PATTERNS OF ANIMAL SIZE AND LANDSCAPE COMPLEXITY: CORRESPONDENCE WITHIN AND ACROSS SCALES

By

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"Man possesses four things
which are useless at sea
rudder, oars,
and the fear of going down"
-Antonio Machado

Those whose love I share know
that dedications are just tardy reminders
of what they already live in
This work is dedicated to those
who leave all the trappings of certainty behind,
armor, weapons and the fear of no control,
and who inspire us to live
in the midst of an ever-deepening question
with a wry sense of whimsy

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As biodiversity erodes globally, we wonder how much predictability in successful risk taking is needed to build the trust required to re-establish the migration routes of lost species. A similar question has been tested in my home this past decade. Predictability has eroded over years of waiting for an incomprehensible project to finally close with quicksilver deadlines which shimmered on a mobile horizon. Words cannot express my thanks to my wife, Gisela Bosch and children, Kurt and Lana, for supporting me through times when no definite answers could ease the uncertainty of what, how long, when and where things reach closure and new life begins.

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PATTERNS OF ANIMAL SIZE AND LANDSCAPE COMPLEXITY CORRESPONDENCE WITHIN AND ACROSS SCALES

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Statistical patterns of animal morphometry reflect interactions between animals and landscapes at a number of scales. Uni-modal distributions of morphometry have been used as evidence that animals respond to continuous distributions of environmental variables. A new synthesis - animal body mass lump analysis - tests discontinuous patterns of animal size as evidence of animal interactions with discontinuous patterns of landscape structure. The objective of this thesis was to test both landscape and non-landscape based explanations for their power to predict the generality and consistency of discontinuous patterns of animal size distributions.

Lump analysis is a reliable method for finding discontinuities in animal size distributions. Lump pattern, a pattern of clumps separated by gaps

in an animal community's body mass size distribution is robust to variance in body mass size estimates (within species) and to error in censusing species occurrence. These lump patterns are not artifacts of random sampling from continuous unimodal size distributions.

I discontinuous size distributions in bird and mammal communities in 150 ecosystems in 18 biomes found in a wide variety of climates and landscapes. Landscapes of similar landscape structural complexity consistently exhibited similar lump patterns with a high degree of correspondence in the locations of lumps and gaps. The degree to which lump pattern is common to two communities or biomes erodes as the difference in landscape structure increases. Lump structure predicts the scale and texture of landscape use by mammal species insofar as those species within a body mass lump use similar features of landscape geometry.

I found that non-landscape hypotheses also explain lump pattern, but at different levels than those explained by landscape-based hypotheses. Phylogeny appears to explain broad, coarse levels of lump pattern common to most mammal communities globally. Body size patterns evident at high taxonomic levels (Order) correspond to three zones on the size axis where lumps are commonly found in mammal communities. Competition for resources within a single range of scale appears to explain fine levels of lump pattern, the size distributions within the lumps. Body sizes of species within lumps are more evenly dispersed than expected by chance.

CHAPTER 1
ANIMAL INTERACTIONS WITH LANDSCAPES: REINTEGRATING ECOLOGY OVER MULTIPLE SCALES

Ecosystem complexity is a function of how we choose to describe systems. "Systems become complex when, in seeking understanding or prediction, we invoke levels of organization that are distant in temporospatial scale or are characterized by entities of disparate types." (Allen and Hoekstra 1992)

Introduction

Ecological theory evolves via a series of splits and reintegrations. New avenues of inquiry split the field and burgeon into separate disciplines. Splits are frequently bounded by theoretical and/or logistical constraints, and the gaps between these bounds often provide rich new sources of inquiry which stimulate reintegration (Pickett et al., 1994). Ecology's emergence as a discipline 90 years ago can be viewed as building a bridge between organismal physiology and biogeography (Schimper 1903, McIntosh 1985). Since that time numerous splits and reintegrations reflect efforts to expand the scope of ecological research to explore the ever-widening scales of environmental change or anthropogenic impact. Splits or reintegrations often mark the emergence of a sub-discipline to address questions at specific scales, such as populations, communities, ecosystems, and biomes.

Ecology is currently challenged to address problems of change at unprecedented global scales. Attempts to predict potential climate impacts expose a number of gaps in ecological understanding. One key gap has emerged between community and ecosystem ecology. Strict reliance either on the "organismal focus" of community ecology or on the "process focus" of ecosystem ecology has proven inadequate as a conceptual framework for testing ideas about change over a broad range of time and space scales. This gap offers an opportunity to integrate the latest advances of separate disciplines into a broad synthesis. Increasingly, both disciplines recognize the reciprocal actions of organisms and ecosystems as a critical "frontier of integration" in ecology (Pickett et al. 1994). If disciplinary protocols are relaxed such that neither organisms nor processes are assumed to be constant (Damuth 1987, Cale 1988), what phenomenon integrates the results of their interactions?

One promising synthesis gives a more flexible frame of reference for ecological interactions. It considers organism-process interactions as part of the functional dynamics of "complex adaptive systems" (Brown 1995, Lewin 1992, Kauffman 1993, Holling 1986, 1992). In systems models components may interact over different, distinct temporal and spatial scales. This view departs from research traditions which rigidly frame the space/time scales at which information is envisioned or collected. For example, Karieva (1989) notes that roughly 80 percent of all manipulative ecological field experiments were performed at the scale of one meter quadrats. Since interactions are not studied exclusively at one scale-specific reference (deme, population, community) analysis may consider any appropriate range of scale. This perspective can incorporate both interactions which operate over distinct scale ranges and those which cross scales, such as the contagious processes of fire or pest outbreaks.

A key thread within this synthesis is that statistical patterns of animal behavior and morphometry can be used as indices of important interactions at a number of scales. The shapes and bounds of statistical distributions of such animal size indices are patterns which reflect either "intrinsic, evolutionary or extrinsic, environmental constraints on variation" (Brown 1995). The test of whether intrinsic or extrinsic processes are the primary influences on animal size indices is the subject of this dissertation. I shall first discuss the synthesis of this theory in terms of the development of theory that links patterns of organism size and behavior to those of processes and landscape structure. I shall examine the questions which have emerged during this synthesis and shall conclude by describing the tests I shall use to probe those questions.

Size Patterns of Organisms Evolving in a Non-Hierarchical World

The organism is a common node in many 'traditional' ecological world models and is widely used as a point of departure to integrate ecological theory (Huston et al. 1988). This focus is evident in studies relating morphology (body size) to a wide variety of processes including physiology (Kleiber 1961), developmental and reproductive strategies (Pianka 1974, Kiltie 1984), longevity (Eisenberg 1981), social organization (Jarman 1974, Eisenberg 1981), home range (McNab 1963, Harestad and Bunnell 1979), and community structure (Pianka 1974, Damuth 1981, Robinson and Redford 1986). How ecological theory is integrated depends on the scale at which processes and related organism size distributions are studied. For example, population ecologists look at intra-specific variability of individual sizes and use population size distributions as surrogates for age distributions in populations dynamics studies (Ricker 1975, Hughes and Connell 1987). Small scale population processes (growth rates and mortality) have been compared across different environmental types as potential causes of bi-modality in population size distributions (Huston and DeAngelis 1987).

The focus shifts from intra- to inter-specific size variability when community ecologists define patterns of community organization. Lawton (1989) quantified relationships between population density, species diversity and mean body size. Most such studies have examined community organization rules for terrestrial animals (Peters and Wassenberg 1983, Damuth 1987, Gaston and Lawton 1988, Maurer and Brown 1988, Blackburn et al 1990). Patterns of mammal community structure have been correlated with body size, diet, population biomass, and rate of reproduction (Eisenberg 1980, Eisenberg, O'Connell, and August 1979; Kinnaird and Eisenberg 1989, Robinson and Redford 1986 a. b).

Brown (1995) proposed "macroecology" to explore overarching patterns at larger scales (biome to global scales in space and decadal to millennial in time) in order to bridge gaps in understanding concerning processes defined at smaller scales by population and community ecologists. By forging synthetic links between ecology, biogeography, paleobiology and macro-evolution, the new initiative of macroecology aims to establish a more informed context for smaller scale questions of abundance, distribution and diversity of species as affected by interactions between organisms (inter-specific) and their environment.

Macro-ecological Patterns of Animal Morphometry

Some general trends do relate animal morphometric patterns to large scale evolutionary, ecological and climatic patterns. Mammal body size correlates strongly with seasonality, the amplitude of seasonal climatic variation (Lindstedt and Boyce 1984). For evolutionary lineages, the general trend for body size to increase (Cope's Law) now appears to apply only to the upper size range since many species shrink in size over evolutionary time

(LaBarbera 1989). Regional (sub-continental) trends show that population density scales negatively with body size (Peters 1983). For both temperate and tropical latitudes herbivorous and carnivorous mammal body sizes decline with increasing density. A weak trend (low correlation coefficient) is also evident for birds (Peters 1983).

Numerous regional scale studies of animal body size distributions (Van Valen 1973, May 1978, 1986, 1988, Bonner 1988, Dial and Marzluff 1988, Morse, Stock and Lawton 1988, Lawton 1990, Brown and Nicoletto 1991, Maurer, Brown and Rusler 1992) find the same body size pattern irrespective of the kind of animal (bacteria, trees, fishes, insects and mammals). The regional size pattern is highly modal with a pronounced right skew (see bottom of Figure 1-1) indicating the predominance of small over large organisms. This trend appears related to the greater incidence of small species (May 1988, Lawton 1989) and to the higher densities attained by small organisms (Peters and Wassenberg 1983, Brown and Maurer 1986, Damuth 1987, Lawton 1989).

Hutchinson and MacArthur (1959) suggested that the greater capacity of small animals to access resources explains their greater abundance. A similar prediction is made if the world's structure is viewed as fractal (May 1986, 1988, Morse, Stock and Lawton 1988, Lawton 1990). If environments are self-similar in structure at all scales, then most resources will be available at the tiny scales where they can be most densely packed. However, fractal geometry is not universal, many structures are self-similar only over certain ranges of scales (Holling 1992). Furthermore, the regional size pattern for animals (May 1988) does not display the highest abundances at the smallest sizes. Abundance increases to a modal size (around 100 grams for terrestrial mammals, around 30 grams for land birds (Brown, Marquet and Taper 1993) and then declines with increasing size.

Brown and Nicoletto (1991) found that for mammals the regional unimodal size pattern flattens with decreasing spatial scale. Community size distributions are uniform, and those for biomes are intermediate. They explain the flattening of body size frequencies at local scales as a result of processes at several scales which amplify the frequencies at the large and small size extremes. At small scales the physiological limitations of small animals requires their consumption of high energy resources whose patchy distribution is at scales smaller than most sampling units, resulting in their presence at most sites. Large animals are found at most sites due to their broad home ranges. At all scales local competition excludes similar sized animals.

Macroecology searches over broad scales for patterns which reveal processes which regulate species abundance, distribution and diversity (Brown 1995). However, few such broad scale studies of animal morphometry envision process interactions within the framework of complex adaptive systems, wherein components interact non-linearly and at distinct, different spatio-temporal scales. Most such studies use an implicit 'Gleasonian' world model; they see the world as a multi-axial nexus of overlapping environmental gradients. Processes are inherently "scale invariant" in that their impacts are seen to overlap in space and time (Figure 1-1) such that their effects are simply averaged over the entire range or scales. The degree of overlap implicit in this 'continuous' world view is such that the aggregate distribution of impacts is viewed as unimodal density function which spans all scales. Unimodal size distributions are likely products of

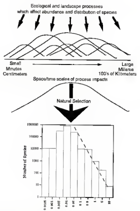


Figure 1-1. Continuous World Model- scale invariant operation of ecological processes selects for a continuous distribution of animal sizes (graph after May 1988)

unimodal models of process impact distributions. It naturally follows that the modal size for any animal group (e g mammals) is considered 'optimal' at all scales for a habitat or ecosystem (Brown 1995, Brown and Nicolleto 1991)

Suggestions of a Discontinuous World

Several lines of evidence from paleobiology and computer simulation of ecosystem behavior run counter to a "continuous" world view The clustering of time series data for meso-scale structuring processes such as insect outbreaks (Clark et al., 1979, McNamee et al 1981, Holling 1988 1992), fires (Clark 1990), and floods (M B Fiering 1983) into small sets of repetitive cycles or periodicities does not appear a likely product of processes randomly overlapping over broad scales Some degree of aggregation of the time behavior of processes is suggested by sharp peaks in time series spectra. Similarly, computer simulation models provide little support for the view of ecosystem behavior as a product of many variables interacting similarly at all scales. Mathematical models of systems as different as African savannas and Canadian boreal forests (McNamee et al , 1981, Holling 1980, Holling 1992, Walker et al., 1969, Steele 1985) suggest that the essentials of ecosystem behavior appear in the dynamics of relatively few variables (Holling, 1992) The differences in variable speeds (cycling times) are about an order of magnitude, again suggesting qualitatively different temporal behavior domains for the key variables driving an ecosystem

Exploration of complex systems behavior (Kauffman 1991 1993, Perry 1995) using computers suggests that a continuous world is an unlikely context for the evolution of complicated entities such as organisms or ecosystems Evolution appears possible only when the behavior of system variables is confined to a small set of relatively stable cycles (attractors) Stability results from hierarchical structure with severe constraints on the number of interactions which are significant to any variable (O'Neill et al 1986, Allen and Starr 1982, Allen 1992). In the continuous world the operation of ecological processes at all scales implies a multitude of potential interactions, many of which are significant. Chaotic collapse occurs in simulated systems with such a liberal density of significant connections (Kauffman 1991, 1993). Structuring process (fire, flood) periodicities suggest the same kind of temporal clustering of attractors which appear in simulated systems in which evolution is possible. Aided by increasing sophistication of computer calculation and remote sensing, larger scale ecological research has added evidence of clustering of behaviors or impacts in space.

Evidence for scale-specific ranges of impact for ecological processes continues to accumulate. Processes important at one scale range may appear insignificant at another. Variance in litter decomposition rates measured at local scales correspond well with micro-scale patterns of the litter and decomposer communities. However, macro- scale climatic patterns explain variance at regional scales (Meentemeyer 1978, Meentemeyer 1984).

These lines of evidence suggested to Holling (1992) that small sets of plant, animal or abiotic processes act in a manner analogous to keystone species (Paine 1966) to organize the spatial distribution and patch sizes of species in terrestrial ecosystems. Holling's (1992) "Extended Keystone Hypothesis" summarized these suggestions by positing that processes "form interacting clusters of relationships, each of which determines the temporal and spatial structure over a constrained range of scales." A landscape's spatial hierarchy is a nesting of smaller structures within larger and larger aggregates. Hierarchical structuring results from the coincidence of processes cycling with different periodicities in spatially nested sets. Thus local areas operating at fast speeds are nested within more slowly cycling regions. The specific space/time scale ranges of these sets of structuring processes define the dimensions of landscape units or "lumps" within the hierarchy. Measuring the dimensions of these lumps and linking them to the fauna which exploit them could establish the parameters for a new model of interactions between organisms and the environment.

Size Patterns of Organisms Evolving in a Hierarchical World

Efforts to define landscape structure and examine its influence on ecological processes coalesced into a discipline within the last four decades (Wiens 1995). Quantitative landscape ecology examines structural (spatial geometry) and functional relations at scales of hectares to square kilometers (Turner 1989). Landscape structure is defined as the spatial distribution of materials, species and energy as they relate to size, shape and number (Turner 1989). Landscape function consists of the interactions between spatial elements. This avenue of inquiry expanded the notion of ecological processes structuring the landscape with evidence that structure in turn influences processes. Turner (1989) demonstrated links between spatial structure (patch size and the distribution of patch sizes) and process rates. For example, critical thresholds in patch density may determine whether the spread of disturbances is related to disturbance intensity (high density) or disturbance frequency (low density) (Turner et al 1989). The effects of landscape structure (patchiness) on organizational processes has been studied at the levels of population and metapopulation structure (Rogers 1987, Bernstein et al. 1991, Gilpin and Hanski 1991) and community and ecosystem dynamics (Pickett and White 1985, Caswell and Cohen 1991). If process periodicities entrain other variables such as vegetation (structure) and animals, then a model of interactions in a discontinuous world is enriched by feedbacks between structure and processes

Attempts to define landscape structure which is linked to animal behavior and community organization continue since MacArthur's (1966a) studies of vertical vegetation complexity and relative abundances of bird species. The question of defining landscape structure at multiple scales in a discontinuous world is more complicated in that it demands that all forms of structure, vegetational and otherwise, be accounted for.

Defining Landscape Structure

Hierarchical definitions of system structure can be criticized as an arbitrarily imposed human organizational bias to filter ecosystem complexity. Human bias can influence the measure of both structure and function. For instance the linear scale adopted for a map determines patch number, size and shape (Gardner et al. 1987). The measure of functional flows between patches are also affected by the spatio-temporal bias of the observer (Turner 1989).

Two approaches are commonly used to avoid scale bias in defining landscape structural patterns. The first (Krummel et al. 1987, Milne 1988) searches for pattern by consciously avoiding a human reference scale in measuring pattern. The measure of ecological pattern is influenced both by how data is bounded and resolved and how spatial and temporal relationships are calculated. The space and time dimensions of data must be explicitly defined because of the current lack of widely accepted sets of spatial scales to define or measure ecological processes or patterns (Holling 1992). Calculation methods are another source of bias in testing spatial and temporal ecological patterns. Bias is minimized by using objective (scale invariant) algorithms at many different scales to derive a cross-scalar measure of pattern complexity (Mandlebrot 1982, Gunderson 1992). Fractal geometry is one such attempt to define objective landscape structure (Krummel et al. 1987, Milne 1988, O'Neill et al. 1988, Turner and Ruscher 1988).

Animals linked to landscapes by scale-dependent patterns of resource perception and utilization.

Another approach avoids human bias in seeking an "organism-centered view" of the environment (Whittaker 1975, Turner 1989). The assumption is that animal survival is linked to its perception of structure at scales which reveal patterns critical to its survival (Turner 1989). This approach follows the intuition of MacArthur that the physical structure of the environment organizes biotic communities and the morphology and behavior of associated animal species (MacArthur and MacArthur 1961, MacArthur et al. 1966a). MacArthur's trend-setting example related vertical stratification of vegetation to avian diversity.

Some attributes of animal perception and response correlate with animal morphometry. Mammalian auditory perception scales with body size (Eisenberg 1990). The frequency range of sound production is lower for large bodied mammals (Calder 1984), and maxima of frequency perception covaries negatively with body mass (Dooling 1980). If those perceptual faculties which mediate animal interaction with landscape scale with size, then size indexes landscape structure.

The study of animal movement patterns has neither the theoretical nor the empirical basis to establish a "mechanistic basis" for landscape ecology that links perception to structure (Ims 1995). However, broader inferences have been drawn from patterns of animal incidence and vegetation structure. Patterns of species distribution, community structure and habitat use are clearly associated with vegetation structure and habitat configuration or "physiognomy." Larger more heterogeneous forests have higher avian species diversity and more bird pairs (Freemark and Merriam 1986). Additionally, body size scales with the size and texture of landscape objects. Mega fauna such as grizzlies discriminate and respond to specific macro- scale structures, for example they seldom use habitat within 100 meters of a highway, whether the road is in use or not (Turner 1989). Dubost (1979) demonstrated that artiodactyl size correlated with the structure of the undergrowth they exploited so as to minimize resistance from vegetation. Demonstrations that landscape elements such as patch size, shape and diversity influence resource use suggest that animal interactions with landscape structure organize communities (Fragoso 1997). However, can organizing rules suggested by studies of community components (single species or guilds) be extrapolated to the entire community?

Evolutionary Patterns, Large Scale Community Stability

Darlington (1957) proposed that extrinsic factors will cause biotic communities to be "complementary" in their organization. According to this "Principle of Complementarity" similar spatial distributions of environmental components, such as soils and climate, will influence natural selection such that the same niches will be filled irrespective of the initial phylogenetic stocks. Paleobiological evidence suggests that vegetative structure (for example, cover) is another environmental factor which organizes communities, making them "complementary" in a fashion analogous to Darlington's principle (Eisenberg 1990). For example, even when carnivore assemblages became extinct, their replacements were remarkably similar in body size and form (Martin 1990). In this example replacement of secondary consumers produces similar body size patterns when communities remain similar in vegetative cover, primary consumers and primary productivity.

Wiens (1984) suggested that the composition of animal communities is so dynamic that such "ephemeral" phenomena are not reliable indices of any rules of ecological organization. Extreme fluctuations in year-to-year species abundances for birds (Wiens and Rotenberry 1981) and mammals (Brown 1995) suggest that there is no "community balance" from which to predict the community's future. If an animal community does not represent some stable equilibrium, how could any association between animals and environmental factors last long enough to influence evolution or even the community's long term organization? If communities are non-equilibrial and reflect fluctuating influences of fast and slow variables, then a static definition of the community, such as a statistical size distribution, is arbitrary. However, evidence of macro-scale "complementarity", measured across biomes (Darlington 1957) or aeons (Martin 1990), suggests that larger scale associations of structure and animal community organization exist in relative equilibrium. Similarly, broad community patterns such as species composition are much more stable than fluctuating abundances.

Ephemerality (Wiens 1984), appears scale dependent. The composition of the local ground foraging bird guild may fluctuate dramatically and show little relation with small scale floristics. But bird communities correlate well with landscape structure when defined at larger scales of aggregation such as "eastern mesic prairies", "xeric shortgrass prairies", and "western shrubsteppe habitat". The question remains, however, at what scales are animal communities stable enough to justify their characterization by a static index, such as a size distribution?

Summary Model of a Lumpy Environment

The sum of data on process cycles, spatial pattern, and organism perception and use of landscapes provides evidence sufficient to complete a testable model of a discontinuous world. In the continuous model animals interact with ecological processes whose impacts are continuously distributed over all scales. The discontinuous model constrains the scales of animal interactions to limited ranges. Two possible scenarios achieve this. The first narrows the space/time scales of process impacts such that they do not overlap (Fig. 1-2). A nested temporal hierarchy of process periodicities entrains variables into aggregates or "lumps" each operating at its own space/time scale. This coupling of process cycling to behavior of ecological variables, such as vegetation, also structures the environment. Entrainment of vegetation and terrain variables by the periodicities of structuring processes produces vegetative and substrate structure unique to the scale range of each lump. For example, dramatic differences in spatial resolution distinguish leaves (micro- scale) from forest stands (meso- scale) from forested valleys (macro- scale).

Lumpiness is not exclusively tied to a hierarchical distribution of exogenous driving forces. The same lumpy world could emerge even if the space/time impacts of process operation were continuously distributed across all scales. In this second scenario lumpiness occurs as an emergent property of system self-organization. Systems which persist and evolve tend to exhibit periodicities (limit cycles) in the behaviors of variables (Kauffman 1991, 1993, Perry 1995), and these can act as attractors which entrain the geometries of structural variables and the morphologies of animals which exploit those

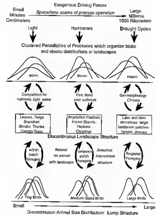


Figure 1-2. Discontinous World Model driven by self-organization of lumpy landscape structures and animal morphologies

structures However, opportunities to feed breed and hide are not simple functions of spatial geometry. The interaction of temporal discontinuities (process periodicities) with spatial hierarchy is a self-organizing process which maintains a lumpy world. Qualitative structural distinctions between lumps could spatially reinforce opportunities presented by the temporally discontinuous hierarchy of choices for animals. For example, seasonal temperature oscillations parallel the trajectories of canopy volume in high latitude deciduous forests. The lumpy model posits that animals interact with an environmental hierarchy which is a discontinuous space/time distribution of process cycling speeds, impacts and physical structures. The combined interaction of animal behavioral choices, landscape structure and atmosphere is shown as a space/time model of the lumpy world (Figure 1-3)

In this study I propose to compare the relative influences of intrinsic and extrinsic factors on animal size as a test of two world views. Intrinsic influences on animal size variation can be quantified as the animal community's composition in terms of trophic level, food niche, or taxonomic categories. Testing extrinsic influences requires quantification of landscape structure. That task begins with the description and ranking of the spatial dimensions of objects in a hierarchical model of animal-landscape interactions

Defining spatial dimensions of ecological objects

Terms describing environmental features (vegetation, land cover) and hierarchical levels of animal association (organism, deme, population) need to be related by a some standard reference frame of spatial dimensions. Currently no such reference frame is commonly accepted by the various ecological disciplines. Community ecologists define community according to the scale demanded by the question at hand (P. Feinsinger, pers. comm.).

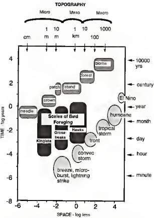


Figure 1-3 Model of discontinuous distribution of space/time dimensions for operation of atmospheric processes, forest structures and bird foraging scales.

and ecosystem ecologists use a similar sliding scale to define ecosystems. So the bacteria in an abandoned aluminum can be considered as a community as may all wolf populations over 1000 square kilometers. The history of flexible use of such terms as 'community' or 'ecosystem' makes it unwieldy to insist on strict delineations for each term, for that forecloses discussion of other efforts to study animal-landscape interactions. However, to avoid confusion, I shall try to follow the spatial scales delineated in Figure 1-4. The dimensions and examples associated with these terms are arbitrary, but they form a clear and objective basis for discussion.

Summary and Overview of Chapters

In this chapter I have striven to establish the bases for the continuous and discontinuous world models. I have set the context for this study as an investigation of both models using patterns of animal size as indices of animal interactions with the environment. In the succeeding chapters I provide the conceptual and methodological bases for my tests. I test the robustness of my pattern detection methodologies and then apply them to a range of animal communities to look for informative differences and similarities of body size pattern. I shall test explanations based both on the continuous and discontinuous world views and then draw my findings into a summary synthesis. The details of each subsequent chapter are as follows.

In Chapter 2, I discuss the conceptual and methodological foundations for using animal body sizes to explore interactions between animals and landscape structure. I describe the advances made since the first attempts to test the existence of multiple modes in body size distributions. These advances establish the existence and generality of lumpy body size

Examples of Landcover Types at each scale Continental Boreal Forest	 Temperate Grassland	Spatial Dimensions (Kilometers) Grain	 Extent	Vegetative/ Spatial Descriptors
Alder Tree	Atriplex sp	0001	01	Physiognomy
Alder thicket	Low shrubs	001	0 1	Habitat
Black spruce bog w/ alder patches	Salt bush flats	01	1	Community
Lacustrine forest lowlands	Shrub/Forest Gallary Stream Swales	0 1	10	Ecosystem
Spruce/Jackpine/ Lake Mosaic	Grass upland/ stream gallenes	1	100	Landscape
Boreal Forest	Shortgrass Prairie	10	500	Biome
Boreal	Temperate	100	1 E3	Super-Biome
North America	North America	500	5 E3	Continent
Northern	Northern	1 E3	10 E3	Hemisphere

Figure 1-4 Arbitrary quantification of scales for spatial terminology with examples at each level of the landscape hierarchy from boreal forest and temperate grassland land covers

distributions and demonstrate a compelling regularity of pattern that sets a favorable context for further research. This context is enriched by recent work which links patterns of landscape structure with those of lump structure. I then describe and discuss the various hypotheses which explain lumpy size distributions based either on a continuous or discontinuous world view. Finally, I describe some of the shortcomings of a variety of prior techniques for determining the number of modes in size distributions so as to highlight the advantages of the GaP Analysis (Restrepo, Renjifo and Marples 1997).

I test the robustness of GaP Analysis methodology for statistical analysis of size distributions before I use it to test landscape and non-landscape hypotheses on actual animal body mass data sets. Specifically I shall test the sensitivity of GaP Analysis to two sources of error. The error sources stem from two types of variability in the body size data sets. The first is related to sampling error due to techniques which inadequately census the space/time dynamics of animal populations. The second error source potentially arises from the size variability inherent within species populations. I strive to sustain the fluidity between the posing of hypotheses (Chapter 2) and application of subsequent tests (Chapters 3 - 5) by placing these qualifying probes of GaP Analysis in Appendix A.

In Chapter 3, I test lump body patterns across a wide variety of biomes for internal consistency (commonality) when comparing animal communities landscapes of similar structure and for uniqueness (singularity) when comparing animal assemblages in different landscapes. I test whether such lump patterns are scale dependent by carrying out these comparisons at several spatial scales, the biome and super-biome levels. I test the robustness and generality of lump structure at several scales by examining whether similarities and differences of lump structure reflect commonalities and uniquenesses, respectively, of landscape geometries.

In Chapter 4, I test extrinsic or environmental explanations of ecosystem-level lump structures I examine whether lump structure reflects the complexity of landscape geometry at different scales (biome, ecosystem, habitat) For a wide variety of structurally distinct ecosystems I quantify and numerically correlate landscape geometry with lump structure (number of lumps) Finally, I test lump structure for its capacity to predict landscape structure use by mammals at the scales of ecosystems and biomes

In Chapter 5, I examine at several levels explanations of ecosystem lump structure based on the continuous world view I arbitrarily distinguish explanations of lumpy size patterns based on animal responses to external structure from those based on inter-organismal interactions as extrinsic vs. intrinsic.' At the level of entire animal communities I examine intrinsic explanations of lump structure as posited by the trophic , morphological and phylogenetic hypotheses At two levels (animal community and animal size distributions within lumps) I test the prediction that competition-induced character displacement causes body masses to be more evenly spaced along the size axis than expected by chance. At the level of entire animal communities the intrinsic-based hypotheses can be rejected if I find commonalities of lump structure with some distinct differences 1) when comparing different trophic levels of the same taxa in the same landscape 2) when comparing different taxa in the same landscape

In Chapter 6, I summarize the findings of the preceding five chapters and I discuss a synthesis of these findings in terms of the potential to expand this line of inquiry beyond the present study

Précis - Concise Overview of Conclusions

The breadth of theory addressed in this work is formidable, the methods used to analyze and present data are novel, and the volume of data processed to test these questions is considerable. The prospect of engaging all three challenges simultaneously brings to mind a Czech film director's comment on enraged farmers who charged with pitchforks at Nazi tanks in 1938, "It is so hard to distinguish between the 1 percent who succeeded and were lauded as heroes and the 99 percent who failed and were regarded as fools." I present the salient conclusions of this work as landmarks to aid the reader in navigating these information-rich territories.

- Gap Analysis is a reliable method for finding discontinuities in animal body size distributions ("lump pattern") which are consistent with most other methods. It is robust to errors introduced in animal size data sets by variance in body mass (within species) and by censusing error of species populations.
- The preponderence of evidence supports the Discontinuous World Model. I found lumpy distributions of animal size in 150 communities in 18 biomes, and my simulation experiments show that such distributions are not likely to be the products of chance.
- Landscape-based hypotheses explain much of the lump pattern which is common within a biome or between different biomes. Two sets of evidence link lumpy body sizes to landscape structure. I consistently find common patterns of lumps shared between animal communities coming from landscapes of similar landscape structure (biomes). I found that the

degree to which lump pattern is common to two communities or biomes erodes as the difference in landscape structure increases

- Non-landscape hypotheses also explain lump pattern, but at different levels than those explained by landscape-based hypotheses Phylogeny appears to explain broad coarse levels of lump pattern common to most mammal communities globally Body size patterns evident at high taxonomic levels (Order) correspond to three zones on the size axis where lumps are commonly found in mammal communities Competition appears to explain narrow, very fine levels of lump pattern, the size distributions within the lumps. Body sizes of species within lumps are more evenly dispersed than expected by chance

CHAPTER 2
TESTING ANIMAL-LANDSCAPE INTERACTIONS USING CONTINUOUS AND DISCONTINUOUS MODELS

Introduction

The theoretical framework for most inquiries into animal responses to the environment has been a landscape of gradients and continuously distributed opportunities which I described as the 'continuous world model (Chapter 1) The clustering of time and space behaviors of ecosystem processes strongly suggests a discontinuous world of separate levels operating in parallel at separate scales. The study of animal size distributions as indices of the interactions of animals with the operation of these processes attempts to test links between the functioning of ecological processes and mechanisms of evolution or community organization. Discontinuous patterns of animal morphometry (lumpiness) have been cited (Holling 1992) as evidence of animal interactions with a world of discontinuously distributed opportunities (discontinuous world model).

Three conditions must be satisfied to show that lumpiness is useful in testing animal landscape interactions. First, lumpiness must have some generality We must regularly find lumpy patterns in a wide variety of different kinds of landscapes, and within each landscape type the lump pattern must be repeatable Second, the technique of finding lumps must reliably find such patterns. And third, some trend should link patterns of animal morphometry or lump structure with patterns of structural complexity in the landscapes the animals inhabit

In this chapter I first marshal the limited but compelling evidence that all three conditions have already been demonstrated sufficiently to establish a firm foundation for this work. Then I present a suite of hypotheses to test a range of explanations, based either on continuous or discontinuous world models, as to why patterns (lump or otherwise) exist in animal size data. Finally, I compare the relative strengths of different methods for examining animal size data sets for discontinuities or for multiple modes (lumps) in order to provide data for testing these hypotheses.

Are There Lumps In Animal Body Mass Size Distributions?

Multiple modes in animal size distributions have been found for birds, mammals and herps and have been taken as evidence of a variety of ecological processes. Valverde (1964) and, later, Legendre (1989) found multi-modal pattern in the size distributions of mammal communities in the form of disjunctions in the cumulative distribution function of mean adult body masses for species. Legendre (1989) associated disjunctions separating two clusters of animal body masses with relatively open habitat and the lack of a disjunction as evidence of closed habitat. Griffiths (1986) found discontinuous size distributions ("polymodality") in numerous taxa (birds, insects, and plankton), which he attributed to three possible, though not mutually exclusive, causes: vegetation structure, avian guild structure and trophic relations ("species stacking"). Allen, Forys and Holling (unpublished manuscript) describe multiple modes in body size distributions of bird, mammal and herp communities in the South Florida everglades landscape and show a trend between "endangered" status and a species' position on the edge of the discontinuities which demarcate modes in the size distribution.

Holling (1992) found multiple modes or "lumps" in adult body size data for birds and mammals in the boreal forest and prairie biomes. Hypotheses based on phylogenetic, trophic or guild categories provided little if any power to explain "lump structure" the presence and location of modes in size distributions. Membership in any of these three categories bore little if any relationship to membership in any lump or group of lumps. The only hypothesis which resisted disproof attributed differences between lump structures of animal communities in separate ecosystems to qualitative differences in landscape structure.

The usefulness of lump analysis in linking animal communities to landscapes is suggested by three sets of observations (Holling 1992). First, comparisons of lump structures between communities of similar landscape structure showed a regularity of pattern or commonality (species in different ecosystems which utilize similar architectures tend to cluster into similar size ranges or lumps). Lump structure commonalities were strongly evident for forest and prairie mammalian and avian data sets, compiled at the biome level from boreal latitudes, and for avian data sets at the boreal forest biome level and at the scale of the North American continent. Second, lump patterns showed a singularity related to the uniqueness of each community's landscape structure (communities with different architectures have lump patterns which differ in the location and/or presence of lumps). Lump structures of avian data sets compiled regionally at boreal latitudes showed stark differences in terrestrial versus pelagic and forest versus prairie comparisons. Third, the complexity of lump structures consistently correlated with that of landscapes. More complicated landscapes, such as terrestrial forests and prairies, had more complicated avian lump structures than those of 'simpler' landscapes, such as pelagic, marine environments.

Restrepo, Renjifo and Marples (1997) found multiple modes in 19 bird communities from 'Upper Lowland' and 'Lower Montane' and 'Upper Montane' forest sites in Columbia. A link between the complexity of lump structure and that of landscapes is suggested by two observations Greater numbers of lumps were found in communities with complete forest cover (as opposed to fragmented, pasture sites) and in sites with greater variability of vertical vegetation structure

Hostetler (1997) found multiple modes in size distributions of bird communities from four temperate eco-regions in North America Both commonality and singularity were evident in comparisons of these avian lump structures Regularity of lump pattern is suggested by identical lump numbers and very similar scale ranges of most lumps when comparing all sites Singularity of lump pattern is evident when inter-site comparisons revealed some degree of lump pattern mismatch in the medium to large size range ($10^{1.3}$ to $10^{3.5}$ grams) The relative similarity of landscape structural complexity between all sites compared precluded any demonstration of a consistent trend between lump and landscapa complexity However, Hostetler's work reveals a unique link between lump structure and landscapa pattern by the demonstration that birds in each size lump respond to at least one aspect of landscapa pattern (tree canopy cover) at different scales

How General is the Incidence of Lumps?

The demonstration of lumpy size distributions in several forest and grassland biomes in North and South America raises the question as to how general the occurrence of lumpiness is To test the range of ecosystem types in which discontinuous body size distributions are evident I applied Holling's (1992) BMDI ("Body Mass Difference Index") method to bird, bat and mammal body size data sets taken from data sets from 75 ecosystems in some 11 biomes on 3 continents Application of Holling's (1992) criterion to identify significant discontinuities (BMDI values larger than the mean plus one standard error) revealed lumpy (multi-modal) body pattern in every single ecosystem. However, if the underlying size distributions are actually continuous, might such lumpy evidence be a false signal created by random or incomplete sampling?

I applied a further test to see what lumpy patterns might be found from random draws from continuous size distributions. For each observed body mass data set I established a continuous, uni-modal size distribution with the same range of body sizes and created a mock data set by randomly drawing from that continuous distribution *n* times where *n* = the number of species in the data set. I then applied the Holling BMDI method to this mock body mass data set using his criterion for 'significance' and counted the number of lumps found. I repeated this process 1000 times for each observed data set to determine mean and standard deviation statistics for number of lumps found in 1000 mock data sets. I then graphed the frequency distributions of lump numbers found in actual data sets and in mock data sets (Figure 2.1). The qualitative differences between the actual and mock lump frequency distributions of lumps suggest it is highly unlikely that observed lump structures result from random sampling from continuous body mass size distributions.

Work to date (Holling 1992, Restrepo Renjifo and Marples 1997, Hostetler 1997) on animal body mass size distributions have established lumpy body mass patterns as a general phenomenon for a variety of taxa over a range of landscape types. Links between lump structure and landscape structure are evident in the similarity between lump patterns found in communities with similar landscapes, in the uniqueness of lump patterns found in communities with contrasting landscape structure, and in similarities of response to landscape pattern by animals in the same lump. The regularity and consistency with which lump pattern has been found is a coarse but intriguing measure of the reliability of lump pattern analysis. Different techniques often give qualitatively similar determinations of lump

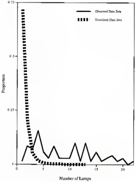


Figure 2-1. Proportion of lumps found using the Holling BMDI on observed and simulated data sets of mean adult body masses for species of birds and mammals.

number and location on the size axis. In addition, my own preliminary investigation casts doubt on the idea that lump pattern results from random sampling error

These observations establish a basis from which to probe further as to why lump body size pattern is found While landscape structure has resisted disproof more consistently than any other explanation of lump pattern, it is premature to ignore other explanations. The complexity of large scale systems derives in part from a diversity of causal processes operating at different scales, and non-linear systems behavior suggests that the relative importance of these processes may change with time (Allen and Starr 1982, Levin 1992) This dynamic uncertainty inherent in complex systems must be embraced not by reducing the scope of investigation so as to cast a strong light on one explanation. Rather uncertainty must be embraced by considering in parallel all sound explanations for ecological pattern The chances of detecting multiple influences on pattern are increased when those influences are represented separately in a suite of hypotheses tested in parallel (Wiens 1984, Marples and Holling, in submission) I now discuss a range of explanations for the existence of pattern in body size distributions and formalize them as testable hypotheses

Hypothetical Explanations of Lumpy Size Distributions

The relatively long history of research based on a Continuous World Model (Chapter 1) has generated a variety of explanations for patterns of animal body size By contrast the novelty of the Discontinuous World Model combined with the imposing challenge of describing the discontinuities and resultant structural forms of such a world have yielded but a single broad explanation to date (Holling 1992) I now describe the basis for these explanations and state them as hypotheses

Hypotheses Based on a Continuous World Model

The study of animal morphometry as an index of animal interactions with ecological processes was given considerable impetus by the contention of Hutchinson (1959) that competition in animal communities is reflected in consistent size ratios between species competing for the same resource. Hutchinson (1959) proposed that an observed minima of bill-size similarity ratio of 1:1.3 represented the results of competition limiting similarity among species. Such size ratios purportedly result from 'character displacement', a shifting in morphometries of the two competing species accompanying a change in the resources sought by either species (resource partitioning). Competition-induced character displacement has also been described as an evenness of spacing of animal morphometries along the size axis. A lively, and often bitter, debate has embroiled attempts to demonstrate (Lack 1947, J. Brown 1975, Schoener 1983, and Moulton and Pimm 1987) or refute (Connell 1980, Arthur 1982) the existence of character displacement as evidence of competition. The possibility that such even spacing of animal sizes could also result from species sorting in the process of community organization is included in the hypothesis statement below. By this token the gaps which separate lumps result from competitive size displacement either at the long term (evolutionary) or short term (community organization) scales.

H1 - Competitive niche and size displacement

> *Animal morphological sizes are spaced on the size axis with a greater degree of evenness than expected by chance. This 'over-dispersion' reflects a divergence of body sizes and resource usage in response to competitive pressures. This divergence could reflect processes which are evolutionary ('character displacement') or community organizational (species sorting).*

Gaps in body size distributions might also result from evolutionary constraints which limit the number of size ranges possible for an organism. Such constraints might act at local scales of community organization (H2) with a limited number of discrete size ranges to choose from, at broad scales of evolutionary rates (H3) limited by physiology or ontogeny, or at broad scales of evolutionary possibilities funneled by a limited set of locomotory modes (H4) which are competitive on land or in the air. I designate H2 as the Macro-Phylogeny hypothesis, to suggest the linkages between size ranges in which lumps are found and membership in higher taxonomic levels such as Family or Order. Paul Marples offered "Noah's Ark" as a more intuitive title for Holling's (1992) "Urtier hypothesis" (H3). And the title 'Limited Morph' (H4) was originally suggested by Holling (1992).

H2 - Macro-Phylogeny

> *The original size ranges of a limited number of ancestral forms have expanded somewhat because of adaptive radiation. These limited expansions result in a global size distribution with a limited number of modes of greater frequencies of species within limited ranges of size. In the process of community organization lumps result from random selection of species from these multiple modes.*

H3 - Noah's Ark ("Urtier")

> *The species of animals have been drawn from a limited number of ancestral forms whose organizational constraints preclude evolution of intermediate sizes even though such sizes would find adaptive possibilities in a landscape with continuously distributed opportunities.*

H4 - Limited Morph

> *There are only a limited number of life-forms (e.g. locomotory modes) possible for animals, each of which is constrained to function*

> *effectively only over a limited range of sizes There are so few of these life-forms possible, that sizes of animal cluster into a small number of clumps even if the spatial attributes of their habitats are continuously distributed*

The possibility that predator-prey relationships require substantial size differences has been suggested as the basis for multi-model size distributions in aquatic environments (Kerr 1974) Gaps in size distributions might also result from position on the food chain, where the size requirements for foraging on low quality resources (herbivores) are significantly greater than those for foragers on more concentrated resources (carnivores) Both trophic interpretations of gaps in size distributions are subsumed in the Trophic Trough hypothesis (H5) below

H5- Trophic Trough

> *Size-dependent trophic interactions will initiate and maintain lumpy patterns of body-mass distributions independent of any other mechanism*

Hypotheses Based on a Discontinuous World Model

Hierarchical world models based on qualitatively different operating speeds of organizing processes were suggested as early as 1973 (H. Simon) as a much more plausible basis of biological evolution than the random organization of opportunities found in a Continuous World However, only recently have the implications of such a model been extended to ecological patterns of animal communities Holling (1992) proposed that a discontinuous world would entrain not only behaviors but ultimately the morphologies of organisms For each distinct range of scales at which objects are apparent (landscape lump) in a discontinuous world, certain body size ranges would be most adaptive, causing morphologies to cluster over time into body size lumps. Holling (1992) posed this idea as 'The Textural Discontinuity' hypothesis.

H6 - Textural discontinuity

> *Animal s should demonstrate the existence of a hierarchical structure and of the discontinuous texture of the landscape they inhabit by having a discontinuous distribution of their sizes, searching scales, and behavioral choices. Landscapes with different hierarchical structures should have corresponding differences in the clumps identified by such a bio-assay.*

Both continuous and discontinuous models are sources for a suite of explanations for lumpy body patterns. An array of methods exist for detecting such patterns in order to test these hypotheses. Controversy over detection methods previously used (Manley 1996) and the sheer number of alternatives require careful selection of the best available method. I now discuss the functioning and relative merits of these detection methods.

Methods to Identify Gaps and Lumps in Size Distributions

For systems as broad and complex as ecosystems finding a robust statistical model for the distribution of a variable such as body size is non-trivial. The non-normality and non-independence of data often make conventional statistics inappropriate for community level questions in ecology (Gotelli and Graves 1996). Current statistical theory provides no rigorously defined models of underlying distributions for variables in multivariate systems. In the absence of known distribution models nonparametric estimates of density functions can be made. Some statistical tools have proven useful in the early, exploratory phases of research to establish the existence of skewness or multimoldality, but the robustness and reliability of methods to estimate the number of modes in size distributions remains debatable In this section I review the methods used to explore animal size distributions and explain the relative advantages of new methods used in this study

Histograms

Ease of application and comprehension make histograms a popular initial method for exploring data density distribution patterns. However, subjective methods of applying and interpreting histograms can bias the detection of multimodal distributions Choices which arbitrarily influence the definition of modality include specification of 1) bin width, 2) data origin and 3) "coordinate direction(s) of the grid of cells" (Silverman, 1986) The degree of smoothing in a size distribution is particularly sensitive to bin width, and such choices lack objective guidelines to protect against biases either for or against multi-modality (Holling, 1992) Silverman (1986) makes a similar criticism of kernal estimates, a flexible and sophisticated method of smoothing histograms. "Subjective choice in sizing the smoothing parameter (h) allows exploration of different interpretations of the density estimate, but no universally accepted objective method is available" Independent confirmation of a size distribution's degree of modality must be sought from other methods

Cumulative Distribution Function

Cumulative Distribution Functions (CDFs) are attractive tools because they are widely used and can quickly convey an intuitive, graphic understanding of a data pattern. Sorting the mean adult body masses of species of a single taxon in ascending size order, a gap is identified where rank increases very little relative to body size (Figure 2.2) By the same token a lump is characterized by a relatively large increase in rank with a small increase in size   The limitations of this method emerge when it is applied to data with inconspicuous discontinuities   CDFs clearly reveal only those gaps of extreme size, discontinuities in most data sets are so difficult to detect that subjective judgment becomes too great a factor

Hierarchical Cluster Analysis

Cluster analysis developed around the challenge to define 'groups' within numerical data without any prior information on the properties or even the existence of the groups   As Silverman (1986) states "   the number of groups and the rules of assignment into these groups have to be discerned solely from the given data, without reference to a training set (p 130)" However, cluster analysis has yet to evolve an objective, generally accepted method for defining modality in statistical distributions   Despite the development of hundreds of clustering algorithms, no single method is regarded as "best" (Manley 1986)   The generality of the clustering method is undermined when different algorithms can produce markedly different results on the same data   Interpreting the results of cluster analysis is highly subjective   For example, cluster analysis performed on univariate data under SAS software can output multiple definitions of the number of clusters found, starting with one cluster and continuing as high as the clustering criteria specified by the user allow (SAS Institute Inc 1988)   Indices (Cubic Clustering Criterion, pseudo F and pseudo t^2 statistics) accompany each interpretation of the number of clusters found in the data set   Proceeding up or down the ranking of cluster number interpretations, a local maximum in such indices suggests a higher likelihood that the number of clusters associated with that maximum is important.   However, there is no independent test for the significance of an interpretation of how many clusters exist in a data set.

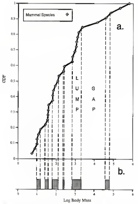


Figure 2.2 - Extrapolation of cumulative distribution function (a) for log10 body masses of shortgrass steppe mammals from southwest Kansas to an interpretation of lump structure (b) wherein each gray box represents a distance along the size axis occupied by a cluster of species of relatively similar size (body size lump). These lumps are separated by "gap" zones on the size axis which are occupied by no or very few species.

Split-Moving Window Analysis

Multi-modality can be defined by identifying data clusters, and it also is indicated by the identification of the discontinuities which separate clusters or modes in the data set. Split moving window boundary analysis (SMW) was developed for location of boundaries separating relatively homogenous soil units along transects (Webster 1973, 1978). SMW detects discontinuities in multivariate data which are ordered in one dimension by comparing dissimilarity metrics derived from two halves of a "window" or a sequential group of samples from the data (Webster 1973, 1978, Ludwig and Cornelius 1987). In two of the many possible applications of SMW by Marples (pers comm) these window halves may reveal discontinuities either in ratio form (equation 2.1) or as an absolute difference (equation 2.2)

$$SMWr_n = 1 - \left[\sum_{i=n-w+1}^{n} s_i \Big/ \sum_{i=n}^{n+w-1} s_i \right] \qquad (2.1)$$

$$SMWd_n = \sum_{i=n}^{n+w-1} s_i - \sum_{i=n-w+1}^{n} s \qquad (2.2)$$

Where s_i is the ith size datum in a univariate series

The utility of SMW is limited by the fact that it only detects "relative" discontinuities (Webster 1973). This can lead to spurious "detection" of discontinuities both at large and small scales, within random data sets (Cornelius and Reynolds 1991). Split Moving Window analysis, as such, lacks objective methods to determine the statistical significance of a discontinuity in a univariate size data set. However, the discontinuities it locates are generally in the same locations on the size axis as those found by other methods such as hierarchical clustering analysis and, as shall be discussed, the Body Mass Difference Index and Gap Pattern Analysis.

Body Mass Difference Index

The lack of objective methods to determine the statistical significance of a discontinuity is shared by the method of Holling (1992) which defines modes in a univariate, serially ordered data set by identifying the discontinuities or "gaps" which separate them. Holling applied this method to find the number of modes or "lumps" in size distributions of birds or mammals inhabiting the boreal prairie and forest biomes. Gaps were quantified by the Body Mass Difference Index (BMDI) as the size difference between the species *n-1* and species *n+1* divided by the body mass of the *nth* species raised to the γ power (Equation 2.3). Various values for γ were explored to detrend the resulting BMDI indices.

$$BMDI = [s_{n+1} - s_{n-1}] / (s_n)^{\gamma} \qquad (2.3)$$

Where s_i is the ith size datum in a univariate series.

A consistent bias is evident in the output of the SMW and the BMDI when applied to a serially ordered univariate size data sets. Using animal body masses derived from species assemblages compiled either at the ecosystem or biome levels, values for either index appear larger for discontinuities within the first and final thirds of a data set and smallest for gaps in the middle. This skew in emphasis to the smallest and largest extremes of a data set manifests itself as a U-shaped pattern (Figure 2.3) further complicating the location of meaningful or significant discontinuities.

The techniques described so far estimate data density patterns without regard for any causative process(es) which potentially could generate these

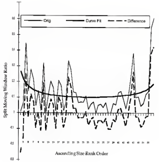


Figure 2-3 Comparison of gap statistics generated using a split moving window ratio algorithm to locate discontinuities in a size distribution of mean adult body masses sorted in ascending order. The body masses were assigned to a species list of non-volant mammals identified in a rainforest community near Belem, Brazil (Medelin 1989). A third order polynomial (thick dark line) is fit to the SMW gap statistics to highlight the U-shaped trend wherein values at the smallest and largest extremes are inflated

patterns. Their prime purpose is to uncover interesting patterns whose properties merit further investigation. Without known distributions for reference there are no standards against which to measure significance and weed out spurious patterns. One criterion for rejecting pattern is to demonstrate that it can be generated in the absence of any process which hypothetically might have created the pattern. Such rejection criteria can be synthesized through the use of null models. Gotelli and Graves (1996) define them as follows:

> *..a pattern-generating model that is based on randomization of ecological data or random sampling from a known or imagined distribution.*

Manley (1995) employed a bump-hunting technique (Silverman 1986) to generate null models to challenge Holling's (1992) finding that the body mass distributions of boreal prairie birds and mammals are lumpy. Manley used statistical simulation to test models of one to progressively greater numbers of modes for their fit to the size distributions of the boreal taxa examined by Holling (1992). Manley (1995) found the best fit with a unimodal model, though he found some evidence for two modes in the underlying size distribution. However, he concluded there was very little evidence to support multimodality or lumpiness beyond two lumps.

GaP Pattern Analysis (GPA)

Marples (in submission) claims that Manley's use of the Silverman bump-hunting technique is so conservative during the exploratory phase of research that it is vulnerable to Type II error. Marples (Restrepo, Renjifo, and Marples 1997) developed Gap Pattern Analysis (GPA), a methodology similar to Silverman's, which allows detection of modes within a size distribution and comparison of their location among multiple data sets. GPA involves generation of null models of species size distribution through computer simulation using a kernel estimate of data density of a species size (n) pool. The species pool is derived from either one or multiple (non-redundant) size data sets and is sorted into ascending size order. A kernal estimate of data density is simply a smoothed histogram of the data. The smoothing window width is adjusted until the kernal estimate of the data density distribution is unimodal. The null distribution has one mode by design so as to establish the size of gaps one would find if the actual, underlying distribution is unimodal.

After ordering the observed data set by ascending size its data density is compared to that found in a null distribution. The basis of comparison is the Relative Discontinuity (D_i). This is a statistic generated by statistical simulation iterated thousands of times. Computer simulation generates thousands of mock distributions drawn at random from the theoretical null. Over all iterations a distribution of gap sizes is generated at each species rank by calculating absolute discontinuities (d_i) for each pair of neighboring species (equation 2.4)

$$d_i = s_{i+1} - s_i \qquad (2.4)$$

The Relative Discontinuity (D_i) is a value found for each species which measures the proportion of absolute discontinuities calculated in all iterations of mock distributions which are smaller than the observed absolute discontinuity. This value establishes how rare a discontinuity would be in a unimodal size distribution, and this rarity is used to determine the significance (alpha) level of the gap (for more information about GPA methodology see Restrepo, Renjifo and Marples 1997).

One salient innovation of GPA is the determination of the significance of gaps with minimal bias through comparison across multiple data sets. The relative rarity of a gap observed in actual size data can be established by its ranking within a simulated null distribution of gap sizes. Significance is determined by equating relative rarity with a probability value. Independent and unbiased determination of gap significance allows comparison of lump structures of data sets from different ecosystems which have different source characteristics such as number of species, minimum and maximum body masses, and range of body masses.

PatternMatching (PM)

The PatternMatching approach runs as a True Basic program, entitled PatternMatcher, written by Paul Marples (Marples, unpublished data). It determines lump structure by examining univariate body size data sets for modes or accumulations of data density as opposed to size ranges of data scarcity (gaps). The PatternMatching method establishes the probability of finding modes in a data set by comparing its lump pattern with those of a group of data sets which share similar characteristics. Marples has grouped data sets based on similarities of landscape characteristics, such as data sets from a region within a biome, however non-landscape characteristics could also be used to group the data sets. The PatternMatching approach statistically tests potential matches between the lump patterns of these different body size data sets within the group. The degree of mismatch (*m*) is a weighted sum of distances along the size axis where lumps in either data set line up with gaps in the other data set. This measure of mismatch distinguishes 'near' from 'complete' misses by establishing a 'distance-from-the-nearest-lump' value at each point along the size axis. Along those size-axis intervals which do not correspond (for example, lump in one data set matched with gap in the other) the distance values are summed to generate an m value.

Each site's body mass data set is modeled as a size distribution with a variable number of modes depending on the resolution (smoothing parameter) of the kernel estimator. The degree of mismatch between the various size distribution models for both sites is tested in a factorial design, beginning with unimodal definitions up to $k \times k$ modes, where k is arbitrarily set by the user. For each model a size distribution is fit to the actual data with the smoothing parameter adjusted to give the number of modes specified by the model. For example, for a 2 x 2 model, mismatch (m_{obs}) would be measured for bimodal approximations of each site's lump structure.

The significance of the mismatch observed for that model is then determined by establishing the likelihood of mismatches if the underlying size distributions of the data sets were actually unimodal though represented as multimodal. For each model a statistical distribution of mismatches is created by sequential calculation of mismatches in 10,000 mock data set pairs. For each site a mock data set is generated by random sampling n times from a continuous unimodal distribution with the same size range as the original data set. A frequency distribution is fit to this derivative data set with the number of modes specified by the model. The locations of lumps and gaps are then established by finding the inflection points in each mock data size distribution. Mismatch is then calculated between the two mock lump patterns. For each model the degree of mismatch expected with a significantly small frequency is determined by finding m_{calc} which is greater than or equal to those m found in the lower 5 percent or 1 percent (depending on the α level desired) of the simulated mismatch distribution. If $m_{obs} <= m_{calc}$ then the degree of mismatch is considered significant. PatternMatcher records the probability values of each model so as to identify those combinations of modes which are most likely to be significant.

Comparing GaP analysis with Pattern Matching

GPA was the first detection method offering reasonable estimates of probability levels for discontinuities in size data. However, these estimates were derived from comparisons of each data set with simulated data based on a continuous null model fit to the actual data. GPA is applied one data set at a time, and when a certain alpha level is chosen, then only one model of the lump structure is estimated. Pattern Matching (PM) offers a novel opportunity to compare a number of models of lump number for a data set with arrays of models for each other data set in a group drawn from landscapes either of similar or dissimilar structure. The PM process establishes a likelihood not for each mode within a size distribution but for each possible model of modes or lumps when compared to models of similar data sets.

In this study I present the results of 4 years of work in determining models of lump numbers for more than 150 ecosystems using GPA. While methodological constraints prevent the use of PM for all of my data, the risk posed by not using the more advanced technique is of interest. To this end I analyzed a subset of my data sets (Table 2-1) using both methods to estimate the best model of lump number for each data set. I examined a total of 688 lumps in some 81 ecosystem body mass data sets from 17 biomes. Table 2-1 lists the biomes by which ecosystem body mass data sets were grouped (column 1), the site names of the ecosystems (columns 2 - 4), the numbers of lumps found in each ecosystem by GaP analysis (columns 5 - 7), the numbers of lumps found by the model with the highest probability value using Pattern

Table 2.1 Comparison between GaP and Alternative mammal lump structure models for probability values of a significant match as calculated by PatternMatcher software (Marples, unpublished data)

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
				Ecosystem lump structure models						Changes in Number of Lumps			Probability that lump pattern match is significant		
				GaP Analysis			Lump Simulation								
Biome	Ecosys1	Ecosys2	Ecosys3	No. of Lumps			No. of Lumps						GaP	Increase Prob w/ Lump Sim	Combined GaP & Lump
African Rain Forest	MontKiau	LaMakoko	Lamto	14	13	19							0.80	0.00	0.80
	Tai	Lamto		16	9		16	8		2	2		0.49	0.35	0.93
Asian Rain Forest	Malaysia	Cape York		19	7								0.64	0.05	0.69
Boreal Forest	New Brunswick	RhoneAlpes		7	6		4	9		3	9		0.52	0.14	0.67
	ManitobaWhite	ManitobaTaiga	DoreLake	7	9	7							0.56	0.00	0.56
	ManitobaNoom	Quebec	New Brunswick	6	7	7	8	4	8	0	3	1	0.07	0.48	0.55
Boreal Forest North	Kluane	NYukonNP		8	7								1.00	0.00	1.00
Tropical Moist Forest	BrazilAtlantic	Sangmalma		9	10								0.30	0.00	0.30
Neotropical Lowland Rainforest1	CerroPelao	RioCenepa	RioSantiago	9	12	7	7	10	3	2	2	4	0.00	0.79	0.79
	AltoRio	CerroPelao	Manu	8	5	10	9	4	8	1	1	1	0.45	0.11	0.56
Neotropical Lowland Rainforest2	Lacandona	BCI	LaSelva	7	7	7	8	6	7	1	2	0	0.15	[illegible]	[illegible]
Neotropical Lowland Rainforest3	KanukuE	KanukuW	Surinam	10	8	11							1.00	0.00	1.00
	KanukuE	Belem	Surinam	10	8	11							0.88	0.00	0.88
Neotropical Montane Rainforest	LaPlanada	Cosco	SierradeChama	4	9	9	8	4	9	1	5	1	0.22	0.25	0.47
	MonteVerd	LaPlanada	Cuzco	8	4	9	9	5	9	2	1	3	0.10	0.18	0.28
Paleo-Grasslands	Transvaal P	Gold	Retrol	11	9	18	9	11	12	2	2	1	0.29	0.40	0.69
Savanna with Forest	Serengeti	Gabon	Amboseli	11	10	10	3	9	11	8	7	1	0.01	0.83	0.84
Scrubland	Colorado	ElKuhaden	Monte Desert	7	6	8	8	9	9	2	6	9	0.89	0.13	0.99
ShortGrass Prairie	Jornada	SWKansas	Bevbore	7	6	7	4	4	8	3	2	2	0.10	0.70	0.80
	Aghtoleigh	CPER	Pawnee	8	9	7	9	3	6	0	2	1	0.44	0.17	0.61
Southern Temperate Forest	Savannah	KathOrleasy	NW Louisiana	8	7	10	12	9	10	2	1	0	0.03	0.04	0.07
TallGrass Prairie	SiteCotton	MontanaRoan	Konza	10	9	9	10	9	5	0	1	3	0.33	0.57	0.91
Temperate Desert	ZionNP	DeathValleyNP	BigBendNP	9	5	7							0.97	0.00	0.97
Tropical Dry Deciduous Forest	Mercilia	CerroBlasco	Juanacha	5	9	5							0.90	0.00	0.99
	Juanacha	Chamela	Banda	9	7	7	9	7	3	0	0	9	0.02	0.13	0.15
Woodland/Savanna	Lokori	Zirano	Jabal	8	9	7	8	9	9	0	0	2	0.42	0.30	0.72
	Rukwa	Ifome	Lokori	16	18	8							0.92	0.00	0.92
Tropical Wet Forest	CoffWFor	Gustopo		6	9		9	10		3	4		0.73	0.14	0.87
	Makokou	MtNimba		11	12								0.62	0.00	0.62
	CoffWFor	MtNimba		8	11		9	6		3	9		0.63	0.10	0.73
SUMMARY															
Average changes in lump no. per ecosystem				1.15											
Avg num lumps per ecosys				0.464											
Avg change in lump number as a proportion				0.135											
Mean probability of a significant match between lump structures													0.69	0.17	0.88
Standard Deviation of probability values													0.37	0.22	0.32

Matching (columns 8 - 10), and the absolute differences between lump numbers found using both methods (columns 11 - 13).

The final three columns list the probabilities determined by Pattern Matching for different lump models for ecosystem body size data sets. Column 14 lists probabilities for lump models found using GaP Analysis. Column 15 lists the probability associated with the best lump model found by Pattern Matching. Column 16 lists the change (increase) in probability associated with any 'superior' lump model found by Pattern Matching. Column 15 merits attention, for while many lump models have high probabilities (>0.8), there are many models with far lower values. Even using Pattern Matching it was often impossible to find a significant lump model. This fact is underscored by the relatively low mean probability value (0.66) and high variance (0.32) of probability values.

GPA considered one data set at a time, while PM looked at each data set in comparison to other data sets from the same biome. The absolute difference between GPA lump number estimates and those provided by PM averaged about 1.15 lumps per data set. This average represents a 13.5 percent change in lump number in absolute (+/-) terms. The overall mean increase (Column 16) in the probability of a significant match between lump patterns of different ecosystems was only 0.17 (from 0.49 to 0.66). This is a notable but not remarkable increase given that a few extreme outlier values boost this number disproportionately. Twenty-three out of thirty values were lower than 0.17.

Therefore, even assuming the superiority of the PM method, one still obtains qualitatively similar results from GPA. Rather than challenge the results already obtained by GPA, these findings give a measure of confidence with the older method. These findings accord with results from most methods listed above which I have explored over the years, the numbers predicted by different methods rarely differed dramatically The dramatic change wrought by the architect of these statistical advances, Paul Marples, is our ability to quantify the probabilities associated with specific discontinuities and the intervening lumps (GPA analysis) and those probabilities associated with models of lumps for entire animal communities when compared with other community body size data sets from similar landscapes (Pattern Matching)

Testing the Robustness of GaP analysis to Error in Size Data Sets

Lump (GaP) analysis is threatened by two sources of error which potentially undermine the reliability of body mass data sets taken from animal communities These two error sources are incomplete censusing of animal communities because of temporally unstable populations and incomplete accounting of intra-species variation in animal body mass sizes In Appendix A I found that GaP analysis is robust to observed levels of these error sources because it reliably found known lump patterns (boreal prairie bird and mammal data sets, Holling (1992)) at simulated error levels which were higher than those observed in the field

I found that observed levels of these error sources in mammal and bird body mass data sets exhibit right-skew (Figure 2-4) frequency distributions For both error sources the frequency distributions are skewed to the right with a long tail to the right signifying that the vast majority of species exhibit little variation in body mass or in temporal abundances in the populations The minority of species which exhibit high variation introduce relatively low levels of stochasticity in determining lump structure which are unlikely to significantly undermine the capacity of lump analysis to find the underlying lump structure.

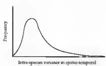


Figure 2-4 Right-skewed frequency distribution characteristic of either error source (temporal population fluctuations or intra-species size variation) in animal body mass data sets.

I found that lump analysis is robust partly because such right-skew distributions of size or abundance variation make animal body mass data sets relatively stable and reliable That is to say that it is unlikely that the species composition or the body masses of a animal community data set would vary drastically over time I could not avoid such conclusions when I found lump analysis marginally robust to extreme scenarios of variation for either error source. I made my computer simulations extreme by allowing not a minority but all species to exhibit the same level of variation in size or in presence/absence When I applied lump analyses to these simulated body mass data sets I found it robust to extreme simulations of census error for both birds and mammals, and not robust to extreme simulations of size variation in birds, though marginally so for mammals. The resistance of lump analysis to such severe simulations of variation supports the hypothesis that it is robust to observed, small-to-moderate levels of variation in species size and population fluctuations

Summary

In this chapter I have cited evidence which establishes a firm basis for further exploration of lump structure as an index of animal landscape interactions. Namely, sufficient demonstrations of the generality of lump structure, the reliability of lump analysis techniques, and links between animal morphometrics and landscape structure have been made to encourage further probes. I have reviewed a suite of hypotheses which allow parallel testing of the continuous and discontinuous world models for their power to explain the existence of lumps or discontinuous size distributions in animals. Lumpiness is found in animal communities from a wide variety of landscapes and is a useful pattern for these tests.

