.5	5	1.70	0.17	10.2	4	7.00	0.41	5.8	5	15.98	0.41	2.6
9	MYADestes GENIBARIS	3	3	1.43	0.12	8.1	3	2.93	0.06	2.0	3	7.80	0.53	6.8	3	14.33	0.12	0.8
10	MONTICOLA CINCLOPHYCHUS	1	1	1.20	0.0	0.0	1	1.90	0.0	0.0	1	7.40	0.0	0.0	1	17.20	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	1.13	0.06	5.1	3	2.57	0.15	6.0	3	6.13	0.12	1.4	3	18.00	0.46	2.5
12	CATHARIS FUSCESCENS	4	4	1.02	0.08	4.9	4	1.82	0.10	5.2	4	6.25	0.79	12.7	4	14.27	0.15	1.1
13	CATHARIS USTULATA	9	9	0.97	0.07	7.3	9	2.11	0.15	6.9	7	6.20	0.17	2.8	9	14.22	0.42	3.0
14	MYLOCECHLA MUSTELINA	7	7	1.17	0.05	4.2	7	2.40	0.14	5.9	7	6.90	0.42	6.1	7	16.26	0.34	2.1
15	TURDUS PHLOMELOS	6	6	2.08	0.10	4.7	6	1.93	0.29	14.5	6	7.02	0.44	6.3	6	17.65	0.30	1.7
16	TURDUS MIGRATORIUS	5	5	1.66	0.09	5.4	5	1.66	0.34	20.7	5	8.44	0.27	3.2	5	18.04	0.25	1.4
17	COSSYPHA	9	9	1.03	0.08	7.7	9	1.97	0.10	4.9	9	6.19	0.10	1.7	9	14.27	0.35	2.4
18	COPSYCHUS	6	6	0.94	0.08	8.9	6	1.80	0.17	9.6	5	6.90	0.41	5.9	6	16.34	0.41	2.5
19	MONTICOLA	4	4	1.17	0.06	4.9	4	2.23	0.15	6.8	4	7.77	0.12	1.5	4	17.60	0.46	2.6
20	CATHARIS	13	13	1.00	0.07	6.6	13	1.97	0.13	6.8	11	6.22	0.48	7.7	13	14.25	0.37	2.6
21	TURDUS	11	11	1.87	0.09	5.0	11	1.80	0.31	17.3	11	7.73	0.38	4.9	11	17.84	0.28	1.6
	GRAND VALUES	55	55	1.12			55	2.06			51	6.51			55	15.64		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species (See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 31 N	PELV-L1 MEAN	S D	C V	V 32 N	PELV-L2 MEAN	S D	C V	V 33 N	PELV-W1 MEAN	S D	C V	V 35 N	PELV-W3 MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	19.15	0.64	3.3	2	12.65	0.07	0.6	2	13.70	0.14	1.0	2	7.90	0.0	0.0
2	COSSYPHA CAFFER	2	2	19.55	0.35	1.8	2	13.05	0.21	1.6	2	13.35	0.35	2.6	2	6.75	0.35	5.2
3	COSSYPHA HUMERALIS	2	2	16.35	0.21	1.3	2	10.65	0.21	2.0	2	12.40	0.00	0.0	2	7.10	0.14	2.0
4	COSSYPHA NIVEICAPILLA	3	3	17.10	0.95	5.6	3	11.00	0.89	6.1	3	11.13	0.59	5.3	3	6.13	0.45	7.4
5	ALETHE CASTANEA	1	1	20.50	0.0	0.0	1	13.10	0.0	0.0	1	14.80	0.0	0.0	1	8.40	0.0	0.0
6	ALETHE PELIOCEPHALA	1	1	19.50	0.0	0.0	1	13.00	0.0	0.0	1	13.70	0.0	0.0	1	8.20	0.0	0.0
7	COPSYCHUS SULARIS	1	1	20.60	0.0	0.0	1	13.10	0.0	0.0	1	14.70	0.0	0.0	1	7.90	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	19.22	0.71	3.7	5	12.28	0.36	3.0	5	12.82	0.33	2.6	5	7.14	0.21	2.9
9	MYAESTES CINIBARRIS	3	3	18.83	0.61	3.2	3	12.53	0.35	2.8	3	14.77	0.25	1.7	3	8.23	0.06	0.7
10	MONTICOLA CINCLORHYNCHUS	1	1	20.70	0.0	0.0	1	12.80	0.0	0.0	1	13.80	0.0	0.0	1	8.30	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	24.03	0.68	2.8	3	15.27	0.50	3.3	3	15.93	0.71	4.5	3	8.53	0.31	3.6
12	CATHARUS FUSCESCENS	4	4	20.42	0.76	3.7	4	13.52	0.78	5.8	4	14.20	0.43	3.0	4	8.22	0.63	7.7
13	CATHARUS USTULATA	9	9	20.28	0.53	3.1	9	13.44	0.39	2.9	9	14.60	0.36	2.4	9	8.19	0.52	6.4
14	MYLOCECHLA MUSTELINA	7	7	24.16	0.91	3.7	7	15.64	0.38	2.4	7	17.63	0.27	1.5	7	9.40	0.59	6.3
15	TURDUS PHILOMELUS	6	6	27.68	0.69	2.5	6	17.85	0.38	2.1	6	18.93	0.41	2.2	6	10.73	0.49	4.6
16	TURDUS MICKATORIUS	5	5	27.66	0.72	2.6	5	17.90	0.49	2.8	5	19.84	0.58	2.9	5	11.12	0.47	4.2