I have also reviewed the relative strengths of a variety of pattern detection techniques and discussed the fundamental robustness of lump analysis, namely, that many of these techniques give relatively similar estimates of lump numbers at an ecosystem site. I have discussed the improvements in recent methodological advances of Paul Marples. For example, by linking gap statistics with alpha levels, GaP analysis offers a sound basis to compare lump patterns at different sites. It is possible that Pattern Matching improves estimates of probabilities of lump pattern, but the lump numbers estimated by both techniques do not differ greatly. I conclude that GaP analysis is a reasonable technique for comparing lump patterns, and shall be the lump pattern method employed in this study. I found GaP Analysis to be robust to the degree of risk introduced by several sources error inherent in animal size data sets. In succeeding chapters I will apply lump (GaP) analysis to bird and mammal body mass data sets to define a lump pattern for each animal community and then will test the power of landscape and non-landscape hypotheses to predict the lump patterns I find

CHAPTER 3
LUMP PATTERN TRENDS IN SIMILAR LANDSCAPES: TESTS OF A DISCONTINUOUS WORLD MODEL

Introduction

Having established that Lump (GaP) Analysis is robust to various sources of error within animal size data sets (Appendix A) I now use it to examine lump pattern similarity within and between biomes and larger scale systems as a test of predictions of the Textural Discontinuity Hypothesis (H6). In tests using lump detection methods similar to GaP analysis, the Textural Discontinuity Hypothesis (H6) has resisted disproof in a limited number of landscapes, primarily boreal prairie (Holling 1992) and forest (Holling 1992, Hostetler 1997), temperate forest (Hostetler 1997, Allen, Forys and Holling, in review) and tropical montane forest and paramo (Restrepo 1997). In all these tests the trend between landscape structure and lump pattern was more compelling than any trend predicted by a non-landscape hypothesis.

Several interesting questions follow on these initial results. How general is this trend, could it be found in a wide variety of landscape types? How consistent are these trends; are there lump patterns which repeatedly characterize particular landscapes and allow one to distinguish between different landscapes? At what scales of landscape might such trends appear general and consistent?

In this chapter I examine lump patterns for their generality and consistency in explicit tests of landscape-based predictions of animal size distributions in a variety of landscapes. However, predictions made by non-landscape explanations of lump pattern (H1 - H5) are implicitly challenged in these tests as well, and I incorporate the results of this chapter with further tests of these non-landscape predictions in Chapter 5.

In this section I discuss what the landscape-based hypothesis (H6) predicts about animal size distributions, review the results of previous tests of this hypothesis and describe the basis for the new tests I shall apply.

Predictions of Lump Pattern Based on a Discontinuous World Model

Broadly speaking, the Textural-Discontinuity hypothesis (H6) posits that lump pattern is a 'bio-assay' of landscape structure, such that discontinuities in animal size distributions will reflect gaps in the hierarchical pattern of landscape architecture. Alternatively the modes or lumps in an animal size distribution can be seen as evidence that groups of similar-sized animals respond to clusters of object sizes in the environment. For example, one might expect three lumps in the size distribution of animals living in a world divided into three ranges of scale (micro-, meso- and macro) for objects (Figure 1-2). Specifically, H6 predicts that lump patterns from animal communities in landscapes of similar architecture should be similar, and that those from communities in structurally different landscapes should be different. Pattern similarity between lump structures is a measure of the degree to which features, such as lumps or gaps, share the same locations on the body size axis when comparing the two lump patterns.

The utility of animal size distributions as bio-assays of landscape structure rests on the consistency or replicability of body size patterns in relation to landscape architecture. If lump pattern similarity can consistently identify features common to animal morphometry in sites in similar landscapes then one can also use this bio-assay to distinguish different landscape types. In this chapter I test H6 by examining lump patterns at different scales for their similarity within groups of landscapes of similar structure I probe the generality of H6's predictions by testing the replicability of the similarity of these patterns over a wide variety of landscape types (biomes) I now discuss how similarities of lump pattern have previously been demonstrated

Previous Tests of a Discontinuous World Model Hypothesis

Holling (1992) found specific support for The Textural-Discontinuity hypothesis in the commonalities and the distinctions between lump patterns of boreal bird communities. For example, a high degree of commonality is found between the lump patterns of boreal prairie birds and boreal forest birds in all scale ranges except those associated with architectural distinctions between the two landscapes: the much greater volume of micro-scale vegetative texture (tree needles, leaves) found in the boreal forest canopy as compared to that found in the prairie (short grasses) Only the boreal forest data set has a lump in the smallest size range, as predicted by H6 Similarly, Holling (1992) found support for the prediction (H6) that the relative lack of micro- (vegetation) and meso-scale (patches) objects in fresh water and pelagic environments would result in a dearth of lumps at all but the largest size ranges for those bird communities However, in comparing macro-scale lump patterns between these aquatic environments one finds 'commonality' in that these latter, large-scale lumps do overlap to a noticeable extent.

Restrepo (1995) did not examine entire bird communities, but in comparisons of frugivorous bird assemblages did find distinct lump pattern similarities in comparisons of different neotropical montane forest and páramo habitats The Textural-Discontinuity hypothesis was supported by the observation of fewer lumps in structurally 'simpler' habitats, based on the assumption that forest is architecturally more complex than pasture, cultivated fields, or páramo

Support for the Textural-Discontinuity hypothesis is also evident in lump pattern commonalities and distinctions between European and North American bird communities compiled for the boreal and temperate forest biomes (Hostetler 1997) Within each biome, lump patterns from both continents strongly overlap at the micro- and macro-scales , but lumps in the meso-scale size range (16.3 - 316 g) do not. This follows the prediction of the Textural-Discontinuity hypothesis that contrasts in meso-scale architecture (fragmented European forests vs. more continuous North America forests) would be reflected in lump pattern differences at meso-scales

All the studies cited above describe similarities and differences in lump pattern at different scale ranges only in qualitative terms Lumps in different systems either overlap or they do not More rigorous tests of commonality and distinctions in lump pattern require careful definition of the parameters by which pattern can be measured. I now describe those parameters in the context of the design of these tests

New Tests of The Textural-Discontinuity Hypothesis

The study of pattern is highly scale dependent What pattern is found strongly depends on the size of window through which it is viewed (extent) and the resolution with which it is defined (grain) Tests of the Textural-Discontinuity hypothesis (H6) compare two patterns, landscape and lump structures, using different levels for grain and extent. Previous tests of H6 mostly relied on robust, qualitative definitions of landscape structure based on assumptions that data sets from the same biome come from landscapes of relatively similar structure Such landscape comparisons varied the spatial extent from continent (Holling 1992), to biome (Holling 1992, Hostetler 1997) to eco-region (Hostetler 1997) to ecosystem (Hostetler 1997, Restrepo 1995). For the description of landscape "objects" grain was varied in coarse jumps between micro- (vegetation physiognomy), to meso- (patches) to macro-scales (geomorphology). The exception to this trend was Hostetler's (1997) fine discrimination between categories of patch size. Previous tests of H6 examined lump pattern with a fixed grain, species mean adult body mass, and a semi-fixed extent, the range of body masses which varied according to the size of the animal community found within the spatial extent used to define landscape structure.

Uncertainties about the scales at which ecological processes operate and at which landscape "objects" are apparent to animals necessitate the comparison of lump and landscape pattern at a number of different scales. There is no single scale at which the landscape is structured or at which animals respond to the environment. Pattern at each scale potentially reveals unique information about space/time dimensions of animal-landscape interactions. For example, if lump pattern is not reliably linked with landscape pattern at the landscape study site level but is at the biome level, this might imply thet the "noise" of local community organization processes distorts the bioassay function of lump pattern, but that this noise is drowned out by integration of pattern at the biome level.

In this chapter I test predictions of the Textural-Discontinuity hypothesis by examining relations between lump and landscape patterns. I test these relations for their generality and consistency over ranges of scale which are unprecedented in their breadth. I test the consistency of lump pattern by quantifying pattern regularities ("commonality") between animal communities in similar landscapes. I test the generality of lump pattern by examining its consistency in a wide variety of landscapes, over 17 different biomes. I do this by varying the grain and extent with which lump pattern is defined over the fullest range of known values For example I vary extent by examining the commonality of lump pattern at different spatial scale ranges, biome, super-biome (similar biomes located on different continents) and near-global levels I vary grain by testing for commonality using various degrees of integration of lump pattern, from lumps to clusters of lumps I begin these tests at the smallest spatial scales, landscape study sites within biomes, and repeat them at the super-biome and near-global levels

Lump Pattern Trends Within Biomes

Hostetler (1997) found sufficient commonality or pattern matching between the lump patterns of three avian communities in the temperate forest biome to characterize the entire group with a ten lump model In this section I address the question of whether lump pattern commonality is general to other biomes In the absence of a recognized standard for consistency in pattern matching between lump structures, I employ both visual and numeric tests of lump pattern commonality I standardize the numeric test to the extent that I quantify the degree of lump pattern commonality found in random collections of animal body mass data sets and then compare numeric results of observed and random collections within biomes.

Graphic Comparisons of Within-Biome Lump Patterns

Lump analysis methods

I determined the lump patterns for bird and mammal communities in 17 biomes by applying lump analysis to their respective body mass data sets (Appendix E) I used a common range of statistical power because it provided a reference standard for interpreting GaP statistics at alpha levels between 0.01 and 0.2 regardless of species number (*n*). When I estimated the significance of a discontinuity value I employed a conservative estimate of statistical effect size (0.2) (Lipsey, 1990). In this way I sought a compromise between Type I and Type II errors by keeping statistical power within middle ranges (0.45 to 0.6 for mammals and 0.5 to 0.7 for birds) (Lipsey, 1990).

Graphic presentation methods.

I present lump patterns of biome groups (all the landscape study sites within a biome) for graphic comparison using StackClumps software (Marples, unpublished data). Lump structure as shown here is univariate in that it is only defined along the $\log_{10}$ body mass size axis. This definition of structure uses the limits or gap-edges of lumps to break the $\log_{10}$ size axis into distances between edges occupied by clusters of species (lumps) and distances occupied by relatively few if any species (gaps). As the name suggests, the univariate lump structures of all study sites within the larger scale context (biome or super-biome) are graphed horizontally and stacked atop one another to aid visual comparison of overlap of lump and gap areas between sites. Each lump is depicted as a box with the degree of shading indicating the density of species in the lump. White boxes usually have less than 4 species, black boxes have upwards of 10 species, and the various shades of gray have intermediate numbers of species. Gaps are indicated by empty spaces which horizontally separate the lump boxes.

Defining similarity in lump pattern comparisons

On what basis can one distinguish similar from dissimilar lump patterns of different animal communities? Since many of my biome groups have four or more body mass data sets, I employ a visual, qualitative comparison scheme for preliminary data exploration and quantify this scheme in more rigorous, subsequent tests. I introduce the qualitative scheme now and describe the quantitative methodology later when I present comparison tests where lump pattern is quantized by indices.

Following precedent (Holling 1992, Restrepo 1995, Hostetler 1997, Allen, Forys and Holling, in review) I define pattern in animal body size distributions by the locations of lumps along the size axis. The bounds of each lump are set by the mean adult body masses of the smallest and largest species in that lump. I determine the extent to which lump pattern is shared between animal communities at landscape sites in a group ("commonality") by the degree to which lumps and gaps of the communities in question overlap on the size axis. Figure 3-1 illustrates both high (Biome 1) and low (Biome 2) degrees of commonality. In Biome 1 the majority of landscape study site lump structures share the same locations for lumps (black boxes) and gaps (horizontal spaces between lumps), while in Biome 2 there is hardly a single location on the size axis (log10 body mass) for which a majority of landscape study sites exhibit a lump or a gap.

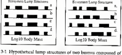


Figure 3-1 Hypothetical lump structures of two biomes composed of four landscape study site animal communities (a - d) illustrating high (Biome 1) and low (Biome 2) degrees of pattern overlap or commonality. Lumps are depicted by black boxes, gaps by spaces horizontally separating lumps.

The amount of taxonomic (species) overlap between sites is shown on the left hand side of each graph by boxed numbers which join the lump patterns in question with brackets. Initial comparisons between landscape animal data sets suggested that Sorenson s Index is sensitive to difference in data set size(n) Marples (unpublished data) determined a simplified version, 'Small Set Similarity' (Equation 3 1), of Sorenson s Index which does reflect the extent of overlap with less sensitivity to n This index appears especially effective when the disparity of data set sizes is extreme

$$SSS = {}^{n_c}\!/_{n_s} \qquad (4\ 1)$$

Where n_s = the number of species in the smaller data set
and n_c – the number of species common to both data sets

Results - Visual Tests of Lump Pattern Commonality and Uniqueness

StackClumps graphics of bird and mammal landscape study site lump patterns within 17 biomes are found in Appendix H I present a subset here for both taxa to show lump pattern in a diverse set of biomes covering a variety of landscape types and climates boreal forest (Figures 3-2 and 3-3), northern temperate forest (Figures 3-4 and 3-5), temperate tallgrass prairie (Figures 3-6 and 3-7), and neotropical rainforest (Figures 3-8 and 3-9)

Pattern commonality is readily evident in all graphs The regularity with which gap and lump zones overlap on the size axis is visually apparent in this subset (Figures 3-2 through 3-9) and in many of the StackClumps graphs presented in Appendix H The shading in the boxes adds another dimension of pattern matching, for lumps of similar shading (species density) often tend to line up This appears in most of the graphs of this subset especially in the $\log_{10}$ body mass size ranges of 1 18 to 1 65 2.6 to 3.6, and 4.6 to

5.5, for boreal forest mammals (Figure 3-1). This shading pattern overlap suggests that species densities tend to line up in addition to discontinuities in the size distribution.

Within the context of lump pattern shared with each biome group, lump structures of individual communities are specific enough to distinguish them from other communities. Uniqueness of lump pattern is evident in that each biome group has lump patterns from certain landscape study sites which differ slightly or moderately from the others. No two landscape study site lump patterns are identical, even with a high degree of species overlap between sites. For example, the lump patterns of mammals from Rocky Mountain and Yellowstone National Parks (Figure 3-3) differ slightly in the meso-scale size range (2.8 to 3.5 $\log_{10}$ body mass) despite a 0.90 index of species similarity. The limited uniqueness of lump pattern supports the Textural Discontinuity hypothesis in that it suggests that lump structure faithfully reflects the unique spatial geometries of each community's landscape as well as the landscape structures common to all communities within the biome.

Many pairs of the landscape study site animal data sets within biome groups have high indices of species similarity. However, visual comparisons suggest that species similarity is not always highly correlated with lump pattern commonality. Relatively high degrees of pattern overlap are evident for some animal communities with low indices of species similarity. Examples of such "good" pattern matches with relatively low similarity indices (indicated here as percentages in parentheses) include: Tallgrass prairie bird communities (Figure 3-6) such as Bridger and Konza(17%), Tallgrass prairie mammal communities (Figure 3-5) such as Konza and Montana Bison (36%), Northern temperate forest mammals (Figure 3-3) such as Itasca and Rocky Mountain National Park (43%).

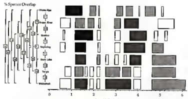


Figure 3-2. Lump structures of mammal communities in boreal forest landscape study sites from France (Rhone Alps), New Brunswick, Canada (Green River) Ontario (Quetico), Manitoba (Nopiming, Taiga, Whiteshell), and Saskatchewan (Doré Lake). Species similarity indices are indicated for each inter-site taxonomic comparison.

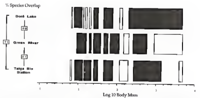


Figure 3-3 Lump structures of bird communities in boreal forest landscape study sites from New Brunswick, Canada (Green River), Manitoba (Taiga), and Saskatchewan (Doré Lake). Species similarity indices are indicated for each inter-site taxonomic comparison.

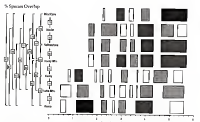


Figure 3-4. Lump structures of mammal communities in northern temperate forest landscape study sites from The Czech Republic (Cesky), Manitoba (Turtle Mountain), Minnesota (Itasca), Colorado (Rocky Mountain N.P.), Montana (Glacier N.P.), Wyoming (Yellowstone N.P.), , and North Dakota (Wind Cave N.P.). Species similarity indices are indicated for each inter-site taxonomic comparison.

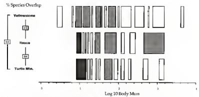


Figure 3-5 Lump structures of bird communities in northern temperate forest landscape study sites from Manitoba (Turtle Mountain) Minnesota (Itasca),and Wyoming (Yellowstone N P) Species similarity indices are indicated for each inter-site taxonomic comparison.

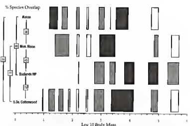


Figure 3-6. Lump structures of mammal communities in North American temperate tallgrass prairie landscape study sites from Kansas (Konza), Montana (Mon. Bison) and South Dakota (Badlands N.P., S. Da. Cottonwood). Species similarity indices are indicated for each inter-site taxonomic comparison.

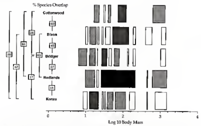


Figure 3-7. Lump structures of bird communities in North American temperate tallgrass prairie landscape study sites from Kansas (Konza), Montana (Bridger, Bison), and South Dakota (Badlands, Cottonwood). Species similarity indices are indicated for each inter-site taxonomic comparison.

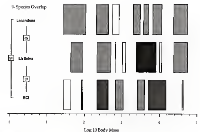


Figure 3-6 Lump structures of mammal communities in neotropical lowland rainforest landscape study sites from Mexico (Lacandona), Panama (BCI), and Costa Rica (La Selva) Species similarity indices are indicated for each inter-site taxonomic comparison

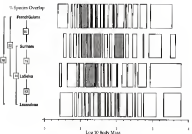


Figure 3-9 Lump structures of mammal communities in neotropical lowland rainforest landscape study sites from French Guiana, Surinam, Mexico (Lacandona), and Costa Rica (La Selva). Species similarity indices are indicated for each inter-site taxonomic comparison.

Numeric Tests of Commonality in Within-Biome Lump Patterns

The human eye is capable of abstruse pattern discriminations whose subtlety becomes more evident as one tries to induce electro-mechanical idiots like computers to approximate them. This dilemma continues to haunt such initiatives as Pattern Analysis and such specific applications as remote sensing (Gonzalez 1987). Therefore, the qualitative, visual sense of pattern commonality between landscape study sites in biomes cannot be dismissed lightly. However, instruments capable of delicate measures may also be highly susceptible to noise. Perhaps during the evolution of the human eye the ability to find subtle pattern was selected for at the expense of the ability to reject spurious pattern, and we infer more pattern matching than actually exists? What is the risk that the qualitative sense of pattern commonality is derived from hyper-sensitive detection and integration of many random events?

Gap pattern commonality

I addressed this risk by developing a simple quantitative measure of pattern commonality and then comparing the results when applying it to stacked lump structures of actual biome groups (Appendix H) and to groups of landscape study site lump structures assemblad at random. I used the mean number (4) of study sites found in my actual biome groups, and assembled random biomes by selecting actual landscape lump structures at random from any biome group and placing them in groups of four.

I measured gap commonality because it is easier to visually discern gaps mutual to lump patterns of different landscape study sites than it is to see mutual lumps, and their quantification is less prone to error. I did this by drawing straight lines vertically through the gaps in the StackClumps graphs to see how many landscape lump patterns the line passed through without touching a lump. I quantify a gap commonality index (*GCI*) as a ratio of the number of gaps shared by a plurality (> 75%) of landscape lump patterns in a biome divided by the total number of gaps in all landscapes in the biome group (Equation 3.2)

$$GCI = {}^{g_c}\!\big/_{g_t} \qquad (4.2)$$

Where

g_c = number of gaps common to 75 percent of all landscapes, and

g_t = total number of gaps in all landscapes in the biome group.

Results - Gap Commonality: Lump pattern commonality does not appear to be the product of random associations of animal size distributions. The gap commonality index (GCI) found between landscapes within actual biomes is more than double that found in random biomes (Table 3-1) for birds or mammals. GCI values for mammal biome groups are distinctly higher than those for biome groups of bird communities. This distinction is visually apparent in that gaps between mammal lumps tend to be wider along the size axis than those between bird lumps, and this increases the likelihood that gaps are shared between mammal communities.

Species similarity indices are higher in actual than in random biomes, but again the overall association between species similarity and pattern commonality is not clear. Mammal biomes have higher GCI values than bird biomes, yet the species similarity indices found in mammal biomes are lower that those found between landscape study sites in bird biomes. The stark contrasts between actual and random biome groups are even more evident when I graph scatter plots of GCI values on species similarity indices (Figure 3-10)

Table 3-1 - Summary statistics of mammal and bird lump structure petterns for groups of landscape data sets sorted by biome and at random.

Gap Commonality Index (GCI) Proportion of gaps common to all landscapes				
Taxon	Birds		Mammals	
	Actual Biomes	Random Assemblages	Actual Biomes	Random Assemblages
Mean	52	.24	69	.34
St Dev	16	.06	17	15
Mean Species Overlap	63	.21	.42	.21

These summary statistics for GCI values suggest a qualitative difference between actual and random biome lump patterns. However, certain factors related to climate, vegetation type or number of landscape study sites in the biome might introduce trends in GCI measures of lump pattern within biomes. To examine these potentials I ranked biome GCI values and list them along with climatic zone (boreal, temperate, tropical) and the number of ecosystem lump structures assembled to represent the biomes for both mammals (Table 3-2a) and birds (Table 3-2b). The majority of observed biome GCI values are beyond the range of GCI values found in random biomes though three mammal biome groups, temperate prairie, tropical wet forest and tropical dry deciduous forest, do fall in that range as indicated by shading in Table 3-2a. For these latter three biomes, the degree of gap commonality is low enough to have been the product of chance. No trend between climate or vegetation type and GCI value is apparent in bird biomes, and the very slight trend between climate and GCI values evident in mammal biomes can be attributed to the fact that tropical biome data sets outnumber all the rest

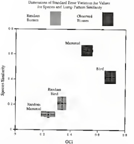


Figure 3-10 Mean values and standard error statistics for species similarity and gap pattern commonality (GCI) measured between pairs of animal communities (bird or mammal) at landscape study sites within observed biomes and biomes created by random assembly of animal data sets.

To test the potential influence on gap pattern detection of the number of landscape study sites in the biome group, I correlated GCI values on number of landscapes in the biome group and found non-significant relationships ($p < 0.33$ for mammals and $p < 0.412$ for birds) with little explanatory power for variance in the data for birds (r = 0.249) and mammals (r = - 0.223), respectively. I conclude that neither climate nor number of study sites in the biome appear to significantly influence the GCI as an index of lump pattern commonality when applied to bird or mammal body mass data sets in groups of three or more data sets from the same biome.

Discussion of gap commonality: The GCI allows more careful pattern comparison between biomes by quantifying my exploratory visual determinations of gap pattern matching within biomes. However pattern matching at larger scales requires a method which is less cumbersome than visual measurement on graphs. Representation of lump pattern with a numeric index would allow easier comparisons between larger spatial scale systems such as between biomes and between super-biomes. This problem is especially acute with bird biome data wherein gap widths are much smaller than those found in mammal lump patterns. To minimize potential pattern matching measurement error I confine subsequent tests to mammal data sets.

An additional problem with these initial pattern tests using the GCI is that my random biomes only partially approximated randomness by confining the pool for random choices to existing landscape study site data sets. This approximation does not truly randomize the location of lumps, just the choice of which landscape study sites to group. In this way it retains whatever collective symmetry that might exist between actual landscape study site lump patterns. A number of landscape and non-landscape factors could contribute to this aggregate lump symmetry. Under this kind of pseudo-randomization these factors might relate lump patterns from different biomes and give inflated indices of pattern commonality. For example, if any of the non-landscape hypotheses (H1 - H5) contributes in

Table 3-2. Designations of climate, landcover, gap commonality index values, and number of ecosystem lump structures associated with biome groups of mammal (A.) and bird (B.) community lump structures. Shaded GCI values fall in the value range found for biome groups of randomly assembled community lump structures.

A. Mammal Community Lump Structures

Biome	*Landcover Type*	*GCI*	*No. Ecosys*
Boreal	Tundra	0.91	3
Temperate	Mediterranean	0.90	2
Tropical	Asian Rain Forest	0.89	7
Temperate	ShortGrass Prairie	0.88	2
Temperate	Northern Forest	0.86	2
Tropical	Savanna with Forest	0.86	2
Boreal	Forest	0.80	5
Tropical	Scrubland	0.80	4
Temperate	Desert	0.77	3
Tropical	Woodland/Savanna	0.75	4
Tropical	Moist Forest	0.70	7
Tropical	Lowland Rainforest 2	0.69	5
Temperate	Southeast Forest	0.68	3
Tropical	Lowland Rainforest 3	0.67	4
Tropical	Montane Rainforest	0.67	3
Temperate	African Grasslands	0.67	5
Tropical	S. African Rain Forest	0.60	6
Tropical	Lowland Rainforest 1	0.57	6
Temperate	TallGrass Prairie	0.48	5
Tropical	Wet Forest	0.39	4
Tropical	Dry Decid Forest	0.38	6

B. Bird Community Lump Structures

Biome	*Landcover Type*	*GCI*	*No. Ecosys.*
Temperate	Southeast Forest	0.79	3
Boreal	Tundra	0.75	2
Temperate	ShortGrass Prairie	0.75	4
Temperate	Northern Forest	0.70	4
Tropical	Lowland Rainforest 1	0.56	2
Tropical	Scrubland	0.48	4
Temperate	TallGrass Prairie	0.47	4
Tropical	Lowland Rainforest 2	0.45	3
Temperate	NW Temp For	0.45	3
Tropical	Low Wet Forest	0.42	2
Boreal	Forest	0.41	3
Tropical	Dry Decid Forest	0.40	7
Tropical	Savanna with Forest	0.31	5

whole or in part to explaining lump pattern, then common traits of ancestry, locomotory mode or trophic level might result in lump pattern commonality between landscape study sites in different biomes. On the landscape level, certain structures or architectures may be quite similar or identical even though they are found in different climates or biomes. For example trees and understory might have very similar forms in forests of radically different climates. I address these concerns now with more comprehensive attempts to define lump pattern commonality and to randomize within-biome lump pattern.

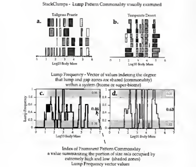
Lump frequency: an index of pattern commonality for gaps and lumps

For simpler numerical comparisons of pattern within and between biomes I reduced lump pattern shared by landscape study sites within biomes to a single vector of numbers. I did this by dividing the size axis into 'bins' of fixed length, 0.01 $\log_{10}$ body mass, and placing in each bin a decimal fraction which I call Lump Frequency. Lump Frequency represents the ratio of the number of landscape study sites with a lump at that location divided by the total number of landscape study sites in the biome. Lump Frequency values vary from 0 (no lumps in any landscape study site at this bin location) to 1 (all landscape study sites have a lump at this bin location). Each data set had a unique range of body size values and therefore a unique vector length. To minimize false readings, numerical comparisons between data sets were made only along those portions of the size axis in which both sets had Lump Frequency values.

I use the Tallgrass Prairie and Temperate Desert biomes to illustrate in Figure 3-11 the transition from visual (stacked lump structures) to numeric (Lump Frequency vectors and Indices of Prominent Pattern Commonality) representations of lump pattern commonality. Both biomes visually exhibit lump pattern commonality because a majority of lumps and gaps line up on the size axis (Figure 3-11 a & b). Very high vector values for Lump Frequency reflect common lump zones and are evident visually as peaks (Figure 3-11 c & d). Low vector values for Lump Frequency reflect common gap zones and are evident visually as valleys.

My attempts to show pattern matching by statistically correlating Lump Frequency vectors of different systems (inter-landscape or inter-biome) showed promising early results. Comparisons of systems with very similar lump pattern graphics had high correlation values (> 0.5), and inter-system comparisons with low lump pattern similarity had low correlation values (< 0). However, it was very difficult to interpret correlation values in the middle range (between 0.15 to 0.3), and randomization of pairings of systems compared showed that this correlation method can give false positive values. For example, random pairings of landscape study sites or biomes with different lump structures often gave relatively high correlation values which were not easily distinguishable from pairings of systems with visually similar lump structures.

These suspiciously high values appear to result from correlation of muddling lump patterns, those patterns which fall between the extremes or prominences of high (lumps) and low (gaps) Lump Frequency values. I revised the definition of prominent lump pattern using these extremes as thresholds to filter out the possibility that such muddling lump patterns introduce the noise of random local historical events. I created an Index of Prominent Lump Pattern Commonality which is a measure of the fraction of the size axis occupied only by the prominent peaks and valleys in Lump Frequency vectors. I define as prominent all Lump Frequency values falling above 0.80 ('strong lumps') or below 0.20 ('strong gaps'). That is to say, I



StackClumps - Lump Pattern Commonality visually examined

Lump Frequency - Vector of values indexing the degree that lump and gap zones are shared (commonality) within a system (biome or super-biome)

Index of Prominent Pattern Commonality a value summarizing the portion of size axis occupied by extremely high and low (shaded zones) Lump Frequency vector values within a system

Figure 3-11. Lump pattern commonality in two biome assemblies of animal community lump structures as measured visually in stacked formation (a & b), as represented numerically by Lump Frequency vectors (c & d) and as summarized by an Index of Prominent Pattern Commonality (bold decimal fractions in c & d), which measures the portion of the size axis occupied by extremely high and low Lump Frequency vector values.

counted as strong lumps or strong gaps only those features shared by 80 percent or more of the landscape study sites in a biome or a super-biome.

I quantified prominent lump pattern as a ratio by counting all the Lump Frequency values above and below these thresholds and dividing each by the total number of bins in the vector. Using the example of the Tallgrass Prairie biome lump structure (Figure 3-11c), 6 percent of the size axis is occupied by prominent lumps and 38 percent is occupied by prominent gaps, giving a total Index of Prominent Lump Pattern value of 0.44. The Temperate Desert biome has a greater portion occupied by prominent lumps, giving it a higher total PLP index value of 0.63. I found no bias or trend between the Prominent Lump Pattern index and the number of study sites in a system when I correlated them. The findings were not significant and had little power to explain the variance in index values for gaps ($r^2 = 0.102$) or lumps ($r^2 = 0.011$).

Can Prominent Lump Pattern Occur by Chance?

I created fake biomes as models of actual biome data sets with randomized lump patterns so as to measure what prominent patterns of Lump Frequency results from chance associations of lumps within biomes. I randomized lump pattern within biomes at the level of each landscape data set. I did this by retaining the same range of body sizes, number of lumps, and size range within each lump as I found in the actual landscape data set. Within the body size range of each landscape data set I randomized the location of these lumps. I assembled each of these randomized landscape lump patterns into a biome group, such that each fake biome had as many landscape data sets as the observed biome group. I measured Lump Frequency vectors for each fake biome and then measured the portions of the vector occupied by prominent gaps and lumps to arrive at a total Index of Prominent Lump Pattern (PLP)

Results. Within-biome lump pattern commonality

Graphic interpretations (GCI values) of significant gap pattern commonality within biomes are supported by statistics of prominent lump and gap pattern index values (Table 3-3). Mean PLP index values suggest that actual biome size axes were occupied on average 34 percent by strong gaps and 17 percent by strong lumps. If I sort actual biomes by PLP index values for gaps or lumps I find no trend relating either type of strong pattern to climate or landcover type.

The very strong degrees of pattern commonality indexed by Prominent Lump Pattern does not appear to be a product of random association of lumps. It occurs slightly less than twice as often along the size axes of actual biomes compared to fake biomes (Table 3-3). When I divide the fake biome by actual biome PLP index values I find ratios of 0.62 (gaps), 0.46 (lumps), and 0.57 (total pattern). The wide disparity between the statistics of real and fake biome PLP indices is evident in the lack of overlap between standard error bars (Figure 3-12). I confirmed this result through a student's t-test which found highly significant ($p < 0.0001$) differences between mean PLP index values for gaps or for lumps in observed and fake biomes.

Summary. Within-Biome Lump Patterns

Both the GCI and the PLP index tests suggest that far higher levels of commonality in lump patterns exist within biomes than expected by chance. These trends appear irrespective of taxon, biome type or number of landscape study sites in the biome. I now examine lump patterns at scales larger than biomes for commonality

Table 3-3 Indices of strong pattern commonality for lumps and gaps measured for 14 biome assemblages of mammal body mass data sets compiled for landscape study sites Strong pattern is measured as Lump Frequency values greater than or equal to 0.8 (lumps) or less than or equal to 0.2 (gaps)

Biome		*No*	*Prominent Lump Pattern*					
			Strong Gap		*Strong Lump*		*Total Strong Pattern*	
Climatic Zone	*Landcover Type*	*Sites*	*Real*	*Fake*	*Real*	*Fake*	*Real*	*Fake*
Neotropical	Montane Rainforest	4	0.22	0.12	0.09	0.01	0.31	0.13
Neotropical	Lowland Rainforest1	5	0.52	0.44	0.17	0.12	0.69	0.56
Neotropical	Lowland Rainforest2	3	0.41	0.22	0.14	0.07	0.55	0.30
Neotropical	Lowland Rainforest3	4	0.20	0.11	0.07	0.03	0.27	0.14
Tropical	African Grasslands	5	0.34	0.28	0.25	0.15	0.59	0.42
Temperate	Shortgrass prairie	6	0.26	0.23	0.08	0.05	0.34	0.27
Temperate	TallGrass prairie	4	0.38	0.16	0.06	0.01	0.44	0.17
Temperate (south)	Decid & Conif Forest	4	0.21	0.10	0.15	0.10	0.36	0.20
Temperate (north)	Decid & Conif Forest	7	0.26	0.18	0.26	0.11	0.52	0.29
Boreal	Forest	7	0.24	0.10	0.20	0.05	0.45	0.16
Arctic or Montane	Tundra	2	0.40	0.24	0.40	0.24	0.79	0.48
Temperate	Desert	8	0.32					
Tropical	Woodland/Savanna	6	0.38					
Tropical	Wet Forest	4	0.56					
		Mean	0.34	0.20	0.17	0.09	0.48	0.29
		SD	0.116	0.1016	0.1022	0.0672	0.1634	0.1457

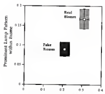


Figure 3-12. Mean and standard error statistics for indices of Prominent Lump Pattern (commonality shared by a super-majority of all sites) within biomes. Values were calculated for observed (real) groups of landscape-level animal lump patterns and for groups of lump patterns which are simulations (fake) of randomized lump patterns. Values index strong or prominent pattern, the proportion of the animal body mass size range occupied by gaps (x-axis) or lumps (y-axis) in 80 percent or more of the landscape data sets within the group.

Lump Pattern Trends at Scales Larger Than Biomes

The consistent trends I found within bird and mammal biomes for lump pattern commonality and uniqueness support the Textural-Discontinuity hypothesis. These findings do not preclude the possibility that animal-landscape interactions are evident at other scales. The likelihood that processes affecting animal morphometry operate at multiple scales (Holling 1992) makes it useful to compare body size patterns over a range of scales (spatial extents and grains). Variation in the degrees of lump pattern matching from scale to scale may help identify the particular processes and the scales at which they affect animal morphometry.

Perhaps processes operating at scales larger than biomes influence animal lump pattern. In this section I test this premise by looking at landscapes over a range of spatial extents larger than biomes. I look at lump pattern within these areas using a variety of grain resolutions. I now describe the assembly of animal data at scales larger than biomes and the different grains resolutions with which to resolve lump pattern.

Spatial extents larger than biomes

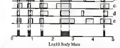
I created super-biomes by aggregating the lump patterns of mammal landscape study sites to spatial extents larger than biomes. I did this by including mammal body mass data from landscape study sites from very similar biomes on different continents or over large geographical ranges on one continent. For example I created a grasslands super-biome by adding mammal landscape study site lump patterns from temperate short and tallgrass prairies to those of African grasslands. Similarly, I created a rainforest super biome by adding neotropical rainforest study sites to those of the paleotropics.

Multiple grain resolutions for lump structure

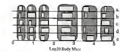
The increased diversity of grain resolutions used to define animal morphometry has significantly expanded the range of hypothetical links between animals and ecological processes. For example, the discovery of multiple modes or lumps (Griffiths 1986, Holling 1992) in size distributions created novel opportunities to test links between animal morphometry to processes organizing landscape architecture in addition to guild structure and trophic relations. The interpretation of these modes for location and number remains an area of intense debate (Marples, in submission). Changing the grain resolution with which lump pattern is defined can significantly alter the number of lumps found. For example, shifting the value of the kernal estimator in smoothing a size distribution can generate a variety of interpretations of lump number in a data set.

To address the variability of possible interpretations of lump structure it is prudent to vary grain as the spatial extent of a system increases. Therefore, over a range of extents I display lump structures using two new grain resolutions in addition to the stacked lump patterns of landscape study sites. I illustrate how I use the two grain resolutions to narrow and expand the lump structure presented by StackClumps (Figure 3-13).

I use needle grain resolution to conservatively narrow the definition of lump pattern common to most study sites in a biome (Figure 3-13 A). With needle grain resolution I use a fixed distance (roughly 0.05 log10 body mass) or "bin-width" along the size axis within which I determine whether a majority of ecosystems exhibit a lump or gap at that location on the size axis. This is shown by the width of the dashed lines extending vertically through



A. Biome lump structure resolved at Needle grain resolution.



B. Biome lump structure resolved at Cloud grain resolution.

Figure 3-13 Three grain resolutions to represent the aggregate lump structure of a hypothetical biome. The middle grain is defined by the sizes of the gaps which separate lumps, and the aggregate lump structure is represented by the stacked lump patterns of 5 animal communities (a-e) within the biome. The narrowest grain ("Needle") shows those zones (gray polygons) common to a majority of all communities at a resolution of 0.1 log10 body mass. The coarsest grain ("Cloud") flexibly encompasses the zones occupied by clusters of lumps.

lump structures of the five communities and delineating the common lump zones as gray polygons on the bottom axis. The conservatism of this approach is evident in the absence of any summary lump structure around 4.0 log10 body mass because there is no zone common to 60 percent or more of all communities in that size range. The same procedure was used to delineate common gap zones (normally represented by white polygons but not shown here so as to maintain the clarity of the illustration).

I use a flexible grain, cloud resolution, to give a more expansive interpretation of biome lump structure by encompassing areas along the size axis where lumps appear to cluster (Figure 3-13 B). By contrast with use of the needle grain, this approach is more liberal and does define a common lump zone around 4.0 log10 body mass. In summary, all three grain resolutions (needle, lump and cloud) are arbitrary renditions of biome lump structure that allow me to vary the focus on patterns of animal morphology as I test their correspondence with patterns resulting from different ecological processes, both landscape and non-landscape.

Graphic Results: Super-Biome Lump Pattern at Three Grain Resolutions

In each graph I present three resolutions for lump patterns of study sites assembled at the super-biome spatial extent. I supplement the stacked lump patterns of ecosystem study sites with needle and cloud resolution lump representations to contrast lump structures of relatively similar biomes such as southern and northern American temperate forests (Figure 3-13), neotropical lowland and montane rainforests (Figure 3-14), north American short and tallgrass prairies and African grasslands (Figure 3-15), and woodland/savannas and savannas with forests (Figure 3-16).

Lump pattern commonality is graphically apparent within and between biomes in each of these comparisons (Figures 3-13 through 3-16). For example, I find conspicuous alignments of lumps around the 1.8 - 2.0, 3.2 - 3.6, 4.0 - 4.2, 4.7 - 4.8, and 5.0 - 5.4 ranges of log10 body mass for mammals in the Woodland - Savanna super-biome (Figure 3-18). In the same graph there is a conspicuous absence of lumps between 2.0 - 3.0 log10 body mass. However, the fact that significant portions of these lump patterns can be rendered at all with either needle or cloud resolution gives additional confirmation of commonality, because these grains can't be employed unless a majority of landscape study sites share pattern. In the absence of pattern commonality the needle and cloud portions of these graphs would be blank.

Needle resolution lump pattern focuses attention at relatively narrow zones of the size axis with high lump densities. Certain common lump zones repeatedly appear in these graphs around log10 3.0 and 3.8 - 4.0. However, lump pattern commonality trends are not uniform across all biomes. Each inter-biome lump pattern comparison shows unique lump and gap zones at needle resolution. Similarly, there is little difference in number (4 to 6) of clouds in all these inter-biome pattern comparisons, but the locations and widths of most of the lump clusters are unique to each biome.

Within the pattern matching trends which clearly suggest commonality, pattern variation between landscape sites and between biomes suggest lump pattern uniqueness at each level. For example, the relative lack of lumps at micro-scales distinguishes tallgrass prairie from shortgrass prairie and African grasslands (Figure 3-15). Comparing two north American biomes, northern temperate forests have less micro-scale and more macro-scale lump structure than southern temperate forests (Figure 3-13).

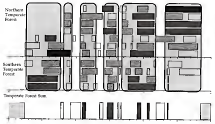


Figure 3-14 - Lump structures of mammal ecosystems in temperate forest biomes at needle lump and cloud resolutions.

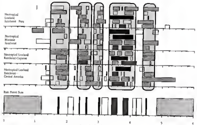


Fig 3-15. Mammal lump pattern for Neotropical Rain Forest biomes shown at lump, cloud and needle resolutions

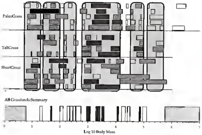


Figure 3-16. Lump structures of mammal ecosystems in grassland biomes at needle, lump and cloud resolutions

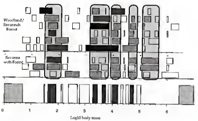


Figure 3-17 Lump structures of mammal ecosystems in savanna and woodland biomes at needle lump and cloud resolutions.

These exploratory tests build a qualitative link between patterns of animal morphometry and landscape structure at scales larger than biomes. Similarities of landscape structure between sites are qualitative benchmarks to the extent that they are commonly recognized (Udvardy 1975, Bailey 1995)) within similar biomes. It stands to reason that grassy savannas with some forest patches are more structurally similar to open, grassy woodlands than to dense forests. Similarly, the graphic demonstrations of inter-biome lump patterns which I just presented suggest a qualitative sense of pattern commonality.

It would help to establish some more rigorous reference point in the relations of two such non-standardized variables as lump and landscapa patterns. One reference point might be to determine how much lump pattern commonality can be found in super-biomes as a product of chance associations of lump pattern within the landscape sites. I carried out such a reference test by enumerating super-biome lump patterns exactly as I did for biome lump patterns. I translated super-biome lump pattern into vectors of Lump Frequency values, which I then used to quantify the degree of strong lump and strong gap pattern within each super-biome. I also randomized super-biome lump pattern and created "fake" super-biomes exactly as I did for biome lump pattern. I then calculated mean and standard deviation statistics for strong lump and gap pattern both in observed and "fake" super-biomes, and tested the statistical difference in these mean values for strong pattern using the student's T-test. I now present results of these tests.

Numeric Tests of Super-biome Lump Patterns

I find significant amounts of correlation or commonality between lump patterns of landscapa study sites within super-biomes (Table 3-3) though somewhat less than was evident for biomes Mean Prominent Lump Pattern (PLP) index values suggest that actual biome size axes were occupied on average 29 percent by strong gaps and 10 percent by strong lumps In scaling up from biomes to super-biomes, the amount of strong gap pattern remains about the same, but the amount of strong lump pattern has fallen by 40 percent, from 17 to 10 percent of the size axis It appears that addition of similar biome lump patterns diminishes the chances of lumps zones being shared by a strong majority (greater than or equal to 80 percent) of all landscape sites in the system.

Strong pattern correlation resulting in high Prominent Lump Pattern (PLP) index values appears less likely in super-biomes to be a product of random association of lumps than it does in biomes As with biomes, overall pattern correlation is much higher in observed as opposed to fake super-biomes, but the difference is much stronger with respect to lump pattern correlation. Strong gap pattern occurs slightly less than twice as often along the size axes of observed super-biomes compared to fake super-biomes (Table 3-3), and strong lump pattern occurs only one fifth as much in fake as in observed super-biomes When I divide the fake super-biome by observed biome PLP index values I find ratios of 0 60 (gaps), 0 20 (lumps), and 0 39 (total pattern).

These mean values are significantly different A graph of mean PLP index values (Figure 3-1F) for observed and fake super-biomes shows no overlap between standard error bars for gap and lump strong pattern I confirmed this result through a student's t-test which found highly significant (p < 0 0001) differences between observed and fake biome mean PLP index values for gaps or for lumps

Table 3-4 Indices of Prominent Lump Pattern (strong pattern commonality for lumps and gaps) measured for 6 super-biome assemblages of mammal body mass data sets compiled for landscape study sites Strong or Prominent pattern is measured as Lump Frequency values greater than or equal to 0.8 (lumps) or less than or equal to 0.2 (gaps)

		Prominent Lump Pattern					
	No. Sites	*Strong Gap*		*Strong Lump*		*Total Pattern*	
		Real	*Fake*	*Real*	*Fake*	*Real*	*Fake*
Boreal Forest	9	0.24	0.06	0.16	0.02	0.41	0.08
Temperate Forest	11	0.20	0.11	0.10	0.05	0.29	0.16
Neotropical Lowland Rainforest	16	0.37	0.14	0.08	0.01	0.45	0.15
Moist/Wet Forest	6	0.39	0.38	0.15	0.04	0.54	0.42
Woodland-Savanna	9	0.25	0.14	0.09	0.00	0.34	0.15
Grasslands	16	0.31	0.24	0.01	0.00	0.32	0.24
Mean		0.29	0.18	0.10	0.02	0.39	0.20
Sd		0.08	0.11	0.05	0.02	0.09	0.12

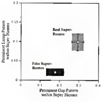


Figure 3-18. Mean and standard error statistics for indices of Prominent Lump Pattern (commonality shared by a super-majority of all sites) within super-biomes. Values were calculated for observed (real) groups of landscape-level animal lump patterns and for groups of lump patterns which are simulations (fake) of randomized lump patterns. Values index strong pattern, the proportion of the animal body mass size range occupied by gaps (x-axis) or lumps (y-axis) in 80 percent or more of the landscape data sets within the group.

Para-Global Lump Patterns

Truly "global" lump pattern would represent the collective morphometries of most species found in a majority of the landscapes recognized within the range of that taxon. The numbers of species and landscape types represented in this study are considerable, but in the aggregate could only be seen as an instructive sub-sample which estimates global pattern. Hence the term "para-global" for the spatial extent of this test of the Textural-Discontinuity hypothesis. I now examine para-global lump patterns for internal consistency or commonality using a variety of graphic resolutions.

Graphic comparisons of lump pattern

There appear to be a limited number of zones over the mammal size range which are shared as gaps or as lumps by a majority of mammal communities over a wide variety of landscape types. I now demonstrate this para-global lump pattern commonality over a range of scales and grain resolutions. I begin with very coarse grain and allow individual visual interpretation of overall lump pattern. I then show aggregate lump patterns which I found at reduced grain sizes but increasing spatial extent.

At a coarse grain, individual lumps, I stack the lump structures of mammal landscape study sites from ten different forest biomes along with a visual interpretation of lump pattern commonality at needle resolution at the bottom (Figure 3-19). The latter suggests common gap zones at 2.0 - 2.2, 2.8, 3.2 - 3.4, and 4.3 log10 body mass and common lump zones at 2.3, 3.0, 3.4 - 3.6, 3.8 - 4.0, and 4.8 log10 body mass.

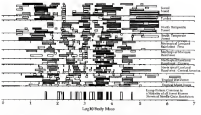


Figure 3-19. Lump patterns of 10 forest biomes as represented by stacked graphs of lump patterns of individual landscape study sites within each biome and as a needle grain resolution interpretation of those lump and gap zones which are common to a majority of biomes. Species density in lump polygons indicated by the darkness of shading.

I approach more closely to global scales by looking at all landscape types, including forests, over larger spatial extents. I do this by aggregating lump pattern from biome to super-biome levels and looking for commonality by marking the lump zones in the size range which are mutual to both super-biomes. I stack graphs of zones of lump overlap between super-biomes (Figure 3-20) and find all the major lump pattern commonality zones which I found in Figure 3-18 as well as some new common lump (1.4 - 1.8 and 5.5 log10 body mass) and gap (4.6 log10 body mass) zones.

As a final estimate of para-global lump pattern, I graph all biome lump patterns as Lump Frequency vectors (Figure 3-21) and find all the above lump and gap commonality zones shown with sharper detail. For example, common lump zones now appear as separate peaks at 1.4 and 1.8 log10 body mass. Similarly, major common gap zones are evident around 1.0, 1.6 and 5.0 log10 body mass. I summarize these findings in Table 3-5.

Table 3-5. Summary of log10 body mass size ranges of gap and lump zones common to lump patterns of most mammal communities in some 14 biomes

Gap	*Lump*
0.9 - 1.1	1.2 - 1.4
1.5	1.6 - 1.7
2.0 - 2.2	2.3
2.5 - 2.9	3
3.2	3.3 - 3.8
4.3	4.7 - 4.9
5	5.2 - 5.4

Implications of para-global lump pattern commonality

The observation of gap and lump zones common to all mammal landscape sites irrespective of biome type suggests that lump structure is a

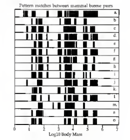


Figure 3-20 Lump pattern common at para-global spatial scales as evident in the pattern shared between mammal lump structures of pairs of super-biomes Lump pattern overlap between super-biomes was determined by visual examination of juxtaposition of pairs of mammal super-biome StackClumps graphs as follows. boreal forest and temperate forest (a), rainforest and moist forest (b), woodland-savanna and grassland (c), boreal forest and grassland (d), rainforest and grassland (e), temperate forest and grassland (f), grassland and moist forest (g) woodland-savanna and moist forest (h), rainforest and woodland-savanna (i), boreal forest and woodland-savanna (j), rainforest and temperate forest (k), temperate forest and woodland-savanna (l) rainforest and boreal forest (m), boreal forest and moist forest (n), temperate forest and moist forest (o)

bioassay of some process(es) which are universal to landscapes all over the world If these processes organize landscape structure into similar patterns in all landscapes, then the Textural-Discontinuity hypothesis (H6) is supported. For example, if plant physiognomies ("a tree is a tree is a tree") or terrain geomorphologies are sufficiently similar across all landscape types, then lump structure still might be the product of engagement by animal communities with landscape architecture

H6 is undermined to some extent if these global processes function independently of landscape structure For example, processes of competition, evolution and trophic relationships are regarded as omnipresent in terrestrial ecosystems However, one must recall that para-global lump commonality is an estimate of what lump pattern is shared among most mammal communities, and it only focuses on zones with higher likelihoods of having a lump or a gap It accounts for the location of the largest gaps which separate zones in which most lumps are found It does not account for the smaller gaps which separate lumps within these zones of higher Lump Frequency The lump patterns created by these smaller gaps and lumps are the identifying features which characterize animal communities body mass morphologies associated with specific landscapes or biomes Any explanation of lump structure must address both levels of lump pattern commonality

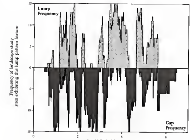


Figure 3-21 Para-global mammal lump pattern as indicated by lump and gap frequency vector values derived from 15 pairwise pattern matches of superbiome lump patterns.

Chapter Summary

In this chapter I have demonstrated that lump pattern is repeatedly found with consistent and common features when looking at bird and mammal body size data from landscapes with similar structure. These features are zones along the body size axis which are characterized by lumps or gaps which are mutual to a majority of sites within a biome or super-biome. This lump pattern commonality is evident at the scale of biomes and super-biomes. I have demonstrated at biome and super-biome scales that it is extremely unlikely that such commonality is the product of chance associations of lumps. I have also failed to find any notable trend which associates my indices of pattern commonality with such variables as the number of landscapes in a spatial extent (biome or super-biome) or climate.

I have also demonstrated broad commonality in lump patterns at near-global spatial scales, by identifying zones on the size axis where lump or gaps are more likely to be found. This does not account for the existence of many small gaps found in size distributions at local spatial scales of specific landscapes, but it does help predict the general locations of lumps at global scales.

Lump pattern commonality within landscapes of similar structure (such as biomes or super-biomes) supports the predictions of the Textural-Discontinuity hypothesis. Lump patterns common at global scales challenge H6 under two conditions. First, there are no landscape structural elements common to all landscapes which are associated with the species in lumps in the global clusters of lumps. Second, there are non-landscape processes which better explain the locations of these global lump clusters.

In the next chapter I address definitions of landscape structure and compare them with lump pattern commonality within and between biomes and super-biomes. In the final chapter I test the ability of non-landscape hypotheses to predict these common lump patterns.

CHAPTER 4
RELATED PATTERNS OF LUMP AND LANDSCAPE STRUCTURE IN LANDSCAPES OF DIFFERENT STRUCTURAL COMPLEXITY

Introduction

The Textural-Discontinuity (H6) hypothesis prediction that similar landscapes are associated with similar lump structures is supported by the internal consistency ('commonality') demonstrated between lump patterns within biomes (Chapter 3). I have demonstrated the generality of lump pattern commonality for birds and mammals in a wide variety of biomes. This demonstration rests on the assumption that intra-biome landscape comparisons share more similarity in structure than inter-biome comparisons. Before I test predictions of non-landscape hypotheses (H1 - H5) that lump and non-landscape patterns are linked (Chapter 5), the assumption of structural similarity within biomes must be tested.

How dependably do traditional landscape classification schemes link patterns of structure at all scales? Perhaps biome definitions of landscape cover are biased towards micro-scale patterns of plant species associations and ignore pattern at meso- (patch) and macro-scales? In this chapter I probe this risk from two directions. First, I measure the consistency in predictions by several traditional landcover classification schemes. Second, I introduce a novel approach for classifying landscape structure at multiple scales and measure the variability in structural values within traditional landcover classes such as biomes.

This new multi-scalar landscape classification scheme allows me to ordinate sites based on structural complexity. This enables me to test more rigorously the power and generality of H6's prediction that landscape structure is linked to lump structure. Namely, the link between animal morphometry and landscape structure is more general if it can be shown to erode at a rate proportional to the degree to which structure differs. The landscape classification scheme allows me to measure the degree of structural difference between landscape sites, and I can measure the rate of erosion in lump pattern matching between animal body mass data sets. In this chapter I measure and compare indices of structure and lump pattern matching for a wide variety of landscapes at scales from biomes to super-biomes.

Finally, I confront H6's prediction by testing whether lump pattern predicts the scale of landscape architecture which a species exploits. This directly addresses the link between animal size and landscape texture by examining if the mean body size of an animal lump corresponds to the coarseness of the architecture which the animals in that lump use.

In summary, I test the Textural-Discontinuity hypothesis in this chapter by addressing the following questions: How confident are we in grouping ecosystem study sites based on common landscape features? How much variability is there in characterizing landscapes? Does the degree of matching between lump patterns correlate with structural differences between sites? Does lump structure predict use of landscape structure?

Traditional Landscape Classification Methods

Comparing and grouping ecosystems based on similarities of landscape structure requires sufficient data from a standardized system for describing structure. It is difficult to meet these criteria. The quantity and quality of data I found for landscape features (vegetation, fauna, physiography) was highly variable. No single descriptive system for landscape cover or structure is widely accepted (Brown and Gibson 1983; Bell et al. 1991), and misclassification is quite possible due to errors of interpretation and vague terminology.

In this chapter I try to avoid multiple sources of error by employing several classification systems which utilize many factors associated with landscape structure, particularly micro- and meso-scale structural features. Climatic factors (temperature and precipitation) are utilized by Holdridge (1971) to classify regions as "Life Zones." Climate-based schemes such as Köppen (1931) and Trewartha (1968) have been incorporated along with edaphic factors and flora and fauna in the classification of North America into eco-regions (Bailey 1995). A third system (Udvardy 1975) classifies terrestrial zones into "biomes" based on floristic and faunistic associations at different spatial scales(sub-regional, regional, provinces). These associations in turn are loosely related to edaphic, climatic, seral stage, and physiographic patterns.

Data Sources for Biome Classification and Climate

For each site I used the biome classifications and site descriptions found in journal articles from which I derived my animal species lists and in related literature. For North American sites I also consulted a third source (Bailey 1995), which combines climatic, edaphic, vegetative, and faunal data in classifying eco-regions. For sites outside North America I cross-checked classifications using biome maps of Udvardy (1975).

For Life Zone classifications I collected temperature, rainfall and evapotranspiration data for each study site using data from the nearest available weather monitoring station (Earth Info 1996, UNESCO 1978). I checked evapotranspiration and rainfall data against hemispheric maps which displayed such data as isopleth gradient lines (Henning 1989).

Holdridge Lifezone Classification

Holdridge's Life Zone Classification (HLZCS) system (Holdridge 1947, Holdridge et al. 1971) is a classification system which attempts to integrate climatic and vegetative definitions into a single model. The HLZCS consists of three levels of classification which are applied serially. A Holdridge diagram summarizes the system logic at each classification level, visually linking vegetative and climatic data to landscape classifications. Figure 4-1 represents the first or primary level, which is defined by mean annual values for precipitation and biotemperature and the potential evapotranspiration ratio (PET). The second level of the HLZCS refines the classification further by incorporating latitudinal and altitudinal definitions. The third level is based on biome level vegetative cover.

The life zone of a study site is indisputably classified if the first two levels of the classification process clearly indicate the center of a cell in a Holdridge diagram. Classification questions which arise when a boundary area ('transition zone') between cells is indicated in the diagram are addressed by closely re-examining the vegetation type as well as revisiting biotemperature and precipitation values.

Comparing Holdridge and Biome Classifications

For each landscape site I compared two classification systems (life zone and biome) so as to contrast vegetation with climate data in determining the site a landscape structure type. Life Zone designations for all sites (see Appendix C) generally agreed (72 percent of observations) with biome classifications based on literature. Contradictions between both classification systems occurred primarily when Life Zone analysis uncovered a greater

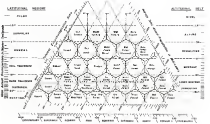


Figure 4-1 Tri-axial schematic of Holdridge Life Zone classification system (after Holdridge 1947)

variety of precipitation values than expected within biome groups. As a consequence, some cases of high between-site variation in precipitation values might warrant reclassification of some sites to other biomes. For example, the Jaureche site (Appendix C) is more humid than a "dry deciduous" biome classification might merit. Clustering of climatic variable values suggest that four biome groupings (Temperate Desert, Tropical Dry Deciduous Forest, Tropical Wet Forest, and Woodland/Savanna Forest) could each be usefully divided into two sub-groups. For example, the Woodland / Savanna Forest biome might be subdivided into a Savanna and a Woodland biome, and the Temperate Desert biome might be subdivided into Sonoran and Great Basin desert biomes.

Assessing the Dependability of Landscape Classifications

Parallel use of several classification schemes decreases the chances that some important factor was omitted in landscape classification. Since no one system is universally accepted as a global standard, balancing between different schemes increases the chance that a reasonable estimate of a site's landscape structure was achieved. For example, Holdridge Life Zone classifications (HLZC) are based on climatic models with parameters that were calibrated primarily in the Neotropics. Consequently, the HLZC model does not predict vegetation types accurately in seasonally dry climates (Schulze and McGee 1978), or account for numerous vegetation types (Brown and Gibson 1983). So while the HLZC is adequate for wet tropical climates, it is prudent to supplement it with other approaches.

Two sources of variation call traditional landcover classifications into question. As discussed in the first chapter, a variety of spatial extents have been applied to classification terms such as ecosystems and biomes. Such flexible use has not converged on any standardization for defining the spatial dimensions of landcover units. The second source of variation is spatial heterogeneity in patterns of disturbance, topography, hydrology, soil, plant associations and climate. After more than a century of study it appears we are only just beginning to appreciate the degree to which these factors interrelate in the operation of ecological systems (Holling 1987, Levin 1992, Wiens 1992) and the maintenance of landscape structure.

My comparison of biome and life zone classifications accounts for a minority of these factors and still shows a notable amount of disagreement (28 percent) based on climatic variability. The extent to which variation in other factors increases the variability of landscape structure between study sites remains undetermined, since the majority of other factors at meso- and macro- scales are, at best, under-appreciated in traditional classifications. The general agreement between the two classification systems suggests that there is relatively little inter-site variation within a landcover type for micro- to meso-scale features like vegetation physiognomy and patch type. However, no one has demonstrated a robust consistency in landscape structure *at all scales* in between-site comparisons using traditional classification methods. I now review some previous attempts to link animal behavior and landscape structure and introduce a new method specifically designed to measure landscape structure at multiple scales.

Classifying Landscape Structure Across Multiple Scales

The Textural-Discontinuity hypothesis (H6) has received modest but consistent support from qualitative associations of lump structure and landscape structure (see review in Chapter 3). A more rigorous test of the linkage between animal morphometry and landscape structure demands that both patterns be quantified Quantification of animal morphometry as lump structure required exhaustive probes into totally novel statistical methods (Marples, in submission) Quantification of landscape structure is no less challenging, for it requires identification of objects or structure in the landscape which are likely to be related to animal behavior Very little is known about what animals actually perceive or respond to Ims (1985) concluded that we lack the empirical or theoretical basis to link structure to perception. However, the history of efforts to link animals to landscapes has marshaled sufficient evidence to form the basis of this probe into community-wide associations between animals and structure

I briefly review the historical basis of theory for my attempts to quantify landscape structure I then describe the methods for quantification of structure over the full range of spatial scales I conclude by testing H6 through comparisons of patterns of lump structure and landscape quanta

Limited Scale Definitions of Community and Structure

A growing body of evidence associates characteristics of animal communities with spatially distributed features in the environment Animal community attributes related to spatial structure include community assembly (Drake et al 1993), population structure (Scribner and Chesser 1993), resilience in predator-prey population dynamics (Huffaker 1958, (but see De Roos, McCauley and Wilson 1991)), population persistence in patchy environments (Hanski 1985, Lande 1987), metapopulation dynamics (Pulliam 1988) and persistence (Hanski 1991), species diversity related to horizontal heterogeneity at within-habitat scales (Wiens 1974, Roth 1976) and between-habitat scales (Whitteker 1965, Cody 1975) In the latter case MacArthur and MacArthur (1961) provided a major impetus by relating vertical stratification of habitat vegetation structure with avian community diversity

Most studies linking animal community organization and landscape structure are based on limited definitions of the animal community and of the scale-range of spatial attributes to which animals may respond. Animal communities are often defined at smaller scales such as phylogenetic subdivisions (order) or guilds. For example, heteromyid rodent species diversity has been linked to increased habitat complexity associated with patchiness on temperate islands (Dueser and Brown 1980) and with vertical vegetation structure and horizontal soil textures in temperate deserts (Rosenzweig and Winakur, 1969).

Similarly, in most studies of animal communities and landscapes, the scales defining landscape structure are usually confined to limited ranges, such as micro- (individual plant species or physiognomies) or meso- (patch sizes, edges, habitats). Habitat structure has most frequently been associated with animal exploitation at micro-scales (Table 4-1). For example, habitat structure and plant species composition have been tied to organization of avian communities in terms of plant abundance and composition (Cody 1985). Tropical bird community composition dynamically follows structural changes associated with plant succession (Loiselle and Blake 1992). Relations between animal abundance and meso-scale horizontal structures such as edges and ecotones have been studied for more than a half century (Leopold 1933, Gardner et al. 1991, Usher 1991).

In a few cases, animal community species diversity increases have been tied to macro-scale landscape complexity. Species diversity in mountainous regions exceeds that of flatlands (Simpson 1964, Cook 1969). This has been attributed to a greater number of isolated valleys or habitats due to the scale and degree of topographic variation allowing more species to be distributed allopatrically (Schluter and Ricklefs 1993).

Table 4-1 Micro-scale definitions of habitat structure associated with animal-structure interactions (after Bell et al, 1991)

Structural Measurement	*Source Studies*
Vertical	
Vegetation Height	Cody and Walter (1976)
Vegetation density at different heights	Cody and Walter (1976) Cody (1978)
Vegetation presence/absence at different heights	Erdelen(1984)
Vertical vegetation density	Wittenberg(1980)
Percent foliage cover at different tree/shrub and understory heights	Karr and Freemark(1983)
Vertical woody and herbaceous foliage density	Dueser and Shugart(1979)
Litter depth	Wiens and Rottenberry(1981) Karr and Freemark(1983)
Percentage cover sufficiently tall to obstruct vision	Ewald et al (1980)
Horizontal	
Inter-plant distances	Vince et al. (1976)
Vegetation spatial variation	Wiens and Rottenberry(1981)
Percent cover	Wiens and Rottenberry(1981) Ewald et al. (1980)
Plant density	Vince et al (1976) Karr and Freemark(1983) Wiens and Rottenberry (1981)
Percent foliage cover at different tree/shrub and understory heights	Karr and Freemark(1983)
Understory tree dispersion	Dueser and Shugart(1979)
Stump sizes and density	Dueser and Shugart(1979)

The breadth of research of most such studies does not usually exceed one scale range (micro-, meso- or macro-) of landscape structure, foreclosing any opportunity to examine animal interactions with landscape pattern across the range of scales found in an ecosystem or landscape.

Landscape Structure Defined at All Scales in a Discontinuous World

The number objects of potential interest to an animal is staggeringly large in a continuous world model. A bird might consider anything from a twig to a cliff edge if it searches at all scales a continuum of all architectures suitable for foraging. Hierarchical models of animal decision making and of landscape structure reduce the diversity of potential linkages of behavior-to-structure to a small number of subsets or hierarchical levels. These subsets can be distinguished by similarities or overlaps in the spatial and temporal scales of the animal behaviors and the regeneration times of "objects" in the landscape (Holling 1992, Holling et al. 1996). For example, three sets of birds (kinglets, grosbeaks, and hawks) are portrayed (Figure 4-2) to have three separate scale ranges to exploit. These scale ranges correspond to tree crowns, forest patches, and forest stands, respectively. Such a hierarchical model highlights hypotheses about the scale ranges of critical importance to survival; it does not preclude exploration or use of objects at other scale ranges.

Most tests of lump structure as an index of animal-landscape interactions have quantified lump structure but addressed landscape structure and animal behaviors only generally. The intriguing qualitative associations between lump and landscape structures discussed above (Holling 1992, Restrepo et al. 1997) offer some of the few scale-specific examples of behavior-structural links over a wide range of spatial scales. Hostetler's (1997)

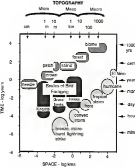


Figure 4-2 Model of discontinuous distribution of space/time dimensions for operation of atmospheric processes, forest structures and bird foraging scales

association of specific body mass ranges of birds with specific scales of tree-canopied patches is the lone example of a link between quanta of animal morphometries and those of landscape structure

While community-wide linkages between each animal species and the scale ranges of objects it responds to are beyond the scope of this study, reasonable estimates of the objects which potentially influence animal behavior can be made *sensu* Holling (1992) This assumption is safest at the macro-scale, where associations between animals and plant physiognomies are long recognized (Table 4-1) Meso-scale linkages between animals and landscape structure are conceivable based on observations of foraging flocks of birds or mammals which move from patch to patch. Animal-landscape associations at the macro-scale are less easy to imagine, but are testable based on simple assumptions of what might be perceived For example, I can count interfaces between major landcover types, such as coasts, large rivers, and mountain ranges, as macro-scale objects likely to influence a wide variety of animal behaviors. I now describe a landscape structure classification scheme based on objects broadly recognized to fit within these scale ranges

Landscape Structure Classification Methods

Overview

One broad purpose within this study is to compare a wide variety of landscapes based on differences in structural complexity. It is readily understandable why this study is unprecedented, because the diversities of landscapes (18 biomes) compounded by the varieties of structural objects within each landscape constitute a vast scope of potential data needs Such overwhelming data demands often confront early, exploratory science, which must resist the temptation to increase the precision of quantification until it has achieved a comprehensive but parsimonious overview which robustly identifies a small, workable set of key features to examine. The variety of possible measures is so great, that the greatest current danger is to narrow the scope of inquiry prematurely. This potentially wastes the investment on careful measures of some subset of objects and risks being trapped by a sense of false precision. In other words, increasing precision would require focusing on one spatial scale range, thereby missing the complexity inherent over a number of scale ranges in the entire landscape.