17*	COSSYPHA	9	9	18.04	0.69	3.8	9	11.84	0.58	4.9	9	12.65	0.41	3.2	9	6.97	0.33	4.8
18*	COPSYCHUS	6	6	19.91	0.71	3.6	6	12.69	0.36	2.9	6	13.76	0.33	2.4	6	7.52	0.21	2.8
19*	MONTICOLA	4	4	27.37	0.68	3.0	4	14.03	0.50	3.6	4	14.87	0.71	4.8	4	8.42	0.31	3.6
20*	CATHARUS	13	13	20.35	0.67	3.3	13	13.48	0.52	3.9	13	14.40	0.38	2.6	13	8.21	0.55	6.8
21*	TURDUS	11	11	27.67	0.70	2.5	11	17.87	0.43	2.4	11	19.39	0.49	2.5	11	10.93	0.48	4.4
	GRAND VALUES	55	55	20.98			55	13.61			55	14.77			55	8.27		
SET #	SET DESCRIPTION	SET N	V 72 N	PELV-W4 MEAN	S D	C V	V 73 N	PELV-W5 MEAN	S D	C V	V 36 N	STERN-L MEAN	S D	C V	V 39 N	STERN-KL MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	3.50	0.42	12.1	2	4.30	0.0	0.0	2	21.90	0.14	0.6	2	19.40	0.99	5.1
2	COSSYPHA CAFFER	2	2	2.85	0.21	7.4	2	3.55	0.07	2.0	2	21.50	1.27	5.9	2	19.55	1.20	6.1
3	COSSYPHA HUMERALIS	2	2	2.60	0.0	0.0	2	3.20	0.14	4.4	2	18.05	0.35	2.0	2	15.70	0.85	5.4
4	COSSYPHA NIVEICAPILLA	3	3	2.20	0.26	12.0	3	2.80	0.10	3.6	3	17.47	0.57	3.3	3	15.17	0.75	4.9
5	ALETHE CASTANEA	1	1	3.50	0.0	0.0	1	4.30	0.0	0.0	1	23.20	0.0	0.0	1	21.90	0.0	0.0
6	ALETHE PELIOCEPHALA	1	1	3.00	0.0	0.0	1	3.90	0.0	0.0	1	21.60	0.0	0.0	1	19.80	0.0	0.0
7	COPSYCHUS SULARIS	1	1	3.50	0.0	0.0	1	4.20	0.0	0.0	1	22.20	0.0	0.0	1	22.20	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	2.28	0.41	17.9	5	3.34	0.26	7.8	5	21.46	1.05	4.9	5	19.98	1.47	7.4
9	MYAESTES CINIBARRIS	3	3	3.73	0.15	4.7	3	3.40	0.10	2.9	2	18.70	0.57	3.0	3	15.93	0.68	4.3
10	MONTICOLA CINCLORHYNCHUS	1	1	2.70	0.0	0.0	1	3.50	0.0	0.0	1	22.80	0.0	0.0	1	22.80	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	3.33	0.06	1.7	3	3.77	0.06	1.5	3	24.77	1.17	4.7	3	22.90	0.66	2.9
12	CATHARUS FUSCESCENS	4	4	3.02	0.10	3.2	4	3.60	0.18	5.1	4	23.12	1.42	6.2	4	21.77	1.31	6.0
13	CATHARUS USTULATA	9	9	3.11	0.18	5.9	9	3.46	0.15	4.4	9	23.38	0.84	3.6	9	21.88	1.30	5.9
14	MYLOCECHLA MUSTELINA	7	7	3.31	0.19	5.6	7	3.99	0.35	8.7	7	27.20	0.56	2.1	7	25.66	1.16	4.5
15	TURDUS PHILOMELUS	6	6	3.75	0.15	4.0	6	4.43	0.22	4.9	6	32.28	1.28	4.0	6	30.90	1.34	4.3
16	TURDUS MICKATORIUS	5	5	3.82	0.18	4.7	5	4.46	0.30	6.8	5	32.44	1.14	3.5	5	32.02	1.36	4.3
17*	COSSYPHA	9	9	2.79	0.27	9.7	9	3.46	0.09	2.7	9	19.73	0.69	3.5	9	17.45	0.92	5.3
18*	COPSYCHUS	6	6	2.89	0.41	14.1	6	3.77	0.26	6.9	6	21.83	1.05	4.6	6	21.09	1.47	7.0
19*	MONTICOLA	4	4	3.02	0.06	1.9	4	3.63	0.06	1.6	4	23.78	1.17	4.9	4	22.85	0.66	2.9
20*	CATHARUS	13	13	3.07	0.16	5.4	13	3.53	0.16	4.5	13	23.25	1.03	4.4	13	21.83	1.30	6.0
21*	TURDUS	11	11	2.78	0.16	4.3	11	4.45	0.26	5.8	11	32.46	1.22	3.8	11	31.46	1.35	4.3
	GRAND VALUES	55	55	3.11			55	3.76			54	23.27			55	21.72		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species (See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 37 N	STERN-D MEAN	S D	C V	V 38 N	STERN-W MEAN	S D	C V	V 40 N	FEMUR-L MEAN	S D	C V	V 41 N	FEMUR-HW MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	6.80	0.28	4.2	2	10.25	0.21	2.1	2	21.65	0.92	4.2	2	3.80	0.0	0.0