I tried to develop a structural complexity index which balances the study's broad scope with attainable goals for data collection and with analysis methods which are transparent but robust. This balancing required sacrificing the comprehensiveness of data acquisition and the precision of object measurement for an achievable measure which reliably indexes the complexity of a hierarchical landscape. Therefore, I expressly avoided data which is costly in time or money to acquire, such as remote sensing. Instead I censused landscape data which, when considered in total, are reasonable estimates of structural complexity over scale ranges which correspond to hierarchical models of animal behavior. And I designed the index such that it can be relatively rapidly quantified at low cost by reading the literature, discussing the area with people with on-site experience, or viewing pictures of the site. I now describe the methods for quantifying structure over three scale ranges.

Structural quantification methods

I obtained verbal and/or pictorial descriptions of landscape structure from literature and by direct interview of researchers or site managers with experience on-site. These descriptions were used to quantify landscape structural complexity over three arbitrary scale ranges (Table 4-2), which roughly correspond to vegetation architecture (micro-scale), land cover patch structure (meso-scale), and geomorphology (macro-scale), respectively The structural elements examined in each scale range reflect hypotheses concerning what architectures animals might exploit given a scale-dependent perceptual grain and extent. This translates to the question, what vertical and horizontal structural elements might be important to animals at these qualitatively different time-space scales?

Dimensions of complexity: Within each scale range the index quantifies structural complexity in two dimensions, vertical and horizontal. Vertical complexity is indexed in the first column, and two aspects of horizontal complexity are indexed in columns two and three, respectively Values in the second column index Horizontal Diversity, and those in the third column index Horizontal Connectivity The structural complexity index for each scale range is the sum of the values in each of the three columns. The structural complexity index for the entire study site is the sum of the values in the three scale ranges I will now show by example how the means of quantification differ in each column

Vertical Complexity In the first column I indexed Vertical Complexity in terms of the height of the dominant structural element within each scale range. This follows the assumption that opportunities to find and exploit structure increase with object height For example, at the micro-scale the dominant structure is defined by plant physiognomy (grass, shrub and tree forms) At the meso-scale the dominant structural element is the height of most common type of vegetation community (desert, grassland, forest), and at the macro-scale the dominant form is defined by the degree of convolution of the landscape surface (flat, undulating, hilly, mountainous)

Table 4-2. Quantification scheme for three kinds of landscape structural complexity (Vertical Complexity, Horizontal Diversity, and Horizontal Connectivity) within three arbitrary ranges (micro-, meso- and macro-) of scale. Within each scale range Vertical Complexity is indexed by a single number associated with the dominant structural form. Horizontal Diversity is indexed by giving each type of form the same value and summing all form types present. Horizontal Connectivity is indexed by both methods: a single number associated with the dominant form in the micro-scale, and by diversity indices at the meso- and macro-scales.

Vertical Complexity		***Horizontal Diversity***		***Horizontal Connectivity***		
			Micro-Scale Landscape Structure			
Score	*Dominant Plant Physiognomy*	*Score*	*Diversity of Plant Physiognomies*	*Score*	*Degree of Connectivity*	*Density of Plant Structures based on Vegetation Type*
1	very short (< 50 cm)	1	graminoids	1	< 5%	Barren, all vegetation scarce
2	short (< 1 m)	1	forbs/ferns/cacti	2	< 25 %	Grassland, shrubs scarce
3	mid (1 - 5 m)	1	shrubs	3	25 - 50 %	Shrubland, shrubs common
4	tall (< 30 m)	1	understory	4	25 - 50 %	Woodland, open forest
5	very tall (30 - 50m)	1	trees	5	> 50 %	Forest, 1 canopy
6	giant (>50 m)	1	very tall trees	6	> 80 %	Forest, 2 canopies
		1	giant	7	> 90 %	Forest, 3 canopies
			Meso-Scale Landscape Structure			
Score	*Dominant Patch Type*	*Score*	*Diversity of Plant Patch Types*	*Score*	*Degree of Wetness*	*Patch Type based on hydrology*
1	Desert	1	Vegetation	1	anhydric	Sahara
2	Steppe	1	Community	1	dry	Sonoran/Steppe
3	Grassland	1	Types based on	1	moist	Hammock
4	Savanna	1	climatic, slope	1	damp	Bottomland
5	Woodland	1	aspect, edaphic	1	wet	Marsh/Swamp
6	Forest	1	factors and disturbance processes	1	liquid	River/Lake
			Macro-Scale Landscape Structure			
Score	*Dominant Terrain Profile*	*Score*	*Diversity of Terrain Profiles*	*Score*	*Degree of Wetness*	*Patch Type based on hydrology*
1	Flat (5m., 1 deg.)	1	Flat	1	anhydric	Barren
2	Undulating (25m., 3 deg.)	1	Undulating	1	dry	Steppe/Grassland
3	Hills/hollows (100 m., 5 deg.)	1	Hills and hollows	1	moist	Woodlands/Savannah
4	High Hills (500 m., 10 deg.)	1	Rolling Piedmont	1	damp	Forest
5	Piedmont (1500m., 15 deg.)	1	Dissected Piedmont	1	wet	Marsh/Swamp
6	Mountains (>1500m, 25 deg.)	1	Mountains	1	liquid	Lakes/Rivers

The value in the first column assigned at each scale is the number corresponding to the dominant structural element. Using the continental boreal forest as an example, the dominant elements at each scale are valued as follows micro-scale (4 points for trees less than 30 meters tall), meso-scale (6 points for forest), and macro-scale (2 points for undulating terrain with average maximum difference in elevation less than 25 meters and slopes less than 3 percent grade)

Horizontal Diversity in the second column Horizontal Diversity is indexed based on the variety of vertical structural forms present This follows the assumption that for some species opportunities to find and exploit structure increase as the diversity of object heights increases over space. Values were assigned by summing the number of vertical elements present on site I assigned a Horizontal Diversity index value at micro-scales based on the number of plant physiognomies present At meso-scales the Horizontal Diversity index value was based on patch diversity by summing the number of patch types resulting from a number of factors (slope, aspect, edaphic patterns, disturbance processes) Ambiguities about patch type diversity related to the number of seral stages present were constrained by the conservative assumption that only two stages existed unless more were explicitly defined in the literature Examples of the manner in which these and other ambiguities were addressed in identifying patch diversity are illustrated for study sites in fourteen different biomes in Table 4-3

I assigned a Horizontal Diversity index value at macro-scales based on the diversity of terrain profiles such as flat undulating, hilly, mountainous. Again, using the continental boreal forest as an example, horizontal diversity at each scale was indexed as follows: micro-scale (5 points for five different physiognomies graminoids, forbs, shrubs, understory, and trees), meso-scale

(8 points for eight different patch types, see Table 4-3), and macro-scale (2 points for flat and undulating terrains)

Horizontal Connectivity. In the third column I indexed Horizontal Connectivity in terms of horizontal distances between key structural elements within each scale range. This follows from the assumption that for some species opportunities to find and exploit structure increase as closer proximity of similar structural types facilitates access to the landscape. This applies especially to species which tend to stay within rather than to cross between structural types. For example, some bird species are known to stay within patch types and move along the boundary rather than cross into another patch type (A. Kratter, pers. comm.)

I calculated a Horizontal Connectivity value in ways unique to each scale range. I calculated a Horizontal Connectivity index at micro-scales based on horizontal and vertical distances between plant structures. For example, I assigned the lowest value to bare substrate with no vegetation, medium values to short profile vegetation with some horizontal closure, and the highest values to dense stands of tall vegetation with multiple canopy layers. At the meso-scale of patch structure, I calculated a Horizontal Connectivity index based on the diversity of patch types related to hydrology. This stems from the idea that connectivity increases with increasing wetness on the landscape because more and more patch types will be linked by water flow. I calculated Meso-scale Horizontal Connectivity values by summing the number of patch types based on their degree of wetness.

At the macro-scale, I created an index of Horizontal Connectivity based on the diversity of landscape cover types related to hydrology which are evident when the landscape is defined with a very coarse grain (1 - 10 kilometers). This builds from the idea that hydrology connects the landscape

Table 4-3 Determinations of Horizontal Diversity indices at meso-scales as related to habitat patch diversity for a variety of terrestrial ecosystems. Any number enclosed by parentheses () indicates a conservative estimate of the number of seral stages

Ecosystem	*Uplands*	*Lowlands*	*No*
FORESTS			
Boreal Forest (Continental)	Jack Pine (2) Black Spruce; Balsam Fir; Aspen/Poplar	Marsh, bog/fen Alder thicket	8
Northern Temperate Forest (Itasca)	Deciduous (Maple /Bass-wood, Oak/Elm): Pine Spruce/Fir grassy meadows, shrub hillside	Marsh Larch/Spruce Bog Wet Sedge meadows alder thicket	10
North Florida Temperate Forest (Ordway)	Oak Hammock Sand Pine (2) Long Leaf Pine Mixed Oak/Pine	Herb. wetlands (ephemeral ponds: marshes) Forested wetland (bays);Pine Flatwoods (2)	10
Multi zonal Rocky Mountain (Yellowstone/ Rocky Mountain NP)	Alpine tundra Sub-alpine (Dwarf spruce/Fir) (mountain meadows) Montane (Ponderosa Pine/Fir) Woodland (rocky slopes, shrub/scrub oak), Shrub/grass (3 elevations)	Willow/coastal	9
Rainforest, Riverine Bottomland (Manu N P Peru)	Terra Firme (3) Bluff top bamboo; Large scale tree fall gaps	Successional Floodplain forest (7) Lake communities (marsh and oxbow): Palm swamp	15
Dry Deciduous (Santa Rosa, C R)	Successional (2) Grassland(2) Riverine Evergreen Ridge Forest; Slope Forest	Floodplain Mangrove	10
Savanna-Forest (Lokori Kenya)	Lava flats, high level scrub	Cordia thickets Salvadora thickets, alluvial flats, delta Ficus stands Hyphaene palms, dense Acacia, riverside Calotropis stands	9
Sour bushveld (Transvaal ?-South Africa)	rocky open areas, relic inland tropical forest fragments	open Faurea trees and sour grass dense bushveld	
DESERTS			
Chihuahuan Desert (Big Bend)	Montane & Sub-Montane Forest (Doug Fir/ Ponderosa Pine/Juniper Open stands (cactus/shrub/ gamma grass) with creosote bush thickets	Cottonwood gallery strands on springs washes streams	4
Sonoran(Organ Pipe)	Valley floor (bare ground, cactus/creosote bush) Bajada (paloverde tree, ocotillo, saguaro)	Mesquite trees along washes and water courses	3
GRASSLANDS			
Shortgrass Prairie (xeric - Colorado)	Shortgrass Shrub (atriplex)' yucca	Cottonwood strands	4
Shortgrass Prairie (hydric Texas)	Shortgrass Shrub (mesquite huisache) Live Oak Hammocks	Marshes (Carex): Riparian Cypress Zones	5
Tallgrass Prairie (Konza)	Tallgrass (2) shrub limestone outcrops	Oak gallery forest	5
Grassland-Desert (Amboseli Basin, Kenya)	Grassy plain open woodland, shrub	swamp, dense woodland	5

by positing that the presence of a landscape type at such a coarse grain is evidence that relatively large portions of the landscape are linked by vegetative cover of one type, and that more opportunities exist for more species as the number of these macro-scale landcovers increases. I calculated a Horizontal Connectivity Index at macro-scales by summing for each site the number of land covers evident at a very coarse spatial grain.

Using the continental boreal forest as an example, Horizontal Connectivity at each scale was indexed as follows: micro-scale (4 points for the sparse tree density of the boreal forest), meso-scale (4 points for four different patch types, moist, damp, wet and liquid), and macro-scale (1 point because only forest is evident at a very coarse spatial grain).

Results. Landscape structure classified in 12 biomes

I list LSCI values for most landscape study sites, complete with index values at each separate scale, in Appendix C. I ranked biomes in decreasing order of structural complexity as suggested by other landscape classification schemes (Holdridge, Koppen, Bailey) as well as my own intuition and then graphed this complexity ordering against mean and standard error statistics for LSCI values (Figure 4-3). The LSCI estimates structural complexity in relatively similar fashion to other classification schemes as indicated by the relatively straight line progression from left to right in the graph. In addition, LSCI values suggest structural similarities which might not be immediately apparent. For example, the LSCI scores for forests across a wide latitudinal band (temperate, neotropical wet and moist) are quite similar. In like manner LSCI values clustered for scrublands, savannas, and woodlands.

Methods for determining lump complexity

I quantified Lump Complexity (LC) as the number of lumps found for an animal body mass data set using lump analysis. I applied lump analysis to animal body mass data derived from on-site measures or from global compendia (Dunning 1993, Silva and Downing 1995) to bird and mammal species lists from some 150 landscape sites in 24 biomes. For each site I sorted the body mass data in ascending order and analyzed for lumps using GaP Analysis (Chapter 2, Restrepo et al. 1997). I present summary lump number statistics for each biome sorted in ascending order of landscape complexity (Table 4-4).

Lump Complexity Compared with Landscape Complexity

Landscape structural complexity appears to predict the complexity of lump structure, as indicated by lump number, though prediction power is higher in bird than in mammal data sets. I regressed Lump Complexity against each biome's rank based on landscape structural complexity and found significant relationships for birds ($r^2 = 0.817$) and mammals ($r^2 = 0.44$) wherein the higher r-squared value for birds indicates greater power to explain the variability in the data. I found similar results when I correlated Lump Complexity against LSCI (Figure 4-4) and found significant relationships with similar differences in explanatory power for birds (Correlation coefficient = 0.763) and mammals (Correlation coefficient = 0.366).

Animal Lump Structure and Landscape Structural Complexity

A number of sources of error potentially undermine the reliability of the Landscape Structural Complexity Index (LSCI). The LSCI was explicitly

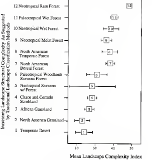


Figure 4-3 Mean and standard deviation values for landscape structural complexity indices calculated for twelve biomes.

Table 4-4 Mean and standard deviation statistics summarized at the biome level of lump numbers found using GaP analysis on landscape study site body mass data sets of birds and mammals.

No	Thermal Zone	Biome Landcover Type	Lump Number Statistics			
			Birds		Mammals	
			Mean	Sd	Mean	Sd
1	Temperate	Desert			5.9	0.6
2	Temperate	Mediterranean			6.0	2.5
3	Temperate	ShortGrass Prairies	7.5	4.0	6.7	1.0
4	Temperate	Tall and Mid Grass Prairies	7.4	2.2	7.8	1.8
5	Boreal	Forest	8.7	2.5	7.3	1.0
6	Boreal	Montane Forest and Tundra	9.0	4.2	6.5	0.7
7	Tropical	Savanna with Forest	10.7	1.5		
8	Temperate	North Eastern Deciduous Forest	11.0	2.8	7.1	1.8
9	Tropical	Lowland Dry Deciduous Forest	11.0	1.4	6.2	0.8
10	Tropical	Scrubland	11.5	2.1	6.0	1.2
11	Tropical	Woodland/Savanna Forest			9.0	1.8
12	PaleoTropical	Grasslands			10.0	2.6
13	Tropical	Savanna with Forest			11.0	1.7
14	Temperate	South Eastern Conif & Decid Forest	12.0	3.0	8.3	1.3
15	Temperate	North Western Conif & Decid Forest	12.0	2.6		
16	Tropical	Wet Forest			8.8	3.2
17	Tropical	Moist Forest			9.5	0.7
18	Tropical	Montane RainForest	12.8	1.8	7.0	2.4
19	Tropical	Lowland Wet Forest	15.0	2.8		
20	NeoTropical	Lowland Rainforest 1	18.8	3.6	8.4	2.7
21	NeoTropical	Lowland Rainforest 2	21.3	3.0	7.0	0.0
22	NeoTropical	Lowland Rainforest 3			9.8	1.0
23	PaleoTropical	Asian RainForast			10.0	4.2
24	PaleoTropical	African Rainforest			12.8	3.4

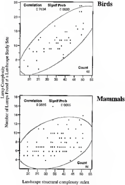


Figure 4-4. Number of lumps found at a study site correlated on landscape structural complexity indices for bird and mammal body mass data sets in ecosystems found in 18 biomes on 5 continents (95 percent confidence limits encircled by gray line)

designed for quick estimates of landscape structure in the absence of remote imagery or direct field observation. Therefore, it explicitly ignores data of those meso-scale structural elements which are costly to acquire, such as size distributions, interval distances and degrees of connectivity associated with patches. In addition to the information knowingly excluded, there is a potentially large data pool which is still unappreciated concerning exactly what landscape structures are meaningful to animals. This uncertainty could lead to errors of omission and commission in the indexing of landscape structure. Between the known and unknown sources of error in determining the LSCI, it is not safe to assume that it is a reliable index of landscape structure. It is novel in the attempt to estimate structural values at three scales, but little empirical evidence confirms the importance to animals of the structures quantified. However, in the face of so many sources of error, the degree of correlation between mammal and bird lump structures and indices of landscape structural complexity (LSCI) is high enough to constitute modest support for the Textural-Discontinuity hypothesis (H6).

So many uncertainties exist in quantifying landscape structural complexity, that the LSCI's greatest contribution may be as a heuristic which identifies scale ranges or particular objects for further testing. Even as a heuristic, however, the possibility exists that structure quantified at certain scales may correlate best with lump structure and thereby dominate determinations of landscape structure. I tested that possibility through multiple regression of number of body mass lumps found at a study site on the structural complexity values (independent variables) for micro-, meso- and macro-scales.

I found different results for mammal and bird data sets. For birds, the overall correspondence between landscape complexity (LSCI) and Lump

Complexity is far higher than for mammals, and it appears that correlation exists primarily at smaller scales of landscape structural complexity. Micro- and meso-scale structural indices are significant predictors (probability > F = 0.0004 and 0.0276, respectively) of avian Lump Complexity while macro-scale structural indices were not significant predictors. For mammals, no independent variable at any scale is a significant predictor of Lump Complexity, while the overall LSCI is a significant predictor even though the explained variance is very low.

While both Lump Complexity values for birds and for mammals correlate well with landscape structural values (LSCI), the degree of correspondence is far higher for birds. Ecological and/or methodological reasons may be involved. Several observations pertain both to the lump and landscape analysis methodologies. First, the number of observations differs greatly between birds and mammals. Increasing the number of bird ecosystem sites might introduce as much variability as observed in the mammal ecosystem sites. Second, with no basis to rank different structural types in the landscape with respect to their importance in animal decisions, equal weighting was given to all types of structure. Increased understanding of animal-structure interactions may eventually allow not only ranking and weighting the values for different structural types but inclusion of types previously unappreciated. For example, meso-scale features such as patch size, inter-patch distances, and connectivity are very costly measures to determine for any site and were expressly avoided in this index. Addition of such features to the index might increase correlation values between lump number and landscape indices. Finally, as with PatternMatcher analysis, these results may be sensitive to the lump analysis methodology.

The differences between birds and mammals in correspondence between landscape and lump complexity values may relate to how the different taxa perceive and respond to landscape structure. Perhaps birds encounter, see' and exploit more of the structural complexity in a landscape than mammals Holling(1992) posits that the birds exploit volumes (3 dimensions) while mammals exploit lines (1 dimension). These different geometries of exploitation might result from differences in perception and/or because their locomotory mode affords access to the landscape over a wider variety of scale ranges than mammals Exploitation of more facets in the landscape might result in more potential niches for birds and cause the bird community lump structure to aggregate into more lumps than the mammals For example, wading birds potentially interact across 5 scales of the south Florida landscape: areal, home range habitat, patch and food (Holling 1992) Mammals may face multiple spatio-temporal scales in their behavioral decisions, but mostly those mammals at the larger end of the size axis For example it is difficult to imagine a shrew interacting with landscape structures as large as a tree stand, let alone a forest However, birds as small as hummingbirds potentially address as wide or wider a range of scales in their annual migrations as do the largest wading birds

Summary of Landscape Complexity Index Results

LSCI values address structure at all spatial scales and suggest structural complexity rankings quite similar to those implicit in traditional landcover classifications This does not confirm their capacity to measure structure, but it provides moderate reassurance that LSCI indices conform with recognized definitions of landscape complexity Significant correlations between LSCI values and Lump Complexity values for birds and mammals over a very wide variety of biomes give broad support to H6's predictions of correspondence between patterns of animal morphometry and landscape structure

The ability to rank systems based on landscape complexity allows me to broaden my tests of the generality of the Textural-Discontinuity hypothesis from intra- to inter-biome lump pattern comparisons. I now describe the theoretical basis and methods for comparing the lump patterns of different biomes in the context of this study's progression of tests of H6

Lump Pattern Matching Between Systems at Scales Larger Than Landscapes

Previous tests (Holling 1992, Restrepo 1995) of the Textural-Discontinuity hypothesis (H6) used a new method of quantifying animal size distributions (lumps) to establish quasi-quantitative links between animal morphometry and landscape structure. In this study I created a series of tests to probe H6 from different angles, escalating the degree to which I endanger H6's predictions about lump structure with each subsequent test. One basis for probing more deeply was to increase the precision of quantifying lump and landscape variables. The next probe of H6 involves a sophisticated methodology which is best understood in the context of the entire series of tests of H6. I now review this test series using a table (4-6) and a graph (4-5) to summarize the entire progression of questions and methods

Review of Lump Pattern Matching Tests of H6

I designed a series of tests of H6 (Table 4-5) to address questions which are increasingly exacting in their probes of H6's predictions. These questions start with general predictions of lump pattern within a system (biome or super-biome) and then focus on more specific predictions related to lump pattern matches between different systems. I matched the increasing

Table 4-5. Questions and related definitions of lump and landscape structure used to probe the predictions of the Textural-Discontinuity Hypothesis.

Chapter Scale	Definitions of			
	Lump Structure		Landscape Structure	
Question	Condition	Description	Condition	Description
Chapter 4 Within a System 1. Are lump patterns similar in landscapes of similar structure?	Qualitative	Lump Pattern Commonality	Qualitative	Biome and Super-Biome
	Quantitative	Lump Frequency	Qualitative	Biome and Super-Biome
Chapter 4 Within a System 2. Is lump pattern commonality the result of random processes?	Quantitative	Gap Commonality Index	Qualitative	Biome and Super-Biome
	Quantitative	Prominent Pattern Commonality	Qualitative	Biome and Super-Biome
Chapter 5 Between Systems 3. Is the degree of lump pattern complexity related to the complexity of landscape structure?	Quantitative	Lump Complexity or The number of lumps found in an animal community	Quantitative	Landscape Structural Complexity Index
Chapter 5 Between Systems 4. Is the degree of lump pattern matching between systems related to differences in landscape structure?	Qualitative	Graphic Overlap of Lump Frequency Indices	Quantitative	Landscape Structural Complexity Index
	Quantitative	Shared Lump Frequency Index	Quantitative	Landscape Structural Complexity Index

specificity of these predictions by progressively adapting the means of indexing lump and landscape structure.

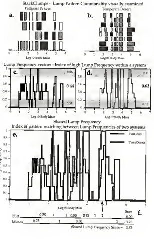
In Chapter 3 I began by testing H6's prediction (Question 1) that similarly structured landscapes are associated with animal communities with similar patterns of lump structure. I did not quantify landscape structure but left it as a qualitative designation, grouping animal data sets by biome classification, and I focused on one aspect of lump pattern complexity 'commonality' or the degree to which lumps and gaps of different ecosystem lump structures align on the size axis. I illustrate the different questions and their tests by comparing their use on two systems of ecosystem lump structures (Figure 4-5), the Temperate Desert and Tallgrass Prairie biomes. The Temperate Desert biome has a higher degree of Lump Pattern Commonality (LPC) than the Tallgrass Prairie, as is evident by the higher frequencies of overlap between lumps and gaps between the lump structures of the ecosystems in each biome (Figure 4-5a and b).

Visual confirmation of (LPC) using StackClumps representations of biomes sets the stage for Question 2: to what extent does LPC result from random events as opposed to landscape structural similarities? Commonality does appear to result from random events when I index LPC only in terms of gaps shared between ecosystem lump structures using the Gap Commonality Index (GCI). I visually determined the number of gaps shared by all ecosystems in a biome, and then repeating the measure for random groupings of actual ecosystem lump structures. The results supported H6 because GC indices were several times larger for actual than random biomes.

I found the same differences in Lump Pattern Commonality patterns between actual and random biomes when I quantify LPC more rigorously in terms of both gaps and lumps by collapsing the shared pattern of LPC into a vector: Lump Frequency (LF). The LF vector is a line of numbers, each number corresponds to a very small interval of the size axis and indicates the frequency of ecosystems in the biome which exhibit a lump over that interval. I illustrate this by graphing Lump Frequency vectors for Tallgrass Prairie and Temperate Desert biomes (Figure 4-5c and d), peaks in these vectors are associated with zones of frequent lump overlap, and valleys are associated with zones of frequent gap overlap in the StackClumps representations above (Figure 4-5a and b). The higher LPC of the Temperate Desert biome is visually evident both in StackClumps and in the greater number of tall peaks and deep valleys found in the Lump Frequency vector representation (Figure 4-5c and d).

To better distinguish between the Lump Frequency (LF) vectors of actual and random biome lump structures I created a derivative index called Prominent Pattern Commonality (PPC). This filters out the noise of moderate values in LF vectors and indexes only those lumps and gaps shared by a super-majority (80 percent) of all ecosystems in a biome. The PPC index represents the proportion of the size axis of a large scale system (biome or super-biome) occupied by significantly high frequencies of common lumps and gaps (see gray areas in Figures 4-5 c and d). For example, six percent of the size axis of the Tallgrass prairie biome shows majority frequencies of lumps and 38 percent of the size axis has majority frequencies of gaps, so the PPC in total is 44 percent (Figure 4-5c). The higher lump pattern commonality of the Temperate Desert biome is indicated by a PPC of 63 percent (Figure 4-5d). PPC indices of actual biomes were significantly higher than those found in biomes with randomized ecosystem lump structures.

Figure 4-5 Lump pattern commonality in two biome assemblies of animal community lump structures as measured visually in stacked formation (a & b), as represented numerically by Lump Frequency vectors (c & d), and as summarized by an Index of Prominent Pattern Commonality (bold decimal fractions in c & d), which measures the portion of the size axis occupied by extremely high and low Lump Frequency vector values. The degree of lump pattern shared between the two biomes is shown visually as the overlap of two Lump Frequency vectors (e), and the degree of overlap is scored (f) as the Index of Shared Lump Frequency.


StackClumps - Lump Pattern Commonality visually examined
Tallgrass Prairie
a.
Temperate Desert
b.
0 1 2 3 4 5 6
Log10 Body Mass
Lump Frequency vectors - Index of high Lump Frequency within a system
c.
0.06
0.44
0.38
d.
0.31
0.63
0.32
Lump Frequency
0 0.2 0.4 0.6 0.8 1
0 1 2 3 4 5 6 7
Log10 Body Mass
Shared Lump Frequency
Index of pattern matching between Lump Frequencies of two systems
e.
TallGrass
TempDesert
Lump Frequency
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1
0 1 2 3 4 5 6 7
Log10 Body Mass
Sum
f.
Hits 0.75 1 1 0.50 0.75 1 1 6.00
Masses 0.75 1 0.50 1 - 3.25
Shared Lump Frequency Score = 2.75

All the visual and numerical tests of Chapter 3 demonstrated significantly high degrees of Lump Pattern Commonality (LPC) within large scale systems of similar landscape structure. While it is unlikely that LPC resulted from random events, these tests did not rule out the possibilities that other processes besides those which determine landscape structure contribute to LPC. If certain evolutionary, trophic or morphological processes create lump patterns common to all systems, then any sub-group related to landscape structure, such as a biome, would also show commonality. Therefore, the results of Chapter 3 broadly support the Textural-Discontinuity hypotheses, but they do not necessarily undermine non-landscape hypotheses (H1 - H5). This ambiguity frames the next challenge: to more rigorously distinguish between the relative powers of these hypotheses to predict lumpy body pattern.

For this chapter I pose two questions (3 and 4 in Table 4-5) which explicitly test H6's predictions and severely challenge all non-landscape hypotheses at the same time. These questions address the ambiguity about causes of lump pattern similarities *within* systems by jumping up in spatial scale and examining which hypothesis best predicts similarities of lump pattern complexity and correspondence between systems.

These questions are the most demanding tests so far of any hypothesis (H1 - H6) because they challenge a hypothesis to predict the correspondence between *rates of change* in pattern matching between lump structures as the difference in landscape structure increases over a range of very different landscape structures, climates, and taxonomic compositions. As I compare pairs of lump structures across all these systems if the degree to which landscape structure differs corresponds to the degree to which lump structures correlate, then H6 gains strong support at the expense of H1 through H5

Comparing quanta of lump and landscape patterns

Comparisons between systems (biomes or super-biomes) requires their classification and ranking in terms of lump structure and landscape structure. This increases the rigor of these tests because it does not hold either landscape or lump variables constant; it allows both to vary independently. I developed the LSCI to rank systems independently based on complexity of landscape structure. I now describe how I used the LSCI and two new quanta for lump structure to address Questions 3 and 4.

Question 3 is a probe of trends in landscape and lump pattern where the complexity of each type of pattern is summarized as an index. I quantified the complexity of lump structure as Lump Complexity (LC), the number of lumps found in an animal body mass data set, and demonstrated significant correlations between LC and the LSCI for mammals and birds. These tests support H6 and endanger non-landscape hypotheses (H1 - H5) because it is very hard to imagine how any non-landscape process affects indices of landscape structure and thereby contributes to such high correlations.

Question 4 escalates the danger for H6 by testing the prediction that the rate of lump pattern matching between systems correlates with the degree of structural or architectural similarity. In this chapter I use the LSCI to determine the degree of structural similarity between landscapes, and I will use Lump Frequency vectors to demonstrate lump pattern matching both visually and numerically. I describe both techniques now.

I illustrate matching between the lump patterns of the Tallgrass Prairie and the Temperate Desert biomes using Lump Frequency vectors in Figure 4-5e. A fair degree of correspondence between lump patterns is visually evident because most of the LF vector peaks (high frequency of lumps) and valleys (low frequency of lumps indicating gaps) coincide. Lack of pattern correspondence is evident where peaks in Tallgrass Prairie LF coincide with valleys in Temperate Desert LF at 1.0 - 1.4, 2.4, and 5.7 log10 body mass.

I developed Shared Lump Frequency (SLF) as an index of pattern matching which I find when I overlap two LF vectors. The SLF is designed to index pattern matches ranging from complete hits to complete misses and account for fractional hits and misses in between. I did not inspect pattern along the size axis at fixed intervals but employed a variable grain which flexibly corresponded to the size of prominent peaks and valleys. The basis for scoring a hit or miss is the relative difference in LF vector values as listed in Table 4-6. Complete hits or misses are determined where either prominent peaks or valleys coincide on the size axis, and I score this numerically when both LF vector values are above 0.7 or below 0.2, respectively. Fractional hits or misses result when one or both vectors exhibit middling rather than prominent stature, as when one or both LF vector values fall in between 0.7 and 0.2. For example, I score a "half hit" when two medium size peaks overlap, i.e. both LF vector values are between 0.5 and 0.7. I score a "three

Table 4-6. System for scoring the degree of pattern matching between values (x) in Lump Frequency vectors of two systems (biomes or super-biomes). Total misses as subtracted from total hits to derive a Shared Lump Frequency Index (SLF).

System 1	*System 2*	*Hit*	*Miss*
x > 0.7	x > 0.7	1	
x > 0.7	0.5 < x < 0.7	3/4	
0.5 < x < 0.7	0.5 < x < 0.7	1/2	
0.2 < x < 0.5	x < 0.2		1/2
0.5 < x < 0.7	x < 0.2		3/4
x > 0.7	x < 0.2		1

quarter miss' (Figure 4-5 e) when a medium size peak and a gap overlap, i.e one LF vector value is between 0.5 and 0.7 (peak) and the other is below 0.2 (gap)

Inter-Biome Lump Pattern Comparisons

The Textural-Discontinuity hypothesis (H6) predicts that the degree of pattern matching between lump structures of two different systems will decline as the contrast in landscape structural complexity increases I first test H6 by graphically demonstrating trends in pattern matching between lump patterns of different biomes (i.e. different levels of landscape structural complexity) Then I describe a method for measuring pattern matching between biome Lump Frequency vectors I apply this method in pattern matches between the Lump Frequency vectors of some 15 biomes representing a range of landscape structural complexity values.

Graphic inter-biome Lump Frequency comparisons

I use three mammal biome Lump Frequency patterns as templates to contrast with Lump Frequency patterns of other mammal biomes from a variety of landscapes (Figures 4-4 through 4-6) In each figure the difference in landscape structure between the template and the contrasting biome increases with each graph from top to bottom For example the template biome lump pattern in Figure 4-4 is boreal forest, and the contrast increases from northern temperate forest (Figure 4-4a) to tropical wet forest (Figure 4-4d)

In each figure the downward progression (a through d) of graphs exhibits a decline in the degree of pattern matching between template and contrasting biome lump patterns. For example, lump patterns of rainforest biomes from two different areas of the Neotropics have a high degree of overlap (Figure 4-5a), with some pattern mismatch around 3 0 log10 body mass By contrast, Woodland-Savanna biome lump patterns show 6 zones of mismatch with those of neotropical rainforest (Figure 4-5c) at 3.5, 4.2, 4.8, 5.0, 5 5-5 8 and 6.3 log10 body mass Similarly, temperate shortgrass prairie biome lump patterns show much more matching with those of African grasslands (Figure 4-6b) than those of tropical wet forest (Figure 4-6d)

The declining degree of lump pattern matching shown in the descending progression of graphs in each figure appears to visually correspond to the increase in landscape structural difference The correspondence of the rates of pattern matching and structural differentiation can be more carefully measured numerically I now quantitatively test differences in lump pattern using the Lump Frequency vector patterns of some 15 biomes to score Shared Lump Frequency indices

Numeric inter-biome lump pattern comparisons

I superimposed pairs of graphs of biome Lump Frequency vectors and visually measured the degree of pattern matching so as to score a Shared Lump Frequency (SLF) index using the scoring system listed in Table 4-6. To standardize my scores I repeated the scoring process until two repeats produced virtually the same score. Some lump pattern pairs had such clear similarities and/or differences that only two repetitions were necessary, whereas some required up to five repetitions

I used SLF index to test the Textural-Discontinuity hypothesis's prediction in two ways, graphically and statistically I stratified the mammal biomes into two groups, listed in the Legend of Figure 4-9, based on the number of study sites in each biome Study site numbers ranged from 3 to 4, and 5 to 8 respectively I did this to avoid pattern matching anomalies arising from differences in Lump Frequency values caused by the number of

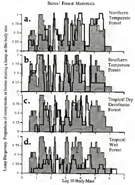


Figure 4-6 Correspondence between mammal lump structure patterns (Lump Frequency vectors) summed for all ecosystems in a biome Boreal forest mammal lump pattern is a gray background template against which black Lump Frequency vector patterns of other biomes are contrasted

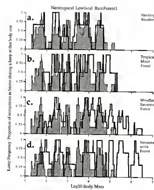


Figure 4-7 Correspondence between mammal lump structure patterns (Lump Frequency) summed for all ecosystems in a biome Neotropical lowland rainforest mammal lump pattern is a gray background template against which black Lump Frequency vector patterns of four other biomes a) Neotropical lowland rainforest2, b) tropical moist forest, c) woodland/savanna forest, d) savanna with forest, are contrasted

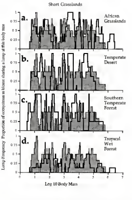


Figure 4-8 Correspondence between mammal lump structure patterns (Lump Frequency vectors) summed for all ecosystems in a biome Shortgrass prairie mammal lump pattern is a gray background template against which black Lump Frequency vector patterns of other biomes are contrasted.

ecosystems in a biome group. As already discussed (Chapter 3), I either found no significant trend or weak but significant trends relating the number of study sites in a biome to indices of pattern commonality (Gap Commonality index, Prominent Pattern Commonality index). There is a small potential that even such weak trends might artificially depress pattern matching values between biomes with very disparate values for number of study sites. Biomes with low numbers of study sites might have higher Lump Frequency values associated with peaks because commonality might be easier to achieve between smaller number of sites. Therefore, even in cases of peak alignment between biomes, when I measure Shared Lump Frequency the chances are more likely for fractional hits rather than full hits.

Within each stratum of biomes I ranked biomes by landscape structural complexity (using mean LSCI values) and sorted them from high to low values along the edges of a matrix. I then measured the degree of lump pattern matching between biomes as Shared Lump Frequency (SLF) indices for all pair combinations of biomes within each stratum's matrix. I graphed trends between landscape structural complexity and SLF values within each matrix (Figure 4-9a & b) with the self matched values forming the diagonal. I found SLF index values ranging between -4 (worst fit) to 7 (best fit) and arbitrarily assigned the number 8 for all 'self-matches', pattern matches of a biome's Lump Frequency vector on itself. Based on visual experience with graphic comparisons, I arbitrarily designate SLF index value ranges into classes of pattern matching as follows: excellent (> 4), very good (3 to 4), good (2 to 3), fair (1 to 2), poor (-1 to 1), very poor (-2 to -1), and execrable (< -2). I applied these classes of pattern matching when I identified zones of similar degrees of lump pattern matching in the matrix by interpolating the SLF values to generate contour lines.

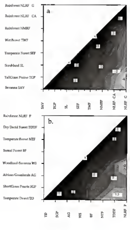
Pattern matching trends in both matrices (Figure 4-9 a and b) support the "Textural-Discontinuity hypothesis" (H6) predictions. H6 posits that the degree of lump pattern matching should decline as the degree of structural difference increases between biomes. For both matrices lump pattern matches are in the 'very good' class only when the biomes matched do not differ in ranking of landscape structural complexity by more than 3, and usually 2 or less. That is to say that on average I found fair to poor lump pattern matches when comparing biomes with differences in rank of landscape structural complexity greater than three. For example, SLF values remained 'good' or better when comparing savannas with tallgrass prairies and scrublands and then declined to the 'fair' range and worse when comparisons extended to forests (Figure 4-9a).

The "Textural-Discontinuity hypothesis" (H6) prediction is more exactly realized when one looks at the contour pattern of Shared Lump Frequency values in each matrix. Briefly, no contours would exist if landscape structure is unrelated to lump structure. That is to say, if the ranking of biomes by structural complexity on the sides of the matrix was irrelevant to the degree of pattern matching between each pair of biomes, then no zones of similar lump pattern matching indices could be found. There would simply be a random mixture of isolated islands of lump pattern matching values. The contours of lump pattern matching values are not isolated or small and show a striking regularity with which they cross the entire matrix in parallel and create, in the aggregate, a fairly consistent downward slope from the diagonal of 'perfect matches' to the lower right hand corner of 'worst matches'. This indicates a more subtle degree of linking between lump and landscape

Legend for Figure 4-9

No	*Symbol*	*No. Sites*	*Biome*
Matrix A			
1	NLRF - G	4	Neotropical Lowland Rainforest - Guyana, Surinam
2	NLRF - CA	3	Neotropical Lowland Rainforest - Central America
3	NMRF	4	Neotropical Montane Rainforest
4	TWF	4	Tropical Wet Forest
5	STF	4	Southern North American Temperate Forest
6	SL	4	Scrubland
7	TGP	4	North American TallGrass Prairie
8	SAV	3	Savanna
Matrix B			
9	NLRF - P	5	Neotropical Lowland Rainforest - Peru
10	TDDF	5	Tropical Dry Deciduous Forest
11	NTF	7	Northern North American Temperate Forest
12	BF	7	North American Boreal Forest
13	WS	6	Woodland - Savanna
14	AG	5	South African Grasslands
15	SGP	6	North American Shortgrass Prairie
16	TD	8	North American Temperate Desert

Figure 4-9 Matrices of values indexing the degree of lump pattern matching between mammal body mass lump patterns of pairs of biomes. The lump pattern of each biome is a vector of Lump Frequency values which signify the proportion of all landscape study sites in the biome which exhibit a lump at that body mass. Each matrix is contoured by interpolation between pattern matching values, which range from 8 (arbitrary designation of perfect match) to 5 (the lowest value observed). Matrix a represents pattern matches between biomes with 3 to 4 landscape study sites, and Matrix b represents biomes with 5 to 8 landscape study sites.


Rainforest NLRF G
Rainforest NLRF CA
Rainforest NMRF
Wet Forest TWF
Temperate Forest STF
Scrubland SL
TallGrass Prairie TGP
Savanna SAV
a
4
4
2
-4
SAV
TGP
SL
STF
TWF
NMRF
NLRF CA
NLRF G
Rainforest NLRF P
Dry Decid Forest TDDF
Temperate Forest NTF
Boreal Forest BF
Woodland-Savanna WS
African Grasslands AG
ShortGrass Prairie SGP
Temperate Desert TD
b.
8
-2
0
1.5
TD
SGP
AG
WS
BF
NTF
TDDF
NLRF P

structures. The downward trend is not simply the product of drastic agreement or disagreement at the extremes, it shows a fairly regular progression through the intermediate differences of landscape structure. However, each matrix map exhibits some irregularities in the downward slope, particularly when pattern matching values are below zero. For example, two anomalous depressions split the slope in the lower right hand corner of Figure 4-9b.

Statistical test of inter-biome lump pattern matches and lump structure

The anomalies in trends in Figure 4-9 suggest some variance in relations between landscape structure and lump pattern matching. I measured this variance statistically by calculating a Landscape Structure Difference Index (LSDI), the absolute difference in landscape structure complexity (LSCI) values between each pair of biomes, and correlating the LSDI with the index of lump pattern matching, the SLF.

This correlation (Figure 4-10) proved highly significant ($p < 0.0001$) with a fair amount of the variance explained by a linear model ($r^2 = 0.420$). This is a relatively low amount of variance given the considerable potential for error to influence the assembly and analysis of animal body mass and landscape structure data sets. The robust association between lump pattern matching and contrasts in landscape structure is firm support for the Textural-Discontinuity hypothesis at the scale of biomes.

Lump Pattern Comparisons Between Super-Biomes

The relatively robust correspondences I found between inter-biome lump pattern matching and landscape structural differences do not confirm that processes linking animals to landscapes operate primarily at the biome level. These results build on the results of previous chapters by extending

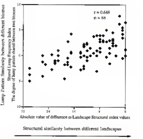


Figure 4-10 Correlation of indices of lump pattern shared between biomes on differences in landscape structural values for pairs of biomes. Landscape structural differences are derived by taking the absolute value of the difference between the indices of landscape structural complexity (LSCI) for two landscape types each of which is typical for each biome as a whole. The degree of structural similarity increases as these difference values decline.

that linkage from the ecosystem or landscape level to the biome level, but they do not eliminate other levels.

It is possible that such linking processes operate at multiple ranges of scale and the clearest signal of correspondence may be most evident at one scale. Such results would identify the importance of that scale at the same time that they help to deepen understanding as to the relative importance of various scale ranges in linking animals to landscapes.

To broaden the hierarchy of scales at which animal-landscape links have been tested, I now examine lump pattern matching and landscape structure at the super-biome level. I aggregate landscape data sets of one biome type which are found on different continents, South America and Africa, for example, into "super-biomes" data. I test H6's predictions exactly as I did for biomes by first graphically examining matches of super-biome lump patterns across a range of landscape structural complexity values and then testing the matches quantitatively.

Graphic comparisons of super-biome lump patterns

I further test H6 by contrasting patterns of Lump Frequency vectors of super-biomes of dissimilar landscape structure (Figure 4-11) and those of similar structure (Figure 4-12). As H6 predicts, the degree of pattern overlap is much higher in the latter than in the former. For example, the peaks and valleys of grassland and woodland/savanna super-biome Lump Frequency patterns overlap over most of the size range except around 3.0 and 3.8 log10 body mass (Figure 4-12c). By contrast, a majority of prominent lump pattern features do not overlap when contrasting Lump Frequency values of rainforests vs. grasslands or boreal forests vs. woodland/savanna (Figures 4-11a and b).

Numeric lump pattern comparisons between super-biomes

Following the same procedure I used for biomes, I constructed a matrix with super-biomes sorted on each side in order of landscape structural complexity, from "simple" grasslands to "very complex" rainforests. I then measured indices of lump pattern matching (Shared Lump Frequency or SLF)

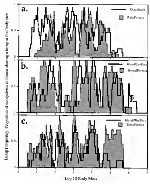


Figure 4-11. Correspondence between mammal lump structure patterns (Lump Frequency vectors) summed for all ecosystems in a super-biome. The super-biome patterns matched are grasslands vs. rainforests (a), woodland savanna forests vs. boreal forest (b), and moist wet forests vs temperate forests(c)

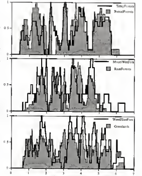


Figure 4-12. Correspondence between mammal lump structure patterns (Lump Frequency vectors) summed for all ecosystems in a super-biome. The super-biome patterns matched are temperate forests vs. boreal forests (a), moist/wets forests vs. rainforests (b) and woodland savanna forests vs grasslands(c)

by super-imposing pairs of graphs of super-biome Lump Frequency vectors and used the scoring system listed in Table 4-6. I found SLF index values ranging between -4 (worst fit) to 6 (best fit) and arbitrarily assigned the number 7 for all self-matches.

I graphed a map of the matrix of super-biome pattern matches which interpolated the SLF values so as to identify zones or contours of similar pattern matching value (Figure 4-13). I found results quite similar to those for biomes in terms of range of SLF values and the general slope and contour of SLF values. In the former case, 'good' or better pattern matches (SLF index values > 2) occurred between pairs of super-biomes with structural rankings differing by 2 at most. For example, the Grasslands lump pattern fit very well with that of Woodland-Savannas, but the fit declined to 'fair' when compared with Boreal Forests (Figure 4-13). The trend linking the degree of lump pattern matching to the difference in structural complexity appears slightly more distinct at the super-biome level than at the biome level. For the matrix graph as a whole the slope of SLF values appears slightly smoother than those found for biome matrices (Figure 4-9a and b), with fewer anomalous zones, especially when compared with biomes with large numbers of landscape study sites (Figure 4-9b).

I statistically confirmed the tightness of the trend linking indices of lump pattern matching and the degree of structural difference in landscapes between pairs of super-biomes. I correlated (Figure 4-14) Landscape Structure Difference Index (LSDI) values with the index of lump pattern matching, the SLF, and found this correlation highly significant ($p < 0.0002$) with a considerable amount of the variance explained by a linear model ($r^2 = 0.671$).

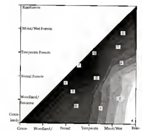


Figure 4-13. Tone-contoured map of a matrix of values indexing the degree of matching (Shared Lump Frequency index) between lump patterns of pairs of super-biomes. The matrix is contoured by interpolation of pattern matching values.

Summary of Lump Pattern Matching Between Different Large Scale Systems

The Textural-Discontinuity hypothesis gains broad and general support from these demonstrations of robust links between lump pattern matching and landscape structural complexity at biome and super-biome scales. Both graphical and numerical tests show a relatively tight fit between the rate of decay in lump pattern matching and rates of increase in the difference in structural complexity between landscapes. The link between landscape and lump patterns suggested by within-system pattern commonality (Chapter 3) is

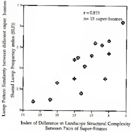


Figure 4-14 Correlation of indices of lump pattern shared between super biomes (Shared Lump Frequency index) on differences in landscape structural values for pairs of biomes. Landscape structural differences are derived by taking the absolute value of the difference between the indices of landscape structural complexity (LSCI) for two landscape types typical of the super-biome as a whole. The degree of structural similarity increases as these difference values decline.

robustly confirmed by this higher level, between-system, trend. I now endanger H6 further by testing its prediction that lump pattern predicts trends in landscape exploitation by animals

Lump Structure as a Predictor of Landscape Structure Use

The Textural Discontinuity hypothesis (H6) posits that patterns of lump structure correspond to patterns of exploitation of landscape structure by animals. Most studies have linked animal behavior to structure using one example of micro-scale architecture such as foliage height (see Table 4-1) Holling (1992) made qualitative associations between avian lump structure and micro-scale (foliage density, tree snags) and meso-scale (patch size) landscape textures Hostetler's (1997) association of bird body mass with forest-canopied patch size remains the sole study linking animal lump structure with landscape structure across a range of scales Lump structure is an intriguing exploratory tool to examine animal morphometry which defines animal size distributions at only one grain resolution lumps These previous studies utilized one taxon (birds) and one grain size (lumps) to resolve animal community morphometry This raises the question as to whether the Textural-Discontinuity's prediction is general enough to apply to other taxa besides birds when using more than one grain resolution to define animal morphometry

I addressed this question by testing H6's prediction using a birds as well as another taxon, mammals, at several resolutions of lump and landscape structure (Table 4-7). I tested three levels of spatial extent intra-landscape inter landscape and inter-biome I used two levels of grain resolution to describe lump structure the individual lump for inter-landscape extent and clouds of lumps for inter-biome extent. I described the use of landscape structure at a coarse, general mesoscale level (habitat) and at multiple scales (architectures ranging from micro-scale vegetation to meso-scale patch or forest stand)

Table 4-7 Grain and extent resolutions for three tests of correspondence between patterns of lump structure and of landscape structure use

Item	Test 1	Test 2	Test 3
Grain resolution used to define body mass size distribution	Individual species body masses and Lumps	Lump	Lump Cloud
Landscape (spatial extent)	Between Landscapes	Between Landscapes	Between Super-Biomes
Landscape Structure Use (grain resolution)	Coarse (meso-scale patch structure)	Multi-scalar fine to very coarse	

Sources of Data for Animal Use of Landscape Structure

I took descriptions of habitat and landscape use by nonvolant mammals from global compendia (Nowak 1991, Macdonald 1993) and regional sources (Emmons 1990, Banfield 1974, Golley 1966). Avian habitat use descriptions were taken from publications describing regional faunal assemblages: Canada (Godfrey 1986) and North America (Ehrlich 1988).

Test 1. Lump Structure and Coarse Landscape Use (Habitat Specialists)

I tested the Textural-Discontinuity hypothesis (H6) at a meso-scale spatial resolution (habitat) of landscape structure using eight avian lump structures derived from North American bird body mass data sets compiled at the landscape level from four different biomes. These included: boreal shortgrass prairie (Alberta), temperate midgrass prairie (Badlands), temperate deciduous forest (Finger Arnot, Yellowstone and Itasca), boreal forest (Taiga

Biological Station, Green River) and temperate tallgrass prairie (Konza) The categories of habitat use I examined were: generalist coniferous forest, deciduous forest, thicket, marsh and grassland

I compared patterns of lump structure with patterns of habitat use I examined patterns of avian habitat use by species to see if they clustered in relation to species' body mass or in relation to membership in a lump I found that no single habitat use category was found exclusively in any lump or group of lumps or constituted a significant majority in any lump With few exceptions every habitat usage category is present in almost every lump This pattern is most pronounced with birds categorized as 'generalist', a group which has the largest proportional representation in most lumps Birds whose habitat usage is mostly in deciduous forest also has broad representation in all lumps

Viewed by degree of representation some categories show slight tendencies to cluster over certain size ranges of lumps. Some vague trends suggest that species which utilize thickets have their greatest representation in lumps of smaller species, while 'water' specialists seem to most represented among lumps of larger sized species. These trends give modest but general support for the prediction by H6 that body size correlates with the fineness of the texture of landscape structure But the predominant trend is representation of all habitat categories across all lumps, a pattern readily explained by the fact that the size distributions of these categories in boreal prairie and temperate forest biomes do not cluster but are spread over most of the avian size range (Figure 4-15)

Methods for comparing patterns of lump structure and landscape use

In Tests 2 and 3 I compared patterns of landscape use with patterns of matching or overlap between lump structures of different systems In each

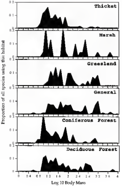


Figure 4-15 Distribution of sizes of birds by proportion of all species using that habitat in boreal forest and temperate forest and prairie ecosystems

test I juxtaposed two lump structures of different systems (either two landscapes in Test 2 or two super-biomes in Test 3) The paired lump structures were very similar except in one part of the size range The lump pattern features distinguishing the two systems were either the presence /absence of lumps or the differences in the size range of lumps In both systems being compared I examined use of habitat structure by species over a range of body sizes which straddled the zone of lump pattern distinctions. That is to say, I looked at patterns of landscape structure use by species within the size zone where lump patterns differed as well as the two neighboring size zones where lump patterns did not differ

Test 2. Landscape Lump Structures and Multi-Scalar Landscape Use

I tested H6 in two landscapes (Gabiro in Rwanda and Amboseli in Kenya) in the savanna/woodland biome by examining habitat usage by mammal species in both systems across a zone in the size axis characterized by a severe difference in size range in the second to smallest lumps (Figure 4-16) The third largest lump (lump 3) is very narrow in the Gabiro lump structure in comparison with lump 3 in Amboseli The neighboring lumps (2 and 4) occupy relatively similar size ranges in both data sets

In either landscape, usage of habitat by species in lumps 2, 3 and 4 are generally similar in a manner predicted by the lump structure First, species in lumps in the same size range use similar habitat structural features irrespective of which site they are found at. Therefore, species of either site in lump 2 use similar landscape textures such as herbaceous mats and grass runways Second the size rank of the lump correlates with the coarseness of the landscape texture, mammals in lumps with smaller mean size utilize finer textures than mammals in lumps with larger mean size For example,

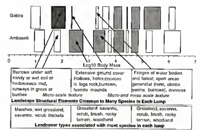


Figure 4-16 Landscape structural elements and cover-types commonly used by mammal species in similar size ranges as revealed in the lump structures of two African Savanna/Woodland Ecosystems: Gabiro, Rwanda and Amboseli, Kenya.

landscape textures utilized progress from micro- to meso-scale as mammals of larger mean body size lumps are examined. Mammals in lump 4 are associated with fringes of forests and water bodies, while mammals in lump 3 use holes and crevices between logs and stones.

These results suggest that lump structure may help predict the landscape structure of a site. In the absence of detailed site descriptions, the differences in size range and species density between species members in lump 3 at both sites might serve to predict that Amboseli has a higher incidence of a certain class of structural features (hollows, holes, crevices, termite mounds) than does Gabiro.

Test 3. Super-Biome Lump Structures and Multi-Scalar Landscape Use

I use a lump structure contrast at the cloud resolution level to compare habitat usage between species in similar size zones of two super- biomes. For example, comparing lump cloud structures of North American super-biomes (Temperate Forest and Temperate Grasslands) reveals a cloud in the forest size range (between 2.3 - 2.8 log10 body mass units) where none exists in the grasslands (Figure 4-17). While lumps are present in this size range in grassland landscapes, their low frequency and low species richness, as indicated by white coloration, suggest a relatively low density of species in this size range. Even if this zone were interpreted as a lump cloud, the difference in species densities between forests and grasslands is distinctive. In like manner to the African savanna/woodland comparison, the Textural-Discontinuity hypothesis gains support from the fact that lump cloud structure does predict similarities in habitat usage despite the fact that there is relatively little taxonomic overlap. Namely, lump clouds 2, 3 and 4 contain species whose habitat usage patterns (identified in the boxes

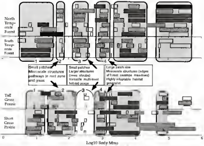


Figure 4-17 Landscape structural elements commonly used by mammal species in similar size ranges as revealed in the lump structure of two Super-biomes: Temperate Forests and Temperate Grasslands in North America.

separating the two super-biome lump patterns) are similar irrespective of which super-biome group they are found For example species found in lump 4 in either super-biome are associated with relatively open landscape architectures such as forest ecotones and meadows

Further support for the Textural-Discontinuity hypothesis is found in thet the coarseness of landscape texture utilized increases with the mean body size of the lump cloud For instance mammals in lump cloud 2 are associated with grass and root-zone pathways while species in cloud 3 are associated with ecotones and open spaces The greater incidence of species in cloud 3 in the temperate forest then in the grasslands could serve to predict that certain structural types (trees and shrubs associated with multi-level habitat usage) are more prevalent in the former region than in the latter

Chapter Summary

In this chapter I have focused on landscape structure in its relation to landscape classification (both traditional and novel), to pattern matching between lump structures of different systems and to animal use of habitat I have found broad similarities of landscape structure within traditional landcover classes such as biomes However three observations suggest that too little is known or measured about landscape structure to safely assume that we can define it and link it to animal behavior First, there is sufficient inter-site variability in landscape structure reported at small scales to question the assumption that traditional landscape designations reliably connote structural similarity between sites Second both the traditional classification schemes and the one I introduced do not rigorously survey or measure meso- and macro-scale structures. Third, very little is known about what structures are important in animal behavioral decisions and survival

Within the limitations of the landscape structural classifications available, I found strong support for the Textural-Discontinuity hypothesis prediction that the degree of matching between lump patterns of different systems correlates closely with differences in landscape structural complexity. Further, I found modest but consistent support for the H6 prediction that lump pattern, or membership in lumps, has power to predict the scale at which mammals exploit landscape structure. Overall, H6 has resisted disproof in tests of lump pattern commonality within systems (Chapter 3), between systems (Chapter 4), and in tests linking lump pattern to landscape structure and to its use (Chapter 4). All non landscape hypotheses (H1 - H5) are implicitly challenged by these observations. In the following chapter, I probe these challenges further.

CHAPTER 5
TESTS OF NON-LANDSCAPE EXPLANATIONS OF LUMP PATTERN

Introduction

The prevailing paradigm of a Continuous World has been increasingly challenged by mounting evidence of a Discontinuous World, an environment marked by discontinuities in space/time behaviors and distributions of ecological processes. The broad focus of this work has been to test animal size distributions for discontinuities as evidence of a Discontinuous World, and, thus far, a landscape-based hypothesis has provided the most compelling explanation of lumpy animal morphologies. Though I have demonstrated consistent trends linking landscape features, such as structural complexity, and discontinuous animal morphologies, that weakens but does not eliminate any other explanation.

Another possibility is that the complexity of process interactions inherent at large scales of landscapes or biomes may involve not one but multiple explanations which emerge from both world views. The soundest approach to such interwoven or co-dependent explanations is not to try to wrest the mantle of authority in one direction or the other. Rather, one must embrace this uncertainty as a whole, unraveling the different threads simultaneously so as to see how much each might contribute to a robust, overall explanation (Wiens 1984, Marples, in submission).

In this study I have demonstrated that lumpy pattern at several scales can be used to test the predictions of non-landscape hypotheses (H1 - H5). I have shown lump pattern at the scale of landscape study sites in a wide variety of biomes, I have demonstrated internal consistency of lump pattern (commonality) between sites of similar structure (Chapter 3), and I have demonstrated in comparisons between landscape sites that the degree of lump pattern matching erodes at a rate proportional to the degree of structural difference (Chapter 4). This chapter is devoted to testing how well non-landscape hypotheses (H1 - H5) predict the lump patterns demonstrated in chapters 3 and 4.

In this section I revisit the manner in which non-landscape hypotheses H1 - H5 predict discontinuous body size distributions. I review the results of previous tests of these hypotheses and describe basis for the new tests I shall apply.

Predictions of Lump Pattern Made By Continuous World Models

To varying extents all organismal or non-landscape hypotheses are challenged if there are similarities in lump pattern associated with similarities in landscape pattern. The Competitive Niche and Size Displacement (H1) hypothesis does not predict lump pattern at the scale of an entire animal community because such evenness of body size spacing is the antithesis of discontinuous size patterns in animal communities (gaps separating size clusters). Finding similar lump patterns in similar landscapes does not fundamentally refute the Macro-Phylogeny (H2), Noah's Ark (H3), Limited Morph (H4) or the Trophic Trough (H5) hypotheses, but one must demonstrate a link between lumpy body size patterns and the criteria used by each hypothesis. For example, when comparing animal communities, lump pattern similarities must be linked with similarities of taxonomic composition at the finest levels (species or genera) (H3) or higher levels (family, order) (H2) or with similar distribution patterns of locomotory modes (H4) or trophic categories (H5). These possibilities become testable when expressed as predictions. I present these predictions as explanations of the frequent findings (Chapters 3 and 4) of similarities in lump structures. For each hypothesis I state its prediction and discuss its implications for testing.

H1. Competitive Niche and Size Displacement

Prediction. *Animal morphological sizes are spaced apart on the size axis with a greater degree of evenness than expected by chance. Similarities in lump structure between ecosystem sites result from similarities in patterns of competitive interaction.*

This prediction has been used to demonstrate at the sub-community level the effects of within-guild competition on such taxa as heteromyid rodents (Brown 1975). At the level of all species and all guilds within an entire animal community, evenness of spacing between species' body sizes appears more likely to fill gaps or discontinuities rather than create them. At community level H1 appears to predict the opposite of lumpiness, and all demonstrations of lumpiness thus far are disproof of these predictions. However, perhaps such spacing occurs at sub-community levels, such as within groups of species of relatively similar body size (lumps). If such were the case, lump structure at the whole community level might be partly a product of spacing of body sizes within each lump. The regularities of even spacing within each lump might make the discontinuities between lumps stand out more clearly.

This interpretation of the Competitive Niche and Size Displacement hypothesis predicts that the lump structure of each landscape study site and the similarities between site data sets are partly due to even size spacing within lumps. Such an explanation does not necessarily challenge the

Textural-Discontinuity hypothesis, for competition between species within lumps may be based on the ability to exploit landscape structure within a limited range of scales If such proves to be the case, then H1 embellishes H6's explanation of lump structure at the sub-community level of lumps

H2. Macro-Phylogeny

Prediction *Similarities in lump structure between landscape study sites result from similarities in macro-scale taxonomic composition (families, orders)*

The Macro-Phylogeny hypothesis posits that phylogenetic pattern influences lump pattern, but as a combination of evolutionary and community organization processes If a limited number of ancestral forms radiated in size to a limited extent, then each radiation might comprise a region of higher density in a size distribution Therefore, limited phenotypic radiation in evolution results in a continuous size distribution around a common ancestor However, if we look at the aggregate picture of all these separate continuous size distribution associated with different ancestors we find a discontinuous size distribution. That is to say that the net result of parallel radiations from a limited set of common ancestors is a discontinuous size distribution with some regions much denser in species than others. These regions of higher species density (modes) might each be associated with broad patterns of phylogeny (macro-phylogeny) at the level of taxonomic Orders or Families As each ecological community organizes, species selected at random from this multi-modal size distribution are more likely to be drawn from the denser regions

Therefore, macro-phylogeny is associated with broad size distribution patterns which constrain the zones where lumps may occur as they form during community organization However, H3 does not explain the occurrence of each gap between lumps at the landscape level, it focuses on the likelihood of finding clusters of lumps in certain portions of the size range

H3. Noah's Ark

Prediction *Similarities in lump structure between ecosystem sites result from similarities in taxonomic composition at the level of species, and genera*

The Noah's Ark ("Urtier" *sensu* Holling 1992) hypothesis posits that gaps do not emerge, they remain in size distributions because of constraints on evolutionary possibilities for a limited set of ancestral forms These limitations constrain size variability even at narrow (species or genus) evolutionary levels to the extent that gaps are not or have yet to be filled in size distributions compiled for mean species body masses. Therefore, H3 predicts that lump pattern similarities stem from taxonomic similarities at the level of species or genus between landscape study sites

H4. Limited Morph

Prediction *Similarities in lump structure between landscape study sites result from similarities in locomotory modes of species in each lump.*

In a world with a limited number of media (air, water, earth) and surfaces (land, vegetation, water), perhaps only a limited number of locomotory modes and structural designs are competitive For example, predation in the air can be accomplished by a limited set of modes such as soaring, hovering and quick strikes from perches Terrestrial terrain can be exploited by a limited set of modes such as leaping, crawling, running, climbing digging, burrowing. Each mode of exploiting the air or ground is possible from a specific wing and body morphology, so the Limited Morph hypothesis suggests that a small set of body sizes arises from the limited set of modes for exploiting the air or ground. H4 posits that lump structure should predict the locations on the size axis of clusters of species of the same locomotory category.

H5. Trophic Trough

Prediction. *Similarities in lump structure between landscape study sites result from similarities in trophic structure. Individual lumps or groups of lumps will have higher frequencies of one trophic category than another.*

If qualitative size differences characterize participants in trophic interactions, then these differences might be associated with the discontinuities in size distributions which identify transitions between trophic levels. Lump structure pattern should predict the locations on the size axis of clusters of trophic categories of one type.

Previous Tests of Non-Landscape Hypotheses

Predictions about lumpy size distributions made by non-landscape hypotheses have generally failed to resist disproof. Holling's (1992) comparisons of lump structures of different taxa in different landscapes challenged predictions made by the Noah's Ark, Trophic Trough and Limited Morph hypotheses. Specifically, finding different lump patterns (in terms of location and number of lumps) for the same taxon in different landscapes challenges the prediction by the Noah's Ark hypothesis that similar ancestry should produce similar lump structures regardless of the landscape. A further challenge to this hypothesis arises with the observation of similar lump structures for different taxa in the same landscape. The radically different ancestry of birds and mammals should not produce similar lump patterns for both taxa. Holling's (1992) finding of similar lump structures for different trophic classes (herbivore/omnivores vs. carnivores) of the same taxa challenges the Trophic Trough hypothesis. Finally, the finding of similar lump patterns in the same landscape for different taxa, birds and mammals challenges the Limited Morph hypothesis

One avenue of inquiry based on the Continuous World Model has continued to use evidence of size dispersion along a continuous size axis as evidence supporting the Competitive Niche and Size Displacement Hypothesis. A broad front of research has found evidence for over-dispersion of animal morphometries in the body sizes of granivorous desert rodents (Brown 1973, 1975, Bowers and Brown 1982, Price and Brown 1983), bill lengths of birds (Schoener 1983, Moulton and Lockwood 1992, Moulton 1993). H1 has never been tested as a predictor of lump structure.

Summary: New probes of continuous world hypotheses

Previous work has tested organismal explanations of animal community morphometry only at the landscape and biome scales in a limited set of landscapes (mostly boreal forest and prairie in North America). In this study I test predictions of lump structure over a wider variety of landscapes and over a broader set of scales (landscape, biome, global). I will use statistical tests to probe more rigorously the qualitative inferences (Holling 1992) that there is little if any relationship between lump structure and membership in various non-landscape categories. I test each hypothesis in the order I introduced them.