2	COSSYPHA CAFFER	2	2	6.30	0.42	6.7	2	10.25	0.21	2.1	2	21.30	0.99	4.6	2	3.75	0.07	1.9
3	COSSYPHA HUMERALIS	2	2	5.10	0.14	2.8	2	9.45	0.49	5.2	2	18.55	0.21	1.1	2	3.15	0.07	2.2
4	COSSYPHA NIVEICAPILLA	3	3	5.23	0.38	7.2	3	9.00	0.26	2.9	3	14.43	0.21	1.1	3	3.47	0.06	1.7
5	ALETHE CASTANEA	1	1	8.00	0.0	0.0	1	10.50	0.0	0.0	1	21.70	0.0	0.0	1	3.90	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	6.40	0.0	0.0	1	11.00	0.0	0.0	1	22.10	0.0	0.0	1	3.90	0.0	0.0
7	COPSYCHUS SULARIS	1	1	7.20	0.0	0.0	1	10.10	0.0	0.0	1	21.20	0.0	0.0	1	4.10	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	6.68	0.30	4.5	5	9.98	0.73	7.3	5	18.94	0.48	2.5	5	3.48	0.08	2.4
9	MYADestes GENIBARBERIS	3	3	5.47	0.06	1.1	3	11.43	0.12	1.0	3	19.43	0.54	3.0	3	3.47	0.06	1.7
10	MONTICOLA CINCLORHYNCHUS	1	1	7.60	0.0	0.0	1	10.80	0.0	0.0	1	21.20	0.0	0.0	1	3.60	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	8.07	0.58	7.2	3	10.60	0.36	3.4	3	24.27	0.32	1.3	3	4.30	0.10	2.3
12	CATHARUS FUSCESCENS	4	4	7.88	0.75	9.5	4	10.12	0.22	2.2	4	20.67	0.92	4.4	4	3.52	0.17	4.8
13	CATHARUS USTULATA	9	9	7.89	0.49	6.2	9	10.36	0.32	3.1	8	20.80	0.73	3.5	8	3.55	0.19	5.2
14	MYLECICHLA MUSTELINA	7	7	9.17	0.70	7.6	7	12.66	0.34	3.1	7	23.76	0.36	1.5	7	4.33	0.05	1.1
15	TURDUS PHILENCELOS	6	6	10.93	0.45	4.1	6	13.12	0.64	4.9	6	26.67	0.61	2.3	6	4.72	0.13	2.8
16	TURDUS MIGRATORIUS	5	5	11.26	0.58	5.1	5	13.48	0.22	1.6	5	27.40	0.98	3.6	5	4.98	0.13	2.6
17*	COSSYPHA	9	9	5.86	0.34	5.7	9	9.74	0.31	3.2	9	20.23	0.63	3.1	9	3.54	0.06	1.6
18*	COPSYCHUS	6	6	6.94	0.30	4.4	6	10.04	0.73	7.3	6	20.07	0.48	2.4	6	3.79	0.08	2.2
19*	MONTICOLA	4	4	7.83	0.58	7.4	4	10.70	0.36	3.4	4	22.73	0.32	1.4	4	3.95	0.10	2.5
20*	CATHARUS	13	13	7.88	0.57	7.2	13	10.24	0.30	2.9	12	20.74	0.79	3.8	12	3.54	0.18	5.1
21*	TURDUS	11	11	11.10	0.51	4.6	11	13.30	0.50	3.7	11	27.03	0.80	3.0	11	4.85	0.13	2.7
	GRAND VALUES	55	55	7.50			55	10.82			54	21.82			54	3.88		
SET #	SET DESCRIPTION	SET N	V 50 N	FEMUR-SW MEAN	S D	C V	V 42 N	TIBIA-L MEAN	S D	C V	V 60 N	TIPIA-SW MEAN	S D	C V	V 57 N	TARGET-L MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	1.70	0.0	0.0	2	37.05	2.19	5.9	2	1.45	0.07	4.9	2	28.90	0.99	3.4
2	COSSYPHA CAFFER	2	2	1.65	0.21	12.9	2	37.35	4.74	12.7	2	1.50	0.14	9.4	2	32.20	0.57	1.8
3	COSSYPHA HUMERALIS	2	2	1.30	0.0	0.0	2	33.35	0.21	0.6	2	1.25	0.07	5.7	2	27.15	0.49	1.8
4	COSSYPHA NIVEICAPILLA	3	3	1.50	0.10	6.7	3	35.10	0.26	0.8	3	1.40	0.10	7.1	3	28.97	0.25	0.9
5	ALETHE CASTANEA	1	1	1.80	0.0	0.0	1	35.00	0.0	0.0	1	1.60	0.0	0.0	1	26.20	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	1.60	0.0	0.0	1	34.70	0.0	0.0	1	1.50	0.0	0.0	1	26.20	0.0	0.0
7	COPSYCHUS SULARIS	1	1	1.80	0.0	0.0	1	37.60	0.0	0.0	1	1.70	0.0	0.0	1	28.60	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	1.62	0.08	5.2	5	33.92	0.74	2.2	5	1.40	0.0	0.0	5	25.94	0.27	1.0
9	MYADestes GENIBARBERIS	3	3	1.40	0.0	0.0	3	33.80	0.95	2.8	3	1.33	0.15	11.5	3	23.50	1.15	4.9
10	MONTICOLA CINCLORHYNCHUS	1	1	1.60	0.0	0.0	1	34.70	0.0	0.0	1	1.40	0.0	0.0	1	24.40	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	1.90	0.10	5.3	3	41.43	0.15	0.4	3	1.73	0.15	8.8	3	29.10	0.46	1.6
12	CATHARUS FUSCESCENS	4	4	1.52	0.13	8.3	4	38.42	1.55	4.0	4	1.35	0.06	4.3	4	29.42	1.10	3.7
13	CATHARUS USTULATA	9	9	1.57	0.10	6.6	9	38.81	1.49	3.8	9	1.34	0.05	3.9	9	29.13	1.15	3.9
14	MYLECICHLA MUSTELINA	7	7	1.99	0.07	3.5	7	41.80	0.65	1.6	7	1.67	0.08	4.5	7	31.47	0.85	2.7
15	TURDUS PHILENCELOS	6	6	2.12	0.08	3.6	6	45.75	1.59	3.5	6	1.83	0.10	5.6	6	32.55	0.62	1.9
16	TURDUS MIGRATORIUS	5	5	2.22	0.15	6.7	5	44.16	1.98	4.3	5	1.96	0.09	4.6	5	32.48	1.54	4.7
17*	COSSYPHA	9	9	1.54	0.11	7.4	9	35.71	2.34	6.6	9	1.40	0.10	7.1	9	29.30	0.58	2.0
18*	COPSYCHUS	6	6	1.71	0.08	4.9	6	35.76	0.74	2.1	6	1.45	0.0	0.0	6	27.27	0.27	1.0
19*	MONTICOLA	4	4	1.75	0.10	5.7	4	38.07	0.15	0.4	4	1.57	0.15	9.8	4	26.75	0.46	1.7
20*	CATHARUS	13	12	1.55	0.11	7.1	13	38.67	1.51	3.9	13	1.35	0.05	4.0	13	29.28	1.13	3.9
21*	TURDUS	11	11	2.17	0.11	5.2	11	45.95	1.82	4.0	11	1.90	0.10	5.1	11	32.51	1.12	3.4
	GRAND VALUES	55	54	1.71			53	37.81			55	1.53			55	28.51		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SFT #	SFT DESCRIPTION	SET N	V 58 N	TARGET-M MEAN	S D	C V	V 43 N	HUM-L MEAN	S D	C V	V 44 N	HUM-HW MEAN	S D	C V	V 45 N	HUM-DCL MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	1.20	0.0	0.0	2	21.65	0.49	2.3	2	6.40	0.14	2.2	2	7.05	0.07	1.0
2	COSSYPHA CAFFER	2	2	1.10	0.14	12.9	2	21.15	0.07	0.3	2	6.30	0.28	4.5	2	6.55	0.78	11.9
3	COSSYPHA HUMERALIS	2	2	1.10	0.0	0.0	2	18.75	0.49	2.6	2	5.55	0.07	1.3	2	5.85	0.07	1.2
4	COSSYPHA NIVIFICAPILLA	3	3	1.17	0.06	4.9	3	18.33	0.14	0.8	3	5.40	0.10	1.9	3	5.73	0.06	1.0
5	ALETHE CASTANEA	1	1	1.30	0.0	0.0	1	23.70	0.0	0.0	1	7.00	0.0	0.0	1	7.40	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	1.30	0.0	0.0	1	22.60	0.0	0.0	1	7.00	0.0	0.0	1	7.10	0.0	0.0
7	CEPSYCHUS SULARIS	1	1	1.30	0.0	0.0	1	22.60	0.0	0.0	1	7.30	0.0	0.0	1	7.10	0.0	0.0
8	CEPSYCHUS MALAFARICUS	5	5	1.06	0.05	5.2	5	21.78	0.23	1.0	5	6.58	0.15	2.3	5	6.72	0.28	4.1
9	MYADISTES GENIFARIS	3	3	1.07	0.06	5.4	3	19.37	0.15	0.8	3	6.10	0.10	1.6	3	5.97	0.25	4.2
10	MONTICOLA CINCLORHYNCHUS	1	1	1.20	0.0	0.0	1	23.10	0.0	0.0	1	7.20	0.0	0.0	1	7.00	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	1.30	0.10	7.7	3	25.37	0.40	1.6	3	7.67	0.15	2.0	3	8.20	0.53	6.5
12	CATHARUS FUSCESCENS	4	4	1.12	0.10	8.5	3	20.50	1.23	6.0	4	6.50	0.42	6.4	4	6.22	0.53	8.4
13	CATHARUS USTULATA	9	9	0.99	0.03	3.4	9	20.76	0.58	2.8	9	6.70	0.24	3.7	9	6.28	0.25	4.0
14	MYLODICHLA MUSTELINA	7	7	1.43	0.19	13.2	7	24.07	0.24	1.0	7	7.79	0.23	2.9	7	7.23	0.30	4.1
15	TURDUS PHILEFLOS	6	6	1.47	0.05	3.5	6	26.78	0.40	1.5	6	8.62	0.36	4.2	6	7.97	0.41	5.2
16	TURDUS MIGRATORIUS	5	5	1.56	0.05	3.5	5	26.72	1.29	4.5	5	9.38	0.45	5.9	5	8.60	0.65	7.6
17*	COSSYPHA	9	9	1.14	0.07	6.4	9	19.47	0.33	1.6	9	5.91	0.16	2.7	9	6.30	0.35	5.6
18*	CEPSYCHUS	6	6	1.18	0.05	4.6	6	22.29	0.73	1.0	6	6.94	0.15	2.1	6	6.91	0.28	4.0
19*	MONTICOLA	4	4	1.25	0.10	8.0	4	24.23	0.40	1.7	4	7.43	0.15	2.1	4	7.60	0.53	7.0
20*	CATHARUS	13	13	1.06	0.06	5.4	12	20.64	0.76	3.7	13	6.60	0.30	4.6	13	6.25	0.35	5.6