Tests of the Competitive Niche and Size Displacement Hypothesis

Over-dispersion of body sizes has been found at sub-community levels, groups or guilds within a community, (Brown 1973, 1975, Bowers and Brown 1982, Price and Brown 1983), Schoener 1982, Moulton and Lockwood 1992, Moulton 1993) and has been cited as evidence of competition. This pattern has been tested at the guild level within a community using a relatively coarse definition of size distributions (size differences between members of a guild) Craig Allen suggested a test of this pattern at a higher level which incorporates all guilds in an animal community, namely, all members of one taxon in a community, and uses a finer definition of size distribution (size differences between species within lumps in the community size distribution) In collaboration with Dr Allen I pooled animal body mass data sets and wrote computer programs to statistically simulate random body size dispersion within body size lumps. I now describe the data sources and detection methods for tests at both these scales

Methods and Sources of Data

I collected mammal, bird and herp data sets of body sizes from sites with reliable, comprehensive species lists I took body mass values for birds and mammals from a source most proximate to each study site, either from studies in the literature or from global compendia (Dunning, 1990, Silva and Downing, 1995) I selected twenty-one sites from six different biomes (Table 5 -1) in the western hemisphere: boreal forest; temperate desert, forest, moist mid-grass prairie and seasonally wet prairie, and neotropical forest

Description of study sites

The 21 sites from which 32 animal data sets were assembled have sufficient size (study areas ranging from hundreds to thousands of hectares) and study history to provide reliable descriptions of animal communities over the past few decades These study sites exhibit a broad range of configurations of landscape structure and climate-related parameters such as rainfall, temperature, incident solar radiation, and evapo-transpiration The diversity of climate parameters and landscape structures tests the generality of animal morphometric pattern over a range of environmental contexts

Table 5-1 Data sources for tests of the Competitive Niche Displacement Hypothesis Locations of animal data sets are given by taxon and number of species related to each study site in six different biomes in the western hemisphere

Bio-geographic Unit			*Number of Species in each Taxon at each site*		
Climatic Zone	*Ecosystem*	*Site Name*	*Birds*	*Mammals*	*Herps*
Temperate	Wet Savannah	South Florida	113	27	30
	Forest	Itasca	73	46	
		Savannah River	80	46	
		Mountain Lake Bio Station	75		
	Prairie	Badlands	26	28	
		Bison	66	22	
		Cottonwood		46	
		Konza	106	39	
	Desert	Bryce		31	
		Canyonlands		29	
		Capitol Reef		39	
		Organ Pipe		28	
		Zion		36	
Boreal	Forest	Doré Lake	129	42	
		New Brunswick	100	36	
		Nopiming	126	42	
		Taiga Bio Sta	84	43	
Neotropical	Forest	Concepcion	39		
		French Guiana	112		
		La Selva		48	
		Lacandona		46	
		Manu Nat Park		63	

Statistical Approaches

I analyzed the data in four stages. First, I used Lump (GaP) Analysis (Chapter 2, Restrepo et al. 1997) to determine the "coarse" body size pattern, the distribution of lumps, in each observed data set. This established a set of lumps for each observed data set, and the number of species(n), the range of body masses, and the body mass of each species within each lump. Second, I measured the spacing between the species within a lump (segment length) by calculating the size differences between neighboring species. I calculated the variance in size differences within each lump to derive an index of the evenness of spacing; high variance connotes little evenness. Third, I used statistical simulation to synthesize a set of mock lumps of identical n and size range as found in the observed lumps, but with the body masses of the species selected at random within the size range. The size distributions within the mock lumps therefore represent a random null against which to compare the distributions within the observed lumps. I then calculated the variance of size spacing between neighboring species in these mock lumps. In the fourth stage I tested the difference between the indices of evenness I found in observed and mock lumps.

Stage one: lump analysis - detection of coarse body patterns

I sorted body mass data for each taxon at each site in ascending order and analyzed for significant discontinuities using GaP Pattern Analysis (Chapter 2). I normalized mass data by taking the logarithmic transform. For each data set a unimodal kernel estimate of the observed data provided a continuous null distribution with the same n and range of body masses as those in the observed data set. This continuous null model helps establish the criterion size range of discontinuities detectable if no gaps exist in the underlying size distribution. Discontinuities larger than the criterion found in analyzing the observed data are deemed "significant." Employing a conservative estimate of effect size (0.2) Type II error was minimized by keeping statistical power within the range of 0.45 to 0.6 (Lipsey, 1990) when estimating the significance threshold for gaps in each data set. Constant power made comparable analysis of all data sets possible regardless of species number (*n*).

Stage two: fine pattern: evenness in species size spacing within lumps

I calculated the size spacing between species within each observed lump (segment length along the size axis) by subtracting the log10 body mass of the *n*th species from that of species *n*+1. I quantified evenness of spacing by calculating the variance of segment lengths within the lump.

Stage three, statistical simulation

For each run I created a mock lump, with *n* and the range of log10 body masses identical to that of the observed lump, by drawing at random *n* times from a uniform distribution, which served as a neutral model for the species pool. Analysis of actual distributions within lumps demonstrated that these distributions are uniform. Furthermore, for any given site it is impossible to ascertain the potential species pool for the entire community, but I conservatively assumed that the size distribution is approximately normal. For relatively small subsets, such as lumps, within that Gaussian community size distribution, the most conservative neutral model against which to test observed distributions is a uniform distribution.

I removed two sources of bias in calculations of variance from the statistical simulation model. Rounding error, such as excessive rounding and differences in the degree of rounding between observed and mock log10 body mass data, was eliminated by rounding all data to three places prior to any calculations. Similarly, I avoided the potential for exaggerated variation in estimates of variance in small lump populations ($n < 5$) by analyzing only those lumps with n greater than 5 Of the 170 lumps occurring in 33 data sets I rejected 27 lumps by this criterion. Since the body masses of the smallest and largest species in each lump are fixed during each simulation run, the species between the ends are the only body masses drawn at random I adopted a conservative protocol that the number of simulated body masses would always exceed the number (2) held fixed

I took special precautions to simulate only the segment length variance between species within lumps Segment length variance exists at the level of the entire animal community and is generated by the major discontinuities or gaps which separate lumps This community-level variance was segregated out during simulations by rejecting any segment lengths which approached the size of the gaps on either side of the lump That is , those segment lengths which exceeded the mean of gap segment lengths defining the ends of the lump Such mean gap sizes were reasonable approximations given that gaps on either side of a lump did not differ greatly in size

Within each mock lump the size spacing between species ("segment length" along the size axis) was calculated by subtracting the log10 body mass of the nth species from that of species n+1 Evenness of spacing was quantified by examining the variance of segment lengths within the lump Probabilities of observed variances occurring by chance were determined from statistical simulation For each lump 1000 simulation runs generated a distribution of mock variances The rank of the observed variance in that distribution of mock variances approximated the p-value of the lump's segment length variance.

Stage 4. Meta-Analysis

Difficulties inherent in field conditions can erode the precision with which animal body masses are determined and introduce variability in animal body mass size data sets. At the coarse, community level of gaps separating lumps, GaP analysis appears robust because the size of discontinuities in vertebrate community body mass data exceed the observed size variation in species mass estimates for 80 percent of boreal prairie birds and all boreal prairie mammals (Appendix A). However, at the finer, within-lump, scale the sources of variation in size estimates due to sampling error make it less likely to find any constancy or evenness of ratios of body sizes, especially at a significance level less than 0.50.

Given the likelihood of distortions introduced by sampling error, detecting meaningful trends required that the scope of investigation be broadened through meta-analysis. Pattern at several levels (overall, within taxon, within biome) was examined using binomial tests as follows. If observed size variances occur at random, I'd expect the frequency distribution of variances to be normal with a mean at 0.5. I created this normally distributed frequency distribution of variances through computer simulation. The observed variance in segment lengths could fall into one of two conditions with respect to the distribution of mock variances generated by simulation, ranked either above the 50 percent rank or below it. With the expectation that random variance would generate near equal numbers of both conditions, I applied the binomial test. Significant numbers of occurrences below the 50 percent rank indicate greater evenness of spacing than expected by chance. The probabilities that the ratio of occurrences above 50 percent to occurrences below might occur at random is generated by the binomial test

Results - Where is Over-dispersion of Sizes Found?

Tests for bias in simulation output

I derived probability values of observed variances occurring at random by ranking them in null distributions of variance Considering all taxa no correlation between species number and probability value was evident (Figure 5-1a) Quite similar curve fit patterns with near-flat regression lines were also found for birds and mammals alone

Tests for uniformity of size distribution within lumps

If species sizes tend to cluster with consistency toward some portion of the size axis within each lump, segment length variance could still be significantly low No size clustering by species within lumps is evident Regression of normalized segment length on normalized relative position within the lump shows no significant trend either for all taxa ((Figure 5-1b)) or for mammals or birds separately

Simulated and observed trends in segment length variance within lumps

Observed segment length variance had a strong tendency to be ranked in the lower half of variance distributions generated by simulation. This is evident (Figure 5-2) in the left-skew of the distribution of rankings for observed segment length variance The distribution of variances expected from a uniform distribution of segment lengths highlights this trend

Binomial test for over-dispersion of segment lengths within lumps

Seventy-four percent of all lumps (106 out of 143) from all sites had variances ranked in the lower half of the null distribution. The chances of such a majority occurring in the low range by random chance are minuscule ($p < 1.6$ E-08) as indicated by the binomial test (Table 5-2) Similar majorities

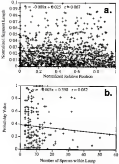


Figure 5-1 Regression of (a) normalized values of within-lump inter-species size differences (segment length) on within-lump position of a species relative to the edge of the lump and (b) rankings of within-lump inter-species size variances relative to 1000 simulated size variances (probability value) against the number of species within the lump.

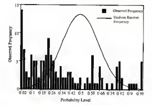


Figure 5-2. Observed frequency distribution of variances in segment lengths or inter-species size differences within lumps in herp mammal and bird data sets compared to a hypothetical normal distribution created when inter-species size differences occur with uniform random frequency

with tiny probabilities are evident for summary binomial tests for each taxon (mammals, birds) and each biome (temperate, boreal, neotropical) When I applied the binomial test to lump sums within each biome, a majority (7 out of 10) had significant p-values Mammal lump data sets, particularly in the neotropical forest and temperate desert and prairie sites, exhibited the lowest variances. Only half the bird lump data sets (boreal forest, temperate prairie) showed significantly low variance at the biome level The sample of herp lumps from South Florida is too small ($n = 6$) to reasonably expect a significant result with the binomial test. Considering each lump separately, sixteen percent (23 out of 143) of all lumps showed low variance of segment lengths at the 0 05 significance level

Table 5-2 Rankings of observed variances of segment lengths within lumps (number of species > 5) within distributions of segment length variances from sets of mock lumps creating by 1000 random draws from uniform random size distribution with the same size ranges as observed lumps

Taxon	Biome	Ecosystem	Number of lumps w/ rank < 50	Mean Rank as a Proportion	Number of lumps w/ rank > 50	Mean Rank as a Proportion	Binomial Probability
Herps	Temperate	Wet Prairie	4	21.1	2	58.5	0.234
Mammals	Temperate	Desert	17	15.6	2	76.5	< 0.001
		Forest	7	15.4	3	63.3	0.117
		Prairie	10	18.1	2	62.5	0.016
	Boreal	Forest	10	18.6	0	0.0	< 0.001
	Neotrop	Forest	12	24.6	3	63.7	0.014
Summary for All Mammals			56	18.7	10	0.0	< 0.001
Birds	Temperate	Forest	16	21.1	11	76.3	0.097
		Prairie	7	11.4	1	85.0	0.044
	Boreal	Forest	13	20.6	5	77.6	0.033
	Neotrop	Forest	9	16.6	7	68.3	0.175
Summary for All Birds			45	17.8	24	73.0	0.004
Summary for all Temperate Sites			61	17.57	21	70.35	< 0.001
Summary for all Boreal Sites			23	16.66	5	77.6	< 0.001
Summary for all Neotropical Sites			21	20.69	10	74.50	0.021
Summary for all sites			105	18.31	36	74.15	< 0.001

Results - Summary

Animal body mass data sets exhibit over-dispersion of mean adult sizes within the size ranges of lumps not within entire communities. I found that observed within-lump segment lengths exhibited much lower variance in a majority of lump data sets, whether sorted by taxon or biome, when ranked against segment length variances derived from lumps created from uniform size distributions. Probability values lower than 0.001 from bi-nomial tests firmly support the conclusion that size spacing within lumps is more even than expected by chance.

Size spacing between species within an entire community is not more even than expected by chance. When I applied the same procedure to animal community body size data sets as a whole in not one case did observed segment lengths exhibit lower variance than simulated segment lengths

Discussion - Implications of Over-dispersion of Sizes

These results challenge the Competitive Niche and Size Displacement Hypothesis at community level body size distributions but support it at the narrower level of lumps Previous tests (Brown 1973, 1975, Bowers and Brown 1982, Price and Brown 1983, Schoener 1982, 1983, Moulton and Lockwood 1992, Moulton 1993) have found confirmation for H1 at the level of sub-groups within a community, however, no previous test has been applied to all species within a taxon of a community Following the predictions of H1, lack of even size spacing community-wide suggests that competition is not operating equally for all species within a community across all scales Rather competition appears to operate between species within lumps, evening the spacing of body sizes through character displacement.

The proposition that competition occurs between species within lumps does not necessarily contradict the predictions of the Textural Discontinuity hypothesis H6. One interpretation of H6 might explain the evolution of lumps through the selection for body sizes within size ranges which are competitive over limited range of spatial scale Another interpretation of the Textural Discontinuity hypothesis might explain lumps as the result of species sorting during community organization Either interpretation is based on the competitiveness of body size in the exploitation of landscape structure at specific scales H6 would be undermined if it can be shown that competition between species within-lumps is not related to exploitation of spatial structure. One example might be if species competed for a food source with a spatial distribution which does not vary across scales.

Summary - Competition Most Likely Within Lumps

I observe morphological over-dispersion in lumps of birds, mammals and herps and not at the level of the entire community. I conclude that H1 is disproved at the level of animal communities and supported at sub-community levels (lumps), and that inter-specific competition is most likely occurring at the spatial scale exploited by species in a lump. The possibility remains untested that over-dispersion of body sizes at sub-community levels, within lumps, might reinforce detection of discontinuities (and therefore lumps) within community level size patterns. I now test the predictions of the remaining organism-based explanations of lump structure.

Tests of Macro-Phylogeny, Trophic Trough and Limited Morph Hypotheses

Previous tests (Holling 1992) have challenged H3, H4, and H5 based on comparisons of lump patterns found in body size data sets of different taxa, trophic levels, or body plans. Such qualitative inference is a robust challenge which is extremely helpful in prioritizing different avenues of inquiry in early exploratory research. In this section I try to test more rigorously these initial challenges of non-landscape hypotheses. In animal community body size data sets I examine patterns of membership in any of the categories specified in H3, H4, and H5 and test their degree of association with patterns of lump membership. That is to say I test the prediction that body sizes cluster in similar ways to clusters of phylogenetic, locomotory, or trophic classes. I now describe the data sources and statistical methods I employed

Methods

Sources of animal body size data

I selected 20 mammal body mass data sets compiled from literature and research station reports for sites in 7 biomes (Table 5-3)

Table 5-3 Locations of study sites from which species lists were used as sources for body mass data sets used in Chi-Square tests of the Macro-Phylogeny, Trophic Troph and Limited Morph Hypotheses.

No	Biome	Continent	Jurisdiction	Site Name
1	Tundra	N America	Canada	Kluane
2				N Yukon N.P
3	Boreal Forest	N America	New Brunswick	Green River
4			Saskatchewan	Prince Albert N P
5			Manitoba	Taiga Bio Station
6	Temperate Forest	N America	Minnesota	Itasca State Park
7			Florida	Katherine Ordway Preserve
8			Wyoming	Yellowstone N P
9	Temperate Desert	N America		Capitol Reef N P
10			California	Death Valley N P
11				Organ Pipe N P
12	Temperate Prairie	N America	South Dakota	Badlands N P
13			Montana	Bison
14			Kansas	Konza Preserve
15	Grasslands	Africa	Kenya	Amboseli
16				Ihema
17			S. Africa	Golden Gate N.P
18	Neotropical Lowland Rainforest	S America	Brazil	Belem
19			Peru	Manu N.P
20		C America	Costa Rica	La Selva

Definitions of niche, taxonomic and lump membership categories

In each data set I assigned each species a set of seven different numbers corresponding to membership in the following categories lumps, niche (trophic and locomotory) and phylogenetic. I arbitrarily assigned a number to each mammalian order and family and applied these phylogenetic indices to each species in each data set. I assigned numbers corresponding to niche categories as follows. It is frequently the case that species within a genus share the same niche requirements in terms of diet or locomotory mode (J. Eisenberg, pers. comm.). Therefore, I classified 585 mammal genera according to niche requirements following the scheme of Eisenberg (1981) (Appendix G). This scheme provides a numeric index for "trophic strategy" or means of procuring food, such as carnivore, granivore, frugivore and "substrate" or locomotory mode, such as terrestrial, fossorial, scansorial, for mammals. I applied these niche indices to each species in the data sets.

I sorted lumps in ascending order(1, 2, 3 ... N). Each species received a number signifying the size rank of the lump in which it is a member. For instance, each species in the lump ranked third largest from the bottom (smallest) of the size order would receive the number 3. Since the number of lumps found by Lump (GaP) Analysis varies with statistical power, I tested the sensitivity of this analysis to the statistical power level used in Lump Analysis. I analyzed each data set three times for lump pattern, each time using a different level of power. The three different power levels were about 0.4, 0.5, and 0.6, respectively. I gave each species three lump numbers corresponding to their lump membership as interpreted under three different statistical power scenarios.

Statistical Methods

To derive expected values for each of the categories within a data set, I calculated the proportions which each niche or taxonomic category represented in that mammal data set. If categories are randomly distributed in a data set, I would expect the same proportional representation within a lump as within the entire data set. I compared these expected values against observed proportions in each lump using a Chi-Square test. Following Chi-

Square protocols I eliminated considerable numbers of lump data prior to the test because the category in question did not occur more than four times in that data set (see "non-testable cases" category shown in Table 5-4).

In such a test the null hypothesis posits that there is a random association between lump pattern (membership in a particular lump) and category pattern (membership in a particular category). Within each lump for each niche or phylogenetic category the test returned a value which represented the probability value associated with rejection of the null. I designated all findings with a probability value equal to or lower than 0.05 as a significant departure from the expected, thereby allowing me to reject the null. For each category I report the number of significant and non-significant findings overall as well as the number of instances where the number of significant findings increased, decreased or did not change as a result of increasing statistical power in determining the number of lumps in Lump Analysis.

Results - Chi-Square Tests

All categories except taxonomic order appear to be randomly related to patterns of lump membership in a majority of cases as evident in the rates at which I fail to reject the null hypothesis (Table 5-4). The failure to reject rate (entitled "Significant Findings" in Table 5-4) is 49, 56, 81 and 69 percent of all testable observations of the order, family, substrate and food categories, respectively. These findings show some sensitivity to the statistical power level used in Lump Analysis. Only in a minority (mean = 23.75 percent of

Table 5-4 Chi square tests of non-random association between membership in lumps and phylogenetic or niche categories of mammals.

Item Description	*Phylogeny*		*Niche Status*	
	Order	*Family*	*Substrate*	*Food*
Tests of All Categories at one level of statistical power				
Total Observations Possible	116	302	109	146
Percent of total possible observations				
Testable Cases. Categories with > 4 Observations	61	26	49	67
Non-testable cases Categories with < 4 Observations	39	74	51	33
Significant Findings	51	44	19	31
Non Significant Findings	49	56	81	69
Tests of influence of statistical power				
Total Observations Possible	24	29	6	28
Percent of total possible observations				
Significant findings increase as power increased	9	31	25	31
Significant findings decrease as power increased	29	14	12	17
No change in significant findings as power increased	67	56	63	52

testable observations) do the numbers of significant findings increase as power increases In a majority of testable observations I find no change or a decrease in the number of significant findings as I increase power Therefore, only in a minority of cases might the rejection of the null increase as a result of a different level of statistical power, and even in these cases the rejection rate does not increase dramatically

Discussion

These results undermine the Trophic Troph and Limited Morph hypotheses In a clear majority of cases associations between categories of lump membership and those of trophic or locomotory mode appear random I find the least support for the locomotory mode category, but trophic classes fare scarcely better, appearing randomly associated with lumps almost 70 percent of time. Other tests of the Trophic Trough and Limited Morph hypotheses (Holling 1992) aggregated the number of categories to far fewer numbers than the ones employed here. For example, Holling utilized only two (carnivore and herbivore/omnivore) trophic categories as opposed to sixteen, and two locomotory modes (volant and nonvolant terrestrial) as opposed to eight(Appendix 6). The degree to which my use of a more diverse group of categories increases the chances of finding non-significant results in a Chi-Square test remains to be tested.

The case for The Macro-Phylogeny (H2) hypothesis is more equivocal, in roughly half of the tests I could reject the null hypothesis. While traditional preoccupation with Type I error would caste this result as complete rejection of H2, broader standards which try to account for Type II might interpret this as a 'mild' rejection. As such it does not decisively topple the suspicion that lump pattern is the product of multiple causes which include phylogeny as well as landscape structure. Macro-scale phylogenetic patterns may contribute broad, almost cryptic, influences on lump membership. I find the highest rejection rate for the null when testing taxonomic order, so it appears to be the right level of the taxonomic hierarchy to seek morphological associations akin to the limited radiation of an ancestral form.

Summary

The Limited Morph and Trophic Trough hypotheses failed to resist disproof at the micro-scale of lumps. However, patterns of taxonomic at high levels (Family and Order) show a weak but intriguing affinity for lumps at this grain resolution of lump pattern. I shall now test the power of narrow (Noah's Ark) and broad (Macro-Phylogeny) patterns of taxonomy in non-landscape hypotheses to predict lump pattern at scales larger than individual animal communities lump pattern commonality within-biomes, super-biomes and at para-global scales

Tests of Noah's Ark and Macro-Phylogeny Hypotheses at Different Scales

The repeated finding of lump pattern commonality which is unique to a particular landscape (such as a biome) challenges the Noah's Ark (H3) hypothesis If limited evolution from a small number of ancestral forms is responsible for gaps in the size distribution, then most lump structures, irrespective of landscape structure should be relatively similar in that they share ancestry Holling's (1992) finding of lump structures unique to the boreal forest and to the boreal prairie clearly undermines Noah's Ark My finding of lump pattern commonality within biomes or "biome signatures" (Chapter 3), lump patterns unique to each of some 12 biomes, makes a more general case for this challenge. However, H3 also predicts that such inter-site pattern similarity within biomes stems from taxonomic similarity at the species or genus level. That is to say that community level lump structure, the location of lumps and gaps, relates to lower level patterns of taxonomy Therefore, Noah's Ark (H3) predicts that an index of lump pattern similarity should correlate with an index of species similarity, and that is how I will test H3 in this section

The Macro-Phylogeny hypothesis (H2) posits that lump pattern similarities arise from macro-scale patterns in animal size distributions This prediction does not focus on individual discontinuities but tries to account for why lumps are found in certain size ranges. In Chapter 3 I identified broad patterns (Figures 3-19 and 3-20) in mammal lump structures where clusters of lumps are more commonly found In this chapter I compare these broad lump and body size patterns as a test of H2

In this section I test predictions of Noah's Ark (H3) and Macro-Phylogeny (H2) over a variety of landscape types and scales. I shall first test H3 by correlating taxonomic similarity indices with measures of lump pattern similarity between landscapes of similar type (commonality). I now discuss data sources and methods for calculating taxonomic similarity.

Tests of H3: Taxonomic Similarity and Lump Pattern Commonality

I assembled lists of mammal genera and species for all landscape study sites which I examined in Chapter 3 for lump pattern commonality both within-biomes and within-super-biomes. Within each biome and super-biome I measured Sorenson's Index of Similarity (5.1) for species and for genera for every matching pair of study site species lists within that spatial extent.

$$I = (2 * sp_c)/(sp_a + sp_b) \qquad (5.1)$$

Where sp_a = Number of species or genera in Site a,

sp_b = Number of species or genera in Site b, and

sp_c = Number of species or genera common to Sites a and b,

I tested the Noah's Ark hypothesis H3 by correlating similarity index values with indices of lump pattern commonality. At both spatial extents and both taxonomic resolutions (species and genus) I found no significance in the relationship between lower level taxonomy and lump pattern commonality (Figure 5-3).

Overall, this test undermines the Noah's Ark hypothesis. Despite numerous graphic observations in Chapter 3 of expectedly strong correlations between high taxonomic similarity and lump commonality, this trend is

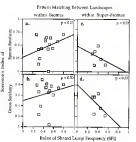


Figure 5-3 Correlations of Sorenson's index of similarity for species (a & c) and genuses (b & d) for pairs of biomes (a & b) and super-biomes (c & d) on indices of pattern correspondence between different systems (biomes or super-biomes), the index of Shared Lump Frequency (SFI). All correlations are not significant (probability values indicated in the upper right hand corner)

vitiated by similar frequencies of reverse or mirror trends, high commonality / low taxonomic similarity and low commonality/high taxonomic similarity. This leaves only broad patterns of size associated with higher level taxonomic categories (Family or Order) as possible predictors of lump pattern.

A Test of Macro-Phylogeny (H2) at Para Global Scales

The Macro-Phylogeny (H2) hypothesis predicts that patterns of similarity in lump structure correlate with broad patterns of animal size associated with taxonomy at the Order or Family levels. In this chapter I used a chi-square test to identify Order as the taxonomic level most closely associated with lump pattern. In Chapter 3 I demonstrated patterns of lump commonality for mammals at the para-global level. I tested the prediction of the Macro-Phylogeny hypothesis by comparing these two broad patterns: lump commonality at para-global scales and size distributions compiled at the level of mammal orders. I randomly sampled the mean adult body masses of 100 randomly selected species of each of the seven most speciose mammalian orders to create an estimate of the size distribution of each order. I then graphically compared both broad lump and taxonomic patterns by juxtaposing the zones of highest lump pattern commonality with each mammal order's size distribution (Figure 5-4).

Results

Every one of this subset of mammal orders has size frequency peaks associated with one (two in the case of Marsupials) of the zones of para-global lump commonality. This correspondence between broad patterns of taxonomy and lump structure becomes even clearer when I aggregate mean adult body masses of all 7 mammal orders into one size distribution and overlay the pattern of common lump zones (Figure 5-5). A size distribution based on mammal order appears bi-model, with a hint of tri-modality, which largely intersects zones of para-global lump commonality.

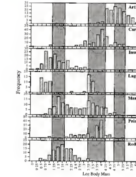


Figure 5-4. Frequency distributions of mean adult body masses of species drawn at random from Silva and Downing(1995) from 7 mammal orders Light gray zones indicate areas of highest matching between lump structures of different mammal communities

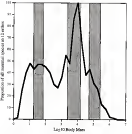


Figure 5-5 Frequency distribution of mean adult body masses expressed as proportion of all species in 12 mammalian orders. Light gray bands identify size ranges where most lump pattern overlap is observed in pattern matches of pairs of mammal super-biomes.

Summary -

The Macro-Phylogeny hypotheses (H2) gains support from distinct overlap between broad patterns of taxonomy (mammalian order) and lump structure (para-global lump pattern). While H2 does not focus on community level lump pattern (the locations of individual gaps and lumps at the landscape level), it does appear to predict the general zones where clusters of lumps are located on the size axis.

Tests of Trophic Trough Hypothesis

Previous comparisons (Eisenberg 1981) of nonvolant terrestrial mammal communities on different continents graphically suggest some degree of discontinuity in the size distributions of some eight trophic categories Holling (1992) found similarities in the patterns of discontinuities in the size distributions of two coarse trophic groupings (carnivores vs herbivore/omnivores) of boreal prairie mammal communities Both categories were present in each lump Finding very similar representation of either trophic category across all the lumps challenges the prediction (H5) that differences in trophic status displace body sizes and create discontinuities in the size distribution.

The generality of this challenge to the Trophic Trough hypothesis would be confirmed by finding similarities in lump patterns for trophic categories in biomes other than the boreal prairie In this section I apply similar tests to nonvolant terrestrial mammal data compiled from six biomes I now describe these data sources and the methods of examining differences of pattern in trophic size distributions

Sources of animal body size data

I assembled species size data at the biome level by compiling body mass data from all landscape study sites I had assembled for a biome and removing redundant species I then separated each biome species assemblage into two trophic groups carnivores and herbivore/omnivores I overlaid graphs of frequency distributions of both trophic categories for each biome

Results - Biome Comparisons of Body Size Distributions of Trophic Levels

Frequency distributions of body mass for carnivores vs herbivore/omnivores overlap along almost the entire range of the size axis (Figure 5-6). The only exception is that log10 body masses of herbivore/omnivores usually extend beyond 5.0, whereas those of carnivores do not. The size distributions of either trophic category do not exhibit any tendency to aggregate exclusively along any part of the size axis.

Discussion

These results give a broad explanation for the general observation (Sendzimir, unpublished data) that carnivores and herbivore/omnivores are mutually present in almost all lumps in data sets. This outcome is likely if the size distributions of both trophic categories span the entire size axis. What remains unclear is why the lump structures of different trophic groups in non-boreal data sets do not align as precisely as Holling (1992) found for boreal data sets. The most likely explanation is that Holling's careful consultation with zoologists with long experience with birds and mammals in the boreal biome created robust and comprehensive species lists for birds and mammals. My compilation of a species lists from a number of study sites within each biome may still have too many omissions to constitute adequate representations of fauna at the biome level.

Chapter Summary

I have tested the predictions of a suite of non-landscape hypotheses which predict lump structure without any reference to landscape structure. I

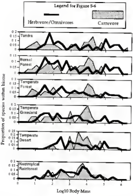


Figure 5-6 Size distributions for mean adult body masses of carnivores and herbivore/omnivores expressed as proportions of all species in sub-samples of mammal communities in 6 biomes

find no support at any level of lump structure for the Noah's Ark (H3), Limited Morph (H4) or Trophic Trough (H5) hypotheses Looking at herps, birds, and mammals I find no support at the level of an animal community lump structure for the Competitive Niche and Size Displacement (H1), but H1 does resist disproof at the sub-community level of within-lump size distributions Looking only at mammals, I also find that trends linking mammal order size distributions with para-global patterns of lump structure similarity support the Macro-Phylogeny (H2) hypothesis.

In total, lump structure appears best explained by three different hypotheses, the Macro-Phylogeny, Textural-Discontinuity and Competitive Niche and Size Displacement hypotheses, each operating at a different spatial scale. The Macro-Phylogeny hypothesis posits that broad long-term processes associated with the evolution of mammalian orders affect local, landscape lump structure through the process of community organization Communities are organized by species selection within broad but limited size ranges, or modes of higher species density, associated with adaptive radiation from a common ancestor of each Order This process increases the likelihood of lumps being located within these modal size ranges

At the level of animal communities in a landscape, the Textural-Discontinuity hypothesis predicts that hierarchical landscape structure is a context in which body sizes are selected for from the pool available after selection from the phylogenetic size distribution The environmental template of landscape architecture is a discontinuous distribution of ranges of scale, and within each scale range resources are apparent to animals Species body sizes are selected for through competition for resources at each different range of spatial scale The breaks in landscape structure which separate ranges of spatial scale are the template which is echoed by gaps in the animal community size distribution. These gaps separate body size lumps in community size distributions, so phylogenetic size distributions are dissected based on animal interactions with landscape structure.

At the sub-community level, within the spatial scale exploited by species within each lump, competition is minimized between species by diversifying their uses of landscape structure. The Competitive Niche and Size Displacement hypothesis predicts that this diversification is aided by separating and spreading the mean species' body sizes as evenly as possible along the size axis within the range of sizes which are effective in using the landscape at that scale, namely, the size range of the lump.

I have concluded this chapter with a brief demonstration of how parallel consideration of three hypotheses can bridge interactions across three ranges of scale to explain lumpy animal community morphometry. These conclusions rely on findings throughout this study, which I bring into a more comprehensive synthesis in the final chapter.

CHAPTER 6
SYNTHETIC INFERENCES FROM TESTS OF CONTINUOUS AND DISCONTINUOUS WORLD MODELS

Introduction

This study pits two world models against one another in an exploration of different explanations of how patterns of ecological processes and landscape structure are linked to patterns of animal size. Questions which encompass such large scales cannot isolate causation, a host of causes must be addressed, and multiple causation is likely. I approached the large scale, multi-causal questions of this study with two main strategies to address my expectation that multiple causation might obscure the signals my tests report. First, I embraced adaptive inference (Wiens 1984, Pickett et al 1995) as a means to test continuous and discontinuous world models in parallel. In this way I hoped that contrasts in results of different, parallel tests of an array of causes, not the results of isolated tests of single causes, might reveal the differences which deepen understanding about the relative importance of each separate cause. Second, I searched for pattern, however faint, across a large collection of animal and landscape data collected from 18 biomes on 5 continents.

In this chapter I try to weave the separate threads of these parallel tests of imposing data arrays into a workable synthesis. I briefly review the underlying theory and initial tests which set the stage for this work and then integrate the results and conclusions of the separate chapters

Animal Size Patterns as Evidence of a Discontinuous World

The premise which opened this avenue of inquiry (Holling 1992) is that the clustering of time and space behaviors of ecosystem processes strongly supports a discontinuous world model in which the world is separated into distinct domains of scale (*sensu* Wiens 1987) over each of which a different set of processes predominates. This sharply contrasts with the Gleasonian view prevailing over the last few decades that all environmental variables have continuous spatial distributions over all scales. The study of animal size distributions as indices of the interactions of animals with the operation of these processes attempts to test links between the functioning of ecological processes and mechanisms of evolution or community organization. The specific means of testing in this study follows the example of Holling (1992) in using discontinuous patterns of animal morphometry ("lumpiness") as evidence of animal interactions with a world of discontinuously distributed opportunities.

How to Test Patterns in Animal Size Distributions?

Lump analysis, as applied through GaP Pattern Analysis (Chapter 2, Restrepo et al. 1997) is an approach with practical and theoretical advantages in defining lump structures. It is relatively rapid and defines lump patterns which are broadly consistent with a variety of techniques (Chapter 2) including Holling's (1992) Body Mass Difference Index (BMDI) and some of the more advanced techniques, 'PatternMatcher', developed by Marples (unpublished results). Lumpiness, as applied with GaP and BMDI analysis, has shown promise in a number of biomes and a variety of taxa (Holling 1992, Restrepo 1995, Hostetler 1997) as an index linking body size pattern to landscape structure. GaP Pattern Analysis is theoretically appealing because it directly attacks the notion that all size distributions are continuous by defining gaps in terms of their probabilities of occurring in data sets derived from continuous body size data.

The promise shown in previous and current work plus my own tests allows me to accept lumps (body size clusters) found in lump analysis as patterns with a number of intriguing properties which may prove useful in testing various world models of ecological processes. I do so despite the ongoing controversy surrounding the hypothesis that lumps reflect modes in size distributions. Manley (1992) challenged the capacity of Holling's BMDI to rigorously show that animal body size clusters reflect modes in a size distribution. However, Marples (in submission) addresses that challenge directly by demonstrating what modal distributions potentially underlie body size clusters and reinforcing the suspicion that Manley's negative results stem in part from Type II error. Furthermore, lumps do not appear to be likely products of chance events causing body size data to appear discontinuous when the underlying size distribution is continuous. My simulations (Chapter 2) of synthetic body size data sets drawn from uni-modal size distributions show that it is highly unlikely that observed lump structures result from random sampling from continuous body mass size distributions.

The Reliability of Lump Analysis

I confirmed the reliability of lump analysis, as applied through GaP Pattern Analysis, by demonstrating that it is robust to observed levels of error in the creation of body mass size data sets (Appendix A). These two error sources are incomplete censusing of animal communities because of temporally unstable populations and incomplete accounting of intra-species variation in animal body mass sizes. I found in literature surveys that the variances of both size and temporal abundances for mammals and birds have right skewed distributions.

I initially estimated that such right skewed distributions of observed levels of both error sources had little potential to render lump analysis unreliable. Rather, a right skewed distribution of size variances should stabilize lump structure in ways analogous to the stabilizing influence of hierarchical organization on computer simulations of system dynamics (O'Neill et al. 1986, Allen and Starr 1982). Systems of components linked by interactions of equal significance and intensity are unstable (Kauffman 1991, 1993). Right skewed distributions of variation frequencies signify that the vast majority of species exhibit little variation in body mass or in temporal abundances in the populations. The minority of species which exhibit high variation introduce relatively low levels of stochasticity in determining lump structure which are unlikely to significantly undermine the capacity of lump analysis to find the underlying lump structure.

I found that lump analysis is robust partly because of stability inherent in such right skewed distributions of size or abundance variation. I determined this by severe probes of lump analysis through simulations of extreme variation scenarios. My computer programs simulated uniform not right skewed distributions of variation in that I allowed all species to exhibit the same level of variation, in size or in presence/absence. Lump analysis is robust to extreme simulations of census error (related to temporal variation in population abundance) for both birds and mammals, and not robust to extreme simulations of size variation in birds, though marginally so for mammals The resistance of lump analysis to such severe simulations of variation supports the hypothesis that it is robust to observed, moderate levels of variation in species size and population fluctuations

Does size variance decouple animals from landscapes?

Variation in animal size may not undermine the robustness of lump analysis, but it may challenge the linkage between animal size and landscape structure In other words the analysis technique may be robust, but the connection assumed in animal interactions with landscape may be weak Size variation may be more than a 'noise' level disrupting the discontinuous landscape signal in mammal sizes Size variation may be evidence of morphological plasticity which adapts successfully either to spatial continua or to discontinuous structures.

The presence of a variety of sizes in a species does not necessarily mean that all sizes are adaptive and result in successful reproduction. Size variance may simply be a strategy which allows populations to persist by increasing the chances that some individuals will be sized such that their scale of foraging will match the spatio-temporal distribution of resources That sub-population which is adaptively sized might have the best chances of reproduction, but its surviving progeny may exhibit the same strategy of a body size diversity

There are indications that species which rely on more heterogenously distributed resources have greater intra-species size variance which relates to their scale of foraging For example, the Queen butterfly (*Danaus gilippus* Cramer) utilizes smaller, less foliose species of milk weeds than do Monarch butterflies (*Danaus plexippus* L) The

Monarch occupies an ecological niche similar to Queen butterflies; it relies on a common species of milk weed (*Asclepias syriaca*). These plants are relatively large resource patches, with a more regular spatio-temporal distribution. The milk weeds (*Asclepias perennis*, *A. longifolia*, *A. lanceolata*, *A. tuberosa*, *A. viridis*) which Queen butterflies rely on are relatively small resource patches that are rapidly exhausted by butterfly foraging. The combination of relatively small plant size and very heterogeneous spatial distribution often forces a Queen butterfly to pupate on site rather than continue to forage (Ray Moranz pers. comm.). The variance of Queen butterfly wing size is high. By comparison wing size variance of Monarchs is very low as a result of stabilizing selection (Arango 1996, Arango and Brower, in prep.).

In this light, size variance is not a 'noise' level within body size metrics which decouples it from landscape structure and renders it a poor index of environmental geometry. Rather it may reflect population-level adaptations to shifting patterns of resource distribution, e.g. landscape structure. This conclusion is supported by evidence (Smith et al. 1997) that in Cameroon sub-populations of the same bird species, the little greenbul (*Andropadus virens*), have significantly different body size and wing size morphometrics which correlate with differences with landscape structure not with genetic drift. As predicted by The Textural Discontinuity hypothesis, birds in more open habitats (the ecotone between the forest and the savanna) have larger body and wing sizes than birds in the more enclosed habitat (forest).

Having established that Lump Analysis is a reliable technique for detecting discontinuities in body size distributions I proceeded to apply it to bird and mammal body size data sets to test predictions of a discontinuous world model.

Tests of the Discontinuous World Model

I found support for the Textural Discontinuity hypotheses in correlations of lump number and landscape complexity, in lump pattern similarities within similar landscapes, in lump pattern contrasts between landscapes of different structure, and in the capacity of lump pattern to predict the scale and texture of landscape used by mammals. I also found evidence which contradicts the Textural Discontinuity hypotheses, namely, that some features of lump pattern are shared by all mammal communities regardless of the type of landscape structure in which they live. That finding suggests that there are several causes of lump structure.

Biome and Super-Biome Scales

Predictions of the Textural Discontinuity hypothesis (H6) are supported by significant trends linking the complexities of lump pattern and of landscape structure. I developed an index (LSCI) which I used to quantify landscape structural complexity over three arbitrary ranges (micro-, meso- and macro-) of scale for each study site. I quantified lump structure complexity as the number of lumps and found correlations (strong for birds, moderate for mammals) between both indices of lump and landscape complexity, e.g. lump number and the LSCI. Confirmation of H6 on such broad levels invites inquiry into how consistent the similarities in lump structure are within similar landscapes and how different they are between different landscapes.

Lump pattern similarities found within systems of similar landscape structure (biomes and super-biomes) confirm the ptedictions of The Textural Discontinuity Hypothesis. My computer simulation tests show that these results are not the products of chance associations of animals or groups of animals (communities). I tested this idea by comparing actual large group (biome or super-biome) lump structures with two kinds of random groups of lump structures. I effected a 'coarse randomization' by selecting actual animal community lump structures at random and then assembling them into groups of 4 which constituted a 'fake' biome lump structure. I effected a 'fine randomization' by randomizing the location of lumps within each actual community's lump structure and then assembling groups of 4 of these 'fake' community lump structures into a 'fake' biome lump structure. In both cases I found much higher degrees of lump pettern similarity within actual biome or super-biome groups of study sites than from groups which are randomized at either level.

Is it possible that indices of lump pattern commonality can be seen as support for non landscape hypotheses? Lump pattern similarities shared by all study sites irrespective of landscape architecture could also produce my observations of high degrees of lump pattern similarity within groups of sites with similar landscape structure. This would seem likely if 'coarse randomization', randomized collections of study site lump structures, had shown levels of pattern similarity which are close to those found in actual groups. In other words, if all animal communities share similar lump pattern for reasons unrelated to landscape structure, then randomizing their associations to form a group should yield pattern commonality indices quite similar to those found in actual biomes. I did not find this, but lump pattern similarity within randomized groups is surprisingly high, and thus suggests some level of pattern similarity which is common to most animal communities These mixed results raise the possibility that lump patterns reflect multiple (landscape and non-landscape) influences

The brunt of the evidence to this point clearly undermines the Continuous World Model and establishes a robust foundation for a Discontinuous World Model The Continuous World Model is seriously challenged by the consistency across 150 ecosystems in 18 biomes with which I find discontinuous size distributions for both birds and mammals and the degree to which lump pattern is shared between communities in similarly structured landscapes However, the evidence of lump pattern commonality does not uniformly and exclusively support landscape-based explanations of lump pattern

The question now becomes what are the relative importances of landscape and non-landscape influences in determining lump pattern in animal body size distributions found in a Discontinuous World The hypotheses posed to explain lump structure (Chapter 2) can be sorted into three groups to clarify the principal concepts underlying each (Table 6-1)

Comparing Lump Patterns Between Large Scale Systems

I tested the possibility of the dominance of organismic and phylogenetic influences on lump pattern by examining two predictions concerning lump pattern similarities at scales larger than biomes, namely pattern matching between rather than within biomes or super-biomes The first prediction is landscape-based and posits that if landscape structure creates a robust signal in lump patterns, then inter-biome pattern

Table 6-1. Two level conceptual organization of hypothetical explanations of discontinuous patterns of animal body size

Base Concepts	***Title***	***Operational Level***
Landscape		
Structural	Textural-Discontinuity (H6)	Space/time patterns of architectures in landscape
Non-Landscape		
Phylogenetic	Noah's Ark (H2)	Genus and Species
	Macro-Phylogeny (H3)	Family and Order
Organismic	Competitive Niche (H1)	Community
	Limited Morph (H4)	Locomotory Modes
	Trophic Trough (H5)	Trophic Level

matches should exhibit differences which correspond to differences in landscape architecture. The second prediction is that if non-landscape processes predominate and give an over riding, common signal in all lump patterns, then most inter-biome pattern matches should show similar levels of similarity.

Both landscape and non-landscape hypotheses are supported by the mix of my findings. I found that the first prediction is mostly true, the second prediction is false, but that two to three zones are consistently found in most mammal community lump structures which contain high densities of lumps. These three zones common to most community lump structures reveal little about most gaps separating lumps but do explain some of the largest gaps separating groups of lumps.

I used the index of landscape structural complexity (LSCI) to order biomes and super-biomes according to rank of complexity. I found that these rankings do predict the values of similarity indices (Shared Lump Frequency index) in pattern matches between pairs of biome and pairs of super-biome lump structures. Indices of pattern matching were high, medium or low when the groups paired represented landscapes of very similar, slightly similar, or dissimilar landscape structural complexity, respectively. This trend is not the product of qualitative structural differences at the extremes (rainforests versus deserts), differences in landscape complexity index (LSCI) predict the index of pattern matching across the entire range of pattern match-ups between biomes or super-biomes. This range of excellent to poor index values for pattern matches completely falsifies the second prediction.

Landscape complexity predicts the degree of pattern matching in comparisons of pairs of animal community lump patterns. However, in the aggregate, patterns of lump pattern matching common to all systems irrespective of landscape type suggest that the Textural Discontinuity hypothesis is an incomplete explanation. I found three regions on the mammal size axis where lumps are found in the majority of all mammal study site lump structures. I determined the bounds of these common lump regions by aggregating the zones of lump pattern matching between every possible match-up of pairs of super-biomes. The zones along the size axis where most lumps are found which are common to most study site lump structures are 1.2 to 1.8, 3.25 to 4.25, and 4.75 to 5.3 log10 body mass.

Lump Structure Predicts Animal Use of Environment

In my most exacting test of the Textural Discontinuity hypothesis I found that lump structure predicts the scale and texture of landscape architecture exploited by mammals. Specifically, mammal species in a lump share certain features in the landscape in their exploitation patterns. Species in lumps with smaller mean body sizes used finer textures over smaller spatial extents than did animal species in larger sized body lumps. I found these results when I classified landscape structure using a range of resolutions from micro-scale (needles in trees) to meso-scale (ecotones). I did not find any correlation between lump structure and patterns of environmental use when the latter was defined only at coarse meso-scale resolutions, such as differences in habitat patch types, for example, thickets versus grasslands.

Tests of the Organismic and Phylogenetic Hypotheses

None of the non-landscape hypotheses showed any significant amount of power to predict the discontinuities which separate lumps in body size distributions of animal communities. However, I found regularities in body size patterns at sub-community levels (groups within the community) and at levels common to many communities found globally. An organismal hypothesis, the Competitive Niche and Size Displacement Hypothesis (H1) predicts the body size patterns at the sub-community level, which I found as the over-dispersion of body sizes within lumps. A phylogenetic hypothesis, the Macro-Phylogeny Hypothesis (H3) predicts the lump patterns common to most mammal communities which matched body size distributions at the taxonomic

Order level All other Organismic or Phylogenetic hypotheses showed no promise in explaining community lump structure

Body Size Distributions Within Lumps

The Competitive Niche and Size Displacement Hypothesis (H1) in normal application does not predict lump structure within an animal community It predicts the antithesis of discontinuities, which is 'over-dispersion', the inter-spacing of body sizes which is more even than expected by chance. In collaboration with Craig Allen, I tested H1 and found no evidence of 'over-dispersion' of body sizes across the entire community. However, we did find that species body masses are over-dispersed within lumps.

If over-dispersion is evidence of competition, then this evidence suggests that the arena of operation for competition is within a single range of scale, not across all scales. Species within lumps exploit landscape 'objects' within the same range of scale, and competition is minimized by size dispersion within lumps with minor shifting of the range of scale exploited Another option might be a significant jump up or down in size to another lump which exploits the landscape at an entirely different scale range.

Lumpy Body Size Distributions Within Communities

No non-landscape hypothesis showed any power to predict lump structure patterns at the community level, specifically the patterns of membership of species within lumps I found only random relations between patterns of species membership in lumps and in any of the categories representing hypotheses 3, 4 and 5 I found the least support for the Limited Morph (H4) and the Trophic Trough (H5) hypotheses. In more general surveys of memberships in trophic categories I found members of both categories (carnivores vs herbivore / omnivores) are present in most lumps, and the size distributions of both categories are continuous over most of the size range, i.e. show no clustering. I found more equivocal support for the Macro-Phylogeny (H2) hypothesis in that relations between membership in specific lumps and membership in specific taxonomic orders was random only 50 percent of the time.

Phylogenetic patterns at the level of species or genera showed no capacity to predict patterns of lump pattern matching within biomes or within super-biomes. I found no support for The Noah's Ark hypothesis (H3) in that there is no significant relationship between indices of similarity (species or genus) and indices of lump pattern commonality (intra-biome) or lump pattern matching (inter-biome).

Lumpy Body Size Distributions Common to Most Communities

I found that phylogenetic patterns at the level of taxonomic Orders can predict lump pattern common to most mammal communities. These common lump zones are too coarse to predict individual gaps but do forecast the size ranges where most lump are found. Of the two phylogeny-based hypotheses (H2 and H3) only The Macro-Phylogeny Hypothesis (H2) showed power to predict patterns of lump pattern matching within and between biomes. This conclusion emerges from the significant overlap between the size distributions of mammal orders and the zones on the size axis with high lump pattern commonality

Synthesis

Lump structure is not the product of a single process; it reflects the multiple effects of several processes operating at the levels of organisms, landscapes and phylogeny (Figure 6-1). These conclusions stem from the support I found for the Competitive Niche and Size Displacement (H1), the Oineria (H3), and the Textural-Discontinuity (H6) Hypotheses. Multiple interpretations are possible, but I offer one synthesis to explain lump pattern by integrating these different levels of process operation.

Animal body mass lump structure results from the interplay between sets of processes operating within three domains. Evolutionary radiation of body sizes at the level of taxonomic orders establishes a roughly bimodal body size distribution. This phylogenetic body size template is the broad context which constrains body size selection opportunities of processes operating at the level of animal communities in specific landscapes. Processes which organize animal communities draw on this bimodal body size distribution and split it into lumps based on competition for available resources, mediated by a discontinuous landscape architecture. That is to say, competitive selection within limited scale ranges will cause species body masses to converge on a limited number of size ranges (lumps) which reflect the discontinuous set of opportunities offered by the landscape structural hierarchy. Competition is minimized by shifting the scale of resource exploitation slightly within a scale domain or greatly by switching to a larger or smaller scale domain. This translates to even dispersion of body sizes within lumps or shifting from one body size lump to another.

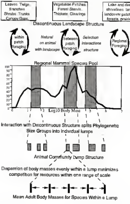


Figure 6-1 Synthetic Model integrating interactions between patterns of phylogeny and landscape structure as mediated through competition

Implications for Ecological Theory and Conservation

Efforts to protect such things as biodiversity or the capacity of natural systems to persist are strained by the tension between the imperatives to conserve what appears to be irretrievably disappearing and to understand systems whose complexity transcends mere numbers, they are dynamic and non-linear in their behavior Understanding must reduce the complexity of nature to some workable subset of processes and actors to give conservation actions an effective focus This work is part of wider efforts to explore the importance of a discontinuous set of architectures in the environment to animal behavior and survival To the extent that this work tests that importance, it helps to develop an important set of simplifying concepts for ecological theory and conservation.

If the discontinuities in animal sizes reflect the persistence of animal communities through interactions with a discontinuous landscape, then animal lumpiness is a useful index of those interactions Furthermore, it identifies subsets of the animal community interacting with subsets of the landscape structure This reduces system complexity from hundreds of species and landscape shapes to a handful of groups This constitutes a dramatic simplifying step for the conceptualization and execution of conservation actions

It also ties groups within the animal community to a small set of processes which operate to structure the landscape Without negating the importance of any other inquiries into the effects on animal survival of temperature, moisture, productivity, disease or economic use of resources, the understanding of animal-landscape interactions establishes some very useful conceptual linkages between animal communities, landscape structure and structuring processes. By doing so in the spirit of adaptive inference, it opens the door to richer understanding through parallel testing of the relative contributions to the resilience of ecological systems of landscape structure in addition to other key sets of factors already being investigated. As shown in this work this may clarify the contributions of non-landscape factors, such as phylogeny. Systems as large and complex as ecosystems are undeniably multi-causal, so insights into the relative importances of various processes and the manner in which they interact are vital both to theory and conservation.

APPENDIX A

TESTING THE SENSITIVITY OF LUMP ANALYSIS TO SOURCES OF ERROR WITHIN DATA SETS

Introduction

Holling (1992) cites discontinuous patterns of animal morphometry (lumpiness) as evidence of animal interactions with a discontinuous world These interactions purportedly are functional links between animals and the landscape, potentially influencing selection either at evolutionary or community organization levels As such animal communities act as a 'bioassay (Holling 1992) of discontinuous landscape structure Trust grows in lumpiness as an index of this bioassay function when one can rule out spurious sources of discontinuities in animal size distributions. In this section I describe two possible sources of spurious lumpiness and discuss their potential to undermine Lump Analysis

Error Source 1. Inadequate Censusing of Animal Populations

Failure to account for all species in a community could create gaps in a size distribution and be a source of spurious lumpiness This failure could emerge from inadequate survey methods, significant variability in the space/time dynamics of species populations, or some combination of the two In the latter case the ephemeral or non-equilibrial nature of animal communities, wherein the species composition of communities appears to fluctuate unpredictably from year to year, is a subject of on-going and lively debate (Connell and Sousa 1983, Wiens 1984, Jaksic et al. 1996).

Error Source 2. Intra-species Body Size Variation

Another source of spurious lumpiness might result from an arbitrarily narrow definition of animal size. Perhaps the integration of the separate intra-species size variabilities of all species' populations actually is a continuous distribution for the entire community. However, the choice of a single number, mean adult body mass, to represent each species might ignore much of the actual variability and create a set of arbitrarily discrete data points. Such incomplete accounting of the full variability in sizes might artificially boost the likelihood of finding significant discontinuities in such an arbitrary size data set. Sexual dimorphism is another source of size variability ignored by the use of mean adult body mass for each species. Consideration of each sex separately might result in a community size distribution which is more or less continuous.

The introduction of spurious lumpy pattern undermines Lump Analysis credibility in several ways. First, if animal community morphometry does indeed bioassay landscape structure, such a 'true' signal might be masked, distorted or swamped. On the other hand, if no bioassay function exists, Lump Analysis merely reflects artifacts of sampling error (Source 1) or size definition error (Source 2). The challenge is to determine the actual occurrence of such error sources and then to probe rigorously for their potential to influence Lump Analysis' ability to detect lump pattern. I now describe the design of the tests of Error Source 1 and Error Source 2.

Testing Influences of Error Sources on Lump Analysis

In this Appendix I test lump analysis for its vulnerability to these two sources of error For each error source I create a test which uses a known data set s lump structure as a template pattern and seeks to define the pattern-masking error level which will make it unlikely for lump analysis to detect the original lump pattern The actual risk to lump analysis posed by either error source relates to whether observed error levels exceed the pattern masking level found in this test I will assess the actual risk by examining whether the pattern-masking error level is likely or unlikely given a frequency distribution of observed error levels Using size variation as an example, if the pattern-masking level of size variation is in the extreme upper tail of the distribution of observed size variations then the risk is low, and lump analysis appears robust to such a source of error

I establish observed error levels by collecting data from literature on the extent and intensity of both error sources. I report on the best estimates for surveying error in animal censuses and on measures of instability in animal community species composition For the second error source I marshal data on size variability and degree of sexual dimorphism in mammals and birds. I then predict the pattern-masking error level based on known characteristics associated with the template data sets For example, I can use the size of discontinuities in the original lump structures to predict how much body size variation might alter the location of those discontinuities and cause lump analysis to fail to find the original lump structure

For the actual tests in this Appendix I create two computer simulation experiments to test the potential of each error source to introduce spurious pattern in Lump Analysis. I set the severity of the test within the computer program design which dictates how to simulate the effects of either error source on lump analysis. Finally, I compare the levels of each error source observed in nature with the simulated error levels (the measured pattern-masking values) associated in my computer experiments with collapse in the reliability of Lump Analysis to find pattern. I now report on the causes and the observed rates for both potential sources of error. I begin with the factors underlying observed error rates in animal censuses.

Determining Known Error Rates in Animal Censuses

Factors which render manunal species lists incomplete and/or unreliable are numerous. Differences in the kind, quality and duration of on-site sampling methods are local error sources which undermine each individual list and lower their inter-site comparability. Each sampling approach is biased toward that fraction of the fauna whose morphology and/or behavior makes it susceptible to capture by that particular method. Multiple inventory techniques such as trapping (conventional, tree and pitfall), diurnal and nocturnal hunting or censusing by sight, mist-netting and interviewing local residents, must be used in combination to comprehensively sample mammal communities. While the list of techniques is shorter, similar limitations are faced by bird censusing techniques (Ralph and Scott 1981). The funding to sustain research efforts of sufficient scope and duration is rare. Lack of standardization in terms of application protocols and duration and intensity of effort make it hard to distinguish real faunal differences between localities. One comparison of mammal censuses in Neotropical lowland rainforests (Voss and Emmons

1996) noted disparities in sampling efforts ranging from one year to several decades.

Most censuses are constrained by practical limitations, but even extraordinary efforts cannot overcome certain challenges of tracking spatially diffuse populations. An obvious and inescapable source of error is that rare species are more likely to be missed than common ones (Hurlbert 1971, Heck et al. 1975, Sudman et al. 1988, Green and Young 1993). An even more demanding challenge than establishing a species' presence is confirming its absence. Belbin (1993) points out that a species' presence can be affirmed by detection of one or more individuals, but failure to detect does not necessarily provide any information. Even if a species' presence is confirmed, the reliability of establishing links between species and landscape features may hinge on determining the degree of presence. Comparisons of bird censuses for species richness are often misleading not only due to differences in quality and quantity of sampling effort but also because of failure to distinguish "core" (resident) from "marginal" (migrant) species (Remsen 1994).

Larger scale sources of error in animal surveys include the geographical and institutional context in which the censuses are carried out. Broad patterns of species distribution can also influence the comparability of bird censuses in that surveyors fail to note that diversity of habitats surrounding a site can influence the number of species observed (Remsen 1994). Other factors contributing to the uncertainty of animal censuses include dependence on occurrence records from institutions like museums. Such data have unknown reliability because sampling probabilities are likely to vary according to what habitat or taxa are investigated (Davis et al. 1990). Other confounding factors include defaunation by hunters, the fact that species accumulation curves are not assymptotic for any fauna, and high inter-site variability in all aspects of fieldwork (Voss and Emmons 1996) The authors conclude that omission error is prevalent in most mammal censuses

> *Comparisons of inventory results with geographic expectations (from range data) suggest that all existing inventories are incomplete*

In addition to detection methodology, the inherent dynamism in space and time of animal populations is another source of error in determinations of animal community species composition. I consider first animal survey accuracy estimates which attempt to quantify the combined effects of both sources I then discuss attempts to quantify the latter source, population dynamism, as an indirect accuracy estimate of animal community surveys.

Sources of Accuracy Estimates for Animal Surveys

I found estimates of the range of error for terrestrial vertebrate population censuses in literature assessing the precision and accuracy of a number of different animal survey research projects. For birds I examined studies of the Breeding Bird Survey (Robbins et al. 1989, Sauer and Droege 1992), and the Christmas Bird Count (Drennan 1981). Mammal community censuses based on range maps in neotropical communities are broadly critiqued without a quantitative assessment of error (Voss and Emmons 1996) I found omission (false negative) and commission (false positive) error rates estimated for those bird and mammal censuses which are based on extrapolations of geographical range overlap in studies of the Gap Analysis Project (Lewellyn and Peterson 1996, Edwards et al. 1996)

Results Error Estimates for Bird and Mammal Community Surveys

Few attempts have been made to assess the inaccuracy of surveys of entire animal communities. The Gap Analysis Program (Burley 1988, Scott et al. 1993) (not to be confused with Marples' GaP Pattern Analysis - see Chapter 2) of the National Biological Survey had among its objectives the mapping of species richness in the United States. Species richness estimates were derived from field observations, range maps, and distributional models relating animal abundance (or presence/absence) to vegetational patterns (Conroy and Noon 1996). A number of accuracy estimates were generated to assess the risks of sampling error. Edwards et al. (1996) estimate error ranges for animals censuses of terrestrial vertebrates to be between 0% and 24% (omission) and 4% to 34% (commission) of the total number of species in the community. The error rates were highest for amphibians and reptiles and lowest for birds and mammals. On the other hand, Lewellyn and Peterson (1996) found higher rates of accuracy of range predictions (89% and 92% for amphibians and reptiles, respectively). These estimates suggest an error range of 0% to 34% for both omission and commission with a median value of 17%.

The paucity of research in this area undermines confidence in error estimates for animal censuses. Another approach to assessing error in estimates of community composition is to study the degree to which populations fluctuate in numbers of individuals over time. Communities characterized by relatively stable species densities have been labeled 'equilibrial' (Chesson and Case, 1986). I use the term 'equilibrial' in a sense (limit cycles, strange attractors) wider than that of classical (point-equilibrium) competition theory (Hutchinson 1959). A community is equilibrial if enough species consistently occupy all niches and habitats such that communities are resource limited (Cody 1974a, Schoener 1974b, Pianka 1976). The absence of equilibrium might suggest such randomness of association either inter-organismal or between organisms and landscapes, that any of the hypotheses posed in Chapter 2 becomes irrelevant.

Are Animal Communities Equilibrial?

Some evidence from structurally simple habitats does not support the equilibrial view. So little covariance was exhibited between habitat types and suites of bird species in shrub steppe ecosystems that Wiens (1984) suggested that these and other ecosystems are 'non-equilibrial'. Specifically, site level comparisons of habitat use by avian ground foraging guilds showed bird populations varying independently of habitat structural features and of density changes of coexisting species. Non-equilibrial properties have been observed for other taxa at other sites as well. Wide fluctuations of species abundance were noted for finches in the Galapagos (Grant 1986) and for dominant insect harbivores in goldenrod (Kareiva, 1986). Wiens (1984) proposed that the study of community organization rules be related to the inherent spatio-temporal variability of populations by identifying where each animal community is on a continuum from non-equilibrial to equilibrial states.

Random changes in presence from year to year are plausible for some individual species or even groups of species in mammals as well. Brown (1975) reports such levels of population fluctuation for desert rodents. Spatio-temporal population fluctuations are evident at the extremes in the animal size range. Larger, broad ranging species may return infrequently. For example, local areas in northern Canada are revisited by caribou every 60+ years as a result of migration cycles (Burkes 1995). Small species, such as microtine rodents, may be undetectable during dramatic lows in population cycles. Local extinctions may require consistent repopulation from outside source areas (Pulliam 1988, Hanski 1991).

The possibility that an animal community is non-equilibrial undermines the reliability of species lists compiled for each landscape, be it a habitat, ecosystem or biome. Since the spatio-temporal variability of populations scales negatively with the size of the area sampled (Connell and Sousa 1983), placing a community on the equilibrium continuum depends on the scale at which the community is defined. For instance, the same ground foraging guild "communities" which appeared non-equilibrial at smaller scales (habitat floristics) did exhibit equilibrial properties over broader spatial categories such as: eastern mesic prairies', 'xeric shortgrass prairies', and 'western shrubsteppe habitat' (Wiens 1984).

One recent study of changes in population abundances at a single site in Chile suggests the ephemeral nature of groups within such communities and cautions against reliance on non dynamic, short term definitions of species composition. Jaksic et al (1996) examined a relatively mobile predator guild (owls, falcons and foxes) at a semi-desert site, Aucó in Chile, and found that the species composition fluctuated sufficiently over time to invalidate biodiversity conservation plans based on static (single year) definitions of predator populations. Similarly, while range estimates predicted their presence, wolverines (*Gulo gulo*) were not detected for more than 20 years at The Taiga Biological Station in Southeastern Manitoba (Bill Pruitt, pers comm.). Whether this represents a serendipitous encounter with an elusive but ever present species or simply a southern migration cycle which periodically brings wolverines to that site, the predictability of a species or group of species occurring at a study site still remains in question.

Non-equilibrium has not been demonstrated as a general property of ecosystem-level animal communities. One survey of the equilibrial properties of populations of various taxa at some fifty ecosystem sites found that the rank order of relative abundances of species remained the same for most sites (Connell and Sousa 1983) but erratic fluctuations without any evident stability were found in several instances. Temporal fluctuation was defined as changes in abundance as measured between two population censuses separated by at least one population turnover. The log transforms of temporal variabilities for population fluctuations were continuously distributed from near 0 to 1.21 standard deviations. Such a continuum does not provide a model with defined statistical parameters to establish bounds of equilibrial behavior. Connell and Sousa (1983) conclude that difficulties in defining equilibria had prevented adequate testing of ideas of community stability based on equilibrium states.

For mammals this question does not apply only to the larger, more free ranging species because the smaller species are elusive, and their population sizes can fluctuate to lows which challenge detection. However, at large enough scales of group size and space/time dimensions of movement, mammal presence appears relatively stable at landscape study sites (Connell and Sousa 1983). Avian mobility brings the presence of almost any species in the entire bird community into question. But the challange of detecting mobile birds is lessened by their vocalizations, a behavior which is shared by many species on a predictable (crepuscular) basis. This is evident in that detection resolution is gauged as the ability to measure avian population abundance changes, not presence or absence. For example, Partners in Flight, an organization that monitors population trends in neotropical migrants, defines an effective monitoring scheme as one that has a 90 percent chance of detecting a 50 percent abundance decline in a species over a 25 year period (Butcher et al., 1993). Such standards make determinations of presence or absence seem relatively risk free. The challenge then falls to differentiating between the "core" breeding species and the transients (Remsen 1994), a risk as yet unquantified.

Summarizing Risks in Censuses of Community Species Composition

Most assessments of the inaccuracy of animal community surveys have been offshoots of large scale (regional and continental) censuses such as the Breeding Bird Survey (Robbins et al. 1989, Sauer and Droege 1992), the Christmas Bird Count (Drennan 1981), the Gap Analysis Project (Lewellyn and Peterson 1996, Edwards et al. 1996) or similar efforts in the Neotropics to estimate animal communities by overlapping range maps (Voss and Emmons 1996). I am unaware of any accuracy estimates for animal population surveys where the census was done in a more intensive manner focused on a single research area, e.g. where an entire animal community was the object of study from an established research center over a number of years.

It is reasonable to assume that site-specific species lists based on relatively continuous observations over a number of years are subject to lower estimate error than species lists synthesized from geographic overlaps in range maps. In the absence of quantification of single site censusing error rates I choose a conservative interpretation of estimates based on range maps, namely the median value, 12 percent, for the range of error attributed to omission (Lewellyn and Peterson 1996, Edwards et al. 1996).

Determining How to Simulate Error Source 1

My survey of census data and time studies suggests that most species abundances in mammal and bird communities are relatively stable over time, and that there is little likelihood that population fluctuations or census errors threaten lump analysis. Only a very small minority of some 50 ecosystem study sites exhibited erratic or "non-equilibrial" population dynamics on a community-wide basis (Connell and Sousa 1983) The relative lack of population fluctuations by most species at a site suggest a measure of integrity in community organization which is sustained over time and across a variety of events such as disturbances

It is difficult to imagine that my computer simulation test will find a pattern-masking value of random change in species abundance below the low levels of temporal fluctuation observed for most species. This suggests that only a strong or extreme test will uncover lump analysis sensitivity to population fluctuations or census error. I propose to probe the stabilizing influence of the integrity of community organization on lump analysis by examining extra-ordinary levels of population fluctuation, which contrast with the relatively persistent abundances of most species. I shall increase the severity of my test by simulating random temporal changes in abundance not for a minority, as observed, but for any species in the entire animal community.