21*	TURDUS	11	11	1.51	0.05	3.5	11	27.75	0.91	3.3	11	9.00	0.45	5.0	11	8.28	0.53	6.4
	GRAND VALUES	55	55	1.23			54	22.43			55	6.97			55	6.94		
SFT #	SFT DESCRIPTION	SET N	V 46 N	HUM-HD MEAN	S D	C V	V 62 N	HUM-SW MEAN	S D	C V	V 47 N	ULNA-L MEAN	S D	C V	V 61 N	ULNA-SW MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	3.70	0.14	3.8	2	1.90	0.0	0.0	2	24.40	0.57	2.3	2	1.75	0.07	4.0
2	COSSYPHA CAFFER	2	2	3.65	0.21	5.8	2	1.75	0.07	4.0	2	23.65	0.64	2.7	2	1.60	0.14	8.8
3	COSSYPHA HUMERALIS	2	2	3.15	0.07	2.2	2	1.50	0.0	0.0	2	21.05	0.92	4.4	2	1.30	0.0	0.0
4	COSSYPHA NIVIFICAPILLA	3	3	3.00	0.0	0.0	3	4.90	5.80	118.4	3	20.13	0.47	2.3	3	1.33	0.06	4.3
5	ALETHE CASTANEA	1	1	4.20	0.0	0.0	1	2.20	0.0	0.0	0	999.99	0.0	0.0	0	999.99	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	4.30	0.0	0.0	1	2.10	0.0	0.0	1	26.60	0.0	0.0	1	1.80	0.0	0.0
7	CEPSYCHUS SULARIS	1	1	4.40	0.0	0.0	1	2.00	0.0	0.0	1	28.50	0.0	0.0	1	1.70	0.0	0.0
8	CEPSYCHUS MALAFARICUS	5	5	3.90	0.25	6.5	5	1.98	0.08	4.2	5	26.56	0.15	0.6	5	1.76	0.09	5.1
9	MYADISTES GENIFARIS	3	3	3.63	0.06	1.6	3	1.80	0.0	0.0	3	25.77	0.64	2.5	3	1.50	0.10	6.7
10	MONTICOLA CINCLORHYNCHUS	1	1	4.50	0.0	0.0	1	2.20	0.0	0.0	1	28.00	0.0	0.0	1	1.90	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	5.10	0.10	2.0	3	2.37	0.06	2.4	3	32.03	0.31	1.0	3	1.97	0.06	2.9
12	CATHARUS FUSCESCENS	4	4	3.95	0.17	4.4	4	1.95	0.66	3.0	4	25.72	1.31	5.1	4	1.67	0.05	3.0
13	CATHARUS USTULATA	9	9	4.16	0.15	3.6	9	1.96	0.05	2.7	9	26.72	0.81	3.0	9	1.69	0.11	4.2
14	MYLODICHLA MUSTELINA	7	7	4.83	0.31	6.5	7	2.34	0.10	4.2	7	29.44	0.54	3.2	7	2.00	0.06	2.9
15	TURDUS PHILEFLOS	6	6	5.35	0.23	4.2	6	2.62	0.10	3.8	6	31.95	0.64	2.0	6	2.22	0.13	8.0
16	TURDUS MIGRATORIUS	5	5	5.68	0.15	2.6	5	2.76	0.15	4.5	5	35.22	1.75	5.0	5	2.40	0.10	4.2
17*	COSSYPHA	9	9	3.37	0.12	3.5	9	2.51	3.67	146.1	9	22.31	0.64	2.8	9	1.50	0.08	5.3
18*	CEPSYCHUS	6	6	4.15	0.25	6.1	6	1.99	0.08	4.2	6	27.53	0.15	0.6	6	1.73	0.09	5.2
19*	MONTICOLA	4	4	4.80	0.10	2.1	4	2.28	0.06	2.5	4	30.02	0.31	1.0	4	1.93	0.04	3.0
20*	CATHARUS	13	13	4.05	0.16	3.9	13	1.95	0.05	2.8	13	26.22	0.97	3.7	13	1.68	0.09	5.6
21*	TURDUS	11	11	5.41	0.20	3.5	11	2.69	0.12	4.6	11	33.58	1.26	3.7	11	2.31	0.12	5.2
	GRAND VALUES	55	55	4.22			55	2.27			54	25.36			54	1.66		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 63 N	CARMET-L MEAN	S D	C V	V 64 N	PHALNX-L MEAN	S D	C V	V 65 N	POLLEX-L MEAN	S D	C V	V 66 N	CORAC-L MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	13.10	0.42	3.2	2	5.65	0.21	3.8	2	3.30	0.14	4.3	2	19.40	0.28	1.5
2	COSSYPHA CAFFER	2	2	13.30	0.42	3.2	2	5.65	0.07	1.3	2	3.05	0.21	7.0	2	18.85	0.07	0.4
3	COSSYPHA HUMERALIS	2	2	11.40	0.42	3.7	2	4.80	0.0	0.0	2	2.80	0.14	5.1	2	16.65	0.35	2.1
4	COSSYPHA NIVICAPILLA	3	3	10.77	0.42	3.9	3	4.67	0.25	5.4	3	2.77	0.06	2.1	3	16.33	0.31	1.9
5	ALETHE CASTANEA	1	1	15.20	0.0	0.0	1	6.50	0.0	0.0	1	3.70	0.0	0.0	1	21.50	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	14.30	0.0	0.0	1	6.20	0.0	0.0	1	3.40	0.0	0.0	1	19.80	0.0	0.0
7	COPSYCHUS SULARIS	1	1	15.00	0.0	0.0	1	6.30	0.0	0.0	1	3.70	0.0	0.0	1	20.10	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	14.04	0.23	1.6	5	5.98	0.22	3.6	5	3.32	0.24	7.2	5	18.96	0.47	2.5
9	MYADestes GENIBARRIS	3	3	13.60	0.36	2.7	3	6.13	0.31	5.0	3	2.80	0.20	7.1	3	18.47	0.42	2.3
10	MONTICOLA CINCLORHYNCHUS	1	1	15.30	0.0	0.0	1	7.10	0.0	0.0	1	4.40	0.0	0.0	1	20.90	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	18.17	0.55	3.0	3	8.73	0.23	2.6	3	4.17	0.15	3.7	3	22.40	0.82	3.7
12	CATHARUS FUSCESCENS	4	4	14.82	0.50	3.4	4	7.67	0.13	1.6	3	3.10	0.10	3.2	4	19.75	0.83	4.2
13	CATHARUS USTULATA	9	9	15.77	0.59	3.9	9	7.84	0.32	4.1	9	3.33	0.29	8.6	9	20.11	0.55	2.7
14	MYLECICHLA MUSTELINA	7	7	16.54	0.33	2.0	7	8.07	0.45	5.6	6	3.58	0.25	6.9	7	23.29	0.90	3.9
15	TURDUS PHILEMELOS	6	6	18.90	0.53	2.8	6	8.92	0.26	3.0	4	3.62	0.22	6.1	6	24.97	0.76	3.0
16	TURDUS MIGRATORIUS	5	5	20.72	1.17	5.7	5	9.72	0.36	3.7	3	4.03	0.23	5.7	5	26.32	0.85	3.2
17	COSSYPHA	9	9	12.14	0.42	3.5	9	5.19	0.19	3.6	9	2.98	0.14	4.5	9	17.81	0.28	1.4
18	COPSYCHUS	6	6	14.52	0.23	1.6	6	6.14	0.22	3.5	6	3.51	0.24	6.8	6	19.53	0.47	2.4
19	MONTICOLA	4	4	16.73	0.55	3.3	4	7.92	0.23	2.9	4	4.28	0.15	3.6	4	21.65	0.82	3.8
20	CATHARUS	13	13	15.05	0.57	3.8	13	7.76	0.28	3.7	12	3.22	0.26	8.1	13	19.93	0.64	3.2
21	TURDUS	11	11	19.81	0.88	4.4	11	9.32	0.31	3.3	7	3.63	0.23	5.9	11	25.64	0.80	3.1
	GRAND VALUES	55	55	15.03			55	6.87			49	3.44			55	20.49		
SET #	SET DESCRIPTION	SET N	V 67 N	CORAC-HW MEAN	S D	C V	V 68 N	CORAC-SW MEAN	S D	C V	V 69 N	CORA-CRL MEAN	S D	C V	V 70 N	PYGO-H MEAN	S D	C V
1	COSSYPHA CYANOCAMPTER	2	2	3.35	0.07	2.1	2	1.10	0.14	12.9	2	8.00	0.71	8.8	2	6.75	0.07	1.0
2	COSSYPHA CAFFER	2	2	3.60	0.14	3.9	2	0.95	0.07	7.4	2	8.00	0.0	0.0	1	7.80	0.0	0.0
3	COSSYPHA HUMERALIS	2	2	2.60	0.42	16.3	2	1.00	0.0	0.0	2	6.90	0.14	2.0	2	6.25	0.07	1.1
4	COSSYPHA NIVICAPILLA	3	3	3.10	0.10	3.2	3	0.87	0.06	6.7	3	7.17	0.58	8.1	2	5.20	0.28	5.4
5	ALETHE CASTANEA	1	1	3.80	0.0	0.0	1	1.20	0.0	0.0	1	8.00	0.0	0.0	0	999.99	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	3.50	0.0	0.0	1	1.20	0.0	0.0	1	8.10	0.0	0.0	1	5.40	0.0	0.0
7	COPSYCHUS SULARIS	1	1	3.80	0.0	0.0	1	1.20	0.0	0.0	1	8.00	0.0	0.0	1	8.70	0.0	0.0
8	COPSYCHUS MALABARICUS	5	5	3.28	0.16	5.0	5	1.12	0.04	4.0	5	7.64	0.35	4.6	5	7.78	0.30	3.9
9	MYADestes GENIBARRIS	3	3	3.70	0.10	3.1	3	1.00	0.0	0.0	3	7.43	0.59	7.9	3	7.03	0.40	5.7
10	MONTICOLA CINCLORHYNCHUS	1	1	3.80	0.0	0.0	1	1.10	0.0	0.0	1	8.50	0.0	0.0	1	7.00	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	4.40	0.20	4.5	3	1.33	0.06	4.3	3	8.93	0.12	1.3	3	8.67	0.38	4.4
12	CATHARUS FUSCESCENS	4	4	3.60	0.24	6.8	4	1.10	0.08	7.4	4	8.13	0.25	3.1	3	7.67	0.51	6.7
13	CATHARUS USTULATA	9	9	3.54	0.15	4.3	9	1.08	0.08	7.7	9	8.73	0.46	5.2	9	7.46	0.49	6.5
14	MYLECICHLA MUSTELINA	7	7	4.10	0.30	7.3	7	1.33	0.11	8.4	7	9.71	0.49	5.0	7	7.99	0.50	6.3
15	TURDUS PHILEMELOS	6	6	4.57	0.37	8.2	6	1.45	0.10	7.2	6	10.17	0.43	4.2	5	9.02	0.66	7.3