I now survey the underlying causes and literature data of observed levels of the second error source so as to establish the severity of my test of its influence on lump analysis

Determining Known Rates of Animal Body Size Variability

The second source of error in defining animal community body size distributions may emerge from narrowly defining animal morphometry as mean adult body mass. Enough intra-species size variation around that mean body size might fill any discontinuities in the animal community size distribution as detected by Lump Analysis. If the underlying community size distribution is continuous, then the choice of arbitrarily discrete data points might increase the incidence of artificial discontinuities and boost detection of spurious lumps I first discuss sources of size variation and then report on observed levels of size variation for birds and mammals

Sources of Body Mass Variation in Terrestrial Vertebrates

Body size varies within populations for a variety of reasons, ranging from intrinsic (genetic) to extrinsic (environmental). Extrinsic mechanisms which affect body size include "maternal effects" Maternal effects are influences on offspring phenotype resulting from non-genetic contributions of parents or even grandparents or from environmental contributions such a s nutritional, endocrine, defensive or regulatory (Rossiter 1994) The mean adult size of some species can vary over time as a result of maternal effects Species whose population sizes undergo cyclic oscillations often exhibit commensurate shifts in mean body morphometrics (Chitty Effect) For example, microtine rodent adult body sizes are 20 to 30 percent larger during population increases and peaks than during declines or lows (Chitty 1952) Such size surges during peak populations are not functions of increases in age or percent of fat in an individual but of more fundamental changes, namely, skeletal proportions (Krebs 1964) Analysis of heritability on body weight, growth rate, age and weight at sexual maturity in *Microtus pennsylvanicus* shows that most of the variation was non-genetic in origin (Boonstra and Boag 1987) Increases in mean size and growth rate were attributed to maternal effects, and milk quality and quantity

For both birds (especially raptors and insectivores) and mammals most of an individual s growth is a function of parental investment (Reiss 1989) Where parental investment influences growth rate, the age at maturity is proportional to adult body mass raised to 0 3 (Reiss 1989) Since the lower the power the younger the animal is at maturity, and since most growth is related to the relatively brief early interlude of parental investment, it follows that birds and mammals (with the exceptions of some very small species) are at an adult size plateau for a majority of their life span. However, for mammals the number of individuals surviving to adulthood varies from species to species, and often the proportion of a population occupied by adults is a minority (Bill Pruitt, pers. comm.). This increases the likelihood that sampling will mix sub-adults with adults and increase the variation of reported mammal adult body masses.

A genetic source of body size variation within populations is indeterminate growth. Growth rates for some species do not decline to a plateau with adulthood but remain positive throughout an organism's life. Short-lived organisms like microtine rodents exhibit indeterminate growth patterns with weight gain continuing until death (Boonstra and Boag 1987). Larger mammals such as mule deer (*Odocoileus hemionus*) and elephants (*Loxodentia africana*) achieve and remain around a maximal adult size in the first 20 percent of their life spans (Peters, 1983), and birds' growth rates allow them to rapidly achieve adult size. For these reasons as well as the contributions of parental investment it appears that for a majority of mammals and birds large intra-species size variation due to indeterminate growth is not likely.

Another genetic source of size variation in some animal populations is sexual dimorphism. Sexual dimorphism might confer selective advantage for: 1) larger males in inter-male reproductive conflicts (Darwin, 1871; Selander, 1972, Trivers, 1972), 2) larger females with greater reproductive success (Reiss, 1989), and 3) smaller females with lower bioenergetic demands (Erlinge, 1979, Moors, 1980). Sexual dimorphism is more pronounced in larger species, though once the factor of polygyny is eliminated a clear positive trend between size and dimorphism is evident only in primates and small mammals (Peters, 1983). The extent of size variation due to sexual dimorphism cannot presently be determined for ecosystem-level communities because of data scarcity (Dunning 1992, Silva and Downing 1995).

Environmental factors related to the timing of sampling can contribute to variation in the body masses reported for mammals. These factors involve variability in body weights stemming from changes in reproductive status, feeding and general physiological condition (Ralls 1976). Animal weights can shift significantly depending on the phase of pregnancy (females only), time since last meal, current health status, and phase of the feeding season. Quantification of sexual dimorphism can be affected by the latter when weight gain rates during the summer are significantly different between males and females (Ralls 1976). Body weights of small mammals can decline overnight by as much as 10 -20 percent or more due to dehydration after snap trapping, though this varies greatly as a function of ambient temperature (Josh Laerm, Curator of Mammals, Museum of Natural History, University of Georgia, pers. comm.). I now describe my data sources and methods for determining observed ranges of size variability in birds and mammals.

Observed Size Variability in Avian Body Masses

Methods of determining avian body mass size variability

I randomly sampled the size variabilities of 1000 bird species from Dunning (1993) by an iterative process. I selected a page number at random and then a species within that page at random, and if the species had data both for mean and standard deviation statistics for species body mass, then I derived a coefficient of variation value by dividing the standard deviation by mean species body mass and selected another species at random. If mean and standard deviation statistics were not available for a species, then I started the selection sequence again.

Results- frequencies of avian body mass size variabilities

I find relatively low values for intra-species variation in mean adult body masses for birds. This pattern is consistent across all bird species, irrespective of sex or number of observations. For example, the coefficient of variation (CV), expressed as a percent, is 8.35 for all observations combined (Table A-1), and the CV values of all 5 sub-categories ranges only 7 percent on either side of that figure. Highly similar summary CV and standard deviation values characterize every category. Within each sub-category I find little variance in the amount of size variation observed as indicated by the relatively low average values (5.5 percent) of standard deviation statistics for CV values across all sub-categories.

All determinations of mean species body mass face the question of whether sample size (*n*) was adequate to capture the variability of body sizes within the population. This question is appropriate here since more than forty percent of the random samples employed to create these summary statistics involved bird species with body mass values derived from relatively few ($n < 30$) observations. I tested the potential that low CV values are associated with low *n* by measuring CV values in the low *n* sub-category. I find almost no difference between low *n* CV values and those of all other sub-categories despite the fact that most of these samples are very small; mean and standard deviation statistics for *n* are 16.5 and 5.5, respectively.

If a trend links bird mean body mass and CV values such that larger birds have larger CV values, then another spurious source of low body size variance might be the under sampling of larger species. I regressed size variance on mean adult body mass for all 1000 samples and found no significant trend relates CV values to mean bird adult body mass (Figure A-1). A slight increasing slope (3.6 percent) is evident in a regression of CV values on body mass, but an r-squared value (0.022) indicates little explanatory value.

Table A-1. Variation in Mean Adult Avian Body Masses disaggregated into data source categories (data drawn randomly from Dunning 1993)

	Mean CV	*SD*	*Number of*
Data Source Category	*(Percent)*		*Observations*
Males	7.69	3.86	230
Females	8.02	4.00	194
Both Sexes	8.88	4.33	192
Unknown	8.66	7.28	376
< 30 observations	8.85	5.94	433
All Birds	8.35	5.51	994

I developed a sexual dimorphism ratio (SDR) to estimate the amount of body size variance within species contributed by differences in male and female mean body masses. I designed the SDR ratio to normalize this size variance with reference to the mean body mass reported for the species. To do this I calculate the absolute value of the difference in mean male and female body masses and divide by the mean adult body mass value of the species (equation A.1). I calculated mean and standard deviation values for the SDR for each taxonomic order for those species of a taxonomic order for which data was available.

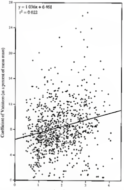


Figure A-1 Variation in adult body masses for 994 species of birds as a function of mean body mass size. Mean size and standard deviation statistics data taken from Dunning 1993

Data availability for both males and females was not consistent across all orders (Dunning 1993) No data were available for both males and females of a species for three orders Gaviiformes, Phoenicopteriformes, and Trogoniformes Numbers of male/female size observations in the remaining 25 orders ranged from 2 to 174 with a mean of 32 and a standard deviation of 41

$$SDR = \frac{abs(M_{Male} - M_{Female})}{M_{Species}} \qquad \text{(A 1)}$$

Where M = Mean Adult Body Mass

I found higher indices of variance in the Sexual Dimorphism Ratio than I did for overall intra-species body size variation The mean SDR for these 25 taxonomic orders was 0 173 with a standard deviation of 0 053 With the exceptions of the Falconiformes and Gruiformes, the mean SDR values of all bird taxonomic orders fell below 0.24, with a mean of 0 162 and a standard deviation of 0.38 I did not find a strong trend linking body size to SDR values. I regressed SDR values on mean log body mass (Figure A-2) and find a very slight increasing trend (r-squared = 0 13) suggesting little difference in SDR between bird species over a broad range of mean body masses found in different orders

Summary-observed variabilities of avian body mass size

In summary, sexual dimorphism potentially contributes much more intra-species size variation then any other cause Mean size variation expressed as percents of mean body mass was 8 4 percent (Standard Deviation

= 5.5 percent) for intra-species size variation and 17.3 percent (Standard Deviation = 5.3 percent) for sexual dimorphism.

Observed Size Variability in Mammalian Body Masses

Methods of determining mammalian body mass size variability

I took data on the size variation inherent in mammal populations (male and female data combined) minimum and maximum CV values for body mass directly from Yablokov (1974). I assembled data on size variation due to sexual dimorphism in mammals for each of seventeen mammal taxonomic orders using a integrative random search procedure similar to that which I used for birds. For each order, I drew one hundred random samples of species with mean adult body masses reported for both males and females from Silva and Downing (1995). I calculated mean and standard deviation values for a sexual dimorphism ratio in the same manner as I did for birds.

Results- frequencies of mammalian body mass size variabilities

Body mass size variance in mammalian taxonomic orders, as expressed by the coefficient of variation, ranges between 10 and 15 percent with a median value of 12.4 percent for body mass (Table A-2). Mammalian body length, another size metric related to body mass, shows a narrower range (4 to 6.2 percent) around a lower median CV value (5.1 percent).

As with birds, if any pattern links mammal mean body mass with body size variance, then larger mammals would have larger intra-species size variance. If I over sampled the small end of the size range I might arrive at an artificially low CV value. I tested the potential for such a skewed CV estimate by regressing the CV values on both body mass and body length and found only slight, non-significant trends in relation to body mass (Figure A-3).

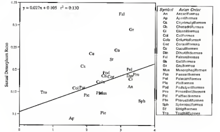


Figure A-2. Sexual Dimorphism Ratio as a function of body mass in 24 bird taxonomic orders

As with birds I found higher body mass size variance due to sexual dimorphism (Sexual Dimorphism Ratio, SDR) in mammalian orders than from observations of intra-specific size variation. SDR values (Table A- 3) average 0.278 across 18 mammal orders with a mean standard deviation of 0.203. The most prominent outliers are insectivores (0.59), marsupials (0.61), primates (0.68) and rodents (0.47). The distribution of SDR values has a left skew, with most values falling below the mean. If calculated as a weighted average mean SDR is much higher, 0.39, however this value may add a bias for those orders for which data exists and may contribute no information about actual SDR values in nature.

Table A-2. Morphometric Variation in Mammal Orders (after Yablokov 1974).

Coefficient of Variation (as a percent)

Mammal Order	Body Length				Body Mass			
	min	max	Median	No. of Observ	min	max	Median	No. of Observ
Insectivora	4.6	8.4	6.5	110	8.1	11.5	9.8	77
Lagomorpha	3.7	4.5	4.1	3	9.6	11.3	10.6	2
Rodentia	4.6	6.9	5.7	209	8.2	13.7	10.9	151
Artiodactyla	3.2	5.1	4.1	6	9.0	20.7	14.9	36
Carnivora	3.1	5.5	4.3	24				
Marsupialia	5.0	7.1	6.1	2				
Primates					14.8	17.4	16.1	2
All Orders	4.0	6.2	5.1	356	10.0	14.9	12.4	268

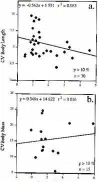


Figure A-3 Coefficient of variation in morphometrics (a. mean body length, b. mean body mass) of mammal species regressed on log mean body mass.

Table A-3 Size variance due to sexual dimorphism and body mass ranges in mammalian orders (data from Silva and Downing 1995)

Taxonomic	Mean Body Mass		Sexual Dimorphism			Body Mass		
Order	count	Log10 (g)	count	Ratio	SD	count	Range	SD
1 Artiodactyla	139	5.026	100	0.243	0.173	100	0.407	0.263
2 Carnivora	170	4.234	104	0.261	0.208	104	0.634	1.105
3 Chiroptera	150	1.533	104	0.114	0.109	103	0.436	0.242
4 Dermoptera	1	NA	0		NA	1		NA
5 Hydracoidea	10	3.447	8	0.145	0.114	8	0.485	0.320
6 Insectivora	125	1.875	78	0.592	2.100	81	0.958	2.201
7 Lagomorpha	66	3.249	41	0.375	1.704	44	0.750	1.747
8 Macroscelidea	19	1.811	17	0.078	0.061	15	0.412	0.133
9 Marsupialia	138	3.576	103	0.611	1.823	103	0.977	1.953
10 Monotremata	7	3.536	8	0.318	0.135	2	0.700	0.582
11 Perissodactyla	20	5.826	9	0.133	0.113	14	0.244	0.129
12 Pholidota	8	3.710	3	0.286	0.145	6	0.622	0.474
13 Primates	147	3.870	91	0.685	1.927	66	0.812	2.150
14 Proboscidea	5	3.536	2	0.038	0.028	3	0.390	0.033
15 Rodentia	151	2.470	103	0.467	1.838	109	0.896	1.906
16 Scandentia	11	1.922	3	0.178	0.056	8	0.705	0.240
17 Tubulidentata	3	4.747	2	0.096	0.084	2	0.270	0.165
18 Xenarthra	21	3.753	6	0.116	0.094	15	0.567	0.272

Summary of observations of mammal body size variance

Because of a lack of data showing intra-species size variation around mean values for species adult body mass, I can only report median size variation between mammal orders, expressed as percents of mean body mass, at 12.4 percent As with birds, sexual dimorphism shows much greater potential to contribute variability in size within species I averaged intra-species size variation for sexual dimorphism within mammal orders and found it was 27.8 percent or slightly more than double that of intra-species size variation for all other causes

Determining How to Simulate Error Source 2

In this section I estimate the vulnerability of lump analysis to size variation Recall that I define vulnerability in terms of the 'pattern-masking' error level the level of size variation at which the original lump structure is not reliably detected by lump analysis. I estimate vulnerability by seeing where my estimates of pattern-masking levels of size variation lie in relation to observed frequencies of size variation at the community level If the pattern-masking level of size variation is in the extreme upper tail of the distribution of observed size variations, then the risk is low, and I can make the test relatively severe I will first develop an estimate of the pattern-masking level of size variation I then develop models of size variation in animal communities based on the data previously presented for bird and mammal species on two parameters of size variation related either specifically to sexual dimorphism or to a combination of all factors influencing size.

Estimating pattern-masking values for size variation in birds and mammals

I use the mean size of discontinuities or gaps which separate lumps in a known body mass data set to estimate the pattern masking level of size variation. This follows from the idea that if the rank of a species body mass within an animal community size distribution places it near the edge of a lump, and if its intra-species size variation is near such a pattern-masking level, the species could be located with equal likelihood in that lump or in the neighboring lump or in the gap in between the two lumps. Pattern-masking levels of size variation push lump analysis across the threshold from reliability to unreliability. For example, Figure A-4 shows a hypothetical lump structure and locates the mean body sizes of two species, a and b, on the edges of lumps 1 and 2, respectively. For each species the drawing also illustrates the marginal sizes, the size range of individuals with body masses which differ positively with the mean by more than one standard deviation. The potential to undermine lump analysis is illustrated by the ratio between intra-species size variability and mean gap size. This potential is high where the ratio is high (Gap A) and low where the ratio is low (Gap B).

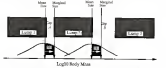


Figure A-4 Hypothetical lump structure and intra-species size distributions of edge species within lumps.

I establish the distribution of known gap sizes for the test by presenting (Table A-4) the gram body masses of edge species in the lump structures of two known data sets, boreal prairie mammals and birds (Holling 1992). I use these data to estimate the pattern-masking size variation value as the mean value of gap sizes expressed as a fraction of edge species body masses. These values are 0.64 for mammals and 0.14 for birds.

Table A-4. Gap sizes as fractions of edge species body masses in the lump patterns of Boreal prairie mammals and birds. The edges of each lump are determined by the average body masses of the smallest (leading edge) and largest (trailing edge) species. All edge body masses are in grams.

A. Boreal Prairie Mammals

	Edge Species Body Mass		Gap Size		
Lump	Lead	Trail	Grams	%of Lead	%of Trail
1	4	13	7.7		0.59
2	21	46	29.1	0.37	0.63
3	75	159	284.2	0.39	1.78
4	444	3357	1837.0	0.64	0.55
5	5194	14061	9933.7	0.35	0.71
6	23995	91966	77677.6	0.41	
7	169643	556557			

B. Boreal Prairie Birds

	Edge Species Body Mass		Gap Size		
Lump	Lead	Trail	Grams	%of Lead	%of Trail
1	10	23	2.1		0.09
2	25	34	3.2	0.08	0.09
3	37	47	5.2	0.09	0.11
4	53	77	19.3	0.10	0.25
5	97	177	37.4	0.20	0.21
6	215	386	54.2	0.17	0.14
7	441	453	65.9	0.12	0.15
8	519	1679	709.0	0.13	
9	2388	4305			

Summary statistics for gap sizes as fractions of edge body masses

	Mammals	Birds
Mean=	0.64	0.14
St Dev=	0.42	0.05

Ranking pattern-masking values within bird and mammal size variation distributions

How one models variation in size across all species in a community greatly determines the probabilities associated with error values which mask lumps or gaps   Mean statistics are but single parameters in any comprehensive picture of size variation within an entire animal community I use the previous data (birds) and new data (mammals) to establish frequency distribution models of size variation in mammal and birds (Figure A-5)   The mean values of size variation I use as estimates of the pattern-masking error values are clearly in the upper tails of observed distributions of coefficients of variation for both taxa. Evan if I extend standard deviation error bars these estimated ranges of values for pattern-masking levels of size variation are in the upper tail, indicating that existing variation in body size is unlikely to mask gap/lump pattern

Establishing the severity of the test

Observed frequencies of animal size variation appear to have a left-skewed distribution which clusters animals into two groups   The majority of species exhibit little size variation resulting in little likelihood of change in their size rank or in lump membership   A minority of species, less than 7 percent of all bird species, for example, exhibit sufficient intra-species size variation that their size rank might fall by chance into another lump or into a gap   The integrity of lumps is protected by the fact that within-species size variance of most species would most likely shuffle species within a lump rather than land it in a gap or another lump

The pattern-masking level of size variance required to cause an 'edge species' to land in a gap or in another lump might be compared to an 'escape velocity' which liberates a species from a lump's orbit Against the

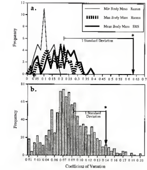


Figure A-5: Distributions of coefficients of variation for mean adult body masses for a) mammal species in Russia (Yablokov 1974) and the Savannah River Site, South Carolina (Cothran et al. 1991), and b) in 994 avian species drawn at random from Dunning (1993). * Arrow marks the pattern-masking value of size variation in boreal prairie mammals or birds needed to make it equally likely for edge species to be in gaps or in neighboring lumps, as calculated by expressing mean gap size as a fraction of the mean body mass of edge species background of stability conferred on lump structure by the majority of species, large size variations within a minority of species could as easily land them in another lump as create a new gap This suggests that only a minority of species might generate new gaps or significantly alter original ones, and only the fraction of that minority are likely to do so The mean value of this escape-level of size variance is indicated by a starred arrow in each diagram (Figure A-5)

Lump analysis does not appear threatened when a majority of species exhibit size variation below the levels which might mask pattern. This prompts the question. "How robust is lump analysis because of this left-skewed distribution of size variation wherein most species vary little in size and a minority varies a great deal?" I can test this by using a uniform distribution of size variation, wherein every species is equally likely to show a specific level of size variation, as the pattern of community level size variation which I will simulate in my test. I can clearly establish the robustness of lump analysis if it can detect the original lump pattern under such radical conditions However, the level of size variation at which lump analysis fails to find the original pattern will aid my estimate of how stabilizing left-skewed patterns of size variation are to lump analysis and to the animal community as a whole I now describe the methods of incorporating such severe protocols in the computer programs of my simulation tests.

Methods for Measuring the Sensitivity of Lump Analysis to Error

This Appendix explores the probabilities that patterns found by lump analysis are spurious because of sensitivity to either of two error sources within animal body mass data sets random species presence and random size variation. In this section I will test the capacity of either error source to prevent lump analysis from detecting an original lump structure. For original data I used two body mass data sets (one bird and one mammal) from the boreal prairie biome (Holling 1992) because their lump structures are published and recognized. These lump patterns appear robust because a variety of pattern detection methodologies (Chapter 2) have consistently predicted the same or very similar lump structures for both data sets.

I will distort the original body mass size distribution of each known data set in a way which simulates the action of either one of the error sources. I can then examine these simulated or mock body size data sets to see to what degree Lump Analysis identifies the original lump pattern. At some level of application, an error source will distort the original size data to the point where the lump pattern recognition rate decays or collapses. This is the pattern-masking error level the level at which lump analysis passes the threshold from reliability to unreliability.

I apply this test using a computer simulation methodology in a three-staged analysis process. I now describe the methods at each of the three stages for 1) simulating the effects of error sources on animal size data sets, 2) detecting lump patterns in those simulated data sets, and 3) measuring the differences in lump pattern between the simulated and original body size data sets. The general organization for the analysis process and each of the three stages is shown in Figure A-6. I run the process multiple times to test its sensitivity to different values for parameters used to recognize lump pattern in Stage 2 and correspondence between lump patterns in Stage 3. I now describe the stages of the process and then the methods of the sensitivity analysis.

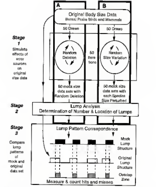


Figure A-6. One run of the computer-aided analysis process. Two alternate analysis paths are shown applying random deletion (Path A) or random size variation (Path B) to generate a set of 50 mock data sets for lump analysis (stage 2) and comparison with the original data sets lump pattern (stage 3)

Stage 1.- Methods for Simulating the Effects of an Error Source

I created synthetic or mock versions of the original data to simulate distortions in body mass data in response to either error source. I organized the synthesis of mock data to capture, at two scales, the variation in response to error by original body mass data. The complete assembly of groups of mock data sets embodies large scale variability, the diversity of responses to a broad range of intensities of each error type. Within the data assembly each group of mock data sets embodies small scale variability, the range of responses to each level of intensity of each error type. I now describe the large and small scale organization of my synthesis of mock data.

Large scale: the assembly of all groups of mock data.

For each error type I synthesized groups of mock data sets, wherein each group represented the response of the original data to a different intensity level of an error source. I tried to capture large scale response variability by examining a wide range of error intensities, organizing them into 14 discrete levels which ranged from 1 to 90 percent as follows: 1, 2, 5, 8, 10, 15, 20, 30, 40, 50, 60, 70, 80 and 90 percent.

Small scale: each group of mock data sets:

Within each group I simulated the intensity level of an error source by approximating its action on the original data. I tried to capture small scale (within-group) response variability by repeating the process fifty times to create a distribution of responses. Therefore, for each group I synthesized fifty mock data sets at a particular level of error operation on the original data.

Random Deletion: I approximated the distortion of error source 1 by randomly deleting species from the original data set and expressed each level as a percent fraction of the original number of species. For example at the ten percent level I created 50 mock data sets by 50 iterations of randomly deleting 10 percent of the species from the original data set.

Random Variation. I approximated error source 2 by randomly varying the size of each species. I simulated random intra-species size variation by determining a new body mass for each species through a random draw from a Gaussian size distribution. The mean body size value of the distribution was the body mass for that species given in the original data set. The error intensity level established the size variation (standard deviation) within the distribution. For example, at the ten percent error level I created 50 mock data sets by 50 iterations of randomly selecting a body mass value for each species from a Gaussian distribution with the original data set's mean size value and a standard deviation set at ten percent of said mean.

Applying the random size variation process created mock data sets with identical numbers of species (n) as that of the original data set, but the mean body mass value of each mock species would differ by some random amount within the range of variation set by the error intensity level. Applying the random deletion process created mock data sets containing body masses identical to those of the root data set but with n differing by an amount set by the error level of the deletion process.

Stage 2 - Methods for Detecting Lumps in Size Distributions

To identify the number and location of modes (lumps) in a size distribution of mean values for adult body masses of each species, I analyzed each original and each mock body size data set using GaP Pattern Analysis (Chapter 2, Restrepo et al. 1997), a process generally referred to as Lump Analysis in this study.

Stage 3 - Measuring Pattern Correspondence Between Lump Structures

I applied the analysis process to calculate measures of correspondence between the original lump structure and those of mock data sets in two ways: numerical differences (mean and variance of lump number counted), and pattern comparison. Pattern correspondence between the original and mock lump data sets is measured by lining up both lump structures on the $\log_{10}$ size axis and comparing the degree of overlap using lump edges as reference points (Figure A-7). Each lump is bounded by two edges, the body mass of the smallest species in the lump is designated the 'leading' edge, and the largest species body mass in the lump is designated the 'trailing' edge. Edge-to-edge comparisons for mutuality are confined by these 'leading-trailing' class designations. I matched leading edges in mock data sets only to leading edges of lumps in the original data set, and likewise, original trailing edges to mock trailing edges.

Without a known statistical model for pattern correspondence to help distinguish significant matches from misses, I devised an arbitrary set of measures which captured the categories of fit that I found in visual comparisons of original and mock lump patterns (Figure A-5). I consider an edge of a mock lump 'mutual' to an original edge if its body mass value falls within a critical tolerance range (Epsilon or ϵ) around the original lump edge's body mass value. I sorted mock lumps into categories-of-fit using a conservative rule that lump edges fit closely when they lie within half the average gap width (epsilon) of the original data set.

I derived epsilon by calculating the value for half the width of each gap in the original data set, wherein the width is the difference between the $\log_{10}$ body masses of leading and trailing edges of neighboring lumps. I normalized each width by dividing both by the leading and by the trailing edge body masses and taking the average of both measures. I found mean (and standard deviation) epsilon values as 0.110 (.061) for mammals and 0.032 (0.012) for birds in the lump structures of the original boreal prairie data sets.

The criteria for classifying lumps into various categories for degrees of fit are based on multiples of epsilon. For instance, the difference between a relatively tight fit ("match") and a less exact one ("straddle") hinges on whether at least one edge in a mock lump is within one or two epsilon of an original edge. Straddles are further defined as "loose" if the distance between its remaining edge and either edge of an original lump is farther than two epsilon.

I calculated overall pattern correspondence between a mock lump data set and the original by aggregating these categories into two groups: "hits" and "misses". I designated as "misses" four categories which indicate little lump pattern correspondence: "No overlap", "Loose Match", "Loose Straddle" and "Inner Lump". All other categories I counted as "hits".

Testing Sensitivity to Different Parameter Values for Pattern Detection

Pattern is detected and measured in Stage 2 (Lump Analysis) and in Stage 3 (lump pattern correspondence). The resolution at which pattern is detected is controlled by a single parameter specific to each method. For Lump Analysis the parameter is the gap statistic criterion level (Criterion Level), and for lump pattern correspondence the parameter is epsilon.

I tested the analysis process for its sensitivity to limited value ranges of each parameter in a nested group of simulations (Table A-4) which tested each of four possible combinations in as many sets of iterations. These 4 tests

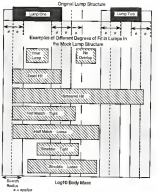


Figure A-7. Correspondence measures between lump structures of original and derivative mock data sets of boreal prairie animals.

Figure A-7 Legend

Elements Measuring Correspondence in Lump Structure

Element	*Description*
Exact Hit	Both mock edges within search radius (epsilon) of the original edge
Smeared Hit	Mock edges match leading and trailing edges of two different lumps in the original data set
Half Match - Tight	One mock edge matched, other edge is within twice the search radius(*e*) of the original edge
Half Match - Loose	One mock edge matched, other edge is greater than twice the search radius(*e*) away from the original edge
Inner Lump	Neither mock edge matches, but mock lump size range falls within that of original lump
Straddle - Tight	Both mock edges are within twice the search radius(*e*), but mock lump size range only partially overlaps that of the original lump size range.
Straddle - Loose	One mock edge is within twice the search radius(*e*), and the other mock edge is more than twice the search radius(*e*) away from the original edge
No Overlap	No part of a mock lump size range overlaps that of any original lump

order the pairings of parameters from most conservative to most liberal combinations, where conservative means avoiding Type I error. The different definitions for the Stage 3 parameter (epsilon) were conservative: epsilon = half the mean gap size (0.13 for mammals, 0.032 for birds), and liberal: epsilon = the median gap size (0.22 for mammals, 0.058 for birds).

Table A-4 Different combinations of input parameters to test sensitivity of the analysis process to output of pattern matching statistics

		Basis of Epsilon Values	
		Conservative	Liberal
Statistical Power Levels		Mean Gap Size	Median Gap Size
Conservative (Low Power)	High Criterion Level	Test 1	Test 2
Neutral (Mid Power)	Mid Criterion Level	Test 3	Test 4
Liberal (High Power)	Low Criterion Level	Test 5	Test 6

In Stage 2 of the analysis process I varied the Criterion Level used in Lump Analysis to test the influence on the lump pattern found of different interpretations of what signifies a 'real gap'. I did this by using different statistical power levels to define the criterion line above which a gap statistic is considered significant. I established the central or 'neutral' point between 'liberal' and 'conservative' Criterion Level definitions following the precedent of Holling (1992). I define the neutral point by selecting a power level which places the criterion line immediately above the 'noise', the range of gap statistic values over which the number of lumps detected sharply increases as the Criterion Line is lowered. This intermediate power level was 0.59 for boreal prairie mammals and 0.68 for boreal prairie birds. For each taxon additional sets of runs were executed at power levels which bracketed

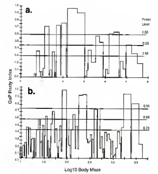


Figure A-8. Interpretations of lump structures derived from Lump Analysis (Gap Detector 2.7) at different levels of statistical power for boreal prairie a. mammals, and b. birds. Each statistical power level line is used as a Criterion level for interpreting gap statistic values to determine lump structure.

the intermediate power level 0.50 and 0.68 (mammals), 0.58 and 0.79 (birds). I visually determined these bracketing power levels by placing criterion lines on graphs of the boreal prairie mammal and bird lump structures (Figure A-8) so as to approximate three interpretations of noise levels of lump analysis: low, intermediate, and high.

Assessing Lump Analysis Sensitivity to Error

I applied random deletion and random size variation as error approximation mechanisms within the analysis process to boreal prairie mammal and bird data sets at three power levels. I report on results of the mid-power level simulations first as a test of the general case. I then report on simulation runs which test sensitivity to higher and lower values of both power as per Table A-4. I do not report on tests using liberal values of epsilon because these results did not differ significantly from conservative epsilon values.

Methods of Graphic Presentation

I present graphic results of visual and numeric comparisons of pattern correspondence between the original and mock lump structures. I created graphs (Figures A-9, A-10, A-12, and A-13) for visual comparison of the general case (mid-power simulations). These graphs present the original lump structure at the bottom with five clusters of mock data sets stacked above. Each cluster of five mock data sets is a sub-sample of a group of 50 which represents the results of applying a specific error level. The shading within each polygon (lump) indicates species data density, darker polygons represent lumps with relatively more species. Visual comparison between the original and mock lump structure is enhanced by extension of the original lump structure vertically with stippled boxes through the areas with clusters of mock lump structures

For numeric tests of the effects of increasing error levels on correspondence between the original and mock lump patterns I quantify an Index of Lump Pattern Recognition (ILPR) as a proportion of the original lump pattern. I do this by taking the difference between hits and misses (see Stage 3 and Figure A-7) and dividing it by the number of lumps in the original data set I graph the ILPR index against error level for all three statistical power levels listed in Table A-4

Within each graph I define two regions which represent conservative and liberal interpretations of robustness in lump pattern recognition For the liberal interpretation I use a gray box with the lower y-axis boundary arbitrarily set at 80 percent of the original lump pattern recognized I set the x-axis boundary by the error level at which the frequency of indices of lump pattern mismatches (misses) is consistently high, as indicated by a sharp decline in the variance in the frequency of misses This signifies that lump pattern recognition is clearly lost. A white box outlines a conservative interpretation based on visual observation of inflection points in the curves of the ILPR index and of graphs of clusters of mock lump structures (Figures A-9, A-10, A-12, A-13) I do not report on tests 2, 4 and 6 because I found little difference in results using either value for the epsilon parameter

Tests to Find the Pattern-masking Level of Random Species Deletion

Random species deletion, graphic comparisons at mid-power simulations

Mammals The pattern-masking error levels associated with significant loss of pattern recognition are between 15 and 20 percent random species deletion.

Mismatch between the original and mock lump patterns is already evident (Figure A-9) at random deletion error levels greater than 15 percent. The overall degree of pattern matching between the original and mock lump structures dramatically declines by the 20 percent deletion error range. Mock lump pattern in the smaller size range (mean log10 body mass < 2) retains its fidelity to the original up to the 25 percent deletion level. Mock lump pattern in the larger size range (mean log10 body mass > 2) shows significant mismatch with the original lump pattern by the 20 percent deletion level.

Birds. The pattern-masking error levels associated with collapse of pattern recognition between bird mock lump patterns and the original occur at random species deletion error levels between 10 percent and 20 percent (Figure A-10). Beginning at that range of error levels striking increases occur in the degree of mismatch between the original and mock lump size ranges. This decay trend is first evident at lower deletion error levels in mock lumps in the smaller size range (mean log10 body mass < 2) and becomes general at error levels above 15 percent. The larger size range (mean log10 body mass > 2) of mock lump data sets retains much of the original lump structure to higher (20 to 25 percent) deletion error levels.

Summary of graphic results. Simulated increases in random deletion of species above those levels found in censuses eliminate some of the original gaps. Increasing deletion intensity above these error levels creates mock data sets composed of fewer lumps with larger body mass size ranges than those lumps in the original data set. These "wider lumps" overlap one or more original gaps with greater frequency as the level of random deletion increases. This effect occurs over different size ranges for bird and mammal lump structures despite the similarity in the range of deletion error levels over which lump pattern decays. Lumps of larger bird species are robust up to

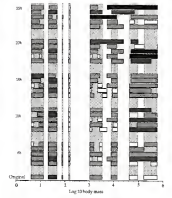


Figure A-9 Lump structure of the original boreal prairie mammal data set with 5 sets of subsamples of mock lump structures created by random size deletion error at levels of 6 10, 15, 20 and 25 percent The pattern of the original lump structure is extended vertically from the bottom of the graph by stippled rectangles higher (20 %) levels of deletion, while lump pattern decay is evident at low (10 %) deletion levels for small birds ($\log_{10}$ body mass < 2) The situation is reversed for mammals. Robust lump recognition occurs at higher deletion intensities for smaller species gap crossing by widening of lumps is evident sooner for species with $\log_{10}$ body mass greater than 2. For both birds and mammals the same region around 2.0 $\log_{10}$ body mass divides the robust and non-robust regions of lump pattern

Random species deletion, numeric comparisons for all simulations

Numeric results (Figure A-11) generally agree with visual interpretations (Figures A-9 and A-10) for both mammals and birds In the case of mammals (Figure A-11a) inflection and decline of indices of pattern recognition occur between 15 and 20 percent random deletion levels, though the pattern-masking deletion level is lower (~12 percent) for low power simulation runs For birds, simulations at all three power levels show indices of pattern recognition passing a threshold at deletion levels around 15 percent. In this case, medium power simulations exhibited declines in pattern recognition at the lowest deletion levels, but the overall trends are fairly similar for all three levels of statistical power For both taxa the loss of robustness over this deletion error range stems from dramatic decreases in indices of pattern matching (hits) and increases in indices of pattern mismatch (misses) accompanied by sharp declines in variance (CV values) for misses. As deletion error levels increase further frequency of misses remains consistently high, and variance of misses remains low suggesting persistent loss of pattern recognition

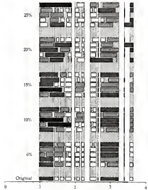


Figure A-10 Lump structure of the original boreal prairie bird data set with 5 sets of subsamples of mock lump structures created by random size deletion error at levels of 6 10, 15, 20 and 25 percent The pattern of the original lump structure is extended vertically from the bottom of the graph by stippled rectangles

Discussion - Is lump analysis robust to random species deletion?

Existing error levels in censuses are not sufficient to affect the reliability of lump analysis. For mammals pattern-masking error levels associated with collapse of pattern recognition occur at the 18 percent level, 6 percent higher than the observed value (12 percent) for omission error. For birds the pattern-masking error levels associated with lump pattern decay occur around 15 percent, but since bird censuses have qualitatively more stringent standards than do those for mammals, it is reasonable to assume that omission error in bird censuses is below 12 percent. The slight differences in pattern-masking deletion error values found at different power levels suggest that the analysis process is somewhat sensitive to power. However, these differences do not change the overall conclusions about the levels at which deletion error rates mask pattern in lump analysis for birds or mammals.

Summary: sensitivity of lump analysis to censusing error

Lump analysis appears robust to census error even when tested using conservative (to Type I error) estimates of census error and unrealistically unstable simulation scenarios of temporal fluctuations in species populations. Lump analysis reliably detected the original pattern at simulated error levels which are higher than observed in nature even when subjected to this extreme simulation of randomized species abundances, wherein the abundance of any species could vary randomly. Simulation of more realistic scenarios of temporal fluctuations of species abundances would probably show robust lump pattern recognition at even higher levels of random species deletion.

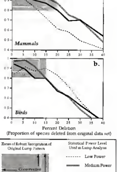


Figure A-11 Lump pattern correspondence between boreal prairie bird and mammal lump structures and mock lump structures Correspondence is indexed as the proportion of the original lump structures still recognized by lump analysis at various levels of random deletion of species

Tests to Find the Pattern-masking Level of Random Variation in Body Size

I used the lump pattern analysis process (Figure A-6) on the same original boreal prairie data sets (Holling 1992) to test the sensitivity of lump analysis to the influence of error source 2. intra-species size variation on body mass data sets. I applied random size variation within the analysis process in exactly the same series of steps used for random deletion. I approximated error source 2 by randomly varying the size of each species in the creation of synthetic or mock data sets, wherein the degree of variation a species' body size might exhibit in a mock data set corresponded to the intensity level of the size variation error. In this manner I used random size variation as a error approximation mechanism to modify boreal prairie mammal and bird data sets and create mock data sets. I analyzed these mock data sets for their lump structures and compared these mock lump structures with the originals to measure the degree of lump pattern correspondence.

I report on results of the mid-power level simulations first as a test of the general case. I then report on simulation runs which test sensitivity to higher and lower values of both powers as per Table A-4. Results are as follows.

Random size variation, graphic comparisons of mid-power simulations

I created graphs (Figures A-12 and A-13) for visual comparison of original and mock lump structures, which were interpreted by lump analysis at middle levels of power. These graphs present the original lump structure at the bottom with five clusters of mock data sets stacked above. Each cluster of five mock data sets is a sub-sample of a group of 50 which represents the results of applying a specific error level of random variation of body size

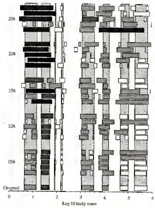


Figure A-12. The lump structure of the original boreal prairie mammals data set with 5 sets of subsamples of mock lump structures created by random size variation error levels of 5,10,15,20 and 25 percent. The pattern of the original lump structure is extended vertically from the bottom by stippled rectangles

Mammals: Mammal mock lump structures show marked declines in lump pattern correspondence with the original lump structure at random size variation error levels between 10 and 15 percent (Figure A-12). Lump pattern analysis crosses the threshold from reliable to unreliable by the 15 percent size variation error level. At these error levels decay in lump pattern correspondence is equally evident across all body sizes in mammal mock lump structures.

Birds. The pattern-masking error level of random variation of body size is much lower in birds than in mammals. Bird mock lump structures begin to show visual pattern mismatch with the original lump structure around the 5 percent random size variation error level (Figure A-13). The increase in pattern mismatch is so precipitous that lump analysis no longer seems robust by the 8 percent size variation error level. Decay in lump pattern is equally evident across all body sizes in bird mock lump structures.

Random size variation, numeric comparisons for all simulations

I test the effects of increasing size variation error levels numerically by quantifying the correspondence between the original and mock lump patterns. I quantify an index of decay in lump pattern recognition as the proportion of the original lump pattern which I find. Within each graph I define two regions which represent conservative (white box) and a liberal (gray box) interpretations of robustness in lump pattern recognition.

Numeric results (Figure A-14) suggest pattern-masking error levels slightly lower than those indicated by graphic comparisons. For mammals the index of lump pattern recognition declines below robust levels in the 10 to 15 percent range of error due to random variation in body size (Figure A-14a). For birds lump pattern correspondence declines below acceptable levels at or below the 5 percent level of random size variation error (Figure A-14b).

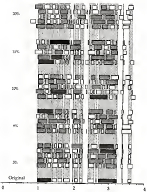


Figure A 13 The lump structure of the original boreal prairie birds data set with 5 sets of subsamples of mock lump structures created by random size variation error levels of 5 10,15,20 and 25 percent The pattern of the original lump structure is extended vertically from the bottom by stippled rectangles

Lump analysis is not robust as error intensity levels increase beyond my visual estimates of a pattern-masking error value for both bird and mammals. At these and higher levels of size variation correspondence between the original and mock lump patterns appears to 'lock in' to persistent and unvarying degrees of mismatch. This conclusion is supported by the observation that the frequency of misses becomes less variable (steep declines in the coefficients of variation) and the frequency of hits becomes more variable as the pattern-masking value of error is surpassed.

In determining pattern-masking error levels of size variation I found taxon-specific sensitivities to statistical power similar to those found for error source 1, random species deletion. Mammal pattern-masking error values showed greater sensitivity than did birds to differences in statistical power levels used in determining lump structure. However, these sensitivities to power appear slight, because the differences in pattern-masking error levels determined at each power level were not so great as to change the overall conclusions

Discussion - Is lump analysis robust to random variation in body size ?

Robustness of lump analysis deteriorates at higher random size variation error levels for boreal prairie mammals than for birds. The pattern-masking levels of size variation error associated with declines in indices of lump pattern recognition are 12 percent for mammals and around 5 percent for birds. The decline in robustness over these pattern-masking levels is confirmed by dramatic changes in the variance of frequency indices of pattern matching (hits) and of pattern mismatching (misses). Specifically, frequency and dependability decline for hits and increase for misses as the pattern-masking level of size variation is surpassed. These trends suggest that the degree of pattern correspondence between mock data sets and the original

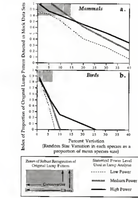


Figure A-14. Lump pattern correspondence between boreal prairie bird and mammal lump structures and mock lump structures. Correspondence is indexed as the proportion of the original lump structures still recognized by lump analysis at various levels of random variation in species body size.

remains consistently low at random size variance levels higher than the pattern-masking levels identified here.

Simulated random variance in body size creates novel gaps in mock lump structures, resulting in more lumps with narrower body mass size ranges than those found in the original lump structure. Visual comparison (Figure A-13) of bird data sets suggests that a majority of the original gaps are evident in the mock lump structures created by 10 percent size variation. On this basis, avian lump analysis still seems somewhat more robust than indicated by numeric indices of pattern correspondence. However decay in lump pattern recognition results from the novel gaps in mock data which now split the size ranges of the original lumps. Similar conclusions can be drawn from comparisons of original and mock mammal lump structures with the added observation that increasing random size variation creates novel lumps which fill the relatively large gaps in the original mammal lump structure.

Summary: Sensitivity of Lump Analysis to Variance in Body Size

Lump analysis is marginally robust for mammals and not at all for birds when I apply a severe simulation of random size variation. I identified pattern-masking levels of size variation error which are just at observed levels of size variation for mammals (12 percent) and below those levels observed in birds (< 5 percent versus 8 percent observed). This simulation of size variation is explicitly severe to try to identify the limits of lump analysis robustness because lump analysis did not initially appear vulnerable to observed frequency distributions of variation in animal size. In this test I allowed the size of *any* species, not the minority observed in nature, to vary as much as any other species.

Lump analysis may be more robust to body size variation in mammals than birds because gaps in mammal lump structures occupy a larger fraction of the size axis than do those of birds It may require higher levels of intra-species size variation to fill the relatively wider mammal gaps The identified pattern-masking levels of size variation are far below those observed because of sexual dimorphism The possibility that each sex in strongly dimorphic species exploits distinct landscape scale ranges and the consequential effects on lump structure deserves further consideration In conclusion, for lump analysis to appear robust, even marginally, under such extreme conditions is clear evidence that it can reliably detect lump pattern in the face of known levels of intra-species size variation

Appendix Summary

I confirmed the reliability of lump analysis, as applied through GaP Pattern Analysis, by demonstrating that it is robust to observed levels of error in the creation of body mass size data sets. I found in literature surveys that the variances of both size and temporal abundances for mammals and birds have left-skewed distributions I found that lump analysis is robust partly because of stability inherent in such distributions of size or abundance variation. I determined this by severe probes of lump analysis through simulations of extreme variation scenarios. Lump analysis is robust to extreme simulations of census error for both birds and mammals and not robust to extreme simulations of size variation in birds, though marginally so for mammals It is quite likely that lump analysis is robust to observed error levels if it shows reliability under such extreme conditions.

APPENDIX B
SPECIES LISTS FOR BIRD OR MAMMAL COMMUNITIES FOUND AT STUDY SITES

DIRECTORY OF SPECIES LISTS FOR EACH TAXON COMPILED BY BIOME

BIRD APPENDICES

MAMMAL APPENDICES

note The literature reference for each animal community species list is included at the top of each of these sub-directories of species lists

BIRD APPENDICES

1. BIRDS OF TEMPERATE FOREST SITES IN NORTH AMERICA AND EUROPE

No.	SITE NAME	REFERENCE
1	Arnot	Birds Observed at the Arnot Teaching and Research Forest, Tompkins and Schuyler Counties, New York, 1983, Dunning, Jr. J.B., 1993.
2	Eglin	Hill, G.E., N. Holler and J. Tucker, Jr., 1994, Dunning, Jr., J.B. 1993.
3	Finger	Smith C.R., 1992, Dunning, Jr. J.B., 1993
4	Hubbard	Holmes R.T., T.W. Sherry and F.W. Sturges, 1986, Dunning, Jr., J.B. 1993
5	Mountain Lake	Angleberger, M.A. 1987, Dunning, Jr., J.B., 1993.
6	Katharine Ordway Preserve	Franz, R., 1991. Dunning, Jr. J.B., 1993
7	Turtle Mountain	Turtle Mountain Resource Inventory. Parks Branch, Natural Resources Division, Manitoba Department of Mines, Natural Resources and Environment, 1979. Dunning, Jr. J.B., 1993
8	Yellowstone NP	McEneaney, T., 1988. Dunning, Jr., J.B., 1993

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
1	Accipiter cooperii	2.647	1		1		1	1	1	1
2	Accipiter gentilis	3.017			1				1	1
3	Accipiter striatus	2.148	1		1		1		1	1
4	Actitis macularia	1.606			1				1	
5	Aechmophorus occidentalis	3.169								1
6	Aegolius acadicus	1.910								1
7	Aeronautes saxatalis	1.507								1
8	Agelaius phoeniceus	1.727	1		1			1	1	1
9	Aimophila aestivalis	1.305		1				1		
10	Aix sponsa	2.821	1		1			1		1
11	Ammodramus bairdii	1.243							1	
12	Ammodramus henslowii	1.117	1		1					
13	Ammodramus lecontei	1.127							1	
14	Ammodramus savannarum	1.230	1		1				1	
15	Anas acuta	3.011							1	1
16	Anas americana	2.878							1	1
17	Anas clypeata	2.789							1	1
18	Anas crecca	2.545							1	1
19	Anas cyanoptera	2.590								1
20	Anas discors	2.587							1	1
21	Anas platyrhynchos	3.034	1		1				1	1
22	Anas rubripes	3.115	1		1					
23	Anas strepera	2.966							1	1
24	Anhinga anhinga	3.092						1		
25	Anthus spinoletta	1.378								1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
26	Anthus spraguei	1.403							1	
27	Aquila chrysaetos	3.603								1
28	Archilochus colubris	0.507	1	1	1	1	1		1	
29	Ardea herodias	3.361						1	1	1
30	Asio flammeus	2.468								1
31	Asio otus	2.414							1	1
32	Athene cunicularia	2.194								1
33	Aythya affinis	2.913							1	1
34	Aythya americana	3.028							1	1
35	Aythya collaris	2.853							1	1
36	Aythya valisineria	3.090							1	
37	Bartramia longicauda	2.172			1					
38	Bombycilla cedrorum	1.512	1		1		1		1	
39	Bonasa umbellus	2.758	1		1		1		1	1
40	Botaurus lentiginosus	2.845	1						1	
41	Branta canadensis canadensis	3.558	1						1	1
42	Branta canadensis moffitti	3.642	1						1	1
43	Bubo virginianus	3.132	1		1			1	1	1
44	Bubulcus ibis	2.529						1		
45	Bucephala albeola	2.627							1	1
46	Bucephala clangula	2.956							1	
47	Bucephala islandica	2.923								1
48	Buteo jamaicensis	3.050	1		1		1	1	1	1
49	Buteo lineatus	2.758	1	1	1		1	1		
50	Buteo platypterus	2.657	1	1	1		1		1	
51	Buteo swainsoni	3.001								1
52	Butorides striatus	2.326	1		1			1		
53	Cardinalis cardinalis	1.650	1	1	1			1		
54	Carduelis pinus	1.164							1	1
55	Carduelis tristis	1.112	1		1		1		1	1
56	Carpodacus cassinii	1.423								1
57	Carpodacus mexicanus	1.330	1		1					
58	Carpodacus purpureus	1.396	1		1	1			1	
59	Casmerodius albus	2.946						1		
60	Cathartes aura	3.160	1		1		1	1	1	
61	Catharus fuscescens	1.494	1		1	1	1		1	1
62	Catharus guttatus	1.491	1		1	1				1
63	Catharus ustulatus	1.489				1				1
64	Catoptrophorus semipalmatus	2.429							1	1
65	Certhia americana	0.924	1		1	1	1			1
66	Ceryle alcyon	2.170			1				1	1
67	Chaetura pelagica	1.373	1				1			
68	Charadrius vociferus	1.980			1			1	1	1
69	Chlidonias niger	1.815							1	1
70	Chondestes grammacus	1.462								1
71	Chordeiles minor	1.789							1	1
72	Cinclus mexicanus	1.764								1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
73	Circus cyaneus	2.636	1		1				1	1
74	Cistothorus palustris	1.051							1	1
75	Cistothorus platensis	0.954							1	
76	Coccyzus americanus	1.806	1	1	1		1			
77	Coccyzus erythropthalmus	1.708	1		1		1		1	
78	Colaptes auratus	2.122	1	1	1		1	1	1	1
79	Colinus virginianus	2.250					1	1		
80	Columba livia	2.551						1		1
81	Columbina passerina	1.479						1		
82	Contopus borealis	1.507								1
83	Contopus sordidulus	1.107								1
84	Contopus virens	1.149	1	1	1	1	1		1	
85	Coragyps atratus	3.318						1		
86	Corvus brachyrhynchos	2.651	1	1	1		1	1	1	1
87	Corvus corax	3.083					1			1
88	Corvus ossifragus	2.455		1				1		
89	Cyanocitta cristata	1.939	1	1	1	1	1	1	1	
90	Cyanocitta stelleri	2.107								1
91	Cygnus buccinator	4.029								1
92	Dendragapus obscurus	3.013								1
93	Dendroica caerulescens	1.004	1		1	1	1			
94	Dendroica cerulea	0.972			1					
95	Dendroica coronata	1.097	1			1				1
96	Dendroica discolor	0.886		1			1			
97	Dendroica dominica	0.973						1		
98	Dendroica fusca	0.987	1		1	1	1			
99	Dendroica magnolia	0.941	1		1					
100	Dendroica pensylvanica	0.984	1		1		1			
101	Dendroica petechia	0.980	1		1				1	1
102	Dendroica pinus	1.076	1	1				1		
103	Dendroica townsendii	0.947								1
104	Dendroica virens	0.944	1		1	1	1			
105	Dolichonyx oryzivorus	1.655	1		1				1	
106	Dryocopus pileatus	2.428	1	1	1		1	1		
107	Dumetella carolinensis	1.567	1	1	1		1		1	1
108	Egretta caerulea	2.536						1		
109	Egretta thula	2.569						1		
110	Egretta tricolor	2.607						1		
111	Empidonax alnorum	1.107	1		1					
112	Empidonax difficilis	1.000								1
113	Empidonax hammondii	1.004								1
114	Empidonax minimus	1.013	1		1	1	1		1	
115	Empidonax oberholseri	1.017								1
116	Empidonax traillii	1.126	1		1					1
117	Empidonax virescens	1.111		1			1			
118	Eremophila alpestris	1.499			1				1	1
119	Eudocimus albus	2.965						1		

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
120	Euphagus cyanocephalus	1.801							1	1
121	Falco columbarius	2.288							1	1
122	Falco mexicanus	2.882								1
123	Falco peregrinus	2.914								1
124	Falco sparverius	2.067	1		1				1	1
125	Fulica americana	2.816							1	1
126	Gallinago gallinago	2.087								1
127	Gallinula chloropus	2.479						1		
128	Gavia immer	3.616								1
129	Geothlypis trichas	1.006	1	1	1		1	1	1	1
130	Glaucidium gnoma	1.806								1
131	Grus canadensis	3.501						1	1	1
132	Haliaeetus leucocephalus	3.677						1		1
133	Hesperiphona vespertina	1.773								1
134	Hirundo pyrrhonota	1.334								1
135	Hirundo rustica	1.203	1		1		1		1	
136	Hirundo rustica rustica	1.260	1		1		1			1
137	Histrionicus histrionicus	2.797								1
138	Hylocichla mustelina	1.720	1		1	1				
139	Icteria virens	1.404		1						
140	Icterus galbula	1.529	1							
141	Icterus galbula galbula	1.539			1				1	1
142	Icterus spurius	1.292			1					
143	Junco hyemalis	1.299	1		1	1	1			1
144	Lanius ludovicianus	1.676		1				1		
145	Larus argentatus	3.063			1					
146	Larus californicus californicus	2.778								1
147	Larus delawarensis	2.714							1	1
148	Larus pipixcan	2.447							1	
149	Leucosticte arctoa atrata	1.423								1
150	Limosa fedoa	2.566								1
151	Lophodytes cucullatus	2.780			1				1	
152	Loxia curvirostra	1.562								1
153	Megaceryle alcyon	2.170	1							
154	Melanerpes carolinus	1.806		1	1			1		
155	Melanerpes erythrocephalus	1.855		1				1		
156	Melanerpes lewis	2.064								1
157	Melanitta fusca deglandi	3.121							1	
158	Meleagris gallopavo	3.763	1		1		1	1		
159	Melospiza georgiana	1.230			1					
160	Melospiza lincolnii	1.241								1
161	Melospiza melodia	1.318	1		1		1		1	1
162	Mergus merganser	3.173								1
163	Mimus polyglottos	1.686	1	1	1			1		
164	Mniotilta varia	1.031	1		1		1			
165	Molothrus ater	1.645	1		1		1		1	1
166	Myadestes townsendi	1.531								1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
167	Mycteria americana	3.421						1		
168	Myiarchus crinitus	1.525	1		1		1		1	
169	Nucifraga columbiana	2.137								1
170	Numenius americanus	2.782								1
171	Nycticorax nycticorax	2.946							1	
172	Oporornis formosus	1.150					1			
173	Oporornis philadelphia	1.101	1		1				1	
174	Oporornis tolmiei	1.017								1
175	Oreoscoptes montanus	1.630								1
176	Otus asio naevius	2.268	1				1	1	1	
177	Otus kennicottii kennicottii	2.223								1
178	Oxyura jamaicensis	2.730							1	1
179	Pandion haliaetus	3.176						1	1	1
180	Parula americana	0.934	1	1			1	1		
181	Parula pitiayumi	0.844					1			
182	Parus atricapillus	1.033	1		1	1			1	1
183	Parus bicolor	1.334	1	1	1		1	1		
184	Parus carolinensis	1.004		1			1	1		
185	Parus gambeli	1.088								1
186	Passer domesticus	1.443	1		1				1	
187	Passerculus sandwichensis	1.306	1		1				1	1
188	Passerella iliaca	1.509								1
189	Passerina amoena	1.196								1
190	Passerina cyanea	1.163	1		1		1		1	
191	Pelecanus erythrorhynchos	3.845							1	1
192	Perisoreus canadensis	1.863								1
193	Phalacrocorax auritus	3.224						1	1	1
194	Phasianus colchicus	3.107	1		1					
195	Pheucticus ludovicianus	1.659	1		1	1	1		1	
196	Pica pica	2.259							1	1
197	Picoides arcticus	1.846								1
198	Picoides borealis	1.639						1		
199	Picoides pubescens	1.431	1	1	1	1	1	1	1	1
200	Picoides tridactylus	1.827								1
201	Picoides villosus	1.631	1		1	1	1	1	1	1
202	Pinicola enucleator	1.751								1
203	Pipilo chlorurus	1.468								1
204	Pipilo erythrophthalmus	1.610	1	1	1		1	1		
205	Piranga ludoviciana	1.449								1
206	Piranga olivacea	1.456	1		1	1	1			
207	Piranga rubra	1.450		1						
208	Podiceps auritus	2.656							1	1
209	Podiceps grisegena	3.010							1	
210	Podiceps nigricollis	2.465							1	1
211	Podilymbus podiceps	2.645						1	1	1
212	Polioptila caerulea	0.778		1			1	1		
213	Pooecetes gramineus	1.414			1				1	1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
214	Porzana carolina	1.873							1	1
215	Progne subis	1.694	1		1				1	
216	Quiscalus major	2.281						1		
217	Quiscalus quiscula	2.065	1	1	1		1	1	1	
218	Rallus elegans	2.537						1		
219	Rallus limicola	1.932								1
220	Regulus calendula	0.825								1
221	Regulus satrapa	0.794								1
222	Riparia riparia	1.164								1
223	Salpinctes obsoletus	1.217								1
224	Sayornis phoebe	1.297	1		1		1		1	
225	Sayornis saya	1.326								1
226	Scolopax minor	2.290	1		1		1	1		
227	Seiurus aurocapillus	1.288	1		1	1	1		1	
228	Seiurus motacilla	1.305	1		1		1			
229	Seiurus noveboracensis	1.250	1						1	
230	Selasphorus platycercus	2.864								1
231	Selasphorus rufus	0.544								1
232	Setophaga ruticilla	0.918	1		1	1	1		1	1
233	Sialia currucoides	1.471							1	1
234	Sialia sialis	1.500	1	1	1		1	1	1	
235	Sitta canadensis	0.991	1		1					1
236	Sitta carolinensis	1.324	1		1	1	1		1	1
237	Sitta pusilla	1.009		1						
238	Sphyrapicus nuchalis	1.662								1
239	Sphyrapicus thyroideus	1.678								1
240	Sphyrapicus varius	1.702	1		1	1			1	
241	Spizella breweri	1.037								1
242	Spizella pallida	1.079							1	
243	Spizella passerina	1.090	1	1	1		1		1	1
244	Spizella pusilla	1.097	1		1		1			
245	Steganopus tricolor	1.745							1	1
246	Stelgidopteryx serripennis	1.201	1							1
247	Stellula calliope	0.417								1
248	Sterna caspia	2.818								1
249	Sterna hirundo	2.079							1	1
250	Strix nebulosa	2.997								1
251	Strix varia	2.860	1		1		1	1		
252	Sturnella magna	1.973	1		1		1	1		
253	Sturnella neglecta	2.014							1	1
254	Sturnus vulgaris	1.920	1		1		1	1	1	1
255	Tachycineta bicolor	1.303	1		1				1	1
256	Tachycineta thalassina	1.151								1
257	Thryothorus ludovicianus	1.272		1	1		1	1		
258	Toxostoma rufum	1.838	1	1	1		1	1	1	
259	Tringa macularia	1.606			1					1
260	Troglodytes aedon	1.037	1		1				1	1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3	4	5	6	7	8
261	Troglodytes troglodytes	0.949			1	1	1			
262	Turdus migratorius	1.888	1		1	1	1		1	1
263	Tympanuchus phasianellus	2.946							1	
264	Tyrannus tyrannus	1.639	1	1	1				1	1
265	Tyrannus verticalis	1.598							1	1
266	Tyto alba	2.723			1					
267	Vermivora celata	0.954								1
268	Vermivora pinus	0.924	1		1					
269	Vermivora ruficapilla	0.941	1		1					
270	Vireo flavifrons	1.258	1				1		1	
271	Vireo gilvus	1.170			1				1	1
272	Vireo griseus	1.057		1				1		
273	Vireo olivaceus	1.223	1	1	1	1	1		1	
274	Vireo philadelphicus	1.086				1				
275	Vireo solitarius	1.210	1		1	1	1			
276	Wilsonia canadensis	0.839	1		1		1			
277	Wilsonia citrina	1.017		1	1		1			
278	Wilsonia pusilla	0.886								1
279	Xanthocephalus xanthocephalus	1.751							1	1
280	Zenaida macroura	2.319	1	1	1			1	1	1
281	Zonotrichia albicollis	1.413	1						1	
282	Zonotrichia leucophrys	1.468								1

2. BIRDS OF QUASI-BOREAL FOREST SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Chilkat Valley, Haines, Alaska	Bertsch, D. 1994
2	Kluane	Theberge, J.B. 1976, Dunning, Jr., J.B., 1993
3	Northern Yukon National Park, Yukon, Canada	Jingfors, K., 1989; Dunning, Jr., J.B., 1993

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3
1	Accipiter gentilis	3.017	1		
2	Accipiter striatus	2.148	1	1	
3	Aegolius acadicus	1.910	1		
4	Agelaius phoeniceus	1.727	1		
5	Anas acuta	3.011	1		1
6	Anas americana	2.878	1		
7	Anas clypeata	2.799	1		
8	Anas crecca	2.545	1		
9	Anas discors	2.587	1		
10	Anas platyrhynchos	3.034	1		
11	Anas strepera	2.966	1		
12	Anser albifrons	3.413			1
13	Anthus spinoletta	1.378		1	
14	Aquila chrysaetos	3.603	1		1
15	Ardea herodias	3.381	1		
16	Asio flammeus	2.468	1		
17	Aythya affinis	2.913	1		1
18	Aythya marila	2.970	1		1
19	Aythya valisineria	3.090	1		
20	Bartramia longicauda	2.172	1		
21	Brachyramphus brevirostris	2.350	1		
22	Brachyramphus marmoratus	2.346	1		
23	Branta bernicla	3.116			1
24	Branta canadensis canadensis	3.538	1		1
25	Branta canadensis moffitti	3.642	1		1
26	Bubo virginianus	3.132	1		
27	Bucephala clangula	2.956	1		
28	Bucephala islandica	2.923	1		
29	Buteo jamaicensis	3.050	1		
30	Buteo lagopus	2.974			1
31	Calcarius lapponicus	1.436			1
32	Calidris melanotos	1.834			1
33	Calidris minutilla	1.365	1		
34	Calidris pusilla	1.406			1
35	Carduelis flammea	1.116	1		1
36	Carduelis hornemanni	1.104	1		
37	Carduelis pinus	1.164	1		
38	Carpodacus purpureus	1.396	1		
39	Catharus guttatus	1.491	1	1	
40	Catharus minimus	1.516	1	1	
41	Catharus ustulatus	1.489	1	1	
42	Cepphus columba	2.688	1		

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3
43	Certhia americana	0.924	1		
44	Chordeiles minor	1.789	1		
45	Cinclus mexicanus	1.764	1		
46	Circus cyaneus	2.636	1		
47	Clangula hyemalis	2.942	1		1
48	Colaptes auratus	2.122	1	1	
49	Contopus borealis	1.307	1	1	
50	Contopus sordidulus	1.107	1	1	
51	Corvus caurinus	2.603	1		
52	Corvus corax	3.083	1		
53	Cyanocitta stelleri	2.107	1		
54	Cygnus buccinator	4.029	1		
55	Cygnus columbianus	3.821			1
56	Dendragapus canadensis	2.673	1		
57	Dendragapus obscurus	3.013	1		
58	Dendroica coronata	1.097	1	1	
59	Dendroica petechia	0.980	1		
60	Dendroica striata	1.214		1	
61	Dendroica townsendi	0.947	1		
62	Empidonax alnorum	1.107	1	1	
63	Empidonax hammondii	1.004	1		
64	Eremophila alpestris	1.499	1	1	
65	Euphagus carolinus	1.774	1	1	
66	Falco columbarius	2.288	1		
67	Falco peregrinus	2.914	1		1
68	Falco rusticolus	3.187			1
69	Falco sparverius	2.067	1	1	
70	Fratercula cirrhata	2.892	1		
71	Fratercula corniculata	2.792	1		
72	Gallinago gallinago	2.097	1	1	
73	Gavia immer	3.616	1		
74	Gavia pacifica	3.220			1
75	Gavia stellata	3.191	1		1
76	Geothlypis trichas	1.006	1		
77	Glaucidium gnoma	1.808	1		
78	Haliaeetus leucocephalus	3.677	1		
79	Hirundo rustica	1.209	1		
80	Hirundo rustica rustica	1.260	1		
81	Histrionicus histrionicus	2.797	1		
82	Junco hyemalis	1.299	1	1	
83	Lagopus lagopus	2.754	1		1
84	Lagopus leucurus	2.550	1		
85	Lagopus mutus	2.623	1		1
86	Larus argentatus	3.063	1		
87	Larus canus	2.610	1		
88	Larus glaucescens	3.004	1		
89	Larus hyperboreus	3.160			1
90	Leucosticte arctoa atrata	1.423	1		
91	Limnodromus griseus	2.058	1		
92	Lophodytes cucullatus	2.790	1		
93	Loxia curvirostra	1.562	1		