16	TURDUS MIGRATORIUS	5	5	5.04	0.25	5.0	5	1.62	0.13	8.0	5	10.62	0.41	3.9	3	10.23	0.38	3.7
17	COSSYPHA	9	9	3.16	0.21	6.7	9	0.98	0.08	8.1	9	7.52	0.49	6.5	7	6.50	0.17	2.7
18	COPSYCHUS	6	6	3.54	0.16	4.6	6	1.16	0.04	3.9	6	7.82	0.35	4.5	6	8.24	0.30	3.7
19	MONTICOLA	4	4	4.10	0.20	4.9	4	1.22	0.06	4.7	4	8.72	0.12	1.3	4	7.83	0.38	4.8
20	CATHARUS	13	13	3.57	0.18	5.1	13	1.09	0.08	7.6	13	8.43	0.41	4.9	12	7.56	0.49	6.5
21	TURDUS	11	11	4.80	0.32	6.7	11	1.53	0.12	7.6	11	10.39	0.42	4.1	8	9.63	0.58	6.0
	GRAND VALUES	55	55	3.71			55	1.17			55	8.38			48	7.06		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species (See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 71 N	PYGO-W MEAN	S D	C V	V 49 N	<EDW-SF MEAN	S D	C V	V 50 N	<DPN MEAN	S D	C V	V 51 N	<SF-MID MEAN	S D	C V
1	CESSYPHA CYANOCAMPTER	2	2	2.90	0.0	0.0	2	51.50	2.12	4.1	2	53.00	9.90	18.7	2	35.00	14.14	40.4
2	CESSYPHA CAFFER	2	1	3.30	0.0	0.0	2	50.00	7.07	14.1	2	42.00	7.07	16.8	2	45.00	0.0	0.0
3	CESSYPHA HUMERALIS	2	2	2.80	0.0	0.0	2	52.50	10.61	20.2	2	55.00	0.0	0.0	2	40.00	0.0	0.0
4	CESSYPHA NIVIFICAPILLA	3	2	2.20	0.57	25.7	3	60.00	0.0	0.0	3	53.33	4.73	8.9	3	27.33	4.93	18.0
5	ALETHE CASTANEA	1	0	999.99	0.0	0.0	1	55.00	0.0	0.0	1	60.00	0.0	0.0	1	25.00	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	2.70	0.0	0.0	1	55.00	0.0	0.0	1	60.00	0.0	0.0	1	20.00	0.0	0.0
7	CORPUSCULUS SULARIS	1	1	3.40	0.0	0.0	1	45.00	0.0	0.0	1	55.00	0.0	0.0	1	50.00	0.0	0.0
8	CORPUSCULUS MALAPARTICUS	5	5	3.42	0.16	4.8	5	48.00	4.47	9.3	5	53.60	7.19	4.1	5	42.60	5.27	12.4
9	MYAESTES GENIPARENSIS	3	3	3.47	0.15	4.4	3	43.67	3.21	7.4	3	65.67	1.15	1.8	3	29.00	1.00	3.4
10	MONTICOLA CINCLORHYNCHUS	1	1	3.20	0.0	0.0	1	55.00	0.0	0.0	1	50.00	0.0	0.0	1	20.00	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	3.83	0.15	4.0	3	56.67	5.77	10.2	3	55.67	1.15	2.1	3	20.67	4.04	19.6
12	CATHARUS FUSCESCENS	4	3	3.07	0.40	13.2	4	75.00	4.08	5.4	4	64.50	1.00	1.6	4	15.50	3.70	23.9
13	CATHARUS USTULATA	9	9	2.97	0.21	7.2	9	71.44	3.36	4.7	9	62.78	2.33	3.7	9	19.22	4.52	23.5
14	MYLOCICHLA MUSTELINA	7	7	3.26	0.24	7.5	7	82.14	4.88	5.9	7	64.57	2.44	3.8	6	3.50	3.51	100.2
15	TURDUS PHILOMELUS	6	5	3.94	0.27	6.9	6	71.67	6.76	8.4	6	58.00	2.45	4.2	6	0.50	6.66	0.0
16	TURDUS MICRATORIUS	5	3	4.33	0.55	12.7	5	77.00	4.47	5.8	5	66.40	4.67	7.0	5	-9.40	3.36	35.0
17	CESSYPHA	9	7	2.80	0.33	11.7	9	53.50	5.78	10.8	9	50.83	6.21	12.2	9	36.83	7.05	19.1
18	CORPUSCULUS	6	6	3.41	0.16	4.8	6	46.50	4.47	9.6	6	54.30	2.19	4.0	6	46.30	5.27	11.4
19	MONTICOLA	4	4	3.42	0.15	4.3	4	55.83	5.77	10.3	4	52.83	1.15	2.2	4	20.33	4.04	19.9
20	CATHARUS	13	12	3.02	0.26	8.7	13	73.22	3.57	4.9	13	63.64	2.06	3.2	13	17.36	4.31	24.8
21	TURDUS	11	8	4.14	0.39	9.4	11	74.33	5.41	7.3	11	62.20	3.61	5.8	11	-4.45	5.44	0.0
	GRAND VALUES	55	48	3.05			55	59.35			55	57.47			54	24.00		
SET #	SET DESCRIPTION	SET N	V 52 N	<MP-MID MEAN	S D	C V	V 53 N	<ZY-POP MEAN	S D	C V	V 54 N	<SF-POP MEAN	S D	C V	V 75 N	DLF PRO MEAN	S D	C V
1	CESSYPHA CYANOCAMPTER	2	1	30.00	0.0	0.0	2	42.50	3.54	8.3	2	48.50	2.12	4.4	2	1.00	0.0	0.0