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3
94	Loxia leucoptera	1.425	1		
95	Megaceryle alcyon	2.170	1		
96	Melanitta fusca	3.245	1		
97	Melanitta perspicillata	2.980	1		1
98	Melospiza lincolnii	1.241	1		
99	Melospiza melodia	1.318	1		
100	Mergus merganser	3.173	1		
101	Mergus serrator	3.011	1		
102	Molothrus ater	1.645	1		
103	Motacilla flava flava	1.246			1
104	Myadestes townsendi	1.531		1	
105	Oenanthe oenanthe oenanthe	1.339			1
106	Oporornis tolmiei	1.017	1		
107	Pandion haliaetus	3.176	1		
108	Parus atricapillus	1.030	1		
109	Parus rufescens	0.987	1		
110	Passerculus sandwichensis	1.306	1	1	1
111	Passerella iliaca	1.509	1		
112	Phalacrocorax auritus	3.224	1		
113	Phalacrocorax pelagicus	3.282	1		
114	Phalaropus lobatus	1.572			1
115	Pica pica	2.259	1		
116	Picoides pubescens	1.431	1		
117	Picoides tridactylus	1.827	1		
118	Picoides villosus	1.831	1		
119	Pluvialis dominica	2.161			1
120	Podiceps auritus	2.656	1		
121	Podiceps grisegena	3.000	1		
122	Regulus calendula	0.805	1	1	
123	Regulus satrapa	0.794	1		
124	Riparia riparia	1.164	1		
125	Selasphorus rufus	0.544	1		
126	Sialia currucoides	1.471	1		
127	Sitta canadensis	0.991	1		
128	Somateria mollissima	3.309			1
129	Sphyrapicus ruber daggetti	1.659	1		
130	Spizella arborea	1.303	1	1	
131	Spizella passerina	1.090	1	1	
132	Stercorarius longicaudus	2.468			1
133	Stercorarius parasiticus	2.653			1
134	Sterna paradisaea	2.041	1		1
135	Strix nebulosa	2.997	1		
136	Sturnus vulgaris	1.930	1		
137	Surnia ulula	2.506	1		
138	Tachycineta bicolor	1.303	1		
139	Tachycineta thalassina	1.151	1		
140	Tringa flavipes	1.908	1	1	
141	Tringa macularia	1.606	1		
142	Tringa melanoleuca	2.233	1		
143	Troglodytes troglodytes	0.949	1		
144	Turdus migratorius	1.888	1	1	

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site Number 1	2	3
145	Vermivora celata	0.954	1	1	
146	Vireo gilvus	1.170	1		
147	Wilsonia pusilla	0.886	1	1	
148	Zonotrichia atricapilla	1.474	1	1	
149	Zonotrichia leucophrys	1.468	1	1	1

3. BIRDS OF BOREAL GRASSLAND SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Delta Marsh, Manitoba	Cuthbert, C.W. R.E. Jones 1983
2.	Matador Saskatchewan, Canada	Maher W.J. 1974 Dunning, Jr. J.B. 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
1	Accipiter cooperii	2.647	1	1	45	Catharus fuscescens	1.494	1	1
2	Accipiter striatus	2.148		1	46	Catoptrophorus semipalmatus	2.429	1	1
3	Actitis macularia	1.606	1		47	Chaetura pelagica	1.373	1	
4	Aechmophorus occidentalis	3.146	1	1	48	Charadrius melodus	1.742	1	1
5	Aegolius acadicus	1.910		1	49	Charadrius vociferus	1.980	1	1
6	Agelaius phoeniceus	1.727	1	1	50	Chlidonias niger	1.815	1	1
7	Aix sponsa	2.831	1		51	Chondestes grammacus	1.462	1	1
8	Ammodramus bairdii	1.243		1	52	Chordeiles minor	1.799		1
9	Ammodramus leconteii	1.127	1		53	Circus cyaneus	2.636	1	1
10	Ammodramus savannarum	1.230		1	54	Cistothorus palustris	1.071	1	
11	Anas acuta	3.011	1	1	55	Cistothorus platensis	0.954	1	
12	Anas americana	2.878	1	1	56	Coccyzus erythropthalmus	1.708	1	1
13	Anas clypeata	2.788	1	1	57	Colaptes auratus	2.122	1	1
14	Anas crecca	2.545	1	1	58	Colaptes auratus	2.152	1	
15	Anas discors	2.587	1	1	59	Columba livia	2.551	1	
16	Anas platyrhynchos	3.034	1	1	60	Contopus sordidulus	1.107		1
17	Anas strepera	2.966	1	1	61	Contopus virens	1.149	1	
18	Anthus spragueii	1.403	1	1	62	Corvus brachyrhynchos	2.651	1	1
19	Aquila chrysaetos	3.603		1	63	Coturnicops noveboracensis	1.713	1	
20	Ardea herodias	3.381		1	64	Cyanocitta cristata	1.939	1	
21	Asio flammeus	2.468	1	1	65	Dendroica castanea	1.100	1	
22	Asio otus	2.434	1	1	66	Dendroica coronata	1.097		1
23	Athene cunicularia	2.194	1	1	67	Dendroica petechia	0.980	1	1
24	Aythya affinis	2.913	1	1	68	Dolichonyx oryzivorus	1.655	1	1
25	Aythya americana	3.028	1	1	69	Dumetella carolinensis	1.567	1	1
26	Aythya valisineria	3.090	1	1	70	Empidonax alnorum	1.107	1	
27	Bartramia longicauda	2.172	1	1	71	Empidonax minimus	1.033	1	1
28	Bombycilla cedrorum	1.512	1	1	72	Eremophila alpestris	1.499	1	1
29	Bonasa umbellus	2.758	1		73	Euphagus cyanocephalus	1.801	1	1
30	Botaurus lentiginosus	2.849	1	1	74	Falco columbarius	2.288		1
31	Branta canadensis canadensis	3.558	1	1	75	Falco mexicanus	2.882		1
32	Branta canadensis moffitti	3.642	1	1	76	Falco sparverius	2.067	1	1
33	Bubo virginianus	3.132	1	1	77	Fulica americana	2.816	1	1
34	Bucephala clangula	2.956	1	1	78	Gallinago gallinago	2.087	1	1
35	Buteo jamaicensis	3.050	1	1	79	Geothlypis trichas	1.006	1	1
36	Buteo regalis	3.039		1	80	Grus canadensis	3.501		1
37	Buteo swainsoni	3.001		1	81	Haliaeetus leucocephalus	3.677		1
38	Calamospiza melanocorys	1.575		1	82	Hirundo pyrrhonota	1.334	1	1
39	Calcarius mccownii	1.365		1	83	Hirundo rustica	1.225	1	
40	Calcarius ornatus	1.276	1	1	84	Hirundo rustica rustica	1.260	1	1
41	Caprimulgus vociferus	1.722	1		85	Icteria virens	1.404		1
42	Carduelis pinus	1.164	1	1	86	Icterus galbula galbula	1.529	1	1
43	Carduelis tristis	1.112	1	1	87	Icterus spurius	1.292	1	
44	Cathartes aura	3.166		1	88	Ixobrychus exilis	1.860	1	

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
89	Larus ludovicianus	1.676	1	1	124	Porzana carolina	1.873	1	1
90	Larus argentatus	3.063	1		125	Progne subis	1.694	1	
91	Larus californicus californicus	2.778		1	126	Quiscalus quiscula	2.065	1	1
92	Larus delawarensis	2.714	1	1	127	Rallus limicola	1.932	1	
93	Larus pipixcan	2.447	1	1	128	Recurvirostra americana	2.500	1	1
94	Limosa fedoa	2.566	1	1	129	Riparia riparia	1.164	1	1
95	Lophodytes cucullatus	2.730	1		130	Sayornis phoebe	1.297	1	
96	Melanerpes erythrocephalus	1.855	1		131	Sayornis saya	1.326		1
97	Melanitta fusca	3.245		1	132	Setophaga ruticilla	0.918		1
98	Melospiza melodia	1.318	1	1	133	Sialia currucoides	1.471		1
99	Mergus merganser	3.173	1		134	Sitta carolinensis	1.324	1	
100	Mimus polyglottos	1.686	1		135	Sphyrapicus varius	1.702		1
101	Molothrus ater	1.645	1	1	136	Spizella pallida	1.079	1	1
102	Myiarchus crinitus	1.525	1		137	Spizella passerina	1.090		1
103	Numenius americanus	2.792		1	138	Steganopus tricolor	1.745	1	1
104	Nycticorax nycticorax	2.946	1	1	139	Stelgidopteryx ruficollis	1.182		1
105	Otus asio naevius	2.288	1		140	Sterna caspia	2.816	1	
106	Oxyura jamaicensis	2.730	1	1	141	Sterna forsteri	2.199	1	
107	Parus atricapillus	1.083	1	1	142	Sterna hirundo	2.079	1	1
108	Passer domesticus	1.443	1	1	143	Sturnella neglecta	2.014	1	1
109	Passerculus sandwichensis	1.306	1	1	144	Sturnus vulgaris	1.930	1	1
110	Pelecanus erythrorhynchos	3.845	1		145	Tachycineta bicolor	1.303	1	1
111	Perdix perdix	2.592	1	1	146	Toxostoma rufum	1.838	1	1
112	Phalacrocorax auritus	3.224	1	1	147	Tringa macularia	1.606		1
113	Phasianus colchicus	3.107		1	148	Troglodytes aedon	1.037	1	1
114	Pheucticus ludovicianus	1.659	1		149	Turdus migratorius	1.888	1	1
115	Pica pica	2.259	1	1	150	Tympanuchus phasianellus	2.946	1	1
116	Picoides pubescens	1.431	1		151	Tyrannus tyrannus	1.639	1	1
117	Picoides villosus	1.801	1	1	152	Tyrannus verticalis	1.598	1	1
118	Pipilo erythrophthalmus	1.619		1	153	Vermivora celata	0.954		1
119	Podiceps auritus	2.656	1	1	154	Vireo gilvus	1.170	1	
120	Podiceps grisegena	3.010	1	1	155	Vireo olivaceus	1.223	1	1
121	Podiceps nigricollis	2.465	1	1	156	Xanthocephalus xanthocephalus	1.751	1	1
122	Podilymbus podiceps	2.645	1	1	157	Zenaida macroura	2.319	1	1
123	Pooecetes gramineus	1.414	1	1					

4. BIRDS OF NEOTROPICAL DRY DECIDUOUS FOREST SITES IN CENTRAL AND SOUTH AMERICA

No	SITE NAME	REFERENCE
1	Parque Nacional Machalilla	Parker III T.A. 1992; Dunning, Jr. J.B., 1993

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1
1	Adelomyia melanogenys	0.580	1	90	Mionectes oleagineus	1.083	1
2	Amaurospiza concolor	1.114	1	91	Molothrus bonariensis	1.541	1
3	Amazilia amazilia	0.633	1	92	Momotus momota aequatorialis	2.199	1
4	Amazilia tzacatl	0.699	1	93	Momotus momota conexus	2.037	1
5	Amblycercus holosericeus	1.820	1	94	Momotus momota lessoni	2.124	1
6	Ara ambigua	3.114	1	95	Muscigralla brevicauda	1.100	1
7	Arremon abeillei	1.413	1	96	Myiarchus phaeocephalus	1.435	1
8	Arremon aurantiirostris	1.538	1	97	Myiarchus tuberculifer	1.299	1
9	Atlapetes brunneinucha	1.668	1	98	Myiobius atricaudus	1.000	1
10	Aulacorhynchus haematopygus	2.332	1	99	Myioborus miniatus	0.978	1
11	Basileuterus fraseri	1.064	1	100	Myiodynastes bairdii	1.653	1
12	Buteo brachyurus	2.695	1	101	Myiodynastes maculatus	1.662	1
13	Buteogallus urubitinga	3.009	1	102	Myiopagis subplacens	1.217	1
14	Butorides striatus	2.326	1	103	Myiophobus fasciatus	0.996	1
15	Cacicus cela	1.984	1	104	Myiozetetes similis	1.447	1
16	Campephilus gayaquilensis	2.383	1	105	Myrmotherula schisticolor	0.992	1
17	Camptostoma obsoletum	0.903	1	106	Nyctibius griseus	2.267	1
18	Campylorhamphus trochilirostris	1.392	1	107	Nyctidromus albicollis	1.726	1
19	Campylorhynchus fasciatus	1.398	1	108	Odontophorus erythrops	2.447	1
20	Capsiempis flaveola	0.886	1	109	Ortalis erythroptera	2.801	1
21	Cathartes aura	3.166	1	110	Otus roboratus roboratus	2.174	1
22	Catharus dryas	1.545	1	111	Pachyramphus homochrous	1.544	1
23	Ceryle torquata	2.501	1	112	Parabuteo unicinctus	2.918	1
24	Chaetura brachyura	1.262	1	113	Parula pitiayumi	0.844	1
25	Chaetura cinereiventris	1.143	1	114	Penelope purpurascens	3.314	1
26	Chloroceryle americana	1.574	1	115	Phaeomyias murina	1.000	1
27	Chlorophanes spiza	1.279	1	116	Phaethornis superciliosus	0.778	1
28	Chlorospingus canigularis	1.235	1	117	Phyllomyias griseiceps	0.857	1
29	Ciccaba nigrolineata	2.649	1	118	Piaya cayana	2.033	1
30	Claravis pretiosa	1.828	1	119	Piculus rubiginosus	1.747	1
31	Coereba flaveola	0.973	1	120	Picumnus olivaceus	1.025	1
32	Columba cayennensis	2.380	1	121	Picumnus sclateri	1.029	1
33	Columba speciosa	2.398	1	122	Pionus chalcopterus	2.332	1
34	Columba subvinacea	2.240	1	123	Pipra mentalis	1.176	1
35	Contopus cinereus	1.068	1	124	Piranga flava	1.580	1
36	Contopus fumigatus	1.314	1	125	Platyrinchus mystaceus	0.987	1
37	Coragyps atratus	3.319	1	126	Polioptila plumbea	0.778	1
38	Cranioleuca erythrops	1.226	1	127	Polyborus plancus	2.946	1
39	Crotophaga sulcirostris	1.913	1	128	Progne chalybea	1.632	1
40	Crypturellus soui	2.338	1	129	Pulsatrix perspicillata	2.943	1
41	Crypturellus transfasciatus	2.452	1	130	Pyrocephalus rubinus	1.158	1
42	Cyanocompsa cyanoides	1.512	1	131	Ramphastos swainsonii	2.810	1
43	Cyclarhis gujanensis	1.459	1	132	Ramphocaenus melanurus	0.987	1
44	Dacnis lineata	1.040	1	133	Rhodospingus cruentus	1.033	1
45	Damophila julie	0.519	1	134	Sakesphorus bernardi	1.483	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1
46	Dendrocincla fuliginosa	1.571	1	135	Saltator albicollis	1.567	1
47	Dryocopus lineatus	2.270	1	136	Saltator maximus	1.676	1
48	Dysithamnus mentalis	1.107	1	137	Sarcoramphus papa	3.531	1
49	Egretta alba	2.932	1	138	Scaphidura oryzivora	2.311	1
50	Egretta thula	2.569	1	139	Schiffornis turdinus	1.501	1
51	Elaenia flavogaster	1.393	1	140	Sittasomus griseicapillus	1.148	1
52	Elanoides forficatus	2.645	1	141	Spizaetus ornatus	3.104	1
53	Eubucco bourcierii	1.525	1	142	Spizaetus tyrannus	3.011	1
54	Euphonia laniirostris	1.176	1	143	Sporophila americana	1.059	1
55	Euphonia xanthogaster	1.114	1	144	Sporophila telasco	0.924	1
56	Euscarthmus meloryphus	0.833	1	145	Stelgidopteryx ruficollis	1.182	1
57	Falco peregrinus	2.914	1	146	Streptoprocne zonaris	1.992	1
58	Falco rufigularis	2.190	1	147	Synallaxis brachyura	1.262	1
59	Falco sparverius	2.067	1	148	Synallaxis tithys	1.199	1
60	Formicarius nigricapillus	1.780	1	149	Tachyphonus luctuosus	1.114	1
61	Forpus coelestis	1.418	1	150	Tangara gyrola	1.322	1
62	Geothlypis aequinoctialis	1.117	1	151	Tangara icterocephala	1.342	1
63	Geranospiza caerulescens	2.529	1	152	Tapera naevia	1.717	1
64	Glaucidium brasilianum	1.821	1	153	Taraba major	1.829	1
65	Glyphorynchus spirurus	1.164	1	154	Thalurania colombica	0.653	1
66	Grallaria guatimalensis	1.974	1	155	Thraupis episcopus	1.544	1
67	Heliomaster longirostris	0.820	1	156	Thraupis palmarum	1.591	1
68	Hemithraupis guira	1.079	1	157	Tiaris obscura	1.049	1
69	Henicorhina leucophrys	1.247	1	158	Tityra semifasciata	1.899	1
70	Herpetotheres cachinnans	2.821	1	159	Todirostrum cinereum	0.806	1
71	Hylocryptus erythrocephalus	1.667	1	160	Tolmomyias sulphurescens	1.173	1
72	Icterus mesomelas	1.601	1	161	Troglodytes aedon	1.037	1
73	Ictinia plumbea	2.393	1	162	Troglodytes solstitialis	1.072	1
74	Lepidocolaptes souleyetii	1.410	1	163	Trogon collaris	1.807	1
75	Leptodon cayanensis	2.695	1	164	Trogon melanurus	2.076	1
76	Leptopogon superciliaris	1.068	1	165	Trogon violaceus	1.712	1
77	Leptotila verreauxi	2.185	1	166	Turdus reevei	1.785	1
78	Leucopternis occidentalis	2.810	1	167	Tyrannus melancholicus	1.573	1
79	Lophotriccus pileatus	0.866	1	168	Tyto alba	2.723	1
80	Lurocalis semitorquatus	1.948	1	169	Veniliornis callonotus	1.398	1
81	Malacoptila panamensis	1.629	1	170	Veniliornis kirkii	1.565	1
82	Manacus manacus	1.176	1	171	Vireo olivaceus	1.223	1
83	Mecocerculus calopterus	0.845	1	172	Volatinia jacarina	0.987	1
84	Megarynchus pitangua	1.870	1	173	Xenops minutus	1.025	1
85	Melanerpes pucherani	1.807	1	174	Xenops rutilans	1.086	1
86	Melanopareia elegans	1.204	1	175	Xiphorhynchus erythropygius	1.673	1
87	Micrastur ruficollis	2.252	1	176	Zenaida asiatica	2.160	1
88	Microcerculus marginatus	1.238	1	177	Zenaida auriculata	2.057	1
89	Mimus longicaudatus	1.823	1	178	Zimmerius viridiflavus	1.090	1

5. BIRDS OF NEOTROPICAL CHACO AND CERRADO SITES IN SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Bolivian Chaco: Santa Cruz, Bolivia	Parker III, T.A., 1993; Dunning, Jr., J.B., 1993.
2	Cerrado Localities, SE Bolivia	Parker III, T.A. and J.V. Remsen Jr., 1993, Dunning, Jr., J.B., 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
1	Accipiter bicolor	0.508	1	
2	Accipiter striatus	0.643	1	
3	Amazona aestiva	0.663	1	
4	Amazonetta brasiliensis	0.740	1	
5	Ammodramus humeralis	1.225	1	1
6	Anhinga anhinga	0.844	1	
7	Anthus lutescens	0.851	1	
8	Ara chloroptera	3.087	1	1
9	Aramides cajanea	0.903	1	
10	Aramus guarauna	0.924	1	
11	Aratinga aurea	0.924	1	
12	Aratinga leucophthalmus	0.987	1	
13	Arremon flavirostris	1.455	1	1
14	Asthenes baeri	0.996	1	
15	Bartramia longicauda	1.000	1	
16	Basileuterus flaveolus	1.161	1	1
17	Basileuterus hypoleucus	0.978		1
18	Batara cinerea	1.013	1	
19	Brotogeris versicolurus	1.037	1	
20	Bubo virginianus	3.132	1	1
21	Bubulcus ibis	1.041	1	
22	Buteo albicaudatus	2.946	1	1
23	Buteo brachyurus	1.057	1	
24	Buteo magnirostris	2.438	1	1
25	Buteogallus urubitinga	1.079	1	
26	Cacicus solitarius	1.086	1	
27	Cairina moschata	1.089	1	
28	Callonetta leucophrys	1.090	1	
29	Campephilus leucopogon	1.090	1	
30	Campephilus melanoleucos	2.386	1	1
31	Camptostoma obsoletum	0.903	1	1
32	Campylorhamphus trochilirostris	1.128	1	
33	Campylorhynchus turdinus	1.130	1	
34	Caprimulgus parvulus	1.141	1	
35	Caprimulgus rufus	1.148	1	
36	Carduelis magellanica	1.159	1	
37	Cariama cristata	1.161	1	
38	Casiornis rufa	1.170	1	
39	Cathartes aura	3.166	1	1
40	Cathartes burrovianus	1.173	1	
41	Catharus ustulatus	1.173	1	
42	Celeus lugubris	2.155	1	1
43	Certhiaxis cinnamomea	1.170	1	
44	Ceryle torquata	1.182	1	
126	Megarhynchus pitangua	1.870	1	1
127	Melanerpes cactorum	1.816	1	
128	Mesembrinibis cayennensis	1.821	1	
129	Micrastur ruficollis	1.829	1	
130	Micrastur semitorquatus	1.859	1	
131	Milvago chimachima	2.506		1
132	Mimus saturninus	1.863	1	
133	Mimus triurus	1.870	1	
134	Molothrus badius	1.900	1	
135	Molothrus bonariensis	1.924	1	
136	Momotus momota aequatorialis	2.199	1	1
137	Momotus momota comenus	2.037	1	1
138	Momotus momota lessoni	2.128	1	1
139	Myiarchus ferox	1.948	1	
140	Myiarchus tuberculifer	1.976	1	
141	Myiarchus tyrannulus	1.641	1	1
142	Myiodynastes maculatus	1.992	1	
143	Myiopagis caniceps	1.013		1
144	Myiopagis viridicata	2.004	1	
145	Myiopagis viridicata minima	2.016	1	
146	Myiophobus fasciatus	0.996	1	1
147	Myiopsitta monachus	2.037	1	
148	Myrmorchilus strigilatus	2.057	1	
149	Nandayus nenday	2.067	1	
150	Nemosia pileata	2.096	1	
151	Notiochelidon cyanoleuca	2.097	1	
152	Nyctibius grandis	2.106	1	
153	Nyctibius griseus	2.107	1	
154	Nyctidromus albicollis	1.726		1
155	Ortalis canicollis	2.130	1	
156	Otus choliba	2.146	1	
157	Pachyramphus polychopterus	2.155	1	
158	Pachyramphus viridis	2.172	1	
159	Parabuteo unicinctus	2.173	1	
160	Paroaria coronata	2.173	1	
161	Parula pitiayumi	0.844	1	1
162	Phacellodomus ruber	2.190	1	
163	Phacellodomus rufifrons	2.190	1	
164	Phacellodomus sibilatrix	2.196	1	
165	Phaeomyias murina	2.196	1	
166	Phaeoprogne tapera	1.558		1
167	Phalacrocorax brasilianus	2.220	1	
168	Pheucticus aureoventris	1.816	1	1
169	Phytotoma rutila	2.234	1	

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
45	Chaetura andrei	1.190	1		170	Piaya cayana	2.033	1	1
46	Chauna torquata	1.201	1		171	Piaya minuta	1.604		1
47	Chloroceryle amazona	1.204	1		172	Picoides mixtus	2.252	1	
48	Chloroceryle americana	1.205	1		173	Piculus chrysochloros	2.267	1	
49	Chlorostilbon aureoventris	1.223	1		174	Picumnus cirratus	1.061	1	1
50	Chondrohierax uncinatus	1.225	1		175	Pionus maximilliani	2.326	1	
51	Chunga burmeisteri	1.230	1		176	Pipra fasciicauda	1.201		1
52	Cnemotriccus fuscatus	1.236	1		177	Piranga flava	1.580	1	1
53	Coccyzus melacoryphus	1.260	1		178	Pitangus sulphuratus	2.344	1	
54	Colaptes melanochloros	1.265	1		179	Podager nacunda	2.344	1	
55	Columba cayennensis	1.279	1		180	Polioptila dumicola	2.362	1	
56	Columba picazuro	1.290	1		181	Polyborus plancus	2.380	1	
57	Columbina picui	1.699	1	1	182	Poospiza melanoleuca	2.386	1	
58	Columbina talpacoti	1.299	1		183	Poospiza torquata	2.421	1	
59	Conirostrum speciosum	0.924	1	1	184	Progne chalybea	2.422	1	
60	Coragyps atratus	3.318	1	1	185	Psarocolius decumanus	2.362	1	1
61	Coryphistera alaudina	1.313	1		186	Pseudoseisura lophotes	2.444	1	
62	Coryphospingus cucullatus	1.173	1	1	187	Pulsatrix perspicillata	2.941	1	1
63	Cranioleuca pyrrhophia	1.302	1		188	Pyriglena leuconota	1.509	1	1
64	Crax fasciolata	1.330	1		189	Ramphastos toco	2.732	1	1
65	Crotophaga ani	2.016	1	1	190	Rhea americana	2.318	1	
66	Crypturellus parvirostris	1.350	1		191	Rhinocrypta lanceolata	2.529	1	
67	Crypturellus tataupa	1.371	1		192	Rhynchotus rufescens	2.954		1
68	Crypturellus undulatus	2.732	1	1	193	Rostrhamus sociabilis	2.529	1	
69	Cyanocompsa brissonii	1.314	1	1	194	Saltator aurantiirostris	2.532	1	
70	Cyanocorax chrysops	1.380	1		195	Saltator coerulescens	2.558	1	
71	Cyanocorax cyanomelas	2.346	1	1	196	Saltator similis	1.679	1	1
72	Cyclarhis gujanensis	1.459	1	1	197	Saltatricula multicolor	2.577	1	
73	Cypsnagra hirundinacea	1.462		1	198	Sarcoramphus papa	2.599	1	
74	Dendrocolaptes picumnus	1.948	1	1	199	Satrapa icterophrys	1.307	1	1
75	Dendrocygna autumnalis	1.431	1		200	Schoeniophylax phryganophila	2.604	1	
76	Dendrocygna bicolor	1.433	1		201	Serpophaga munda	0.663	1	1
77	Dendrocygna viduata	1.446	1		202	Sicalis flaveola	2.695	1	
78	Donacobius atricapillus	1.447	1		203	Sirystes sibilator	1.522		1
79	Drymornis bridgesii	1.450	1		204	Sittasomus griseicapillus	1.141	1	1
80	Dryocopus lineatus	2.270	1	1	205	Spiziapteryx circumcinctus	2.723	1	
81	Egretta thula	1.455	1		206	Sporophila caerulescens	1.041		1
82	Elaenia albiceps	1.456	1		207	Sporophila collaris	2.732	1	
83	Elanoides forficatus	1.489	1		208	Sporophila lineola	2.760	1	
84	Emberizoides herbicola herbicola	1.496	1		209	Sporophila plumbea	1.064		1
85	Emberizoides herbicola sphenurus	1.497	1		210	Stelgidopteryx ruficollis	2.771	1	
86	Eucometis penicillata	1.431	1	1	211	Stigmatura budytoides	2.821	1	
87	Euphonia chlorotica	1.041	1	1	212	Streptoprocne zonaris	1.992	1	1
88	Euscarthmus meloryphus	0.833	1	1	213	Sublegatus modestus	2.829	1	
89	Falco deiroleucus	2.616		1	214	Suiriri suiriri	1.185	1	1
90	Falco femoralis	1.525	1		215	Synallaxis albescens	1.176	1	1
91	Falco rufigularis	1.541	1		216	Synallaxis frontalis	1.176	1	1
92	Falco sparverius	2.067	1	1	217	Synallaxis gujanensis	2.920	1	
93	Florida caerulea	1.556	1		218	Tachycineta leucorrhoa	2.933	1	
94	Fluvicola pica	1.558	1		219	Tapera naevia	2.941	1	
95	Furnarius rufus	1.567	1		220	Taraba major	1.829	1	1
96	Gallinago paraguaiae	1.573	1		221	Thalurania furcata	0.643		1
97	Gallinula chloropus	1.574	1		222	Thamnophilus caerulescens	1.330	1	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
98	Gampsonyx swainsonii	1.378	1		223	Thamnophilus doliatus	1.446	1	1
99	Geothlypis aequinoctialis	1.580	1		224	Thamnophilus punctatus	1.373		1
100	Geranospiza caerulescens	1.589	1		225	Theristicus caerulescens	2.979	1	
101	Glaucidium brasilianum	1.831	1	1	226	Thraupis bonariensis	3.009	1	
102	Gnorimopsar chopi	1.591	1		227	Thraupis sayaca	1.505	1	1
103	Guira guira	1.592	1		228	Thryothorus guarayanus	1.130	1	1
104	Harpyhaliaetus coronatus	3.470	1	1	229	Tiaris obscura	1.049		1
105	Heliomaster furcifer	1.633	1		230	Tigrisoma lineatum	3.092	1	
106	Hemithraupis guira	1.079	1	1	231	Tolmomyias sulphurescens	1.173	1	1
107	Hemitriccus margaritaceiventer	0.924	1	1	232	Troglodytes aedon	1.097	1	1
108	Herpetotheres cachinnans	1.662	1		233	Trogon surrucura	1.718	1	1
109	Himantopus mexicanus	1.667	1		234	Turdus amaurochalinus	1.800		1
110	Hirundinea ferruginea	1.380		1	235	Turdus leucomelas	1.836		1
111	Hirundo rustica rustica	1.681	1		236	Tyrannus melancholicus	3.328	1	
112	Hydropsalis brasiliana	1.767	1	1	237	Tyto alba	3.808	1	
113	Hylocharis chrysura	0.643	1	1	238	Vanellus chilensis	3.421	1	
114	Hymenops perspicillatus	1.695	1		239	Veniliornis passerinus	1.497	1	1
115	Icterus cayanensis	1.581	1	1	240	Vireo olivaceus	3.505	1	
116	Icterus icterus	1.712	1		241	Volatinia jacarina	0.987	1	1
117	Jacana jacana	1.718	1		242	Vultur gryphus	3.802	1	
118	Knipolegus aterrimus	1.740	1		243	Xenops rutilans	3.681	1	
119	Lathrotriccus euleri	1.744	1		244	Xiphocolaptes major	3.802	1	
120	Leistes superciliaris	1.752	1		245	Xiphorhynchus guttatus	4.053	1	
121	Lepidocolaptes angustirostris	1.496	1	1	246	Xolmis cinerea	1.775		1
122	Leptodon cayanensis	1.781	1		247	Xolmis irupero	4.362	1	
123	Leptopogon amaurocephalus	1.068		1	248	Zenaida auriculata	2.107	1	
124	Leptotila verreauxi	2.185	1	1	249	Zonotrichia capensis	1.313	1	1
125	Machetornis rixosus	1.800	1						

6. BIRDS OF NEOTROPICAL GRASSLAND SITE IN SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Lower River Heath, Bolivia/Peru	Parker III T.A., 1990; Dunning, Jr., J.B., 1993.
2	Ixiamas Area, Bolivia	Parker III T.A., 1991; Dunning, Jr. J.B., 1993.

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
1	Accipiter bicolor	2.532	1		49	Campylorhamphus trochilirostris	1.592	1	
2	Ajaia ajaja	3.183	1		50	Campylorhynchus turdinus	1.591	1	1
3	Amazilia lactea	0.665	1		51	Capito niger	1.728	1	
4	Amazona farinosa	2.795	1		52	Caprimulgus maculicaudus	1.470	1	
5	Amazona ochrocephala	2.708	1	1	53	Cathartes aura	3.166	1	1
6	Ammodramus humeralis	1.225		1	54	Cathartes burrovianus	2.979	1	1
7	Ancistrops strigilatus	1.588	1		55	Cathartes melambrotus	3.079	1	
8	Anhima cornuta	3.498	1		56	Celeus elegans	2.068	1	
9	Anhinga anhinga	3.092	1		57	Celeus flavus	2.303	1	
10	Anthracothorax nigricollis	0.843	1		58	Celeus grammicus	1.886	1	
11	Anthus lutescens	1.100	1	1	59	Celeus torquatus	2.127	1	
12	Ara ararauna	3.051	1	1	60	Cercomacra cinerascens	1.301	1	
13	Ara chloroptera	3.097	1	1	61	Cercomacra manu	1.264	1	
14	Ara couloni	2.306	1		62	Cercomacra nigrescens	1.217	1	
15	Ara macao	3.006	1		63	Certhiaxis cinnamomea	1.170		1
16	Ara manilata	2.386	1	1	64	Ceryle torquata	2.501	1	1
17	Ara nobilis	2.134	1		65	Chaetura brachyura	1.262	1	
18	Ara severa	2.633	1	1	66	Charadrius collaris	1.452	1	
19	Aramides cajanea	2.599	1	1	67	Chauna torquata	3.681		1
20	Aramus guarauna	3.033		1	68	Chelidoptera tenebrosa	1.528	1	
21	Aratinga aurea	1.934	1	1	69	Chloroceryle aenea	1.173	1	
22	Aratinga leucophthalmus	2.196	1	1	70	Chloroceryle amazona	2.096	1	1
23	Aratinga weddellii	2.336	1		71	Chloroceryle americana	1.574	1	
24	Ardea cocoi	3.508	1	1	72	Chloroceryle inda	1.505	1	
25	Ardeola ibis	2.305	1		73	Chlorophanes spiza	1.279	1	
26	Atticora fasciata	1.146	1		74	Chondrohierax uncinatus	2.468	1	
27	Attila bolivianus	1.653	1		75	Chrysoptilus punctigula	1.782	1	
28	Attila spadiceus	1.592	1		76	Ciccaba virgata	2.398	1	
29	Aulacorhynchus prasinus	2.186	1		77	Circus buffoni	2.706		1
30	Automolus infuscatus	1.517	1		78	Cistothorus platensis	0.954		1
31	Automolus ochrolaemus	1.604	1		79	Claravis pretiosa	2.326	1	1
32	Automolus rufipileatus	1.525	1		80	Cnemotriccus fuscatus	1.125	1	1
33	Barypthengus martii	2.179	1		81	Coereba flaveola	0.973	1	1
34	Brotogeris cyanoptera	1.826	1		82	Columba cayennensis	2.340	1	1
35	Bubulcus ibis	2.529		1	83	Columba plumbea	2.316	1	
36	Bucco macrodactylus	1.398	1		84	Columba speciosa	2.389	1	
37	Busarellus nigricollis	2.954	1		85	Columba subvinacea	2.240	1	
38	Buteo albicaudatus	2.946	1	1	86	Columbina talpacoti	1.667	1	1
39	Buteo magnirostris	2.420	1	1	87	Conopophaga peruviana	1.262	1	
40	Buteogallus urubitinga	3.009	1		88	Coragyps atratus	3.319	1	1
41	Butorides striatus	2.306	1		89	Corythopis torquata	1.167	1	
42	Cacicus cela	1.954	1	1	90	Cotinga maynana	1.839	1	
43	Cacicus solitarius	1.981	1		91	Cranioleuca gutturata	1.140	1	
44	Cairina moschata	3.392	1	1	92	Crotophaga ani	2.016	1	1
45	Calliphlox amethystina	0.398		1	93	Crypturellus bartletti	2.284	1	
46	Campephilus melanoleucos	2.306	1		94	Crypturellus cinereus	2.633	1	
47	Campephilus rubricollis	2.330	1		95	Crypturellus parvirostris	2.206	1	1
48	Camptostoma obsoletum	0.903	1	1	96	Crypturellus soui	2.338	1	

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
97	Crypturellus undulatus	2.732	1	1	152	Geotrygon montana	2.061	1	
98	Cyanerpes caeruleus	1.079	1		153	Geranospiza caerulescens	2.529	1	
99	Cyanocompsa cyanoides	1.512	1		154	Glaucidium brasilianum	1.881	1	1
100	Cyanocorax cyanomelas	2.344		1	155	Glaucidium minutissimum	1.679	1	
101	Cyanocorax violaceus	2.418	1		156	Glaucis hirsuta	0.845	1	
102	Cyclarhis gujanensis	1.459	1	1	157	Glyphorynchus spirurus	1.164	1	
103	Cymbilaimus lineatus	1.540	1		158	Gnorimopsar chopi	1.900	1	1
104	Cymbilaimus sanctaemariae	1.456	1		159	Gubernetes yetapa	1.686		1
105	Cyphorhinus arada	1.308	1		160	Gymnoderus foetidus	2.439	1	
106	Dacnis cayana	1.114	1		161	Gymnopithys salvini	1.398	1	
107	Dacnis flaviventer	1.114	1		162	Gymnostinops yuracares	2.536	1	
108	Dacnis lineata	1.041	1		163	Habia rubica	1.517	1	
109	Daptrius americanus	2.788	1		164	Harpagus bidentatus	2.315	1	
110	Daptrius ater	2.534	1		165	Harpia harpyja	3.792	1	
111	Deconychura longicauda	1.377	1		166	Heliomaster longirostris	0.880	1	
112	Dendrexetastes rufigula	1.843	1		167	Heliornis fulica	2.133	1	
113	Dendrocincla fuliginosa	1.571	1		168	Hemithraupis flavicollis	1.114	1	
114	Dendrocincla merula	1.613	1		169	Hemitriccus johannis	1.000	1	
115	Dendrocolaptes certhia	1.808	1		170	Hemitriccus zosterops	0.954	1	
116	Dendrocolaptes picumnus	1.948	1		171	Herpetotheres cachinnans	2.821	1	1
117	Dichrozona cincta	1.204	1		172	Heterocercus linteatus	1.383	1	
118	Donacobius atricapillus	1.542	1		173	Hoploxypterus cayanus	1.878	1	
119	Dromococcyx pavoninus	1.605	1		174	Hydropsalis climacocerca	1.531	1	
120	Dromococcyx phasianellus	1.927	1		175	Hylocharis cyanus	0.556	1	1
121	Dryocopus lineatus	2.270	1	1	176	Hylopezus berlepschi	1.681	1	
122	Egretta alba	2.993	1	1	177	Hylophilus hypoxanthus	1.230	1	
123	Egretta thula	2.086	1		178	Hylophylax poecilinota	1.223	1	
124	Elaenia chiriquensis	1.207	1		179	Hypocnemis cantator	1.064	1	
125	Elaenia flavogaster	1.390	1	1	180	Hypocnemoides maculicauda	1.114	1	
126	Elanoides forficatus	2.645	1	1	181	Icterus cayanensis	1.591	1	
127	Elanus caeruleus	2.532		1	182	Ictinia plumbea	2.383	1	
128	Electron platyrhynchum	1.781	1		183	Iodopleura isabellae	1.203	1	
129	Emberizoides herbicola herbicola	1.447	1	1	184	Jabiru mycteria	3.882	1	
130	Emberizoides herbicola sphenurus	1.403	1	1	185	Jacamerops aurea	1.814	1	
131	Eubucco richardsoni	1.544	1		186	Lanio versicolor	1.230	1	
132	Eupetomena macroura	0.940	1		187	Laterallus exilis	1.519	1	1
133	Euphonia chlorotica	1.043	1	1	188	Lathrotriccus euleri	1.079	1	
134	Euphonia chrysopasta	1.146	1		189	Legatus leucophaius	1.387	1	
135	Euphonia laniirostris	1.176	1		190	Leistes superciliaris	1.646		1
136	Euphonia minuta	1.000	1		191	Lepidocolaptes albolineatus	1.519	1	
137	Euphonia rufiventris	1.146	1		192	Lepidocolaptes angustirostris	1.496		1
138	Eurypyga helias	2.346	1		193	Leptodon cayanensis	2.695	1	
139	Falco femoralis	2.536	1	1	194	Leptopogon amaurocephalus	1.089	1	
140	Falco rufigularis	2.100	1		195	Leptotila rufaxilla	2.196	1	1
141	Florisuga mellivora	0.869	1		196	Leucopternis schistacea	3.000	1	
142	Formicarius analis	1.794	1		197	Lipaugus vociferans	1.915	1	
143	Formicarius colma	1.667	1		198	Lophostrix cristata	2.715	1	
144	Forpus sclateri	1.398	1		199	Machaeropterus pyrocephalus	0.881	1	
145	Frederickena unduligera	1.519	1		200	Malacoptila semicincta	1.643	1	
146	Furnarius leucopus	1.642	1	1	201	Manacus manacus	1.176	1	
147	Galbula cyanescens	1.400	1		202	Megarynchus pitangua	1.870	1	1
148	Galbula dea	1.438	1		203	Melanerpes cruentatus	1.771	1	
149	Gallinago paraguaiae	1.948		1	204	Mesembrinibis cayennensis	2.920	1	1
150	Gampsonyx swainsonii	1.966	1	1	205	Micrastur gilvicollis	2.310	1	
151	Geothlypis aequinoctialis	1.117	1	1	206	Micrastur ruficollis	2.252	1	

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
207	Microcerculus marginatus	1.238	1	
208	Milvago chimachima	2.536	1	
209	Mionectes macconnelli	1.130	1	
210	Mionectes oleagineus	1.083	1	
211	Momotus momota aequatorialis	2.199	1	
212	Momotus momota conexus	2.037	1	
213	Momotus momota lessoni	2.126	1	
214	Monasa morphoeus	2.035	1	
215	Monasa nigrifrons	1.907	1	1
216	Morphnus guianensis	3.243	1	
217	Mycteria americana	3.421	1	1
218	Myiarchus ferox	1.452	1	1
219	Myiopagis caniceps	1.013	1	
220	Myiopagis gaimardii	1.100	1	
221	Myiophobus fasciatus	0.996	1	1
222	Myiornis ecaudatus	0.778	1	
223	Myiozetetes cayanensis	1.413	1	
224	Myiozetetes granadensis	1.467	1	
225	Myiozetetes similis	1.447	1	
226	Myospiza humeralis	1.732	1	
227	Myrmeciza atrothorax	1.185	1	
228	Myrmeciza goeldii	1.623	1	
229	Myrmeciza hemimelaena	1.204	1	
230	Myrmeciza hyperythra	1.613	1	
231	Myrmoborus leucophrys	1.337	1	
232	Myrmoborus myotherinus	1.301	1	
233	Myrmothera campanisona	1.672	1	
234	Myrmotherula axillaris	0.924	1	
235	Myrmotherula brachyura	0.863	1	
236	Myrmotherula hauxwelli	2.807	1	
237	Myrmotherula leucophthalma	0.973	1	
238	Myrmotherula longipennis	0.973	1	
239	Myrmotherula menetriesii	0.934	1	
240	Myrmotherula ornata	0.973	1	
241	Myrmotherula sclateri	0.924	1	
242	Myrmotherula surinamensis	0.907	1	
243	Nannopsittaca dachilleae	1.818	1	
244	Neochen jubata	3.097	1	
245	Notharchus macrorhynchos	1.982	1	
246	Nyctibius grandis	2.760	1	
247	Nyctibius griseus	2.287	1	1
248	Nycticorax nycticorax	2.966		1
249	Nyctidromus albicollis	1.726	1	1
250	Nyctiphrynus ocellatus	1.627	1	
251	Nystalus chacuru	1.796	1	1
252	Nystalus striolatus	1.672	1	
253	Ochthornis littoralis	1.124	1	
254	Odontophorus stellatus	2.491	1	
255	Onychorhynchus coronatus	1.146	1	
256	Opisthocomus hoazin	2.900	1	
257	Ornithion inerme	0.845	1	
258	Ortalis motmot	2.690	1	
259	Oryzoborus angolensis	1.090	1	1
260	Otus choliba	2.130	1	1
261	Otus watsonii	1.090	1	
262	Pachyramphus marginatus	1.255	1	
263	Pachyramphus polychopterus	1.334	1	1
264	Panyptila cayennensis	1.324	1	
265	Paroaria gularis	1.342	1	
266	Penelope jacquacu	3.108	1	
267	Percnostola lophotes	1.447	1	
268	Phacellodomus ruber	1.589		1
269	Phaeomyias murina	1.000	1	
270	Phaeoprogne tapera	1.558	1	
271	Phaethornis hispidus	0.690	1	1
272	Phaethornis philippii	0.681	1	
273	Phaethornis ruber	0.362	1	
274	Phaetusa simplex	2.365	1	
275	Phalacrocorax brasilianus	3.065	1	
276	Philydor erythrocercus	1.422	1	
277	Philydor erythropterus	1.477	1	
278	Philydor pyrrhodes	1.490	1	
279	Philydor ruficaudatus	1.396	1	
280	Philydor rufus	1.427	1	
281	Phlegopsis nigromaculata	1.648	1	
282	Piaya cayana	2.033	1	1
283	Piaya minuta	1.604	1	
284	Piculus chrysochloros	1.944	1	
285	Picumnus rufiventris	1.322	1	
286	Pilherodius pileatus	2.744	1	1
287	Pionites leucogaster	2.190	1	
288	Pionopsitta barrabandi	2.146	1	
289	Pionus menstruus	2.393	1	1
290	Pipra chloromeros	1.217	1	
291	Pipra coronata	0.939	1	
292	Pipra fasciicauda	1.201	1	
293	Pipra rubrocapilla	1.079	1	
294	Piprites chloris	1.301	1	
295	Pitangus sulphuratus	1.798	1	1
296	Platyrinchus coronatus	0.778	1	
297	Polyborus plancus	2.946	1	1
298	Polytmus guainumbi	0.663	1	1
299	Polytmus theresiae	0.538	1	
300	Porzana albicollis	2.049	1	1
301	Progne chalybea	1.632	1	
302	Psarocolius angustifrons	2.295	1	
303	Psarocolius decumanus	2.362	1	1
304	Psophia leucoptera	2.996	1	
305	Pteroglossus beauharnaesii	1.860	1	
306	Pteroglossus castanotis	2.491	1	1
307	Pteroglossus inscriptus	2.100	1	
308	Pteroglossus mariae	2.146	1	
309	Pulsatrix perspicillata	2.941	1	1
310	Pygiptila stellaris	1.393	1	
311	Pyrrhura rupicola	1.875	1	
312	Querula purpurata	2.035	1	
313	Ramphastos culminatus	2.567	1	1
314	Ramphastos cuvieri	2.866	1	
315	Ramphastos toco	2.732	1	1
316	Ramphocelus carbo	1.447	1	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
317	Ramphotrigon ruficauda	1.253	1		364	Thraupis episcopus	1.544	1	1
318	Rhynchotus rufescens	2.954	1	1	365	Thraupis palmarum	1.591	1	
319	Rhytipterna simplex	1.554	1		366	Threnetes leucurus	0.748	1	
320	Rynchops niger	2.477	1		367	Thryothorus genibarbis	1.286	1	
321	Saltator coerulescens	1.761	1	1	368	Thryothorus guarayanus	1.130		1
322	Saltator maximus	1.679	1		369	Thryothorus leucotis	1.290	1	
323	Sarcoramphus papa	3.531	1		370	Tigrisoma lineatum	2.933	1	1
324	Scaphidura oryzivora	2.311	1		371	Tinamus guttatus	2.778	1	
325	Schiffornis major	1.491	1		372	Tinamus major	3.022	1	
326	Schiffornis turdinus	1.505	1		373	Tityra cayana	1.869	1	
327	Schistochlamys melanopis	1.519	1	1	374	Tityra inquisitor	1.630	1	
328	Sirystes sibilator	1.322	1		375	Todirostrum chrysocrotaphum	0.845	1	
329	Sittasomus griseicapillus	1.141	1		376	Todirostrum latirostre	0.908	1	
330	Spizaetus ornatus	3.106	1		377	Todirostrum maculatum	0.845	1	
331	Spizaetus tyrannus	3.011	1		378	Tolmomyias assimilis	1.250	1	
332	Sporophila castaneiventris	0.886	1		379	Tolmomyias flaviventris	1.086	1	
333	Sporophila collaris	1.130		1	380	Tolmomyias poliocephalus	1.061	1	1
334	Sporophila plumbea	1.064	1	1	381	Tolmomyias sulphurescens	1.173	1	
335	Stelgidopteryx ruficollis	1.182	1		382	Touit huetii	1.778	1	
336	Sterna superciliaris	1.667	1		383	Troglodytes aedon	1.037	1	1
337	Streptoprocne zonaris	1.992	1	1	384	Trogon collaris	1.807	1	
338	Synallaxis albescens	1.176		1	385	Trogon curucui	1.718	1	
339	Synallaxis frontalis	1.179		1	386	Trogon melanurus	2.076	1	
340	Synallaxis gujanensis	1.258	1	1	387	Trogon violaceus	1.712	1	
341	Synallaxis rutilans	1.243	1		388	Trogon viridis	1.943	1	1
342	Syrigma sibilatrix	2.568		1	389	Turdus albicollis	1.733	1	
343	Tachornis squamata	1.008		1	390	Turdus hauxwelli	1.839	1	
344	Tachycineta albiventer	1.248	1		391	Turdus ignobilis	1.792	1	
345	Tachyphonus cristatus	1.279	1		392	Turdus lawrencii	1.861	1	
346	Tachyphonus luctuosus	1.114	1		393	Tyranneutes stolzmanni	0.954	1	
347	Tangara cayana	1.251		1	394	Tyrannopsis sulphurea	1.752	1	
348	Tangara chilensis	1.362	1		395	Tyrannulus elatus	0.892	1	
349	Tangara mexicana	1.320	1		396	Tyrannus melancholicus	1.573	1	1
350	Tangara schrankii	1.279	1		397	Tyto alba	2.733		1
351	Tangara velia	1.302	1		398	Vanellus chilensis	2.515		1
352	Tapera naevia	1.717	1		399	Veniliornis affinis	1.564	1	
353	Taraba major	1.637	1		400	Veniliornis passerinus	1.497	1	
354	Terenotriccus erythrurus	0.863	1		401	Volatinia jacarina	0.987	1	
355	Terenura humeralis	1.114	1		402	Xenopipo atronitens	1.130	1	
356	Tersina viridis	1.462	1		403	Xenops milleri	1.083	1	
357	Thalurania furcata	0.643	1		404	Xenops minutus	1.025	1	
358	Thamnomanes ardesiacus	1.248	1		405	Xiphorhynchus guttatus	1.695	1	
359	Thamnomanes schistogynus	1.230	1		406	Xiphorhynchus obsoletus	1.591	1	
360	Thamnophilus aethiops	1.386	1		407	Xiphorhynchus picus	1.615	1	
361	Thamnophilus doliatus	1.446	1	1	408	Xiphorhynchus spixii	1.494	1	
362	Thamnophilus schistaceus	1.322	1		409	Zimmerius gracilipes	0.908	1	
363	Theristicus caudatus	3.190		1					

7 BIRDS OF NEOTROPICAL MOIST FOREST SITES IN SOUTH AMERICA

No	SITE NAME	REFERENCE
1	Jauneche, Ecuador	Parker III, T.A., 1992, Dunning, Jr., J.B. 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1
1	Amazilia amazilia	0.633	1	46	Elanoides forficatus	2.645	1
2	Amazilia tzacatl	0.699	1	47	Euphonia laniirostris	1.176	1
3	Amazona autumnalis	2.619	1	48	Euscarthmus meloryphus	0.833	1
4	Amazona farinosa	2.788	1	49	Falco rufigularis	2.190	1
5	Amblycercus holosericeus	1.830	1	53	Geranospiza caerulescens	2.520	1
6	Ara ambigua	3.114	1	54	Glaucidium brasilianum	1.821	1
7	Arremon abeillei	1.433	1	55	Harpagus bidentatus	2.315	1
8	Arremon aurantiirostris	1.538	1	56	Hemithraupis guira	1.079	1
9	Automolus ochrolaemus	1.604	1	57	Herpetotheres cachinnans	2.831	1
10	Basileuterus fraseri	1.064	1	58	Herpsilochmus rufimarginatus	1.033	1
11	Buteo magnirostris	2.430	1	59	Lepidocolaptes souleyetii	1.410	1
12	Buteogallus urubitinga	3.009	1	60	Leptopogon superciliaris	1.068	1
13	Cacicus cela	1.934	1	61	Leptotila verreauxi	2.185	1
14	Campephilus gayaquilensis	2.383	1	62	Leucopternis occidentalis	2.826	1
15	Camptostoma obsoletum	0.903	1	63	Leucopternis plumbea	2.683	1
16	Campylorhamphus trochilirostris	1.592	1	64	Lophotriccus pileatus	0.880	1
17	Campylorhynchus zonatus	1.556	1	65	Malacoptila panamensis	1.629	1
18	Capsiempis flaveola	0.886	1	66	Manacus manacus	1.176	1
19	Cathartes aura	3.166	1	67	Megarynchus pitangua	1.870	1
20	Cercomacra nigrescens	1.217	1	68	Melanerpes pucherani	1.807	1
21	Ceryle torquata	2.501	1	69	Micrastur ruficollis	2.252	1
22	Chaetura cinereiventris	1.143	1	70	Mionectes oleagineus	0.985	1
23	Chloroceryle americana	1.574	1	71	Mionectes oleagineus	1.083	1
24	Chlorophanes spiza	1.279	1	72	Molothrus bonariensis	1.541	1
25	Ciccaba nigrolineata	2.649	1	73	Momotus momota aequatorialis	2.199	1
26	Ciccaba virgata	2.398	1	74	Momotus momota conexus	2.037	1
27	Claravis pretiosa	1.808	1	75	Momotus momota lessoni	2.124	1
28	Cnipodectes subbrunneus	1.365	1	76	Myiarchus tuberculifer	1.299	1
29	Coereba flaveola	0.973	1	77	Myiobius atricaudus	1.000	1
30	Columba cayennensis	2.380	1	78	Myiodynastes maculatus	1.662	1
31	Columba subvinacea	2.240	1	79	Myiopagis subplacens	1.217	1
32	Coragyps atratus	3.318	1	80	Myiopagis viridicata	1.090	1
33	Crotophaga ani	2.016	1	81	Myiopagis viridicata minima	1.004	1
34	Crotophaga major	2.179	1	82	Myiophobus fasciatus	0.996	1
35	Crotophaga sulcirostris	1.913	1	83	Myiozetetes similis	1.447	1
36	Crypturellus soui	2.336	1	84	Notharchus tectus	1.422	1
37	Crypturellus transfasciatus	2.452	1	85	Nyctibius griseus	2.267	1
38	Cyanocompsa cyanoides	1.512	1	86	Nyctidromus albicollis	1.726	1
39	Cyclarhis gujanensis	1.459	1	87	Odontophorus erythrops	2.447	1
40	Dacnis lineata	1.041	1	88	Ornithion brunneicapillum	0.851	1
41	Damophila julie	0.519	1	89	Ortalis erythroptera	2.801	1
42	Dendrocincla fuliginosa	1.571	1	90	Otus roboratus roboratus	2.374	1
43	Dryocopus lineatus	2.270	1	91	Pachyramphus albogriseus	1.241	1
44	Dysithamnus mentalis	1.107	1	92	Pachyramphus homochrous	1.544	1
45	Elaenia flavogaster	1.383	1	93	Panyptila cayennensis	1.324	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1
94	Parula pitiayumi	0.844	1	120	Synallaxis brachyura	1.262	1
95	Penelope purpurascens	3.314	1	121	Tachyphonus luctuosus	1.114	1
96	Phaethornis longuemareus	0.477	1	122	Tangara cyanicollis	1.230	1
97	Phaethornis superciliosus	0.778	1	123	Tapera naevia	1.717	1
98	Phyllomyias griseiceps	0.837	1	124	Taraba major	1.829	1
99	Piaya cayana	2.033	1	125	Thalurania colombica	0.653	1
100	Piaya minuta	1.604	1	126	Thraupis episcopus	1.544	1
101	Piculus rubiginosus	1.747	1	127	Thraupis palmarum	1.591	1
102	Picumnus olivaceus	1.025	1	128	Tinamus major	3.072	1
103	Pionus chalcopterus	2.322	1	129	Tityra semifasciata	1.899	1
104	Pitylus grossus	1.690	1	130	Todirostrum cinereum	0.806	1
105	Platyrinchus mystaceus	0.987	1	131	Tolmomyias sulphurescens	1.173	1
106	Polioptila plumbea	0.778	1	132	Troglodytes aedon	1.037	1
107	Polyborus plancus	2.946	1	133	Trogon melanurus	2.076	1
108	Progne chalybea	1.632	1	134	Trogon violaceus	1.712	1
109	Pulsatrix perspicillata	2.941	1	135	Turdus reevei	1.785	1
110	Pyrocephalus rubinus	1.158	1	136	Tyrannulus elatus	0.892	1
111	Ramphocaenus melanurus	0.987	1	137	Tyrannus melancholicus	1.573	1
112	Rhodospingus cruentus	1.033	1	138	Tyto alba	2.723	1
113	Saltator maximus	1.676	1	139	Veniliornis callonotus	1.298	1
114	Schiffornis turdinus	1.501	1	140	Veniliornis kirkii	1.565	1
115	Sittasomus griseicapillus	1.141	1	141	Vireo olivaceus	1.223	1
116	Spizaetus tyrannus	3.011	1	142	Volatinia jacarina	0.987	1
117	Sporophila americana	1.029	1	143	Xenops minutus	1.029	1
118	Stelgidopteryx ruficollis	1.182	1	144	Xenops rutilans	1.086	1
119	Streptoprocne zonaris	1.992	1				

6. BIRDS OF NEOTROPICAL WET, MONTANE FOREST SITES IN SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Cabeceras de Bilsa, Ecuador	Parker III, T.A. 1993; Dunning, Jr. J.B. 1993.
2	Calabatea, Bolivia	Parker III, T.A. 1991; Dunning, Jr. J.B. 1993.
3	Carpanta, Colombia	Andrade, G.I. et al. 1993; Dunning, Jr. J.B. 1993.
4	Cerro Blanco, Ecuador	Parker III, T.A. 1991; Dunning, Jr. J.B. 1993
5	Cerro Pirre, Darién, E. Panama	Robbins, M.B., T.A. Parker III and S.E. Allen 1985; Dunning, Jr. J.B. 1993
6	La Planada	Fundacion para la Educacion Superior pamphlet, 1990; Dunning, Jr. J.B. 1993.
7	Six Forests of Western Ecuador	Parker III, T.A. 1993; Dunning, Jr. J.B. 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7
1	Accipiter bicolor	2.337				|	|	|	
2	Accipiter striatus	2.188			|				
3	Accipiter superciliosus	1.864					|		
4	Acestrura fanniae	0.500		|					
5	Acropternis orthonyx	1.950			|				
6	Adelomyia melanogenys	0.530		|	|				|
7	Aglaiocercus kingi	0.605		|	|				
8	Amaurolimnas concolor	2.128							|
9	Amaurospiza concolor	1.134						|	|
10	Amazilia amabilis	0.630					|		
11	Amazilia amazilia	0.632				|			
12	Amazilia edward	0.672					|		
13	Amazilia franciae	0.682						|	
14	Amazilia tzacatl	0.690	|					|	|
15	Amazona autumnalis	2.679	|			|	|		|
16	Amazona farinosa	2.705							|
17	Amazona mercenaria	2.511		|	|			|	
18	Amblycercus holosericeus	1.830							|
19	Ampelioides tschudii	1.807							
20	Ampelion rubrocristatus	1.832			|				
21	Ampelion rufaxilla	1.882		|					
22	Anabacerthia striaticollis	1.396						|	
23	Anas flavirostris	2.597			|				
24	Androdon aequatorialis	0.813					|		
25	Anisognathus flavinucha	1.623		|				|	
26	Anisognathus igniventris	1.531			|				
27	Anthracothorax prevostii	0.906							|
28	Aphanotriccus audax	1.033					|		
29	Ara ambigua	3.114				|	|		|
30	Ara ararauna	3.051					|		
31	Ara chloroptera	3.097			|				
32	Ara militaris	3.036		|					
33	Ara severa	2.633							|
34	Arremon abeillei	1.412				|			|
35	Arremon aurantiirostris	1.358					|		|
36	Atlapetes atricapillus	1.640					|		
37	Atlapetes brunneinucha	1.608			|		|	|	|
38	Atlapetes pallidinucha	1.590			|				
39	Atlapetes torquatus	1.612		|	|				
40	Attila spadiceus	1.592	|				|	|	
41	Aulacorhynchus derbianus	2.382		|					
42	Aulacorhynchus haematopygus	2.332						|	|
43	Aulacorhynchus prasinus	2.485			|		|		
44	Automolus ochrolaemus	1.606					|		|
45	Automolus rubiginosus	1.575					|		|
46	Baryphthengus martii	2.379	|				|		|
47	Baryphthengus ruficapillus	2.342					|		
48	Basileuterus bivittatus	1.146		|					
49	Basileuterus coronatus	1.207						|	
50	Basileuterus fraseri	1.064				|			|
51	Basileuterus fulvicauda	1.173						|	
52	Basileuterus luteoviridis	1.217			|				
53	Basileuterus nigrocristatus	1.160			|				
54	Basileuterus tristriatus	1.104						|	|
55	Boissonneaua flavescens	0.905			|			|	
56	Bolborhynchus lineola	1.729						|	
57	Brachygalba lugubris	1.230					|		
58	Brotogeris jugularis	1.798					|		
59	Brotogeris pyrrhopterus	1.797							|

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7
60	Bucco macrodactylus	1.582					|		
61	Bucco tectus	1.519					|		
62	Buteo albonotatus	2.890				|			|
63	Buteo brachyurus	2.595		|		|			|
64	Buteo leucorrhous	2.467						|	
65	Buteo magnirostris	2.430		|	|			|	|
66	Buteogallus urubitinga	3.008	|			|	|		|
67	Buthraupis montana	1.887			|				
68	Cacicus cela	1.954					|		
69	Campephilus gayaquilensis	2.385	|						
70	Campephilus haematogaster	2.373					|		
71	Campephilus melanoleucos	2.366					|		
72	Campephilus rubricollis	2.330		|					
73	Camptostoma obsoletum	0.950	|			|			|
74	Campylopterus falcatus	0.888							
75	Campylorhamphus pusillus	1.598					|		
76	Campylorhamphus trochilirostris	1.592					|		|
77	Campylorhynchus albobrunneus	1.512					|		
78	Campylorhynchus fasciatus	1.396							|
79	Campylorhynchus zonatus	1.388	|						|
80	Capito maculicoronatus	1.679							
81	Caprimulgus longirostris	1.685			|				
82	Capsiempis flaveola	0.880							|
83	Caryothraustes canadensis	1.538					|		
84	Catamblyrhynchus diadema	1.185			|			|	
85	Cathartes aura	3.100	|	|	|		|		
86	Catharus dryas	1.545							
87	Catharus fuscater	1.480			|		|		
88	Catharus ustulatus	1.480					|		
89	Celeus elegans	1.884	|				|		
90	Cephalopterus penduliger	2.595	|						|
91	Cercomacra nigrescens	1.257							|
92	Cercomacra nigricans	1.238					|		
93	Cercomacra tyrannina	1.212	|						|
94	Ceryle torquata	2.501				|			
95	Chaetura brachyura	1.262				|			|
96	Chaetura cinereiventris	1.145	|			|			|
97	Chaetura spinicauda	1.182							
98	Chalybura buffonii	0.806							|
99	Chamaepetes goudotii	2.939			|			|	
100	Chamaeza campanisona	1.882		|					
101	Chiroxiphia boliviana	1.348		|					
102	Chloroceryle aenea	1.175					|		
103	Chloroceryle americana	1.578				|	|	|	
104	Chlorochrysa calliparaea	1.230		|					
105	Chlorophanes spiza	1.279	|	|			|		|
106	Chlorophonia cyanea	1.146		|					
107	Chlorophonia pyrrhophrys	1.200							
108	Chloropipo holochlora	1.150							|
109	Chlorornis riefferii	1.734							
110	Chlorospingus canigularis	1.295							|
111	Chlorospingus semifuscus	1.467							
112	Chlorospingus ophthalmicus	1.342			|				
113	Chlorostilbon mellisugus	0.455						|	
114	Chlorothraupis olivacea	1.591							
115	Chlorothraupis stolzmanni	1.605						|	
116	Chondrohierax uncinatus	2.486						|	
117	Chordeiles acutipennis	1.807							
118	Chrysothlypis chrysomelas	1.114					|		

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	1	2	3	4	5	6	7
119	Ciccaba huhula	2.599		1					
120	Ciccaba nigrolineata	2.649							1
121	Ciccaba virgata	2.438	1				1	1	1
122	Cinclus leucocephalus	1.647			1			1	
123	Cinnycerthia unirufa	1.386			1				
124	Claravis mondetoura	1.953		1					
125	Claravis pretiosa	1.810				1	1		1
126	[illegible]	1.274			1				
127	Cnipodectes subbrunneus	1.365					1		
128	Coeligena coeligena	2.310		1					
129	Coeligena [illegible]	0.811			1				
130	Coeligena torquata	0.851			1			1	
131	Coereba flaveola	0.973	1	1		1	1	1	1
132	Colibri coruscans	2.620		1	1			1	
133	Colibri delphinae	0.790		1				1	
134	Colibri thalassinus	0.771						1	
135	Colonia colonus	1.207					1		
136	Columba cayennensis	2.380				1	1	1	1
137	Columba fasciata	2.518			1			1	
138	Columba nigrirostris	2.246					1		
139	Columba plumbea	2.316		1				1	
140	Columba speciosa	2.348	1				1		1
141	Columba subvinacea	2.240	1				1	1	1
142	Conirostrum albifrons	1.000			1				
143	Conirostrum leucogenys	1.045					1		
144	Conirostrum sitticolor	1.017			1			1	
145	Contopus albogularis	1.107	1						1
146	Conopophaga ardesiaca	1.400		1					
147	Contopus borealis	1.507	1						1
148	Contopus cinereus	1.060				1			1
149	Contopus fumigatus	1.314		1	1			1	1
150	Contopus sordidulus	1.107							1
151	Coragyps atratus	3.330	1		1	1	1	1	1
152	Corythopis torquata	1.095					1		
153	Cranioleuca curtata	1.200		1					
154	Cranioleuca erythrops	1.200					1	1	1
155	Crax rubra	3.416					1	1	
156	Creurgops verticalis	1.300						1	
157	Crotophaga ani	2.036	1	1			1	1	1
158	Crotophaga major	2.179					1		
159	Crotophaga sulcirostris	1.913				1			
160	Crypturellus cinnamomeus	2.681		1					
161	Crypturellus soui	2.438	1				1		1
162	Crypturellus transfasciatus	2.618				1			1
163	Cyanerpes caeruleus	1.079	1	1					
164	Cyanerpes lucidus	1.100					1		
165	Cyanocompsa cyanoides	1.312	1				1		1
166	Cyanocorax affinis	2.248					1		
167	Cyanocorax yncas	1.885		1	1				
168	Cyanolyca viridicyana	2.303			1				
169	Cyclarhis gujanensis	1.459		1		1			1
170	Cyclarhis nigrirostris	1.501						1	
171	Cymbilaimus lineatus	1.540	1				1		1
172	Cyphorhinus phaeocephalus	1.276	1				1		1
173	Cyphorhinus thoracicus	1.490		1					
174	Cypseloides rutilus	1.309		1	1			1	
175	Dacnis cayana	1.114	1	1			1		1
176	Dacnis lineata	1.061	1	1					1
177	Dacnis venusta	1.207	1				1		1
178	Damophila julie	0.510	1						1
179	Daptrius americanus	2.710					1		
180	Deconychura longicauda	1.377					1		
181	Dendrocincla fuliginosa	1.571	1				1		1
182	Dendrocincla tyrannina	1.590			1			1	
183	Dendrocolaptes certhia	1.800	1				1		1
184	Dendrocolaptes picumnus	1.800		1	1				
185	Dendroica petechia	1.100							1
186	Dendroica fusca	0.987							1
187	Diglossa albilatera	1.000			1			1	
188	Diglossa baritula	1.000		1					
189	Diglossa caerulescens	1.114			1			1	
190	Diglossa cyanea	1.230			1			1	
191	Diglossa glauca	1.079		1					
192	Diglossa lafresnayii	1.204			1				
193	Diglossa sittoides	0.954						1	
194	Donacobius atricapillus	1.542					1		
195	Doryfera ludovicae	0.736						1	
196	Drymophila [illegible]	1.079						1	
197	Dryocopus lineatus	2.320	1			1	1		1
198	Dryocopus [illegible]	2.428							1
199	Dubusia taeniata	1.565			1				
200	Dysithamnus mentalis	1.137				1	1		1
201	Elaenia chiriquensis	1.205						1	
202	Elaenia flavogaster	1.393	1	1		1		1	1
203	Elaenia frantzii	1.300			1				
204	Elaenia [illegible]	1.200		1					
205	Elaenia pallatangae	1.275		1				1	
206	Elanoides forficatus	2.643	1			1	1	1	1
207	Electron platyrhynchum	1.782					1		1
208	Empidonax virescens	1.111	1						1
209	Eriocnemis cupreoventris	0.768			1				
210	Eriocnemis vestitus	0.800			1				
211	Eubucco bourcierii	1.505					1	1	1
212	Eubucco versicolor	1.503		1					
213	Euphonia chlorotica	1.061	1						1
214	Euphonia thoracica	1.176	1			1			1
215	Euphonia mesochrysa	1.311		1					
216	Euphonia xanthogaster	1.114	1	1			1	1	1
217	[illegible]	2.636				1			1
218	Eutoxeres aquila	1.043	1				1		1
219	Falco peregrinus	2.916							1
220	Falco rufigularis	2.180				1	1		1
221	Falco sparverius	2.305			1	1			1
222	Florisuga mellivora	2.300	1						1
223	Formicarius analis	1.794					1		
224	Formicarius nigricapillus	1.780	1						1
225	Formicarius rufipectus	1.893					1	1	
226	Forpus coelestis	1.418				1			1
227	Fregata magnificens	3.300				1			
228	Galbula ruficauda	1.421							1
229	Gallinago nobilis	2.636			1				
230	Gampsonyx swainsonii	1.956					1		
231	Geothlypis aequinoctialis	1.117							1
232	Geothlypis semiflava	1.230						1	1
233	Geotrygon frenata	2.535						1	
234	Geotrygon goldmani	2.412					1		
235	Geotrygon linearis	2.686			1				
236	Geotrygon saphirina	2.063	1				1		1
237	Geranoaetus melanoleucus	2.920			1				
238	Geranospiza caerulescens	2.559				1			1
239	Glaucidium brasilianum	1.825				1			1
240	Glaucidium jardinii	1.752		1					
241	Glaucidium minutissimum	1.671					1		
242	Glaucis aenea	0.681	1						1
243	Glaucis hirsuta	0.845					1		
244	Glyphorynchus spirurus	1.164	1				1	1	1
245	Goethalsia bella	0.544					1		
246	Grallaria guatemalensis	1.978					1		1
247	Grallaria ruficapilla	1.897						1	
248	Grallaria rufula	1.585			1				
249	Grallaricula flavirostris	1.230					1	1	
250	Grallaricula nana	1.292			1				
251	Gymnocichla nudiceps	1.486					1		
252	Gymnopithys leucaspis	1.493					1		
253	Habia rubica	1.517		1					
254	Hapalopsittaca amazonina	2.305			1				
255	Haplophaedia aureliae	0.714		1			1		
256	[illegible]	1.153		1					
257	Harpagus bidentatus	2.333	1			1			1
258	Harpia harpyja	3.792					1		
259	Heliangelus amethysticollis	0.724			1				
260	Heliodoxa jacula	0.907	1				1		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Size 1	2	3	4	5	6	7
261	Heliodoxa leadbeateri	0.869							
262	Heliomaster longirostris	0.830							
263	Heliothryx aurita	0.731							
264	Heliothryx barroti	0.740							
265	Hemispingus atropileus	1.361							
266	Hemispingus frontalis	1.206							
267	Hemispingus superciliaris	1.146							
268	Hemispingus verticalis	1.130							
269	Hemithraupis flavicollis	1.114							
270	Hemithraupis guira	1.079							
271	Henicorhina leucophrys	1.167							
272	Henicorhina leucosticta	1.196							
273	Herpetotheres cachinnans	2.831							
274	Herpsilochmus rufimarginatus	1.031							
275	Hylocharis grayi	0.771							
276	Hylocryptus erythrocephalus	1.667							
277	Hyloctistes subulatus	2.031							
278	Hylomanes momotula	1.281							
279	Hylopezus fulviventris	1.653							
280	Hylopezus perspicillatus	1.629							
281	Hylophilus decurtatus	0.946							
282	Hylophilus ochraceiceps	1.057							
283	Hylophylax naevioides	1.229							
284	Icterus chrysater	1.720							
285	Icterus mesomelas	1.677							
286	Ictinia plumbea	2.393							
287	Iridophanes pulcherrima	1.139							
288	Iridosornis rufivertex	1.384							
289	Ixobrychus exilis	1.918							
290	Klais guimeti	0.415							
291	Knipolegus poecilocercus	1.346							
292	Lafresnaya lafresnayi	0.726							
293	Laniocera rufescens	1.588							
294	Laterallus albigularis	1.508							
295	Lathrotriccus euleri	1.058							
296	Legatus leucophaius	1.358							
297	Lepidocolaptes affinis	1.544							
298	Lepidocolaptes souleyetii	1.433							
299	Lepidothrix coronata	0.991							
300	Leptopogon superciliaris	1.188							
301	Leptotila cassini	2.205							
302	Leptotila verreauxi	2.186							
303	Leucopternis albicollis	2.796							
304	Leucopternis melanops	2.630							
305	Leucopternis plumbea	2.601							
306	Leucopternis princeps	2.930							
307	Leucopternis semiplumbea	2.459							
308	Lipaugus fuscocinereus	2.146							
309	Lipaugus unirufus	1.914							
310	Lipaugus vociferans	1.909							
311	Lipaugus vociferans	1.910							
312	Lophornis delattrei	0.447							
313	Lophostrix cristata	2.715							
314	Lophotriccus pileatus	0.881							
315	Lurocalis semitorquatus	1.940							
316	Malacoptila panamensis	1.470							
317	Manacus manacus	1.176							
318	Manacus vitellinus	1.161							
319	Margarornis bellulus	1.301							
320	Margarornis squamiger	1.206							
321	Masius chrysopterus	1.084							
322	Mecocerculus calopterus	0.888							
323	Mecocerculus leucophrys	1.145							
324	Megarynchus pitangua	1.203							
325	Melanerpes cruentatus	1.775							
326	Melanerpes pucherani	1.807							
327	Melanopareia elegans	1.204							
328	Merganetta armata	2.510							
329	Metallura tyrianthina	1.288							
330	Micrastur mirandollei	2.745							
331	Micrastur ruficollis	2.231							
332	Micrastur semitorquatus	2.809							
333	Microbates cinereiventris	1.130							
334	Microcerculus marginatus	1.276							
335	Micromonacha lanceolata	1.303							
336	Microrhopias quixensis	0.988							
337	Mimus longicaudatus	1.305							
338	Mionectes oleagineus	1.050							
339	Mionectes olivaceus	1.215							
340	Mionectes striaticollis	1.208							
341	Mitrephanes phaeocercus	0.939							
342	Mitrospingus cassinii	1.383							
343	Molothrus bonariensis	1.344							
344	Momotus momota aequatorialis	2.199							
345	Momotus momota conexus	2.091							
346	Momotus momota lessonii	2.136							
347	Monasa morphoeus	2.025							
348	Muscigralla brevicauda	1.100							
349	Myadestes coloratus	1.461							
350	Myadestes ralloides	1.462							
351	Myiarchus cephalotes	1.471							
352	Myiarchus ferox	1.431							
353	Myiarchus phaeocephalus	1.485							
354	Myiarchus tuberculifer	1.299							
355	Myiobius atricaudus	1.080							
356	Myiobius barbatus	1.081							
357	Myiobius sulphureipygius	1.076							
358	Myiobius villosus	1.137							
359	Myioborus miniatus	0.978							
360	Myiodynastes bairdii	2.051							
361	Myiodynastes chrysocephalus	1.607							
362	Myiodynastes maculatus	1.652							
363	Myiopagis caniceps	1.053							
364	Myiopagis subplacens	1.217							
365	Myiopagis viridicata	1.196							
366	Myiopagis viridicata minima	1.201							
367	Myiophobus fasciatus	0.984							
368	Myiophobus flavicans	1.106							
369	Myiophobus pulcher	0.954							
370	Myiornis atricapillus	0.778							
371	Myiotheretes striaticollis	1.588							
372	Myiotriccus ornatus	1.130							
373	Myiozetetes cayanensis	1.413							
374	Myiozetetes granadensis	1.329							
375	Myiozetetes similis	1.386							
376	Myrmeciza berlepschi	1.388							
377	Myrmeciza exsul	1.420							
378	Myrmeciza laemosticta	1.480							
379	Myrmornis torquata	1.661							
380	Myrmotherula axillaris	0.934							
381	Myrmotherula brachyura	0.860							
382	Myrmotherula fulviventris	1.077							
383	Myrmotherula longicauda	0.919							
384	Myrmotherula schisticolor	0.980							
385	Myrmotherula surinamensis	0.987							
386	Neochelidon tibialis	1.095							
387	Neomorphus geoffroyi	2.514							
388	Nonnula ruficapilla	1.342							
389	Notharchus macrorhynchos	1.949							
390	Notharchus tectus	1.301							
391	Notiochelidon cyanoleuca	1.080							
392	Nyctibius griseus	2.801							
393	Nyctidromus albicollis	1.726							
394	Nystalus radiatus	1.588							
395	Nystalus striolatus	1.672							
396	Ochthoeca cinnamomeiventris	1.101							
397	Ochthoeca fumicolor superciliosa	1.167							
398	Ochthoeca rufipectoralis	1.035							
399	Ocreatus underwoodii	0.477							
400	Odontophorus erythrops	2.447							
401	Odontophorus gujanensis	2.501							
402	Oncostoma olivaceum	0.820							

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site						
			1	2	3	4	5	6	7
403	Onychorhynchus coronatus	1.146					1		
404	Ornithion brunneicapillum	0.85	1				1		1
405	Ortalis cinereiceps	2.695					1		
406	Ortalis erythroptera	2.801	1			1			1
407	Oryzoborus funereus	1.080					1		
408	Otus choliba	2.086			1				
409	Otus clarkii	2.086					1		
410	Otus guatemalae	2.026					1		
411	Otus roboratus roboratus	2.134							1
412	Oxyruncus cristatus	1.623		1			1		
413	Pachyramphus albogriseus	1.241				1		1	1
414	Pachyramphus castaneus	1.290		1					
415	Pachyramphus cinnamomeus	1.307	1				1		1
416	Pachyramphus homochrous	1.344	1			1	1		1
417	Pachyramphus polychopterus	1.346	1	1			1	1	1
418	Pachyramphus versicolor	1.297			1			1	
419	Pandion haliaetus	3.176			1				1
420	Panyptila cayennensis	1.328					1		1
421	Parabuteo unicinctus	2.911				1			
422	Parula pitiayumi	0.864		1		1	1	1	1
423	Penelope jacquacu	3.109	1	1					
424	Penelope montagnii	3.043			1				
425	Penelope purpurascens	3.318	1				1		1
426	Phaenostictus mcleannani	1.728					1		
427	Phaeomyias murina	1.000				1			1
428	Phaeothlypis fulvicauda	1.188					1		1
429	Phaethornis guy	0.799					1		
430	Phaethornis longuemareus	0.477	1			1	1		1
431	Phaethornis superciliosus	0.778	1	1		1	1		1
432	Phaethornis syrmatophorus	0.771						1	
433	Phaethornis yaruqui	0.771	1						1
434	Pheucticus chrysopeplus	1.797						1	
435	Pheucticus ludovicianus	1.689							1
436	Philydor erythrocercus	1.430					1		
437	Philydor rufus	1.467		1				1	
438	Phrygilus unicolor	1.336			1				
439	Phyllomyias griseiceps	0.857	1						1
440	Phylloscartes ventralis	0.908		1					
441	Piaya cayana	2.055	1	1		1	1	1	1
442	Piaya minuta	1.608	1				1		1
443	Piculus leucolaemus	1.690	1				1	1	1
444	Piculus rivolii	1.934			1				
445	Piculus rubiginosus	1.747	1	1		1		1	
446	Picumnus olivaceus	1.039					1		
447	Picumnus sclateri	1.326				1			
448	Pionopsitta haematotis	2.173					1		
449	Pionus chalcopterus	2.335	1			1		1	1
450	Pionus menstruus	2.390	1				1		1
451	Pionus tumultuosus	2.436		1					
452	Pipra coronata	0.929					1		1
453	Pipra erythrocephala	1.188					1		
454	Pipra mentalis	1.176	1						1
455	Pipraeidea melanonota	1.282		1	1			1	
456	Pipreola riefferii	1.700			1			1	
457	Piprites chloris	1.301		1					
458	Piranga flava	1.380		1					1
459	Piranga leucoptera	1.204		1				1	
460	Piranga rubra	1.450	1						1
461	Pittasoma michleri	2.057					1		
462	Pitylus grossus	1.690	1				1		1
463	Platycichla leucops	1.780						1	
464	Platyrinchus coronatus	0.975	1				1		1
465	Platyrinchus mystaceus	0.987		1			1	1	1
466	Polioptila plumbea	0.778				1			1
467	Polyborus plancus	2.946				1			1
468	Popelairia conversii	0.477	1				1		1
469	Premnoplex brunnescens	1.223		1	1		1	1	
470	Premnornis guttuligera	1.201			1			1	
471	Progne chalybea	1.430	1			1			1
472	Psarocolius decumanus	2.507		1					
473	Psarocolius wagleri	2.378					1		
474	Pseudocolaptes lawrencii	1.679			1				
475	Pseudotriccus pelzelni	1.000					1	1	
476	Pseudotriccus ruficeps	1.079			1			1	
477	Pteroglossus torquatus	2.364					1		
478	Pulsatrix perspicillata	2.945	1			1	1		1
479	Pyriglena leuconota	1.500		1					
480	Pyrocephalus rubinus	1.158							1
481	Pyrrhomyias cinnamomea	1.309		1	1			1	
482	Querula purpurata	2.053					1		1
483	Ramphastos culminatus	2.597		1					
484	Ramphastos sulfuratus	2.636					1		
485	Ramphastos swainsonii	2.850	1				1		1
486	Ramphocaenus melanurus	0.981				1			1
487	Ramphocelus carbo	1.447		1					
488	Ramphocelus dimidiatus	1.447					1		
489	Ramphocelus flammigerus	1.519					1		
490	Ramphomicron microrhynchum	2.086			1				
491	Rhodospingus cruentus	1.289				1			1
492	Rhynchocyclus brevirostris	1.350	1				1		1
493	Rhynchocyclus fulvipectus	1.431						1	
494	Rhynchocyclus olivaceus	1.330					1		
495	Rhynchortyx cinctus	2.176					1		1
496	Rhytipterna holerythra	1.560					1		1
497	Rupicola peruviana sanguinolenta	2.365		1				1	
498	Sakesphorus bernardi	1.483				1			1
499	Saltator albicollis	1.587				1			1
500	Saltator striatipectus	1.721						1	1
501	Saltator maximus	1.670	1	1		1	1		1
502	Sapayoa aenigma	1.318					1		
503	Sarcoramphus papa	3.531	1			1	1		1
504	Sayornis nigricans	1.368						1	
505	Scaphidura oryzivora	2.318	1						1
506	Schiffornis turdinus	1.303	1	1			1		1
507	Schistochlamys melanopis	1.318		1					
508	Schizoeaca fuliginosa	1.262			1				
509	Sclerurus guatemalensis	1.580					1		1
510	Sclerurus mexicanus	1.778					1	1	1
511	Scytalopus latebricola	1.356			1				
512	Scytalopus unicolor	1.246			1			1	
513	Seiurus noveboracensis	1.250							1
514	Selenidera spectabilis	2.076					1		
515	Sericossypha albocristata	2.077			1				
516	Serpophaga cinerea	0.898						1	
517	Setophaga ruticilla	0.903							1
518	Sicalis flaveola	1.299				1			1
519	Sirystes sibilator	1.519					1		
520	Sittasomus griseicapillus	1.141		1		1	1		1
521	Smaragdolanius leucotis	1.398		1					
522	Spizaetus ornatus	3.104					1		1
523	Spizaetus tyrannus	3.001				1	1		1
524	Spizastur melanoleucus	2.929					1		
525	Sporophila americana	1.033	1			1			1
526	Sporophila americana aurita	0.996					1		1
527	Sporophila atrirostris	1.057				1			1
528	Sporophila caerulescens	1.061		1					
529	Sporophila corvina	0.893					1		
530	Sporophila nigricollis	0.982					1	1	
531	Sporophila schistacea	1.176						1	
532	Sporophila telasco	0.924				1			1
533	Steatornis caripensis	2.627		1	1				
534	Stelgidopteryx ruficollis	1.130	1			1	1	1	1
535	Streptoprocne zonaris	1.972		1	1	1	1	1	1
536	Sturnella magna	1.973			1				
537	Synallaxis azarae	1.228		1	1			1	
538	Synallaxis brachyura	1.262	1				1	1	1
539	Synallaxis cabanisi	1.190				1			1
540	Synallaxis sclateri	1.260			1			1	
541	Syndactyla rufosuperciliata	1.442		1					
542	Syndactyla subalaris	1.464					1	1	
543	Tachyphonus delatrii	1.301	1						1
544	Tachyphonus luctuosus	1.134	1			1	1		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Bio 1	2	3	4	5	6	7
545	Tachyphonus rufiventer	1.279		1					
546	Tachyphonus rufus	1.833						1	
547	Tangara arthus	1.342		1					
548	Tangara chilensis	1.303		1					
549	Tangara cyanicollis	1.230		1					1
550	Tangara cyanotis	1.176		1					
551	Tangara florida	1.389	1				1		1
552	Tangara [illegible]	1.325					1		
553	Tangara guttata	1.308					1		
554	Tangara gyrola	1.301	1	1			1	1	1
555	Tangara [illegible]	1.322						1	
556	Tangara icterocephala	1.342	1				1	1	1
557	Tangara inornata	1.236					1		
558	Tangara labradorides	1.176						1	
559	Tangara larvata	1.301	1				1		1
560	Tangara meyerdeschauenseei	1.613		1					
561	Tangara nigroviridis	1.290		1	1			1	
562	Tangara palmeri	1.303	1				1		1
563	Tangara parzudakii	1.467						1	
564	Tangara punctata	1.176		1					
565	Tangara [illegible]	1.279						1	
566	Tangara vassorii	1.305			1			1	
567	Tangara xanthocephala	1.279		1				1	
568	Tangara xanthogastra	1.176		1					
569	Tapera naevia	1.717				1			1
570	Taraba major	1.825	1				1	1	1
571	Terenotriccus erythrurus	0.845					1		1
572	Terenura callinota	1.000					1	1	
573	Tersina viridis	1.462		1			1		
574	Thalurania colombica	0.633	1					1	1
575	Thamnistes anabatinus	1.316	1				1		
576	Thamnophilus doliatus	1.387		1					
577	Thamnophilus punctatus	1.373					1		
578	Thamnophilus unicolor	1.384						1	
579	Thraupis cyanocephala	1.556			1			1	
580	Thraupis episcopus	1.544	1			1	1	1	1
581	Thraupis palmarum	1.591	1	1			1	1	1
582	Thraupis sayaca	1.505		1					
583	Threnetes ruckeri	0.806	1				1		1
584	Thripadectes flammulatus	1.740			1				
585	Thryothorus fasciatoventris	1.305					1		
586	Thryothorus genibarbis	1.306		1					
587	Thryothorus nigricapillus	1.305	1				1		1
588	Thryothorus thoracicus	1.246	1						1
589	Tiaris obscura	1.049							1
590	Tiaris olivacea	0.949						1	
591	Tigrisoma lineatum	3.036						1	
592	Tinamus major	3.022	1				1		1
593	Tinamus tao	3.301		1					
594	Tityra inquisitor	1.636	1						1
595	Tityra semifasciata	1.895	1	1			1		1
596	Todirostrum cinereum	0.828		1		1	1		1
597	Todirostrum nigriceps	0.813					1		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Bio 1	2	3	4	5	6	7
598	Todirostrum plumbeiceps	0.756		1					
599	Tolmomyias assimilis	1.188					1		
600	Tolmomyias sulphurescens	1.175				1			1
601	Touit dilectissima	1.815					1		
602	Trichothraupis melanops	1.288		1					
603	Troglodytes aedon	1.057	1	1	1	1	1		1
604	Troglodytes ochraceus	0.955					1		
605	Troglodytes solstitialis	1.072			1			1	1
606	Trogon collaris	1.807	1	1			1		1
607	Trogon comptus	2.017	1						1
608	Trogon curucui	1.718		1					
609	Trogon massena	2.149					1		
610	Trogon melanurus	1.988	1			1	1		1
611	Trogon personatus	1.808		1	1			1	
612	Trogon rufus	1.720	1				1		1
613	Trogon violaceus	1.752				1			1
614	Trogon viridis	1.943	1				1		1
615	Turdus albicollis	1.733	1						1
616	Turdus assimilis	1.837					1		
617	Turdus fuscater	2.146			1				
618	Turdus leucomelas	1.830		1					
619	Turdus obsoletus	1.805					1		
620	Turdus reevei	1.785				1			1
621	Turdus serranus	1.937		1	1			1	
622	Tyrannulus elatus	0.881	1						1
623	Tyrannus melancholicus	1.573	1	1		1	1	1	1
624	Tyto alba	2.720				1		1	1
625	Uropsalis lyra	1.505			1			1	
626	Veniliornis affinis	1.584		1					
627	Veniliornis callonotus	1.398				1			1
628	Veniliornis dignus	1.575						1	
629	Veniliornis fumigatus	1.540			1			1	
630	Veniliornis kirkii	1.565	1				1		1
631	Vireo leucophrys	1.097						1	
632	Vireo olivaceus	1.255				1	1		1
633	Vireolanius [illegible]	1.415	1						1
634	Volatinia jacarina	0.985				1			
635	Vultur gryphus	4.033			1				
636	Xenerpestes minlosi	1.041					1		
637	Xenops minutus	1.031	1				1		1
638	Xenops rutilans	1.086		1		1			1
639	Xiphocolaptes promeropirhynchus	2.134						1	
640	Xiphorhynchus erythropygius	1.670	1				1		1
641	Xiphorhynchus guttatus	1.681					1		
642	Xiphorhynchus lachrymosus	1.754	1				1		1
643	Xiphorhynchus triangularis	1.585		1					
644	Zenaida asiatica	2.100				1			1
645	Zenaida auriculata	2.057			1				1
646	Zimmerius bolivianus	1.009		1					
647	Zimmerius [illegible]	0.885					1		
648	Zimmerius viridiflavus	1.006	1					1	1
649	Zonotrichia capensis	1.303		1	1			1	

8 BIRDS OF NEOTROPICAL CLOUD FOREST SITES IN SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Maquipucuna? Marco Real, Ecuador	Parker III T.A., 1992 Dunning, Jr. J.B. 1993
2	Monteverde Cloud Forest Preserve, Costa Rica	Fogden, M. and P. Fogden, 1993 Dunning, Jr. J.B., 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
1	Accipiter bicolor	2.532		1	49	Catharus aurantiirostris	1.431		1
2	Accipiter superciliosus	1.904		1	50	Catharus dryas	1.545	1	
3	Amaurolimnas concolor	2.124		1	51	Catharus fuscater	1.509		1
4	Amaurospiza concolor	1.114		1	52	Celeus loricatus	1.884	1	
5	Amazilia tzacatl	0.690	1	1	53	Cephalopterus glabricollis	2.585		1
6	Amazona autumnalis	2.619		1	54	Cephalopterus penduliger	2.529	1	
7	Amblycercus holosericeus	1.580		1	55	Cercomacra tyrannina	1.212		1
8	Ampelioides tschudii	1.907	1		56	Chaetura cinereiventris	1.143	1	1
9	Anthracothorax prevostii	0.806		1	57	Chamaepetes unicolor	3.095		1
10	Ara ambigua	3.114		1	58	Chloroceryle amazona	2.388		1
11	Ara severa	2.635	1		59	Chloroceryle americana	1.574		1
12	Aramides cajanea	2.596		1	60	Chlorophanes spiza	1.279	1	1
13	Aratinga finschi	2.176		1	61	Chlorospingus canigularis	1.226	1	
14	Arremon aurantiirostris	1.538	1	1	62	Chlorospingus flavigularis	1.442	1	
15	Arremonops conirostris	1.594		1	63	Chlorospingus ophthalmicus	1.342		1
16	Atlapetes brunneinucha	1.648	1	1	64	Chlorothraupis carmioli	1.591		1
17	Atlapetes gutturalis	1.599		1	65	Chlorothraupis stolzmanni	1.608	1	
18	Atlapetes tricolor	1.470	1		66	Chondrohierax uncinatus	2.444		1
19	Attila spadiceus	1.592		1	67	Ciccaba virgata	2.380	1	1
20	Aulacorhynchus haematopygus	2.332	1		68	Cinclus mexicanus	1.764		1
21	Aulacorhynchus prasinus	2.158		1	69	Claravis pretiosa	1.808	1	
22	Automolus ochrolaemus	1.806		1	70	Cnipodectes subbrunneus	1.800	1	
23	Baryphthengus martii	2.179	1		71	Coereba flaveola	0.973	1	1
24	Baryphthengus ruficapillus	2.343		1	72	Colibri delphinae	0.799		1
25	Basileuterus culicivorus	1.021		1	73	Colinus leucopogon	2.136		1
26	Basileuterus fraseri	1.064	1		74	Colonia colonus	1.288		1
27	Basileuterus rufifrons	1.037		1	75	Columba cayennensis	2.380	1	
28	Basileuterus tristriatus	1.106	1	1	76	Columba fasciata	2.535		1
29	Brotogeris jugularis	1.790		1	77	Columba flavirostris	2.511		1
30	Brotogeris pyrrhopterus	1.797	1		78	Columba nigrirostris	2.246		1
31	Buteo albicaudatus	2.946		1	79	Columba plumbea	2.310	1	
32	Buteo albonotatus	2.300		1	80	Columba subvinacea	2.240	1	1
33	Buteo brachyurus	2.695		1	81	Columbigallina passerina	1.512		1
34	Buteo jamaicensis	3.080		1	82	Columbina inca	1.677		1
35	Buteo magnirostris	2.439	1		83	Contopus cinereus	1.099		1
36	Buteo nitidus	2.622		1	84	Coragyps atratus	3.318	1	1
37	Buteogallus anthracinus	2.980		1	85	Corapipo leucorrhoa	1.093		1
38	Buteogallus urubitinga	3.006		1	86	Cotinga amabilis	1.834		1
39	Cacicus cela	1.954	1		87	Cranioleuca erythrops	1.228	1	
40	Cacicus uropygialis	1.784		1	88	Crax rubra	3.616		1
41	Campephilus gayaquilensis	2.343	1		89	Crotophaga ani	2.016	1	
42	Campephilus guatemalensis	2.384		1	90	Crotophaga sulcirostris	1.913		1
43	Camptostoma obsoletum	0.903	1		91	Crypturellus soui	2.308	1	1
44	Campylorhamphus trochilirostris	1.592	1		92	Cyanerpes caeruleus	1.079	1	
45	Campylorhynchus zonatus	1.500	1	1	93	Cyanerpes cyaneus	1.146		1
46	Capsiempis flaveola	2.388	1		94	Cyanerpes lucidus	1.057		1
47	Caryothraustes poliogaster	1.621		1	95	Cyanocompsa cyanoides	1.512	1	1
48	Cathartes aura	3.168	1	1	96	Cyanocorax morio	2.310		1

		Mean Log10					Mean Log10		
		Body	Site				Body	Site	
No.	SCIENTIFIC NAME	Mass	1	2	No	SCIENTIFIC NAME	Mass	1	2
97	Cyclarhis gujanensis	1.459	1	1	152	Hyloctistes subulatus	1.524	1	
98	Cyphorhinus phaeocephalus	1.393	1	1	153	Hylopezus fulviventris	1.613		1
99	Cypseloides niger	1.659		1	154	Hylophilus decurtatus	0.944		1
100	Dacnis lineata	1.041	1		155	Hylophilus ochraceiceps	1.017		1
101	Dacnis venusta	1.207		1	156	Icterus dominicensis prosthemelas	1.452		1
102	Damophila julie	0.519	1		157	Icterus mesomelas	1.601	1	
103	Deconychura longicauda	1.307		1	158	Ictinia plumbea	2.393		1
104	Dendrocincla fuliginosa	1.571	1	1	159	Jacana spinosa	1.971		1
105	Dendrocincla homochroa	1.622		1	160	Klais guimeti	0.415		1
106	Dendrocolaptes certhia	1.876		1	161	Lanio leucothorax	1.502		1
107	Dendrocolaptes picumnus	1.948		1	162	Laterallus albigularis	1.676		1
108	Dendroica occidentalis	0.967		1	163	Laterallus exilis	1.519		1
109	Diglossa sittoides	0.954		1	164	Legatus leucophaius	1.387		1
110	Drymophila caudata	1.076	1		165	Lepidocolaptes souleyetii	1.417	1	1
111	Dryocopus lineatus	2.270	1	1	166	Leptopogon superciliaris	1.166	1	
112	Dysithamnus mentalis	1.107		1	167	Leptotila cassinii	2.301		1
113	Dysithamnus striaticeps	1.076		1	168	Leptotila verreauxi	2.198		1
114	Elaenia flavogaster	1.393	1	1	169	Leucopternis albicollis	2.796		1
115	Elanoides forficatus	2.645	1	1	170	Leucopternis occidentalis	2.920	1	
116	Elanus caeruleus	2.532		1	171	Lophornis helenae	0.415		1
117	Electron platyrhynchum	1.781	1	1	172	Lophostrix cristata	2.715		1
118	Euphonia anneae	1.173		1	173	Lophotriccus pileatus	0.849	1	
119	Euphonia laniirostris	1.178	1		174	Lurocalis semitorquatus	1.940		1
120	Euphonia luteicapilla	1.114		1	175	Lysurus crassirostris	1.589		1
121	Euphonia minuta	1.134		1	176	Malacoptila panamensis	1.629	1	
122	Euphonia xanthogaster	1.114	1		177	Manacus candei	1.267		1
123	Eurypyga helias	2.348		1	178	Manacus manacus	1.176	1	
124	Eutoxeres aquila	1.045		1	179	Masius chrysopterus	1.024	1	
125	Falco rufigularis	2.190	1	1	180	Megarhynchus pitangua	1.870	1	1
126	Falco sparverius	2.087		1	181	Melanerpes pucherani	1.807	1	1
127	Florisuga mellivora	0.869	1	1	182	Micrastur ruficollis	2.302	1	1
128	Formicarius nigricapillus	1.780	1		183	Micrastur semitorquatus	2.826		1
129	Forpus coelestis	1.415	1		184	Microbates cinereiventris	1.076	1	1
130	Galbula ruficauda	1.423		1	185	Microcerculus marginatus	1.236	1	
131	Geothlypis aequinoctialis	1.117	1		186	Microcerculus philomela	1.256		1
132	Geothlypis poliocephala	1.188		1	187	Microchera albocoronata	0.431		1
133	Geothlypis semiflava	1.220		1	188	Micromonacha lanceolata	1.279	1	
134	Geotrygon montana	2.041	1		189	Microrhopias quixensis	0.898	1	
135	Glaucidium brasilianum	1.981	1		190	Mionectes oleagineus	1.083	1	1
136	Glaucidium minutissimum	1.679		1	191	Mionectes olivaceus	1.215		1
137	Glyphorhynchus spirurus	1.164	1	1	192	Molothrus aeneus	1.806		1
138	Grallaria guatimalensis	1.974	1		193	Momotus momota aequatorialis	2.198	1	1
139	Gymnopithys leucaspis	1.493		1	194	Momotus momota conexus	2.038	1	1
140	Habia rubica	1.317		1	195	Momotus momota lessonii	2.124	1	1
141	Haplospiza rustica	1.193		1	196	Monasa morphoeus	2.019		1
142	Harpagus bidentatus	2.315	1	1	197	Myadestes melanops	1.307		1
143	Harpyhaliaetus solitarius	3.477		1	198	Myadestes ralloides	1.442	1	
144	Heliodoxa jacula	0.803	1	1	199	Myiarchus tuberculifer	1.289	1	1
145	Heliothryx barroti	0.740	1	1	200	Myiobius atricaudus	1.004	1	
146	Hemithraupis guira	1.079	1		201	Myiobius barbatus	1.049	1	
147	Henicorhina leucophrys	1.247	1	1	202	Myiobius sulphureipygius	1.076		1
148	Henicorhina leucosticta	1.190		1	203	Myioborus miniatus	0.978	1	1
149	Herpetotheres cachinnans	2.821	1	1	204	Myiodynastes chrysocephalus	1.607	1	
150	Hylocharis eliciae	0.556		1	205	Myiopagis viridicata	1.096	1	
151	Hylocichla mustelina	1.770		1	206	Myiopagis viridicata minima	1.064	1	

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2	No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
207	Myiophobus fasciatus	0.996	1		262	Procnias tricarunculata	2.322		1
208	Myiotriccus ornatus	1.120	1		263	Progne chalybea	1.632	1	1
209	Myiozetetes granadensis	1.467		1	264	Psarocolius wagleri	2.230		1
210	Myiozetetes similis	1.447	1	1	265	Pteroglossus torquatus	2.386		1
211	Myrmeciza exsul	1.423	1	1	266	Pulsatrix perspicillata	2.941	1	1
212	Myrmeciza immaculata	1.658	1	1	267	Pyrocephalus rubinus	1.158	1	
213	Myrmeciza nigricauda	1.340	1		268	Quiscalus mexicanus	2.190		1
214	Myrmotherula fulviventris	1.017	1	1	269	Ramphastos sulfuratus	2.530		1
215	Myrmotherula schisticolor	0.942	1		270	Ramphastos swainsonii	2.810	1	
216	Notharchus tectus	1.422	1		271	Ramphocaenus melanurus	0.987		1
217	Notiochelidon cyanoleuca	0.987		1	272	Ramphocelus passerinii	1.805		1
218	Nyctibius griseus	2.267	1		273	Ramphocelus sanguinolentus	1.615		1
219	Nycticorax nycticorax	2.946		1	274	Rhynchocyclus brevirostris	1.388		1
220	Nyctidromus albicollis	1.726	1	1	275	Rhynchortyx cinctus	2.178		1
221	Nystalus radiatus	1.785	1		276	Rhytipterna holerythra	1.566		1
222	Odontophorus erythrops	2.447	1		277	Saltator atriceps	1.901		1
223	Odontophorus leucolaemus	2.429		1	278	Saltator atripennis	1.751	1	
224	Ornithion brunneicapillum	0.851	1	1	279	Saltator coerulescens	1.740		1
225	Ortalis cinereiceps	2.695		1	280	Saltator maximus	1.676	1	1
226	Ortalis erythroptera	2.801	1		281	Sarcoramphus papa	3.531		1
227	Oryzoborus funereus	1.090		1	282	Scaphidura oryzivora	2.311		1
228	Otus choliba	2.150		1	283	Schiffornis turdinus	1.501	1	
229	Pachyramphus aglaiae	1.477		1	284	Scytalopus argentifrons	1.230	1	
230	Pachyramphus albogriseus	1.281	1		285	Selenidera spectabilis	2.350		1
231	Pachyramphus cinnamomeus	1.309	1	1	286	Serpophaga cinerea	0.908		1
232	Pachyramphus homochrous	1.544	1		287	Setophaga ruticilla	0.919		1
233	Panyptila cayennensis	1.314	1	1	288	Sittasomus griseicapillus	1.141	1	
234	Parula pitiayumi	0.844	1	1	289	Spizaetus ornatus	3.106		1
235	Penelope jacquacu	3.108	1		290	Spizaetus tyrannus	3.011	1	1
236	Penelope purpurascens	3.314	1	1	291	Sporophila americana	1.009	1	
237	Phaenostictus mcleannani	1.706		1	292	Sporophila americana aurita	0.996	1	1
238	Phaeothlypis fulvicauda	1.180		1	293	Sporophila americana aurita	1.050	1	
239	Phaethornis guy	0.799		1	294	Stelgidopteryx ruficollis	1.180		1
240	Phaethornis longuemareus	0.477	1	1	295	Stelgidopteryx serripennis	1.201		1
241	Phaethornis superciliosus	0.778	1		296	Streptoprocne zonaris	1.992		1
242	Phaethornis yaruqui	0.778	1		297	Sturnella magna	1.973		1
243	Pheucticus tibialis	1.794		1	298	Synallaxis brachyura	1.262	1	1
244	Phyllomyias griseiceps	0.857	1		299	Syndactyla subalaris	1.461	1	
245	Piaya cayana	2.033	1	1	300	Tachyphonus luctuosus	1.134	1	
246	Picoides villosus	1.881		1	301	Tangara arthus	1.342	1	
247	Piculus rubiginosus	1.747	1		302	Tangara cyanicollis	1.230	1	
248	Piculus simplex	1.740		1	303	Tangara florida	1.286		1
249	Picumnus olivaceus	1.025	1		304	Tangara guttata	1.088		1
250	Pionopsitta haematotis	2.173		1	305	Tangara gyrola	1.323	1	1
251	Pionus chalcopterus	2.332	1		306	Tangara icterocephala	1.342	1	1
252	Pionus senilis	2.308		1	307	Tangara larvata	1.301		1
253	Piranga leucoptera	1.204	1	1	308	Tangara lavinia	1.086		1
254	Piranga ludoviciana	1.449		1	309	Tapera naevia	1.727	1	
255	Pitangus sulphuratus	1.785		1	310	Taraba major	1.595	1	
256	Pitylus grossus	1.690	1	1	311	Terenotriccus erythrurus	0.863	1	1
257	Platycichla leucops	1.795	1		312	Terenura callinota	0.845	1	
258	Platyrinchus coronatus	0.973		1	313	Tersina viridis	1.462	1	
259	Platyrinchus mystaceus	0.987	1	1	314	Thalurania colombica	0.635	1	1
260	Polioptila plumbea	0.775	1		315	Thamnistes anabatinus	1.316		1
261	Polyborus plancus	2.946	1		316	Thamnophilus doliatus	1.446		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	Site 2
317	Thamnophilus punctatus	1.375		1
318	Thamnophilus unicolor	1.384	1	
319	Thraupis bonariensis	1.506		1
320	Thraupis episcopus	1.544	1	1
321	Thraupis palmarum	1.591	1	1
322	Threnetes ruckeri	0.808	1	1
323	Thryothorus atrogularis	1.411		1
324	Thryothorus modestus	1.272		1
325	Thryothorus nigricapillus	1.342	1	1
326	Thryothorus rufalbus	1.423		1
327	Thryothorus rutilus	1.215		1
328	Thryothorus thoracicus	1.246		1
329	Tiaris obscura	1.049	1	
330	Tiaris olivacea	0.949		1
331	Tigrisoma lineatum	2.939		1
332	Tinamus major	3.002	1	1
333	Tityra inquisitor	1.636		1
334	Tityra semifasciata	1.890	1	1
335	Todirostrum cinereum	0.806	1	1
336	Todirostrum nigriceps	0.813	1	1
337	Todirostrum sylvia	0.851		1
338	Tolmomyias sulphurescens	1.170	1	1
339	Troglodytes aedon	1.037	1	1
340	Trogon clathratus	2.114		1
341	Trogon collaris	1.765	1	
342	Trogon massena	2.149		1
343	Trogon melanurus	2.076	1	
344	Trogon violaceus	1.712		1
345	Turdus assimilis	1.829		1
346	Turdus fumigatus	1.854		1
347	Turdus grayi	1.868		1
348	Turdus obsoletus	1.798	1	
349	Tyrannulus elatus	0.892	1	
350	Tyrannus forficatus	1.638		1
351	Tyrannus melancholicus	1.573	1	1
352	Tyto alba	2.723		1
353	Veniliornis callonotus	1.398	1	
354	Veniliornis fumigatus	1.340		1
355	Vireo flavoviridis	1.255		1
356	Vireo leucophrys	1.097	1	1
357	Vireo olivaceus	1.223	1	
358	Vireolanius leucotis	1.415	1	
359	Vireolanius pulchellus	1.380		1
360	Volatinia jacarina	0.987	1	1
361	Xenops minutus	1.005	1	1
362	Xenops rutilans	1.086	1	
363	Xiphorhynchus erythropygius	1.671	1	1
364	Zimmerius vilissimus	0.937		1
365	Zonotrichia capensis	1.313		1

14. BIRDS OF NEOTROPICAL RAIN FOREST SITES IN SOUTH AND CENTRAL AMERICA

No.	SITE NAME	REFERENCE
1	Alto Madidi Region of Northwest Bolivia	Parker III, T.A., 1991; Dunning, Jr. J.B., 1993
2	Anchicaya Valley, Colombia	Hilty, S.L., 1975
3	Cocha Cashu, Peru	Terborgh, J. et al. 1990; Dunning, Jr. J.B., 1993
4	Guiana	Thiollay, J.M., 1994
5	La Selva	McDade, L.A. et al. 1994; Dunning, Jr. J.B., 1993
6	Reserva de la Biosfera Azules, Selva Lacandona	Vasquez Sanchez, M.A. and M.A. Ramos Olmos, 1992; Dunning, Jr., J.B., 1993
7	Surinam interior forests (including river fringe)	Haverschmidt, F. 1968; Dunning, Jr. J.B., 1993
8	Upper Rio Urucu, Amazonas, Brazil	Peres, C.A. and Whittaker, A., 1991; Dunning, Jr. J.B., 1993

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8
1	Abeillia abeillei	0.471						1		
2	Accipiter bicolor	2.351	1		1		1			
3	Accipiter superciliosus	1.944		1	1	1	1			1
4	Actitis macularia	1.606		1						
5	Agamia agami	2.716					1	1		
6	Agelaius phoeniceus	1.719						1		
7	Amaurolimnas concolor	2.144					1			
8	Amazilia amabilis	0.638		1			1			
9	Amazilia beryllina	0.672						1		
10	Amazilia candida	0.580						1		
11	Amazilia cyanocephala	0.763						1		
12	Amazilia franciae	0.699		1						
13	Amazilia lactea	0.585	1							
14	Amazilia tzacatl	0.580		1			1	1		
15	Amazilia leucogaster	0.613								1
16	Amazilia yucatanensis	0.591						1		
17	Amazona autumnalis	2.637					1	1		1
18	Amazona farinosa	2.785	1	1	1		1	1		1
19	Amazona ochrocephala	2.700	1		1					
20	Amblycercus holosericeus	1.810					1	1		
21	Ampelioides tschudii	1.857		1						
22	Ancistrops strigilatus	1.355	1							1
23	Androdon aequatorialis	0.813		1						
24	Anhima cornuta	3.498	1							
25	Anhinga anhinga	3.087	1				1	1		
26	Anthracothorax nigricollis	0.845	1							1
27	Aphanotriccus capitalis	1.072					1			
28	Aphelocoma unicolor	2.053						1		
29	Ara ambigua	3.116					1			
30	Ara ararauna	3.051	1		1				1	1
31	Ara chloroptera	3.093	1		1					1
32	Ara couloni	2.346			1					
33	Ara macao	3.006	1		1			1		1
34	Ara manilata	2.568	1		1					1
35	Ara severa	2.587	1		1					1
36	Aramides cajanea	2.599	1				1	1		1
37	Aramus guarauna	3.033						1		
38	Aratinga finschi	2.176					1			
39	Aratinga leucophthalmus	2.149	1		1					
40	Aratinga nana	1.886					1	1		
41	Aratinga weddellii	1.933	1		1					
42	Ardea cocoi	3.505	1							
43	Ardeola ibis	2.531	1							
44	Arremon aurantiirostris	1.514		1			1	1		
45	Arremon taciturnus	1.425	1		1				1	
46	Arremonops chloronotus	1.436						1		
47	Arremonops conirostris	1.594					1			
48	Aspatha gularis	1.705						1		
49	Atlapetes atricapillus	1.649		1						
50	Atlapetes brunneinucha	1.668		1						
51	Atlapetes leucopis	1.471		1						
52	Atticora fasciata	1.146	1							1
53	Attila bolivianus	1.653	1							
54	Attila cinnamomeus	1.547								1
55	Attila spadiceus	1.592	1	1	1		1	1		1
56	Aulacorhynchus haematopygus	2.332		1						
57	Aulacorhynchus prasinus	2.184	1		1					
58	Automolus dorsalis	1.543	1							
59	Automolus infuscatus	1.517	1		1	1			1	1
60	Automolus ochrolaemus	1.474	1		1		1	1		
61	Automolus rubiginosus	1.573		1		1				
62	Automolus rufipileatus	1.525	1							1
63	Baryphthengus martii	2.179	1							1
64	Baryphthengus ruficapillus	2.265		1			1			
65	Basileuterus culicivorus	1.021		1				1		
66	Basileuterus flaveolus	1.173								1
67	Basileuterus rivularis	1.130	1	1		1			1	
68	Basileuterus rufifrons	1.037						1		
69	Basileuterus tristriatus	1.104		1						
70	Brotogeris chrysopterus	1.716				1				
71	Brotogeris cyanoptera	1.816	1		1					
72	Brotogeris jugularis	1.846					1			
73	Brotogeris sanctithomae	1.771			1					
74	Brotogeris versicolurus	1.781								1
75	Bubulcus ibis	2.535					1	1		1
76	Bucco capensis	1.738								1
77	Bucco macrodactylus	1.536			1					1
78	Bucco macrorhynchos	1.951					1	1		
79	Bucco tamatia	1.530								1
80	Busarellus nigricollis	2.854								1
81	Buteo albonotatus	2.752							1	
82	Buteo albicaudatus	3.046						1		
83	Buteo brachyurus	2.693			1			1		
84	Buteo jamaicensis	3.050						1		
85	Buteo magnirostris	2.420	1	1			1	1		
86	Buteo nitidus	2.561						1		1
87	Buteogallus anthracinus	2.980					1	1		
88	Buteogallus urubitinga	3.006	1							1
89	Butorides striatus	2.311	1	1			1	1		
90	Cacicus cela	1.954	1		1					1
91	Cacicus haemorrhous	1.978	1							
92	Cacicus solitarius	1.943	1		1					
93	Cacicus uropygialis	1.784		1			1			
94	Cairina moschata	3.392	1				1	1		1
95	Campephilus guatemalensis	2.398					1			
96	Campephilus melanoleucos	2.366	1		1					
97	Campephilus rubricollis	2.350	1		1	1			1	1
98	Camptostoma obsoletum	0.910	1							1
99	Campylopterus curvipennis	0.792						1		
100	Campylopterus hemileucurus	1.021						1		
101	Campylopterus largipennis	0.918			1	1			1	1
102	Campylorhamphus procurvoides	1.556				1			1	1
103	Campylorhamphus pusillus	1.596		1						
104	Campylorhamphus trochilirostris	1.602	1		1					

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	1	2	3	4	5	6	7	8
105	Campylorhynchus albobrunneus	1.517		1						
106	Campylorhynchus turdinus	1.591	1		1					1
107	Campylorhynchus zonatus	1.539					1	1		
108	Capito maculicoronatus	1.979		1						
109	Capito niger	1.720	1		1	1				1
110	Capsiempis flaveola	0.886					1			
111	Carduelis notata	1.107						1		
112	Carpodectes nitidus	2.108					1			
113	Caryothraustes canadensis	1.530				1			1	1
114	Caryothraustes humeralis	1.560	1							
115	Caryothraustes poliogaster	1.633					1	1		
116	Casmerodius albus	2.946						1		
117	Cathartes aura	3.180		1			1			1
118	Cathartes burrovianus	3.120						1	1	
119	Cathartes melambrotus	3.079	1		1				1	1
120	Catharus aurantiirostris	1.431						1		
121	Catharus mexicanus	1.510						1		
122	Catharus ustulatus	1.489		1						
123	[illegible]	1.732							1	
124	Celeus castaneus	1.938					1	1		
125	Celeus elegans	2.068	1		1				1	1
126	Celeus flavus	2.100	1		1					1
127	Celeus grammicus	1.896	1		1					1
128	Celeus flavescens	1.886		1			1			
129	Celeus spectabilis	2.087	1							
130	Celeus torquatus	2.137	1		1				1	1
131	Celeus undatus	1.888							1	
132	Cephalopterus ornatus	2.580								1
133	Cephalopterus penduliger	2.580		1						
134	Cercibis oxycerca	2.903	1		1	1			1	1
135	Cercomacra manu	1.264	1							
136	Cercomacra nigrescens	1.227	1		1					1
137	Cercomacra serva	1.270	1		1					
138	Cercomacra tyrannina	1.213		1			1	1		
139	Ceryle torquata	2.491	1				1	1		1
140	Chaetura brachyura	1.262	1		1					
141	Chaetura chapmani	1.303								1
142	Chaetura cinereiventris	1.163	1	1	1		1			1
143	Chaetura spinicauda	1.182		1		1				1
144	Chaetura vauxi	1.201						1		
145	Chalybura urochrysia	0.808					1			
146	Chamaepetes goudotii	2.838		1						
147	Chamaeza nobilis	2.090	1		1					1
148	Charadrius collaris	1.490	1							
149	Chauna torquata	3.691	1							
150	Chelidoptera tenebrosa	1.528	1							1
151	Chiroxiphia pareola	1.217								1
152	Chloroceryle aenea	1.173	1			1	1	1		1
153	Chloroceryle amazona	2.030	1				1			1
154	Chloroceryle americana	1.574	1				1	1		1
155	Chloroceryle inda	1.690	1			1	1			1
156	Chlorochrysa nitidissima	1.371		1						
157	Chlorophanes spiza	1.279	1	1	1	1	1		1	1
158	Chlorophonia cyanea	1.146			1					
159	Chlorophonia flavirostris	1.041		1						
160	Chlorospingus flavigularis	1.447		1						
161	Chlorospingus flavovirens	1.390		1						
162	Chlorospingus ophthalmicus	1.362						1		
163	Chlorostilbon mellisugus	0.455								1
164	Chlorothraupis carmioli	1.591					1			
165	Chlorothraupis olivacea	1.591		1						
166	Chlorothraupis stolzmanni	1.605		1						
167	Chondrohierax uncinatus	2.444				1		1		1
168	Chordeiles acutipennis	1.698						1		
169	Chrysoptilus punctigula	1.782	1							
170	Columba speciosa	2.398					1	1		
171	Columba subvinacea	2.260	1		1					1
172	Columba subvinacea	2.171							1	
173	Columbina inca	1.677						1		
174	Columbina passerina	1.479						1		
175	Columbina talpacoti	1.667	1				1	1		1
176	Conioptilon mcilhennyi	1.954			1					
177	Conopias parva	1.287								1
178	Conopophaga aurita	1.300				1			1	1
179	Conopophaga castaneiceps	1.441		1						
180	Conopophaga peruviana	1.362	1		1					
181	Chrysuronia oenone	0.715			1					
182	Circus buffoni	2.597								1
183	Ciccaba nigrolineata	2.649					1	1		
184	Ciccaba virgata	2.398	1	1	1		1	1		
185	Cinclus leucocephalus	1.640		1						
186	Cissopis leveriana	1.811	1							1
187	Claravis pretiosa	1.828	1				1	1		
188	Cnemotriccus fuscatus	1.128	1							1
189	Cnipodectes subbrunneus	1.365								1
190	Coccyzus melacoryphus	1.681			1					
191	Cochlearius cochlearius	2.708								1
192	Coeligena wilsoni	1.580		1						
193	Coereba flaveola	0.973		1		1	1	1		1
194	Colibri delphinae	0.799		1						
195	Colinus virginianus	2.156						1		
196	Colonia colonus	1.207		1						
197	Columba cayennensis	2.361	1		1		1	1		
198	Columba fasciata	2.511					1	1		
199	Columba nigrirostris	2.246					1	1		
200	Columba plumbea	2.316		1	1	1			1	1
201	Conothraupis speculigera	1.298	1							
202	Contopus fumigatus	1.068					1			
203	Contopus fumigatus	1.314		1						
204	Coragyps atratus	3.310	1	1	1		1	1		1
205	Corapipo gutturalis	0.914				1				
206	Corythopis torquata	1.167	1		1					1
207	Corythopis torquata	1.290							1	
208	Cotinga cayana	1.808				1				1
209	Cotinga cayana	1.799							1	
210	Cotinga cotinga	1.724							1	
211	Cotinga maynana	1.839	1		1					
212	Cranioleuca erythrops	1.225		1						
213	Cranioleuca gutturata	1.180	1							
214	Crax alector	3.531							1	
215	Crax salvini	3.486			1					1
216	Crax rubra	3.616					1	1		
217	Crotophaga ani	2.016	1	1						1
218	Crotophaga major	2.179			1					1
219	Crotophaga sulcirostris	1.913					1	1		
220	Crypturellus atrocapillus	2.656			1					

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	1	2	3	4	5	6	7	8
221	Crypturellus bartletti	2.381	1		1					
222	Crypturellus boucardi	2.644					1	1		
223	Crypturellus cinereus	2.509	1		1					1
224	Crypturellus cinnamomeus	2.621						1		
225	Crypturellus soui	2.338	1	1	1		1	1		1
226	Crypturellus undulatus	2.731	1		1					1
227	Crypturellus variegatus	2.584	1		1	1				1
228	Cyanerpes caeruleus	1.088	1		1	1			1	1
229	Cyanerpes cyaneus	1.146						1	1	1
230	Cyanerpes lucidus	1.057					1			
231	Cyanerpes nitidus	0.954								1
232	Cyanicterus cyanicterus	1.285								1
233	Cyanocompsa cyanoides	1.530	1	1			1	1		1
234	Cyanocorax cayanus	2.369							1	
235	Cyanocorax morio	2.519					1	1		
236	Cyanocorax violaceus	2.416	1		1					1
237	Cyanocorax yncas	1.995						1		
238	Cyclarhis gujanensis	1.439	1					1		
239	Cymbilaimus lineatus	2.509	1		1	1	1		1	1
240	Cyphorhinus arada	1.338	1		1	1			1	1
241	Cyphorhinus phaeocephalus	1.391					1			
242	Cypseloides rutilus	2.509		1						
243	Dacnis cayana	1.114	1	1	1		1			1
244	Dacnis flaviventer	1.114	1							
245	Dacnis lineata	1.041	1		1					
246	Dacnis venusta	1.207		1						
247	Daptrius americanus	2.800	1		1	1	1			1
248	Daptrius ater	2.534	1		1					1
249	Deconychura longicauda	1.377	1		1	1				1
250	Deconychura stictolaema	2.519								1
251	Dendrexetastes rufigula	1.845	1		1	1			1	
252	Dendrocincla anabatina	1.461						1		
253	Dendrocincla fuliginosa	1.571	1	1	1	1	1		1	1
254	Dendrocincla homochroa	1.303						1		
255	Dendrocincla merula	1.613	1		1					1
256	Dendrocolaptes certhia	1.808	1	1	1		1	1		1
257	Dendrocolaptes picumnus	1.948	1		1					1
258	Dendrocolaptes picumnus	1.962							1	
259	Dendrocygna autumnalis	2.920						1		
260	Deroptyus accipitrinus	2.364								1
261	Dichrozona cincta	1.204	1		1					
262	Discosura longicauda	0.501							1	
263	Dives dives	1.980						1		
264	Donacobius atricapillus	1.542	1							
265	Doryfera ludoviciae	0.756		1						
266	Dromococcyx pavoninus	1.898	1							
267	Dromococcyx phasianellus	1.927	1							
268	Drymophila devillei	1.033								1
269	Dryocopus lineatus	2.519	1	1	1		1	1	1	1
270	Dysithamnus mentalis	1.107						1		
271	Dysithamnus puncticeps	1.080					1			
272	Egretta alba	2.999	1							
273	Egretta caerulea	2.556						1		
274	Egretta thula	2.569	1					1		
275	Elaenia flavogaster	1.393		1			1			1
276	Elanoides forficatus	2.549		1	1			1		
277	Elanus leucurus	2.537					1	1		
278	Electron platyrhynchum	1.781	1	1	1		1			1
279	Empidonax albigularis	1.149						1		
280	Empidonax flaviventris	1.098						1		
281	Eubucco bourcierii	1.555		1						
282	Eubucco richardsoni	1.544	1		1					1
283	Eubucco tucinkae	1.613	1		1					
284	Eucometis penicillata	1.433						1		1
285	Euphonia minuta	2.632						1		
286	Euphonia affinis	1.000						1		
287	Euphonia cayennensis	1.204							1	
288	Euphonia chrysopasta	1.146	1		1					1
289	Euphonia fulvicrissa	1.041		1						
290	Euphonia gouldi	1.146					1	1		
291	Euphonia hirundinacea	1.146						1		
292	Euphonia laniirostris	1.170	1							1
293	Euphonia luteicapilla	1.114					1			
294	Euphonia minuta	2.589	1	1	1		1			1
295	Euphonia rufiventris	1.146	1		1					1
296	Euphonia xanthogaster	1.116	1	1	1					
297	Eurypyga helias	2.369	1				1			1
298	Eutoxeres aquila	1.045		1			1			
299	Eutoxeres condamini	0.973			1					
300	Falco rufigularis	2.380	1		1		1	1		1
301	Falco sparverius	2.369		1						
302	Florisuga mellivora	2.509	1	1	1	1	1	1		1
303	Formicarius analis	1.796	1		1	1	1	1	1	1
304	Formicarius colma	1.667	1		1	1			1	1
305	Forpus sclateri	1.398	1		1					
306	Frederickena unduligera	1.919	1							
307	Frederickena viridis	1.950				1			1	
308	Furnarius leucopus	1.643	1		1					
309	Galbula albirostris	1.366				1				1
310	Galbula cyanescens	1.407	1		1					
311	Galbula dea	1.430							1	1
312	Galbula ruficauda	1.433		1			1	1		
313	Gampsonyx laniirostris	1.068	1							
314	Geothlypis aequinoctialis	1.117	1							
315	Geothlypis poliocephala	1.164					1			
316	Geothlypis semiflava	1.230					1			
317	Geotrygon frenata	2.493		1						
318	Geotrygon montana	2.061	1		1	1		1		1
319	Geotrygon veraguensis	2.190					1			
320	Geranospiza caerulescens	2.519	1				1	1		
321	Glaucidium brasilianum	1.811	1		1			1		1
322	Glaucidium minutissimum	1.079	1		1		1			1
323	Glaucis aenea	0.681					1			
324	Glaucis hirsuta	2.569	1		1					
325	Glyphorynchus spirurus	1.164	1	1	1	1	1	1		1
326	Glyphorynchus spinosus	1.168							1	
327	Grallaria varia	2.507				1			1	1
328	Granatellus pelzelni	2.546							1	
329	Gymnocichla nudiceps	1.456					1			
330	Gymnoderus foetidus	2.429	1		1				1	1
331	Gymnopithys leucaspis	1.455		1						
332	Gymnopithys rufigula	1.477							1	
333	Gymnopithys salvini	1.295	1		1					1
334	Gymnostinops yuracares	2.505	1							
335	Habia fuscicauda	2.505					1	1		
336	Habia rubica	1.517	1		1			1		1
337	Haplophaedia aurelia	0.716		1						
338	Harpagus bidentatus	2.315	1	1	1		1	1		1
339	Harpia harpyja	3.702			1		1	1		1
340	Harpia harpyja	3.509							1	
341	Heliomaster longirostris	0.720	1				1			
342	Heliornis fulica	2.133					1	1		
343	Heliodoxa maria	0.699							1	
344	Heliothryx aurita	0.732	1		1					1
345	Heliothryx barroti	0.740		1			1	1		
346	Hemithraupis flavicollis	1.124	1		1				1	1
347	Hemithraupis guira	1.030			1					
348	Hemithraupis guira	1.061							1	
349	Hemitriccus johannis	1.006			1					
350	Hemitriccus minor	0.779								1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	1	2	3	4	5	6	7	8
351	Hemitriccus zosterops	0.954	1		1	1				1
352	Henicorhina leucophrys	1.287		1						
353	Henicorhina leucosticta	1.156		1			1	1	1	
354	Herpetotheres cachinnans	2.821	1	1	1		1	1		1
355	Herpsilochmus axillaris	1.043		1						
356	Herpsilochmus rufimarginatus	1.033								1
357	Herpsilochmus sticturus	1.058				1			1	
358	Heterocercus linteatus	1.408								1
359	Heterospingus xanthopygius	1.875	1							
360	Hydropsalis climacocerca	1.581	1							
361	Hylexetastes perrotii	2.072							1	
362	Hylexetastes perrotii	2.097								1
363	Hylocharis cyanus	0.256	1		1					
364	Hylocharis leucotis	0.544						1		
365	Hyloctistes subulatus	1.554	1		1		1			1
366	Hylomanes momotula	1.467						1		
367	Hylopezus berlepschi	1.085	1		1					
368	Hylopezus fulviventris	1.613		1			1			
369	Hylopezus macularius	1.607				1				1
370	Hylopezus perspicillatus	1.630					1			
371	Hylophilus cinnamomeus	0.944					1	1		
372	Hylophilus hypoxanthus	1.076	1		1					1
373	Hylophilus ochraceiceps	1.017	1		1		1	1	1	
374	Hylophilus semibrunneus	1.307		1						
375	Hylophilus thoracicus	1.051							1	
376	Hylophylax naevia	1.430			1	1			1	1
377	Hylophylax naevioides	1.458					1			
378	Hylophylax poecilinota	1.223	1		1	1				1
379	Hypocnemis cantator	1.084	1		1	1				1
380	Hypocnemoides maculicauda	1.154			1					
381	Icterus cayanensis	1.591	1		1					1
382	Icterus chrysater	1.729		1				1		
383	Icterus dominicensis prosthemelas	1.652					1	1		
384	Icterus mesomelas	1.681					1	1		
385	Ictinia plumbea	2.393		1	1	1				1
386	Iodopleura isabellae	1.301								1
387	Iridophanes pulcherrima	1.176		1						
388	Jabiru mycteria	2.880								
389	Jacamerops aurea	1.814			1		1			1
390	Jacana spinosa	1.971					1	1		
391	Turdus albicollis	1.401							1	
392	Klais guimeti	0.415					1			
393	Knipolegus poecilocercus	1.134								1
394	Lampornis hemileucus	0.905						1		
395	Lampornis viridipallens	0.731						1		
396	Lamprospiza melanoleuca	1.351	1		1				1	1
397	Lanio aurantius	1.544						1		
398	Lanio fulvus	1.561				1			1	
399	Lanio leucothorax	1.603					1			
400	Lanio versicolor	1.536	1		1					1
401	Laniocera hypopyrrha	1.709	1		1					1
402	Laterallus albigularis	1.608					1			
403	Laterallus exilis	1.519	1				1			1
404	Laterallus melanophaius	1.711	1							
405	Lathrotriccus euleri	1.079	1							
406	Legatus leucophaius	1.480			1					1
407	Lepidocolaptes albolineatus	1.516	1		1				1	1
408	Lepidocolaptes souleyetii	1.452					1	1		
409	Leptodon cayanensis	2.681	1				1	1		
410	Leptopogon amaurocephalus	1.068	1					1		
411	Leptopogon superciliaris	1.088		1						
412	Leptotila cassinii	2.051					1	1		
413	Leptotila rufaxilla	2.196	1		1	1				1
414	Leptotila verreauxi	2.201						1		
415	Leucopternis albicollis	2.796	1			1	1	1		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	1	2	3	4	5	6	7	8
416	Leucopternis melanops	1.897							1	
417	Leucopternis princeps	1.088		1						
418	Leucopternis schistacea	2.468	1		1					1
419	Leucopternis semiplumbea	2.478					1			
420	Liosceles thoracicus	1.409			1					
421	Lipaugus unirufus	1.914					1			
422	Lipaugus vociferans	1.515	1		1	1			1	1
423	Lophornis adorabilis	1.480					1			
424	Lophostrix cristata	2.718	1		1		1			
425	Lophotriccus galeatus	0.839								1
426	Lophotriccus pileatus	0.820		1						
427	Lophotriccus vitiosus	0.842							1	
428	Lurocalis semitorquatus	1.483			1		1	1		
429	Machaeropterus pyrocephalus	0.999	1							
430	Machaeropterus regulus	0.975								1
431	Malacoptila panamensis	1.597					1	1		
432	Malacoptila rufa	1.600								1
433	Malacoptila mystacalis	1.643	1		1					1
434	Manacus manacus	1.327					1	1		
435	Manacus vitellinus	1.261		1						
436	Masius chrysopterus	1.024		1						
437	Megarhynchus pitangua	1.870	1				1	1		
438	Melanerpes aurifrons	1.916						1		
439	Melanerpes cruentatus	1.771	1		1					1
440	Melanerpes formicivorus	1.907						1		
441	Melanerpes pucherani	1.807					1	1		
442	Melozone hypoleucus	1.792						1		
443	Melospiza unicolor	1.843						1		
444	Melozone biarcuatum	1.447						1		
445	Mesembrinibis cayennensis	2.800	1				1			
446	Micrastur gilvicollis	2.310	1		1	1			1	1
447	Micrastur mirandollei	2.745								1
448	Micrastur ruficollis	1.870	1	1	1		1	1		1
449	Micrastur semitorquatus	2.809		1	1		1	1		
450	Microbates cinereiventris	1.076		1			1			
451	Microbates collaris	1.053				1				
452	Microcerculus bambla	1.296				1				
453	Microcerculus marginatus	1.238	1	1	1			1		1
454	Microcerculus philomela	1.038					1			
455	Micromonacha lanceolata	1.298		1						1
456	Microrhopias quixensis	0.896		1	1		1	1		
457	Milvago chimachima	2.506		1						
458	Mionectes macconnelli	1.130	1							
459	Mionectes oleagineus	1.401	1					1		
460	Mionectes oleagineus	1.081			1		1			1
461	Mionectes olivaceus	1.225	1	1						
462	Leptopogon phaeocercus	0.934		1						
463	Mitrospingus cassinii	1.605		1			1			
464	Molothrus aeneus	1.405					1	1		
465	Molothrus oryzivorus	1.541	1	1						
466	Momotus momota	2.157							1	
467	Momotus momota aequatorialis	2.196	1		1	1		1		
468	Momotus momota conexus	1.810	1		1	1		1		
469	Momotus momota lessonii	2.126	1		1	1		1		
470	Monasa atra	1.966				1			1	
471	Monasa morphoeus	2.089	1		1		1			1
472	Monasa nigrifrons	1.850			1					1
473	Morphnus guianensis	3.243	1	1	1				1	1
474	Myadestes obscurus	1.499						1		
475	Myadestes ralloides	1.442		1						
476	Myadestes unicolor	1.568						1		
477	Mycteria americana	3.421	1					1		
478	Myiarchus ferox	1.835	1							1
479	Myiarchus tuberculifer	1.298		1	1		1	1		
480	Myiarchus tyrannulus	1.643						1		