2	CESSYPHA CAFFER	2	2	27.50	3.54	12.9	2	45.00	0.0	0.0	2	37.50	3.54	9.4	2	3.50	0.71	20.2
3	CESSYPHA HUMERALIS	2	2	32.50	3.54	10.9	2	40.00	7.07	17.7	2	49.00	5.66	11.5	2	2.00	0.0	0.0
4	CESSYPHA NIVIFICAPILLA	3	3	30.67	4.04	13.2	3	43.33	2.89	6.7	3	59.00	1.73	2.9	3	1.33	0.58	43.3
5	ALETHE CASTANEA	1	1	25.00	0.0	0.0	1	52.00	0.0	0.0	1	60.00	0.0	0.0	1	1.00	0.0	0.0
6	ALETHE POLIOCEPHALA	1	1	23.00	0.0	0.0	1	45.00	0.0	0.0	1	60.00	0.0	0.0	1	3.00	0.0	0.0
7	CORPUSCULUS SULARIS	1	1	20.00	0.0	0.0	1	50.00	0.0	0.0	1	35.00	0.0	0.0	1	1.00	0.0	0.0
8	CORPUSCULUS MALAPARTICUS	5	4	44.75	1.26	2.8	5	44.00	6.52	14.8	5	40.60	3.78	9.3	5	1.00	0.0	0.0
9	MYAESTES GENIPARENSIS	3	3	51.00	1.00	2.0	3	43.33	2.89	6.7	3	53.33	2.89	5.4	3	2.00	0.0	0.0
10	MONTICOLA CINCLORHYNCHUS	1	0	999.99	0.0	0.0	1	30.00	0.0	0.0	1	40.00	0.0	0.0	1	4.00	0.0	0.0
11	MONTICOLA SOLITARIUS	3	3	42.33	7.52	5.9	3	41.00	1.73	4.2	3	45.67	1.15	2.5	3	4.00	0.0	0.0
12	CATHARUS FUSCESCENS	4	3	36.00	3.61	10.0	4	35.00	4.08	11.7	4	57.50	6.45	11.2	4	2.25	0.96	42.6
13	CATHARUS USTULATA	9	9	35.56	2.24	6.3	9	36.67	4.33	11.8	9	60.56	4.64	7.7	9	2.11	0.60	28.5
14	MYLOCICHLA MUSTELINA	7	7	29.00	4.69	16.2	7	45.71	9.76	21.3	7	61.14	5.40	8.8	6	2.17	0.41	18.8
15	TURDUS PHILOMELUS	6	6	33.83	2.04	6.0	6	32.50	2.74	8.4	6	57.50	6.89	12.0	6	2.50	0.55	21.9
16	TURDUS MICRATORIUS	5	5	31.80	2.68	8.4	5	36.00	6.52	18.1	5	58.00	4.47	7.7	5	2.80	0.84	29.9
17	CESSYPHA	9	8	30.17	3.80	12.6	9	42.71	3.98	9.3	9	48.40	3.32	6.8	9	1.96	0.48	24.7
18	CORPUSCULUS	6	5	32.38	1.26	3.9	6	47.00	6.52	13.9	6	37.80	3.78	10.0	6	1.00	0.0	0.0
19	MONTICOLA	4	3	42.33	2.52	5.9	4	35.50	1.73	4.9	4	42.83	1.15	2.7	4	4.00	0.0	0.0
20	CATHARUS	13	12	35.78	2.57	7.2	13	35.83	4.26	11.9	13	59.03	5.20	8.8	13	2.18	0.72	32.8
21	TURDUS	11	11	32.82	2.35	7.2	11	34.25	4.80	14.0	11	57.75	5.94	10.3	11	2.65	0.69	26.1
	GRAND VALUES	55	51	30.81			55	41.38			55	51.46			54	2.23		

APPENDIX TABLE 5 CONTINUED

Univariate statistics for 32 mimid and 14 thrush species
(See table 5.2 for description of characters.)

SET #	SET DESCRIPTION	SET N	V 76 N	PCYM FOR MEAN	S D	C V	V
1	CESSYPHA CYANOCAMPTER	2	2	1.50	0.71	47.1	
2	CESSYPHA CAFFER	2	2	2.00	0.0	0.0	
3	CESSYPHA HUMERALIS	2	2	1.00	0.0	0.0	
4	CESSYPHA NIVEICAPILLA	3	3	1.00	0.0	0.0	
5	ALETHE CASTANEA	1	1	2.00	0.0	0.0	
6	ALETHE POLIOCEPHALA	1	1	1.00	0.0	0.0	
7	COPSYCHUS SULARIS	1	1	2.00	0.0	0.0	
8	COPSYCHUS MALAFARICUS	5	5	2.00	0.71	35.4	
9	MYADestes CENTEAPERTIS	3	3	1.00	0.0	0.0	
10	MONTICOLA CINCLERMYNCHUS	1	1	1.00	0.0	0.0	
11	MONTICOLA SOLITARIUS	3	3	1.00	0.0	0.0	
12	CATHARUS FUSCESCENS	4	4	1.00	0.0	0.0	
13	CATHARUS USTULATA	9	9	1.00	0.0	0.0	
14	MYLOCTICHA MUSTELINA	7	7	1.00	0.0	0.0	
15	TURDUS PHILOMELUS	6	6	1.00	0.0	0.0	
16	TURDUS MISCATORIUS	5	5	1.00	0.0	0.0	
17*	CESSYPHA	9	9	1.3P	0.32	23.0	
18*	COPSYCHUS	6	6	2.00	0.71	35.4	
19*	MONTICOLA	4	4	1.00	0.0	0.0	
20*	CATHARUS	13	13	1.00	0.0	0.0	
21*	TURDUS	11	11	1.00	0.0	0.0	
	GRAND VALUES	55	55	1.28			

--- END OF TABLE

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