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site							
			1	2	3	4	5	6	7	8
481	Myiobius atricaudus	1.097								1
482	Myiobius barbatus	1.080				1			1	
483	Myiobius barbatus	1.041							1	
484	Myiobius sulphureipygius	1.073					1	1		
485	Myiobius villosus	1.137		1						
486	Myioborus miniatus	0.978		1				1		
487	Myiodynastes chrysocephalus	1.687		1						
488	Myiodynastes maculatus	1.662								1
489	Myiopagis caniceps	1.013	1	1						1
490	Myiopagis gaimardii	1.100	1		1					1
491	Myiopagis viridicata	1.090			1			1		
492	Myiopagis viridicata minima	1.004			1			1		
493	Myiophobus fasciatus	1.089	1							
494	Myiornis ecaudatus	0.778	1	1	1					
495	Myiotriccus ornatus	1.130		1						
496	Myiozetetes granadensis	1.467	1		1		1			
497	Myiozetetes similis	1.447	1	1			1	1		
498	Myrmeciza atrothorax	1.195	1							
499	Myrmeciza exsul	1.423		1			1			
500	Myrmeciza ferruginea	1.415				1				
501	Myrmeciza fortis	1.663	1		1					1
502	Myrmeciza goeldii	1.601	1		1					
503	Myrmeciza hemimelaena	1.204	1		1					1
504	Myrmeciza hyperythra	1.613	1		1					1
505	Myrmeciza immaculata	1.489		1						
506	Myrmeciza laemosticta	1.396		1						
507	Myrmoborus leucophrys	1.327	1		1					1
508	Myrmoborus myotherinus	1.301	1		1					1
509	Myrmornis torquata	1.663				1			1	
510	Myrmothera campanisona	1.672	1		1				1	
511	Myrmotherula axillaris	0.924	1		1	1	1			1
512	Myrmotherula brachyura	0.888	1	1	1	1				1
513	Myrmotherula fulviventris	1.057		1			1			
514	Myrmotherula guttata	1.037				1				
515	Myrmotherula gutturalis	0.944				1			1	
516	Myrmotherula haematonota	0.947								1
517	Myrmotherula hauxwelli	1.025	1		1					1
518	Myrmotherula iheringi	0.903			1					
519	Myrmotherula leucophthalma	0.973	1		1					
520	Myrmotherula longipennis	0.973	1		1	1			1	1
521	Myrmotherula menetriesii	0.934	1		1	1			1	1
522	Myrmotherula schisticolor	0.935		1						
523	Myrmotherula sclateri	0.933	1		1					
524	Myrmotherula surinamensis	0.987		1						
525	Nannopsittaca dachilleae	1.636	1							
526	Nasica longirostris	1.684			1					1
527	Nemosia pileata	1.206								1
528	Neochelidon tibialis	0.929	1	1						1
529	Neochen jubata	3.097	1							
530	Neoctantes niger	1.505			1					
531	Neomorphus geoffroyi	1.650			1		1			
532	Neopelma sulphureiventer	1.658							1	
533	Nonnula ruficapilla	1.342	1		1					1
534	Notharchus macrorhynchos	1.892	1		1					1
535	Notharchus tectus	1.455							1	
536	Notiochelidon cyanoleuca	1.080		1						
537	Nyctibius bracteatus	1.897			1					
538	Nyctibius grandis	2.765	1		1		1			1
539	Nyctibius griseus	2.267			1		1			
540	Nyctibius leucopterus	2.217								1
541	Nycticorax nycticorax	1.680	1							
542	Nycticorax violaceus	2.826						1		
543	Nyctidromus albicollis	1.736	1		1		1	1		1
544	Nyctiphrynus ocellatus	1.633	1		1					
545	Nystalus radiatus	1.785		1						
546	Nystalus striolatus	1.672	1		1					
547	Ochthornis littoralis	1.126	1							
548	Ocreatus underwoodii	0.477		1						
549	Odontophorus erythrops	2.447		1			1			
550	Odontophorus gujanensis	2.477				1				1
551	Odontophorus stellatus	2.491	1		1					
552	Odontorchilus branickii	1.080		1						
553	Oncostoma cinereigulare	0.778					1	1		
554	Onychorhynchus coronatus	1.146	1		1		1	1	1	1
555	Onychorhynchus coronatus	1.080							1	
556	Opisthocomus hoazin	2.920	1		1					1
557	Oporornis formosus	1.150						1		
558	Ornithion brunneicapillum	0.863					1			
559	Ornithion inerme	0.845	1		1					
560	Ornithion semiflavum	0.845						1		
561	Ortalis cinereiceps	2.695					1			
562	Ortalis motmot	2.699	1		1					1
563	Ortalis vetula	2.738						1		
564	Oryzoborus angolensis	1.093	1	1						1
565	Oryzoborus funereus	1.090					1	1		
566	Otus choliba	2.130	1							
567	Otus guatemalae	2.020					1	1		
568	Otus petersoni	2.210		1						
569	Otus watsonii	1.680	1		1					1
570	Pachyramphus aglaiae	1.477						1		
571	Pachyramphus castaneus	1.450								1
572	Pachyramphus cinnamomeus	1.307		1			1			
573	Pachyramphus marginatus	1.305	1		1					
574	Pachyramphus minor	1.611	1		1	1				
575	Pachyramphus polychopterus	1.334	1	1			1			
576	Pachyramphus validus	1.653	1							
577	Pandion haliaetus	3.176		1						
578	Panyptila cayennensis	1.204	1	1	1		1	1		1
579	Paroaria gularis	1.382	1						1	1
580	Parula pitiayumi	0.844		1						
581	Passer domesticus	1.447					1			
582	Penelope jacquacu	3.108	1		1					1
583	Penelope marail	3.179				1			1	
584	Penelope purpurascens	3.314					1	1		
585	Percnostola lophotes	1.447	1		1					
586	Percnostola rufifrons	1.484				1			1	
587	Perissocephalus tricolor	2.553				1			1	
588	Phaenostictus mcleannani	1.708					1			
589	Phaeomyias murina	1.100	1							
590	Phaeoprogne tapera	1.551								1
591	Phaeothlypis fulvicauda	1.130					1			
592	Phaethornis bourcieri	0.604				1				
593	Phaethornis hispidus	0.687	1		1					
594	Phaethornis longuemareus	0.477		1		1	1	1		
595	Phaethornis malaris	0.844				1				
596	Phaethornis philippii	0.688								1
597	Phaethornis ruber	0.362	1			1				1
598	Phaethornis stuarti	0.462			1					
599	Phaethornis superciliosus	0.778	1		1	1	1	1		1
600	Phaethornis syrmatophorus	0.771		1						
601	Phaethornis yaruqui	0.778		1						
602	Phaetusa simplex	2.365	1							
603	Phalacrocorax brasilianus	3.180	1							
604	Phalacrocorax olivaceus	3.135					1	1		
605	Philydor atricapillus	1.491		1						
606	Philydor erythrocercus	1.422	1		1	1			1	1
607	Philydor erythropterus	1.477	1		1					1
608	Philydor pyrrhodes	1.602	1		1					
609	Philydor ruficaudatus	1.396			1					1
610	Philydor rufus	1.427	1	1						

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site							
			1	2	3	4	5	6	7	8
611	Phlegopsis nigromaculata	1.666	1		1					
612	Phoenicircus carnifex	1.903							1	
613	Piaya cayana	2.033	1	1	1		1	1		1
614	Piaya melanogaster	1.991	1						1	1
615	Piaya melanogaster	2.018							1	
616	Piaya minuta	1.604	1							1
617	Picoides scalaris	1.481						1		
618	Piculus chrysochloros	1.944	1		1					1
619	Piculus flavigula	1.738							1	1
620	Piculus leucolaemus	1.839	1	1	1					
621	Piculus rubiginosus	1.747		1				1		
622	Piculus simplex	1.786					1			
623	Picumnus exilis	0.954				1				
624	Picumnus lafresnayi	0.979								1
625	Picumnus olivaceus	1.066		1						
626	Picumnus rufiventris	1.322			1					
627	Pilherodius pileatus	2.744	1							
628	Pionites leucogaster	2.190	1		1					1
629	Pionopsitta barrabandi	2.146	1		1					1
630	Pionopsitta caica	2.127							1	
631	Pionopsitta haematotis	2.173		1			1	1		
632	Pionus menstruus	2.393	1	1	1	1	1			1
633	Pionus senilis	2.326					1	1		
634	Pipile cumanensis	3.013							1	
635	Pipra caeruleocapilla	1.079								1
636	Pipra chloromeros	1.237	1		1					
637	Pipra coronata	0.929	1		1					1
638	Pipra erythrocephala	1.125				1				
639	Pipra fasciicauda	1.281	1		1					
640	Pipra mentalis	1.176					1	1		
641	Pipra pipra	1.066		1		1				1
642	Pipra serena	1.352				1				
643	Pipraeidea melanonota	1.302		1						
644	Piprites chloris	1.281	1		1				1	1
645	Piprites griseiceps	1.204					1			
646	Piranga leucoptera	1.204						1		
647	Pitangus lictor	1.433	1							
648	Pitangus sulphuratus	1.788	1				1	1		1
649	Pithys albifrons	1.302				1			1	
650	Pitylus grossus	1.660		1			1			
651	Platycichla leucops	1.799		1						
652	Platypsaris minor	1.574								1
653	Platyrinchus cancrominus	1.000						1		
654	Platyrinchus coronatus	0.975	1		1	1	1			
655	Platyrinchus mystaceus	0.987		1						
656	Platyrinchus platyrhynchos	1.079			1				1	1
657	Platyrinchus saturatus	1.033				1				
658	Podager nacunda	2.236								1
659	Podilymbus podiceps	2.643						1		
660	Polioptila guianensis	0.778							1	1
661	Polioptila plumbea	0.771					1			1
662	Polyborus plancus	2.980						1		
663	Polyplancta aurescens	0.793	1		1					1
664	Popelairia conversii	0.477		1						
665	Popelairia langsdorffi	0.477								1
666	Popelairia popelairii	2.288			1					
667	Porphyrolaema porphyrolaema	1.778			1					
668	Porphyrula martinica	2.380	1				1			
669	Premnoplex brunnescens	1.212		1						
670	Procnias alba	2.330							1	
671	Progne chalybea	1.632					1	1		
672	Psarocolius angustifrons	2.295	1	1	1					1
673	Psarocolius decumanus	2.361	1		1					
674	Psarocolius oseryi	2.176			1					
675	Psarocolius viridis	2.538				1				1
676	Psarocolius wagleri	2.230					1	1		
677	Pseudocolaptes lawrencii	1.713		1						
678	Pseudotriccus pelzelni	2.233		1						
679	Psophia crepitans	3.017				1				
680	Psophia leucoptera	2.986	1		1					1
681	Pteroglossus azara	2.368								1
682	Pteroglossus beauharnaesii	2.290	1		1					1
683	Pteroglossus castanotis	2.481	1		1					
684	Pteroglossus flavirostris	2.130			1					1
685	Pteroglossus inscriptus	2.130	1		1					1
686	Pteroglossus mariae	2.146	1							
687	Pteroglossus torquatus	2.356					1	1		
688	Pteroglossus viridis	2.124							1	
689	Pulsatrix perspicillata	2.943	1		1		1	1	1	1
690	Pygiptila stellaris	1.285	1		1					
691	Pyrocephalus rubinus	1.158						1		
692	Pyrrhura picta	1.813	1		1	1				1
693	Pyrrhura rupicola	1.875	1		1					
694	Querula purpurata	2.025	1	1	1		1		1	1
695	Querula purpurata	1.970							1	
696	Quiscalus mexicanus	2.207						1		
697	Ramphastos culminatus	2.567	1							
698	Ramphastos cuvieri	2.809	1		1					1
699	Ramphastos sulfuratus	2.636					1	1		
700	Ramphastos swainsonii	2.816					1			
701	Ramphastos toco	2.732							1	
702	Ramphastos tucanus	2.734				1				1
703	Ramphastos vitellinus	2.585			1				1	1
704	Ramphocaenus melanurus	0.987					1		1	1
705	Ramphocelus carbo	1.447	1							1
706	Ramphocelus nigrogularis	1.491	1							
707	Ramphocelus passerinii	1.500					1	1		
708	Ramphocelus sanguinolentus	1.613					1	1		
709	Ramphotrigon fuscicauda	1.310			1					
710	Ramphotrigon megacephala	1.146	1							1
711	Ramphotrigon ruficauda	1.283	1		1	1			1	1
712	Rhegmatorhina melanosticta	1.380	1		1					1
713	Rhynchocyclus brevirostris	1.398		1			1	1		
714	Rhynchocyclus olivaceus	1.330	1			1				1
715	Rhynchortyx cinctus	2.176					1			
716	Rhytipterna holerythra	1.566					1	1		
717	Rhytipterna simplex	1.554	1		1	1			1	1
718	Rupicola peruviana sanguinolenta	2.366		1						
719	Rupicola rupicola	2.146				1			1	
720	Rynchops niger	2.479	1							
721	Saltator atriceps	1.901					1	1		
722	Saltator aurantiirostris	1.750		1						
723	Saltator coerulescens	1.740	1				1	1		
724	Saltator maximus	1.676	1	1	1		1	1		
725	Sarcoramphus papa	3.531	1		1		1		1	1
726	Sayornis nigricans	1.264		1						
727	Scaphidura oryzivora	2.311	1				1	1		
728	Schiffornis major	1.491			1					
729	Schiffornis turdinus	1.502	1	1		1	1	1	1	1
730	Sclateria naevia	1.334	1		1					1
731	Sclerurus guatemalensis	1.540					1	1		
732	Sclerurus mexicanus	1.390		1				1		1
733	Scytalopus femoralis	1.354		1						
734	Selenidera culik	2.173				1			1	
735	Selenidera reinwardtii	2.120	1		1					1
736	Selenidera spectabilis	2.250					1			
737	Semnornis ramphastinus	1.889		1						
738	Serpophaga cinerea	0.909		1						
739	Sirystes sibilator	1.502	1		1				1	1
740	Sittasomus griseicapillus	1.161	1		1			1		1
741	Smaragdolanius leucotis	1.502		1						

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8
742	Spizaetus ornatus	3.104		1	1		1	1		1
743	Spizaetus tyrannus	3.011	1		1		1	1	1	
744	Spizastur melanoleucus	3.029		1	1				1	1
745	Sporophila americana	1.059		1						
746	Sporophila americana murallae	0.996						1		
747	Sporophila aurita	1.057					1			
748	Sporophila bouvronides	0.982								1
749	Sporophila castaneiventris	1.080	1							
750	Sporophila minuta	1.281		1						
751	Sporophila nigricollis	1.050		1						
752	Sporophila torqueola	0.940					1	1		
753	Steatornis caripensis	2.617		1						
754	Stelgidopteryx ruficollis	1.282	1	1			1			1
755	Stelgidopteryx serripennis	1.203						1		
756	Sterna superciliaris	1.807	1							
757	Streptoprocne zonaris	1.992	1	1	1		1	1		1
758	Sturnella magna	1.973					1			
759	Synallaxis brachyura	1.248		1			1			
760	Synallaxis erythrothorax	1.210						1		
761	Synallaxis gujanensis	1.256	1							
762	Synallaxis rutilans	1.242	1							
763	Syndactyla subalaris	1.461		1						
764	Tachornis squamata	1.025			1					
765	Tachybaptus dominicus	1.080						1		
766	Tachycineta albilinea	1.243					1	1		
767	Tachycineta albiventer	1.280								1
768	Tachyphonus cristatus	1.379	1			1			1	1
769	Tachyphonus delatrii	1.301		1			1			
770	Tachyphonus luctuosus	1.114	1	1	1		1			
771	Tachyphonus rufiventer	1.279			1					
772	Tachyphonus rufus	1.400		1			1			
773	Tachyphonus surinamus	1.279				1			1	1
774	Tangara arthus	1.310		1						
775	Tangara callophrys	1.423	1		1					
776	Tangara chilensis	1.362	1		1	1			1	1
777	Tangara cyanicollis	1.318		1						
778	Tangara florida	1.280		1						
779	Tangara gyrola	1.320		1					1	
780	Tangara icterocephala	1.342		1						
781	Tangara inornata	1.258					1			
782	Tangara larvata	1.300					1	1		
783	Tangara lavinia	1.080		1						
784	Tangara mexicana	1.230	1		1					1
785	Tangara nigrocincta	1.230	1	1	1					
786	Tangara nigroviridis	1.230		1						
787	Tangara palmeri	1.380		1						
788	Tangara parzudakii	1.447		1						
789	Tangara punctata	1.276							1	
790	Tangara rufigula	1.279		1						
791	Tangara schrankii	1.279	1		1					1
792	Tangara velia	1.310	1		1	1			1	1
793	Tangara vitriolina	1.362		1						
794	Tangara xanthogastra	1.176	1							
795	Tapera naevia	1.717	1				1	1		
796	Taraba major	1.929	1	1	1		1	1		
797	Terenotriccus erythrurus	0.853	1	1	1		1	1	1	1
798	Terenura callinota	0.845		1						
799	Terenura humeralis	1.111	1		1					
800	Terenura spodioptila	0.839								1
801	Tersina viridis	1.462	1						1	1
802	Thalurania colombica	0.653					1			
803	Thalurania furcata	0.643	1	1	1	1			1	1
804	Thamnistes anabatinus	1.356		1			1	1		
805	Thamnomanes ardesiacus	1.280	1		1	1			1	
806	Thamnomanes caesius	1.288				1				1
807	Thamnomanes saturninus	1.310								1
808	Thamnomanes schistogynus	1.230	1		1					
809	Thamnophilus aethiops	1.354	1		1					1
810	Thamnophilus amazonicus	1.304								1
811	Thamnophilus doliatus	1.446	1				1	1		
812	Thamnophilus murinus	1.250				1			1	1
813	Thamnophilus punctatus	1.373					1			
814	Thamnophilus schistaceus	1.322	1		1					1
815	Thamnophilus unicolor	1.364		1						
816	Thraupis abbas	1.559						1		
817	Thraupis episcopus	1.544	1	1			1	1		1
818	Thraupis palmarum	1.591	1	1	1		1			1
819	Threnetes leucurus	0.748	1		1					1
820	Threnetes ruckeri	1.000		1						
821	Thryothorus atrogularis	1.411					1			
822	Thryothorus coraya	1.272				1			1	
823	Thryothorus euophrys	1.217							1	
824	Thryothorus genibarbis	1.300	1		1					1
825	Thryothorus leucotis	1.090	1							
826	Thryothorus maculipectus	1.175						1		
827	Thryothorus modestus	1.279					1			
828	Thryothorus nigricapillus	1.340		1			1			
829	Thryothorus thoracicus	1.245					1			
830	Tiaris olivacea	0.949		1			1			
831	Tigrisoma lineatum	2.933	1			1	1			1
832	Tigrisoma mexicanum	3.089						1		
833	Tinamus guttatus	2.778	1		1					1
834	Tinamus major	3.022	1	1	1	1	1	1		1
835	Tinamus tao	3.309	1		1					1
836	Tityra cayana	1.880	1		1	1				1
837	Tityra inquisitor	1.636					1	1		
838	Tityra semifasciata	1.899	1	1	1		1	1		
839	Todirostrum chrysocrotaphum	0.863	1		1					1
840	Todirostrum cinereum	1.020		1			1			
841	Todirostrum latirostre	0.808	1							
842	Todirostrum maculatum	0.845	1							
843	Todirostrum nigriceps	0.813		1			1			
844	Todirostrum sylvia	1.050					1	1		
845	Tolmomyias assimilis	1.230	1		1		1		1	1
846	Tolmomyias flaviventris	1.086	1		1					
847	Tolmomyias poliocephalus	1.061	1		1					1
848	Tolmomyias sulphurescens	1.173		1			1	1	1	1
849	Topaza pella	1.695							1	
850	Touit huetii	1.813		1						
851	Touit purpurata	1.778				1				1
852	Troglodytes aedon	1.037	1	1				1		
853	Trogon clathratus	2.104					1			
854	Trogon collaris	1.820	1	1	1	1				
855	Trogon curucui	1.786	1		1					1
856	Trogon massena	2.149		1			1	1		
857	Trogon melanocephalus	1.880						1		
858	Trogon melanurus	1.900	1		1					
859	Trogon melanurus	2.008							1	1
860	Trogon rufus	1.721				1	1		1	
861	Trogon violaceus	1.712	1	1	1		1	1	1	1
862	Trogon violaceus	1.695							1	
863	Trogon viridis	1.963	1	1	1					1
864	Turdus albicollis	1.713	1		1	1				1
865	Turdus assimilis	1.875						1		
866	Turdus grayi	1.846					1	1		
867	Turdus hauxwelli	1.880			1					
868	Turdus ignobilis	1.775		1						
869	Turdus lawrencii	1.841	1							
870	Turdus obsoletus	1.839		1						
871	Turdus serranus	1.897		1						

		Mean Log10 Body	Site							
No.	SCIENTIFIC NAME	Mass	1	2	3	4	5	6	7	8
872	Tyranniscus bolivianus	0.954	1		1					1
873	Tyranniscus vilissimus	0.875							1	
874	Tyranniscus gracilipes	0.842							1	
875	Tyrannulus elatus	0.987	1		1					1
876	Tyrannus melancholicus	1.573	1	1			1	1		1
877	Tyrannus tyrannus	1.630			1					
878	Tyto alba	2.723					1			
879	Uropsila leucogastra	0.987						1		
880	Urochroa bougueri	0.602		1						
881	Veniliornis affinis	1.544	1		1					1
882	Veniliornis cassini	1.006		1						
883	Veniliornis dignus	1.575		1						
884	Veniliornis fumigatus	1.540		1			1	1		
885	Veniliornis passerinus	1.497	1							1
886	Vireo olivaceus	1.134							1	1
887	Vireo gilvus	1.221								1
888	Vireolanius leucotis	1.613			1					1
889	Vireolanius pulchellus	1.360					1	1		
890	Volatinia jacarina	0.987	1	1			1	1		
891	Xenops milleri	1.080	1							1
892	Xenops minutus	1.033	1	1	1		1	1	1	1
893	Xenops rutilans	1.086	1		1					1
894	Xiphocolaptes promeropirhynchus	2.134	1		1			1		1
895	Xipholena punicea	1.830				1			1	1
896	Xiphorhynchus erythropygius	1.681		1			1			
897	Xiphorhynchus flavigaster	1.464						1		
898	Xiphorhynchus guttatus	1.605	1		1		1			1
899	Xiphorhynchus lachrymosus	1.751					1			
900	Xiphorhynchus obsoletus	1.361			1					
901	Xiphorhynchus ocellatus	1.540			1					1
902	Xiphorhynchus pardalotus	1.606				1				1
903	Xiphorhynchus picus	1.615	1		1					1
904	Xiphorhynchus spixii	1.494	1		1					
905	Xiphorhynchus triangularis	1.487		1						
906	Zimmerius gracilipes	0.906	1		1					1
907	Zimmerius vilissimus	0.987					1			
908	Zonotrichia capensis	1.313		1						

11. BIRDS OF TEMPERATE GRASSLANDS SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Badlands National Park	Sieg, C. H., 1991. Dunning Jr., J.B. 1993.
2	Colorado CPER	Porter, D.K. and Ryder, R.A. 1974, USDA, Rocky Mountain Region, 1974. Dunning Jr. J.B., 1993.
3	Konza	Zimmerman, J.L., 1985. Dunning Jr., J.B., 1993.
4	Pawnee	USDA Rocky Mountain Region, 1974, Dunning Jr. J.B. 1993
5	Bison	Morris, M.S. Technical Report No. 37. Dunning Jr. J.B. 1993
6	Bridger	Collins, D., Technical Report No. 38, Dunning Jr. J.B., 1993.

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
1	Accipiter cooperii	2.647			1	1		
2	Accipiter gentilis	3.017		1		1		1
3	Aechmophorus occidentalis	3.169				1		
4	Aeronautes saxatalis	1.507				1		
5	Agelaius phoeniceus	1.727	1		1	1	1	
6	Aimophila cassinii	1.275				1		
7	Aix sponsa	2.821			1		1	
8	Alectoris chukar	2.761					1	
9	Ammodramus bairdii	1.243		1				
10	Ammodramus henslowii	1.117			1			
11	Ammodramus savannarum	1.220	1		1	1	1	
12	Amphispiza belli	1.286		1				
13	Amphispiza bilineata	1.130		1				
14	Anas acuta	3.011	1			1	1	
15	Anas americana	2.878				1		
16	Anas clypeata	2.789	1			1		
17	Anas crecca	2.345	1			1	1	
18	Anas cyanoptera	2.590				1		
19	Anas discors	2.587	1		1	1	1	
20	Anas platyrhynchos	3.034	1		1	1	1	
21	Anas strepera	2.966	1			1	1	
22	Anthus spinoletta	1.379		1				
23	Anthus spragueii	1.403		1				
24	Aquila chrysaetos	3.603	1			1	1	1
25	Archilochus colubris	0.507			1			
26	Asio flammeus	2.468	1		1	1	1	
27	Asio otus	2.434		1		1		
28	Athene cunicularia	2.194	1			1		
29	Aythya americana	3.028	1			1		
30	Aythya marila	2.970		1				
31	Aythya valisineria	3.090		1		1		
32	Bartramia longicauda	2.172	1	1	1	1		
33	Bombycilla cedrorum	1.512		1		1	1	
34	Bonasa umbellus	2.758					1	1
35	Botaurus lentiginosus	2.849	1		1			
36	Branta canadensis canadensis	3.568				1	1	
37	Branta canadensis moffitti	3.642				1	1	
38	Bubo virginianus	3.132	1		1	1	1	1

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
39	Buteo jamaicensis	3.050	1		1	1	1	1
40	Buteo platypterus	2.657			1			
41	Buteo regalis	3.059	1			1		
42	Buteo swainsoni	3.001	1		1	1		
43	Butorides striatus	2.328		1	1	1		
44	Calamospiza melanocorys	1.575	1			1		
45	Calcarius mccownii	1.365				1		
46	Calcarius ornatus	1.276				1		
47	Calcarius pictus	1.430		1				
48	Caprimulgus vociferus	1.722			1			
49	Cardinalis cardinalis	1.650			1			
50	Carduelis pinus	1.164				1		1
51	Carduelis tristis	1.112	1		1	1	1	1
52	Carpodacus cassinii	1.423		1				1
53	Carpodacus mexicanus	1.330				1		
54	Casmerodius albus	2.946			1			
55	Cathartes aura	3.168	1	1	1	1		
56	Catharus fuscescens	1.494		1				1
57	Catharus guttatus	1.491						1
58	Catharus ustulatus	1.489						1
59	Certhia americana	0.924		1				1
60	Ceryle alcyon	2.170			1	1	1	
61	Chaetura pelagica	1.373			1			
62	Charadrius montanus	2.027				1		
63	Charadrius semipalmatus	1.670		1				
64	Charadrius vociferus	1.990	1		1	1	1	
65	Chlidonias niger	1.615				1		
66	Chondestes grammacus	1.462			1	1		
67	Chordeiles minor	1.799	1		1		1	
68	Cinclus mexicanus	1.764					1	1
69	Circus cyaneus	2.636	1		1	1	1	
70	Cistothorus platensis	0.954			1			
71	Coccyzus americanus	1.806			1	1		
72	Coccyzus erythropthalmus	1.708	1		1			
73	Colaptes auratus	2.122	1			1	1	1
74	Colinus virginianus	2.230			1	1		
75	Contopus borealis	1.507		1				1
76	Contopus sordidulus	1.107				1		1
77	Contopus virens	1.149			1			
78	Corvus brachyrhynchos	2.651	1				1	
79	Corvus corax	3.083						1
80	Cyanocitta cristata	1.939	1		1	1		
81	Cyanocitta stelleri	2.107						1
82	Dendragapus obscurus	3.013					1	1
83	Dendroica coronata	1.097					1	1
84	Dendroica magnolia	0.941		1				
85	Dendroica pensylvanica	0.984		1				
86	Dendroica petechia	0.980	1		1	1	1	1
87	Dendroica striata	1.114		1				
88	Dendroica townsendi	0.947		1				

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
89	Dolichonyx oryzivorus	1.533		1	1	1		
90	Dumetella carolinensis	1.507	1		1	1		
91	Egretta thula	2.569				1		
92	Empidonax hammondii	1.004						1
93	Empidonax oberholseri	1.017						1
94	Empidonax traillii	1.126		1	1			
95	Eremophila alpestris	1.499	1		1	1		1
96	Euphagus cyanocephalus	1.801	1			1	1	
97	Falco mexicanus	2.882	1			1		
98	Falco peregrinus	2.914		1				
99	Falco rusticolus	3.187		1				
100	Falco sparverius	2.067	1		1	1	1	
101	Fulica americana	2.816	1		1	1	1	
102	Gallinago gallinago	2.067				1		
103	Gavia immer	3.616		1				
104	Geothlypis trichas	1.306	1		1	1		
105	Glaucidium gnoma	1.806						1
106	Guiraca caerulea	1.458	1		1	1		
107	Gymnorhinus cyanocephalus	2.013		1				
108	Haliaeetus leucocephalus	3.677		1		1		
109	Hesperiphona vespertina	1.773						1
110	Hirundo pyrrhonota	1.334	1		1	1	1	
111	Hirundo rustica	1.205	1			1	1	
112	Hirundo rustica rustica	1.260	1		1		1	
113	Hylocichla mustelina	1.720			1			
114	Icteria virens	1.806	1		1	1		
115	Icterus galbula galbula	1.529	1			1	1	
116	Icterus spurius	1.292	1		1	1		
117	Ictinia mississippiensis	2.424			1			
118	Junco hyemalis	1.299						1
119	Lanius ludovicianus	1.676	1		1	1		
120	Larus californicus californicus	2.778				1		
121	Leucosticte arctoa atrata	1.423		1				
122	Limosa haemastica	2.441		1				
123	Lophodytes cucullatus	2.790					1	
124	Loxia curvirostra	1.562		1			1	1
125	Loxia curvirostra	1.609						1
126	Melanerpes carolinus	1.806			1			
127	Melanerpes erythrocephalus	1.855	1		1	1		
128	Melanerpes lewis	2.064					1	
129	Melospiza lincolnii	1.241		1				1
130	Melospiza melodia	1.318	1		1	1	1	
131	Mergus merganser	3.173					1	
132	Mergus serrator	3.013		1				
133	Micropalama himantopus	1.752		1				
134	Mimus polyglottos	1.686			1	1		
135	Mniotilta varia	1.031	1		1			
136	Molothrus ater	1.645	1		1	1		1
137	Myadestes townsendi	1.531						1
138	Myiarchus cinerascens	1.435		1				

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
139	Myiarchus crinitus	1.525			1			
140	Nucifraga columbiana	2.137		1		1	1	1
141	Numenius americanus	2.782	1			1		
142	Numenius phaeopus	2.582		1				
143	Nyctea scandiaca	3.308		1				
144	Nycticorax nycticorax	2.946				1		
145	Nycticorax violaceus	2.836		1				
146	Oporornis formosus	1.150			1			
147	Oporornis tolmiei	1.017					1	1
148	Otus asio naevius	2.268				1		
149	Oxyura jamaicensis	2.730	1	1		1		
150	Pandion haliaetus	3.176		1				
151	Parula americana	0.934			1			
152	Parus atricapillus	1.033	1		1	1	1	
153	Parus bicolor	1.334			1			
154	Parus gambeli	1.888						1
155	Passer domesticus	1.445	1		1	1	1	
156	Passerculus sandwichensis	1.306				1	1	
157	Passerella iliaca	1.509		1				1
158	Passerina amoena	1.188				1	1	1
159	Passerina cyanea	1.163			1			
160	Perdix perdix	2.582					1	
161	Perisoreus canadensis	1.863						1
162	Phasianus colchicus	3.197	1		1	1	1	
163	Pheucticus ludovicianus	1.659		1	1			
164	Pheucticus melanocephalus	1.623	1			1		1
165	Pica pica	2.259	1			1	1	1
166	Picoides arcticus	1.846						1
167	Picoides pubescens	1.431			1	1	1	
168	Picoides tridactylus	1.827						1
169	Picoides villosus	1.831	1		1	1	1	
170	Pinicola enucleator	1.751		1				1
171	Pipilo erythrophthalmus	1.618	1		1	1	1	
172	Piranga ludoviciana	1.449		1			1	1
173	Piranga olivacea	1.456			1			
174	Plegadis chihi	2.791		1				
175	Podiceps auritus	2.456		1				
176	Podiceps nigricollis	2.465	1			1		
177	Podilymbus podiceps	2.645	1		1	1		
178	Polioptila caerulea	0.778			1			
179	Pooecetes gramineus	1.414				1	1	1
180	Porzana carolina	1.873			1	1	1	
181	Progne subis	1.694		1	1			
182	Quiscalus quiscula	2.065	1		1	1		
183	Rallus limicola	1.932			1			
184	Recurvirostra americana	2.500				1		
185	Regulus calendula	0.825		1			1	1
186	Regulus satrapa	0.794						1
187	Riparia riparia	1.164	1	1		1	1	
188	Salpinctes obsoletus	1.217	1			1	1	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
189	Sayornis phoebe	1.297	1		1			
190	Sayornis saya	1.326	1			1		
191	Seiurus aurocapillus	1.288		1	1			
192	Seiurus motacilla	1.306			1			
193	Seiurus noveboracensis	1.290		1				
194	Selasphorus platycercus	2.864				1		
195	Setophaga ruticilla	0.918			1			
196	Sialia currucoides	1.471	1			1		1
197	Sialia sialis	1.500			1	1		
198	Sitta canadensis	0.991					1	1
199	Sitta carolinensis	1.324			1			
200	Sitta pygmaea	1.025					1	
201	Sphyrapicus thyroideus	1.675						1
202	Sphyrapicus varius	1.702		1			1	
203	Spiza americana	1.437	1	1	1	1		
204	Spizella breweri	1.037				1		
205	Spizella passerina	1.090	1		1	1	1	1
206	Spizella pusilla	1.097			1			
207	Steganopus tricolor	1.745	1			1	1	
208	Stelgidopteryx ruficollis	1.182	1			1		
209	Stelgidopteryx serripennis	1.201			1			
210	Stellula calliope	0.417						1
211	Sterna albifrons	1.756		1				
212	Sterna forsteri	2.199				1		
213	Strix nebulosa	2.997						1
214	Strix varia	2.864			1			
215	Sturnella magna	1.973			1			
216	Sturnella neglecta	2.014	1		1	1	1	1
217	Sturnus vulgaris	1.920	1		1	1	1	
218	Tachycineta bicolor	1.303			1		1	1
219	Tachycineta thalassina	1.151	1				1	1
220	Thryomanes bewickii	0.996			1			
221	Thryothorus ludovicianus	1.272			1			
222	Toxostoma rufum	1.838	1		1	1		
223	Tringa macularia	1.606	1		1	1	1	
224	Troglodytes aedon	1.037	1		1	1	1	
225	Turdus migratorius	1.886	1		1	1	1	1
226	Tympanuchus cupido	2.956			1			
227	Tympanuchus phasianellus	2.946	1					
228	Tyrannus forficatus	1.635		1		1		
229	Tyrannus tyrannus	1.639	1		1	1	1	
230	Tyrannus verticalis	1.598	1		1	1	1	
231	Tyrannus vociferans	1.659		1		1		
232	Tyto alba	2.723			1	1		
233	Vermivora celata	0.954						1
234	Vermivora peregrina	1.001		1				
235	Vireo bellii	0.929			1			
236	Vireo gilvus	1.170		1	1	1	1	1
237	Vireo griseus	1.057			1			
238	Vireo olivaceus	1.223		1	1	1	1	

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5	6
239	Vireo solitarius	1.220		1				
240	Wilsonia canadensis	0.839		1				
241	Wilsonia pusilla	0.886						1
242	Xanthocephalus xanthocephalus	1.751	1		1	1		
243	Zenaida macroura	2.319	1		1	1	1	1
244	Zonotrichia leucophrys	1.468						1
245	Zonotrichia querula	1.560		1				

12. BIRDS OF BOREAL FOREST SITES IN NORTH AMERICA

	SITE NAME	REFERENCE
1	Doré Lake, Prince Albert National Park, Saskatchewan, Canada	Erskine, A J., 1974
2	Green River New Brunswick	Green River Annual Report 1957 Dunning, Jr J B., 1993
3	Nopiming Provincial Park, Manitoba	A Preliminary Floral and Faunal Inventory 1979, Dunning, Jr J.B 1993.
4	Taiga Biological Station, Manitoba	Pruitt W O. 1987 Dunning, Jr. J B. 1993.
5	Wood Buffalo NP Alberta/NW Territories	Official Bird List, Wood Buffalo National Park, Canada, 1978, Dunning, Jr., J.B., 1993

No	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5
1	Accipiter cooperii	2.647	1	1	1	1	
2	Accipiter gentilis	3.017	1		1	1	
3	Accipiter striatus	2.148	1		1	1	1
4	Actitis macularia	1.606	1	1	1	1	1
5	Aechmophorus occidentalis	3.169	1				
6	Aegolius acadicus	1.918				1	
7	Aegolius funereus	2.141	1			1	1
8	Agelaius phoeniceus	1.727	1	1	1	1	1
9	Aix sponsa	2.821			1	1	
10	Ammodramus leconteii	1.127	1		1		1
11	Anas acuta	3.011	1			1	1
12	Anas americana	2.878	1			1	1
13	Anas clypeata	2.789				1	1
14	Anas crecca	2.545	1		1	1	1
15	Anas discors	2.587	1		1	1	1
16	Anas platyrhynchos	3.034	1	1		1	1
17	Anas rubripes	3.115		1		1	
18	Anas strepera	2.966	1			1	
19	Aquila chrysaetos	3.603				1	1
20	Archilochus colubris	0.507	1	1	1	1	
21	Ardea herodias	3.381	1	1	1	1	
22	Asio flammeus	2.468	1			1	1
23	Asio otus	2.414	1				1
24	Aythya affinis	2.913	1			1	1
25	Aythya americana	3.025	1				1
26	Aythya collaris	2.853		1	1	1	1
27	Aythya marila	2.970					1
28	Aythya valisineria	3.090	1				1
29	Bartramia longicauda	2.172	1				1
30	Bombycilla cedrorum	1.512	1	1	1	1	1
31	Bombycilla garrulus	1.781	1				1
32	Bonasa umbellus	2.738	1		1	1	1
33	Botaurus lentiginosus	2.849		1	1		1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5
34	Branta canadensis canadensis	3.558	1	1	1	1	1
35	Branta canadensis moffitti	3.642	1	1	1	1	1
36	Bubo virginianus	3.132	1	1	1	1	1
37	Bucephala albeola	2.627	1			1	1
38	Bucephala clangula	2.936	1	1	1	1	1
39	Buteo jamaicensis	3.890	1	1	1	1	1
40	Buteo platypterus	2.657	1	1	1		
41	Calidris minutilla	1.365					1
42	Carduelis flammea	1.114	1				1
43	Carduelis hornemanni	1.104	1				
44	Carduelis pinus	1.164	1	1	1	1	1
45	Carduelis tristis	1.112		1	1	1	
46	Carpodacus purpureus	1.396	1	1	1	1	1
47	Cathartes aura	3.166			1	1	
48	Catharus fuscescens	1.494		1	1		
49	Catharus guttatus	1.491	1	1	1	1	1
50	Catharus minimus	1.518					1
51	Catharus ustulatus	1.489	1	1	1		1
52	Catoptrophorus semipalmatus	2.429	1				
53	Certhia americana	0.924	1	1	1	1	
54	Hirundo rustica rustica	1.260	1	1	1	1	1
55	Icterus galbula galbula	1.529	1		1	1	
56	Junco hyemalis	1.299	1	1	1	1	1
57	Lanius excubitor	1.817					1
58	Lanius ludovicianus	1.676		1			
59	Larus argentatus	3.063	1			1	1
60	Larus californicus californicus	2.778	1				1
61	Larus canus	2.610					1
62	Larus delawarensis	2.714	1		1	1	1
63	Larus philadelphia	2.326	1				1
64	Larus pipixcan	2.447					1
65	Limnodromus griseus	2.058					1
66	Lophodytes cucullatus	2.790			1	1	
67	Loxia curvirostra	1.562	1			1	1
68	Loxia leucoptera	1.425	1	1	1		1
69	Megaceryle alcyon	2.170			1		
70	Melanitta fusca	3.245					1
71	Melanitta perspicillata	2.980					1
72	Melospiza georgiana	1.230	1	1	1	1	1
73	Melospiza lincolnii	1.241	1		1		1
74	Melospiza melodia	1.318	1	1	1	1	1
75	Mergus merganser	3.173	1	1	1	1	1
76	Mergus serrator	3.011					1
77	Mniotilta varia	1.031	1		1		1
78	Molothrus ater	1.645	1	1	1	1	1
79	Oporornis agilis	1.182	1		1		
80	Oporornis philadelphia	1.101	1	1	1	1	

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5
81	Oxyura jamaicensis	2.730					1
82	Pandion haliaetus	3.178	1	1	1	1	1
83	Parula pitiayumi	0.844		1			
84	Parus atricapillus	1.033	1		1	1	1
85	Parus hudsonicus	0.991	1		1	1	1
86	Passer domesticus	1.443	1	1			1
87	Passerculus sandwichensis	1.306	1	1			1
88	Passerella iliaca	1.509	1	1			1
89	Pelecanus erythrorhynchos	3.845	1				1
90	Perisoreus canadensis	1.863	1		1	1	1
91	Phalacrocorax auritus	3.224	1	1		1	
92	Pheucticus ludovicianus	1.659	1	1	1		1
93	Pica pica	2.259	1				
94	Picoides arcticus	1.846			1	1	1
95	Picoides pubescens	1.431	1		1	1	1
96	Picoides tridactylus	1.827		1	1		1
97	Picoides villosus	1.831	1		1	1	1
98	Pinicola enucleator	1.751	1	1		1	1
99	Piranga ludoviciana	1.449					1
100	Piranga olivacea	1.456		1			
101	Podiceps auritus	2.656	1		1	1	1
102	Podiceps grisegena	3.010	1		1	1	1
103	Podilymbus podiceps	2.645	1	1	1	1	1
104	Ceryle alcyon	2.170	1	1			1
105	Chaetura pelagica	1.373		1			
106	Charadrius semipalmatus	1.670					1
107	Charadrius vociferus	1.980	1		1		1
108	Chlidonias niger	1.815	1		1		1
109	Chordeiles minor	1.789	1	1	1	1	1
110	Circus cyaneus	2.636			1		1
111	Cistothorus palustris	1.051	1			1	1
112	Cistothorus platensis	0.954	1				
113	Coccyzus erythropthalmus	1.708	1	1	1		
114	Colaptes auratus	2.122	1	1	1		1
115	Contopus borealis	1.507	1	1	1	1	1
116	Contopus sordidulus	1.107	1				1
117	Contopus virens	1.149		1	1	1	
118	Corvus brachyrhynchos	2.651	1		1	1	1
119	Corvus corax	3.083	1		1	1	1
120	Coturnicops noveboracensis	1.713					1
121	Cyanocitta cristata	1.939	1		1	1	
122	Dendragapus canadensis	2.673	1		1	1	1
123	Dendroica caerulescens	1.004		1			
124	Dendroica castanea	1.106	1	1	1	1	1
125	Dendroica coronata	1.097	1	1	1		1
126	Dendroica fusca	0.987	1	1	1		
127	Dendroica magnolia	0.941	1	1	1	1	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5
128	Dendroica palmarum	1.013	1		1	1	1
129	Dendroica pensylvanica	0.984	1	1	1	1	
130	Dendroica petechia	0.980	1	1	1	1	1
131	Dendroica striata	1.114	1	1			1
132	Dendroica tigrina	1.041	1	1	1		1
133	Dendroica virens	0.944	1	1	1		1
134	Dolichonyx oryzivorus	1.655		1			
135	Dryocopus pileatus	2.428	1	1	1	1	1
136	Dumetella carolinensis	1.567			1		
137	Empidonax alnorum	1.107	1	1	1	1	1
138	Empidonax flaviventris	1.064		1	1		1
139	Empidonax minimus	1.013	1	1	1	1	1
140	Eremophila alpestris	1.499	1	1			
141	Euphagus carolinus	1.774	1	1			1
142	Euphagus cyanocephalus	1.801					1
143	Falco columbarius	2.288	1	1		1	1
144	Falco peregrinus	2.914					1
145	Falco sparverius	2.067	1	1	1		1
146	Fulica americana	2.816	1				1
147	Gallinago gallinago	2.087	1		1	1	1
148	Gavia immer	3.616	1	1	1	1	1
149	Gavia stellata	3.191					1
150	Geothlypis trichas	1.006	1	1	1	1	1
151	Grus americana	3.765					1
152	Grus canadensis	3.501			1	1	1
153	Haliaeetus leucocephalus	3.677	1	1	1	1	1
154	Hesperiphona vespertina	1.773	1	1	1		1
155	Hirundo pyrrhonota	1.334		1	1		1
156	Hirundo rustica	1.205	1	1	1	1	1
157	Pooecetes gramineus	1.414	1				1
158	Porzana carolina	1.873	1		1	1	1
159	Progne subis	1.694	1		1		
160	Quiscalus quiscula	2.066	1	1	1	1	1
161	Regulus calendula	0.825	1	1	1	1	1
162	Regulus satrapa	0.794	1	1	1	1	1
163	Riparia riparia	1.164	1		1		1
164	Sayornis phoebe	1.297	1		1		1
165	Seiurus aurocapillus	1.288	1	1	1	1	1
166	Seiurus noveboracensis	1.250	1	1	1	1	1
167	Setophaga ruticilla	0.918	1	1	1	1	1
168	Sialia sialis	1.500		1			
169	Sitta canadensis	0.991	1	1	1	1	1
170	Sitta carolinensis	1.324	1	1			
171	Sphyrapicus varius	1.702	1	1	1		1
172	Spizella arborea	1.303					1
173	Spizella pallida	1.075	1		1		1
174	Spizella passerina	1.090	1	1	1	1	1

No.	SCIENTIFIC NAME	Mean Log10 Body Mass	Site 1	2	3	4	5
175	Sterna caspia	2.816					1
176	Sterna hirundo	2.079	1		1	1	1
177	Sterna paradisea	2.041					1
178	Strix nebulosa	2.997	1			1	1
179	Strix varia	2.860	1	1	1	1	
180	Sturnella neglecta	2.014	1		1		
181	Sturnus vulgaris	1.920	1	1			1
182	Surnia ulula	2.506					1
183	Tachycineta bicolor	1.303	1	1	1		1
184	Toxostoma rufum	1.838			1	1	
185	Tringa flavipes	1.908	1				1
186	Tringa melanoleuca	2.233	1				1
187	Tringa solitaria	1.685	1		1		1
188	Troglodytes aedon	1.037	1	1	1		
189	Troglodytes troglodytes	0.949	1	1	1		
190	Turdus migratorius	1.888	1	1	1	1	1
191	Tympanuchus phasianellus	2.946	1		1	1	1
192	Tyrannus tyrannus	1.639	1	1	1	1	1
193	Vermivora celata	0.954	1				1
194	Vermivora peregrina	1.001	1	1	1	1	1
195	Vermivora ruficapilla	0.941	1	1	1	1	
196	Vireo gilvus	1.170	1				1
197	Vireo olivaceus	1.223	1	1	1	1	1
198	Vireo philadelphicus	1.086	1	1	1		1
199	Vireo solitarius	1.220	1	1	1	1	1
200	Wilsonia canadensis	0.838	1	1	1	1	
201	Wilsonia pusilla	0.886		1	1	1	1
202	Xanthocephalus xanthocephalus	1.751	1				
203	Zenaida macroura	2.319	1		1		
204	Zonotrichia albicollis	1.413	1	1	1	1	1
205	Zonotrichia leucophrys	1.468	1				1

MAMMAL APPENDICES

1. MAMMALS OF TEMPERATE DESERT SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Big Bend National Park	Van Gelder R., 1982.
2	Bryce Canyon National Park	Van Gelder R., 1982.
3	Capitol Reef National Park	Van Gelder R., 1982.
4	Canyonlands National Park	Van Gelder R., 1982.
5	Death Valley National Park	Van Gelder R., 1982.
6	Mesa Verde National Park	Van Gelder R., 1982.
7	McKittrick, California	Schultz, J.R. 1938.
8	Mojave Desert, California	Merriam, J.C., 1919
9	Organ Pipe Cactus National Park	Van Gelder R. 1982.
10	Zion National Park	Van Gelder R., 1982.

No.	SCIENTIFIC NAME ORDER	GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8	9	10	ALTERNATIVE MASS	SITE
1	Artiodactyla	Alces	alces	5.604						1				1		
2	Artiodactyla	Antilocapra	americana	4.833	1	1	1		1		1	1	1	1	4.682	7,8
3	Artiodactyla	Bison	bison	5.695		1				1						
4	Artiodactyla	Cervus	canadensis	5.398							1					
5	Artiodactyla	Cervus	elaphus	5.431	1				1	1				1		
6	Artiodactyla	Odocoileus	hemionus	4.964	1	1	1	1	1	1	1		1		4.635	7
7	Artiodactyla	Odocoileus	virginianus	4.876					1	1						
8	Artiodactyla	Oreamnos	americanus	4.888						1						
9	Artiodactyla	Ovis	canadensis	4.999		1	1	1	1	1	1			1	4.905	7
10	Artiodactyla	Ovis	nelsoni	4.833								1				
11	Artiodactyla	Rangifer	tarandus	4.979						1						
12	Carnivora	Antrozous	pallidus	1.199								1				
13	Carnivora	Bassariscus	astutus	2.961	1		1	1	1							
14	Carnivora	Canis	latrans	4.121	1	1	1	1	1	1	1		1	1	4.000	7
15	Carnivora	Canis	lupus	4.633	1	1			1	1						
16	Carnivora	Eptesicus	fuscus	1.090								1				
17	Carnivora	Felis	concolor	4.737	1	1	1	1	1	1	1	1			1.090	7,8
18	Carnivora	Felis	onca	5.061							1					
19	Carnivora	Felis	rufus	3.914	1	1	1	1	1	1			1			
20	Carnivora	Lutra	canadensis	3.939		1				1	1				4.000	7
21	Carnivora	Lynx	lynx	4.239						1						
22	Carnivora	Lynx	rufus	4.201							1			1	10.000	
23	Carnivora	Martes	americana	3.097						1						
24	Carnivora	Martes	pennanti	3.462						1						
25	Carnivora	Mephitis	mephitis	3.356	1	1	1		1	1	1		1		3.474	7
26	Carnivora	Mustela	erminea	1.846		1				1						
27	Carnivora	Mustela	frenata	2.214	1		1		1	1				1		
28	Carnivora	Mustela	nivalis	1.627						1						
29	Carnivora	Mustela	vison	2.936		1			1	1						
30	Carnivora	Myotis	californicus	0.991								1				
31	Carnivora	Procyon	lotor	3.845		1			1	1	1	1			3.866	7
32	Carnivora	Spilogale	putorius	2.954	1	1	1	1	1				1			
33	Carnivora	Taxidea	taxus	3.803	1	1	1	1	1	1	1		1	1	3.900	7
34	Carnivora	Urocyon	cinereoargenteus	3.602	1	1	1	1	1		1		1		3.648	7
35	Carnivora	Ursus	americanus	5.134	1	1			1	1						
36	Carnivora	Ursus	arctos	5.311	1	1				1						
37	Carnivora	Vulpes	macrotis	3.260		1	1	1				1	1			
38	Carnivora	Vulpes	vulpes	3.688		1	1		1	1						

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8	9	10	ALTER-NATIVE MASS	SITE
39	Chiroptera	Gulo	gulo	4.104	1					1						
40	Insectivora	Scapanus	latimanus	1.760							1					
41	Insectivora	Sorex	merriami	0.770										1		
42	Insectivora	Sorex	ornatus	0.697							1					
43	Lagomorpha	Lepus	americanus	3.173		1				1						
44	Lagomorpha	Lepus	californicus	3.491	1	1	1	1	1		1	1	1	1	3.410	7,8
45	Lagomorpha	Lepus	townsendii	3.464	1	1				1				1		
46	Lagomorpha	Ochotona	princeps	2.155						1						
47	Lagomorpha	Sylvilagus	audubonii	2.863	1	1	1	1	1		1	1	1			
48	Lagomorpha	Sylvilagus	bachmani	2.788							1					
49	Lagomorpha	Sylvilagus	nuttallii	2.932	1			1	1					1		
50	Rodentia	Ammospermophilus	leucurus	2.009		1	1	1				1	1		1.978	8
51	Rodentia	Ammospermophilus	nelsoni	2.049							1					
52	Rodentia	Castor	canadensis	4.305	1	1	1		1	1	1			1	4.250	7
53	Rodentia	Cynomys	parvidens	3.013	1	1										
54	Rodentia	Cynomys	gunnisoni	3.013			1		1				1			
55	Rodentia	Cynomys	leucurus	3.013			1									
56	Rodentia	Dipodomys	deserti	2.021								1				
57	Rodentia	Dipodomys	heermanni	1.778							1					
58	Rodentia	Dipodomys	ingens	2.055							1					
59	Rodentia	Dipodomys	merriami	1.611								1				
60	Rodentia	Dipodomys	microps	1.743								1				
61	Rodentia	Dipodomys	nitratoides	1.618							1					
62	Rodentia	Dipodomys	ordii	1.798										1		
63	Rodentia	Dipodomys	panamintinus	1.873								1				
64	Rodentia	Erethizon	dorsatum	4.000	1	1	1	1	1	1			1	1	3.800	10
65	Rodentia	Eutamias	amoenus	1.716						1						
66	Rodentia	Eutamias	dorsalis	1.880	1	1										
67	Rodentia	Eutamias	merriami	1.716							1					
68	Rodentia	Eutamias	minimus	1.632	1	1			1	1				1		
69	Rodentia	Eutamias	quadrivittatus	1.630		1	1		1							
70	Rodentia	Eutamias	ruficaudus	1.833						1						
71	Rodentia	Eutamias	umbrinus	1.799	1											
72	Rodentia	Lagurus	curtatus	1.468										1		
73	Rodentia	Marmota	caligata	3.708						1						
74	Rodentia	Marmota	flaviventris	3.525	1	1								1		
75	Rodentia	Microtus	californicus	1.971							1	1				
76	Rodentia	Microtus	montanus	1.837										1		
77	Rodentia	Microtus	pennsylvanicus	1.562										1		
78	Rodentia	Mus	musculus	1.169										1		
79	Rodentia	Neotoma	albigula	2.297		1	1		1				1			
80	Rodentia	Neotoma	cinerea	2.477		1	1	1	1	1				1		
81	Rodentia	Neotoma	fuscipes	2.281				1			1	1				
82	Rodentia	Neotoma	intermedia	2.233								1				
83	Rodentia	Neotoma	lepida	2.107	1	1	1	1								
84	Rodentia	Neotoma	lepida	2.164							1					
85	Rodentia	Neotoma	mexicana	2.267			1		1							
86	Rodentia	Ondatra	zibethicus	3.037		1	1		1	1				1		
87	Rodentia	Onychomys	leucogaster	1.663										1		
88	Rodentia	Onychomys	torridus	1.808							1	1			1.398	8
89	Rodentia	Perognathus	californicus	1.342							1					
90	Rodentia	Perognathus	fallax	1.204								1				
91	Rodentia	Perognathus	Neotoma	1.279								1				
92	Rodentia	Perognathus	inornatus	1.491							1					
93	Rodentia	Perognathus	longimembris	0.833							1					
94	Rodentia	Perognathus	panamintinus	1.471								1				

		SCIENTIFIC NAME		Mean Log10 Body					Site						ALTER-NATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	6	7	8	9	10	MASS	SITE
95	Rodentia	Perognathus	parvus	1.199										1		
96	Rodentia	Perognathus	penicillatus	1.255								1				
97	Rodentia	Peromyscus	boylii	1.453							1					
98	Rodentia	Peromyscus	californicus	1.516							1					
99	Rodentia	Peromyscus	crinitus	1.349								1				
100	Rodentia	Peromyscus	maniculatus	1.243							1	1		1	1.344	8
101	Rodentia	Rattus	norvegicus	2.531										1		
102	Rodentia	Reithrodontomys	megalotis	1.065							1	1		1	1.114	8
103	Rodentia	Sciurus	aberti	2.795			1		1							
104	Rodentia	Spermophilus	beecheyi	2.781				1			1	1			2.813	7
105	Rodentia	Spermophilus	columbianus	2.766						1						
106	Rodentia	Spermophilus	lateralis	2.348	1	1			1	1						
107	Rodentia	Spermophilus	mohavensis	2.406								1				
108	Rodentia	Spermophilus	richardsonii	2.622						1						
109	Rodentia	Spermophilus	spilosoma	1.949									1			
110	Rodentia	Spermophilus	tereticaudus	2.274				1								
111	Rodentia	Spermophilus	townsendii	2.288										1		
112	Rodentia	Spermophilus	tridecemlineatus	2.204						1						
113	Rodentia	Spermophilus	variegatus	2.912	1	1	1		1				1			
114	Rodentia	Tamiasciurus	hudsonius	2.280	1	1			1	1						
115	Rodentia	Thomomys	bottae	2.049							1					
116	Rodentia	Thomomys	perpallidus	2.114								1				
117	Rodentia	Thomomys	talpoides	2.143										1		

2. MAMMALS OF TEMPERATE GRASSLANDS SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Badlands National Park, South Dakota	Sharps, J.C. and D.W. Uresk, 1990.
2	Bison	*Montana Bison Tech Report*
3	Cottonwood	
4	CPER	W. K. Lauenroth and D.G. Milchunas, 1992.
5	Jornada	Tech report No. 43
6	Konza	Finck, J.F., D.W. Kaufman, G.A. Kaufman, S.K. Gurtz, B.K. Clark, L.J. McLellan, B.S. Clark. 1986.
7	Pantex	Tech report No. 43
8	Pawnee	Terminal report No. 1
9	SW Kansas-NW Oklahoma	Hibbard, C.W. and D.W. Taylor, 1960

		SCIENTIFIC NAME		Mean Log10 Body	Site									ALTERNATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	6	7	8	9	MASS	SITE
1	Artiodactyla	Alces	alces	5.604						1	1	1			
2	Artiodactyla	Antilocapra	americana	4.653	1									4.688	12
3	Artiodactyla	Bison	bison	5.665										5.812	12
4	Artiodactyla	Cervus	canadensis	5.342									1		
5	Artiodactyla	Cervus	elaphus	5.431								1			
6	Artiodactyla	Dicotyles	tajacu	4.326	1										
7	Artiodactyla	Odocoileus	sp.	4.845									1		
8	Artiodactyla	Odocoileus	hemionus	4.964	1			1			1	1			
9	Artiodactyla	Odocoileus	virginianus	4.876	1			1		1		1		4.735	5,6
10	Artiodactyla	Oreamnos	americanus	4.866							1				
11	Artiodactyla	Ovis	canadensis	4.959	1										
12	Artiodactyla	Ovis	dalli	4.864							1				
13	Carnivora	Bassariscus	astutus	2.961	1										
14	Carnivora	Canis	latrans	4.121	1	1		1			1	1		4.097	2
15	Carnivora	Canis	lupus	4.630	1						1				
16	Carnivora	Conepatus	mesoleucus	3.303	1										
17	Carnivora	Felis	concolor	4.737	1						1	1		4.681	4
18	Carnivora	Felis	pardalis	4.079	1										
19	Carnivora	Felis	rufus	3.914	1			1							
20	Carnivora	Lutra	canadensis	3.959							1	1			
21	Carnivora	Lynx	rufus	3.869		1		1		1		1		3.914	8,11
22	Carnivora	Lynx	lynx	3.992						1	1	1		4.239	10,11
23	Carnivora	Martes	americana	3.087						1	1				
24	Carnivora	Martes	pennanti	3.462						1					
25	Carnivora	Mephitis	macroura	3.267	1										
26	Carnivora	Mephitis	mephitis	3.380	1			1		1		1		3.301	5
27	Carnivora	Mustela	erminea	1.806						1	1	1			
28	Carnivora	Mustela	frenata	2.224	1			1		1		1			
29	Carnivora	Mustela	nigripes	2.787											
30	Carnivora	Mustela	nivalis	1.637				1			1	1			
31	Carnivora	Mustela	vison	2.936				1		1	1	1			
32	Carnivora	Nasua	nasua	3.643	1										
33	Carnivora	Procyon	lotor	3.845	1			1		1		1			
34	Carnivora	Spilogale	putorius	2.694	1			1							
35	Carnivora	Taxidea	taxus	3.800	1	1		1				1			
36	Carnivora	Urocyon	cinereoargenteus	3.513	1			1							
37	Carnivora	Ursus	americanus	5.156	1					1	1	1			
38	Carnivora	Ursus	arctos	5.301							1				
39	Carnivora	Vulpes	macrotis	3.297	1										
40	Carnivora	Vulpes	vulpes	3.675				1		1	1	1		3.669	8,10,11
41	Chiroptera	Gulo	gulo	4.138							1				
42	Insectivora	Blarina	brevicauda	1.286						1		1			
43	Insectivora	Blarina	hylophaga	1.342				1							
44	Insectivora	Condylura	cristata	1.737						1					
45	Insectivora	Cryptotis	parva	0.690				1	1					0.750	12
46	Insectivora	Microsorex	hoyi	0.477						1	1	1			

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8	9	ALTER-NATIVE MASS	SITE
47	Insectivora	Notiosorex	crawfordi	0.778		1									
48	Insectivora	Parascalops	breweri	1.732						1					
49	Insectivora	Scalopus	aquaticus	1.796				1						1.699	12
50	Insectivora	Sorex	cinereus	0.609						1	1	1			
51	Insectivora	Sorex	arcticus	0.911								1			
52	Insectivora	Sorex	fumeus	0.916						1					
53	Insectivora	Sorex	[illegible]	0.778											
54	Insectivora	Sorex	nanus	0.845											
55	Insectivora	Sorex	merriami	0.876							1				
56	Insectivora	Sorex	palustris	1.141						1	1				
57	Insectivora	Sorex	vagrans	0.845			1								
58	Lagomorpha	Lepus	californicus	3.362									1		
59	Lagomorpha	Lepus	townsendii	3.464								1		3.175	12
60	Lagomorpha	Lepus	americanus	3.173			1			1	1	1			
61	Lagomorpha	Lepus	californicus	3.691	1	1		1	1						
62	Lagomorpha	Ochotona	princeps	2.185							1				
63	Lagomorpha	Sylvilagus	audubonii	2.863	1	1			1					2.845	12
64	Lagomorpha	Sylvilagus	floridanus	3.066	1			1				1		3.041	12
65	Lagomorpha	Sylvilagus	nuttalli	2.932											
66	Marsupicarnivora	Didelphis	marsupialis	3.323									1		
67	Marsupicarnivora	Didelphis	virginiana	3.301	1			1							
68	Rodentia	Ammospermophilus	harrisi	2.176							1	1			
69	Rodentia	Ammospermophilus	leucurus	2.189	1	1									
70	Rodentia	Castor	canadensis	4.301	1			1		1	1	1		4.300	3,6
71	Rodentia	Clethrionomys	gapperi	1.462			1					1			
72	Rodentia	Clethrionomys	rutilus	1.340							1				
73	Rodentia	Cynomys	ludovicianus	3.097		1								2.976	12
74	Rodentia	Dipodomys	ordii	1.708		1								1.810	12
75	Rodentia	Dipodomys	spectabilis	2.121		1									
76	Rodentia	Erethizon	dorsatum	4.006						1	1	1			
77	Rodentia	Eutamias	amoenus	1.708			1								
78	Rodentia	Eutamias	[illegible]	1.620							1	1			
79	Rodentia	Geomys	bursarius	2.215				1	1					2.016	12
80	Rodentia	Geomys	arenarius	2.549		1									
81	Rodentia	Glaucomys	sabrinus	2.199						1	1				
82	Rodentia	Lagurus	curtatus	1.498											
83	Rodentia	Lemmus	sibiricus	1.651							1				
84	Rodentia	Marmota	flaviventris	3.525											
85	Rodentia	Marmota	monax	3.535				1		1	1	1			
86	Rodentia	Marmota	caligata	3.750							1				
87	Rodentia	Microtus	chrotorrhinus	1.900						1					
88	Rodentia	Microtus	longicaudus	1.740							1				
89	Rodentia	Microtus	montanus	1.657			1								
90	Rodentia	Microtus	ochrogaster	1.661				1							
91	Rodentia	Microtus	oeconomus	1.724							1				
92	Rodentia	Microtus	pennsylvanicus	1.579						1	1	1		1.563	8
93	Rodentia	Microtus	pinetorum	1.400				1							
94	Rodentia	Mus	musculus	1.199				1				1			
95	Rodentia	Napaeozapus	insignis	1.351						1					
96	Rodentia	Microtus	[illegible]	2.423									1		
97	Rodentia	Neotoma	albigula	2.297	1	1									
98	Rodentia	Neotoma	cinerea	2.477			1				1				
99	Rodentia	Neotoma	floridana	2.475				1							
100	Rodentia	Neotoma	mexicana	2.267	1										
101	Rodentia	Neotoma	micropus	2.491	1	1									
102	Rodentia	Ondatra	zibethicus	3.097				1		1	1	1		3.079	12
103	Rodentia	Onychomys	leucogaster	1.443		1			1					1.390	12
104	Rodentia	Pappogeomys	castanops	2.350									1		
105	Rodentia	Perognathus	flavus	0.886									1		
106	Rodentia	Perognathus	hispidus	1.591									1		
107	Rodentia	Perognathus	fasciatus	0.973											

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	6	7	8	9	ALTER-NATIVE MASS	SITE
108	Rodentia	Perognathus	flavescens	1.041					1					1.000	12
109	Rodentia	Perognathus	flavus	0.934		1									
110	Rodentia	Perognathus	hispidus	1.672				1	1						
111	Rodentia	Perognathus	inornatus	0.940					1						
112	Rodentia	Perognathus	penicillatus	1.382		1									
113	Rodentia	Peromyscus	leucopus	1.430									1		
114	Rodentia	Peromyscus	maniculatus	1.193									1		
115	Rodentia	Peromyscus	difficilis	1.505											
116	Rodentia	Peromyscus	crinitus	1.602		1									
117	Rodentia	Peromyscus	leucopus	1.348				1	1					1.301	7
118	Rodentia	Peromyscus	maniculatus	1.373		1	1	1	1	1	1	1			
119	Rodentia	Phenacomys	intermedius	1.447							1				
120	Rodentia	Rattus	norvegicus	2.581				1				1			
121	Rodentia	Reithrodontomys	megalotis	1.176		1		1	1					1.079	12
122	Rodentia	Reithrodontomys	montanus	0.954				1	1					1.000	12
123	Rodentia	Sciurus	niger	2.835									1		
124	Rodentia	Sciurus	carolinensis	2.721						1		1			
125	Rodentia	Sigmodon	hispidus	2.102		1		1	1					2.146	12
126	Rodentia	Spermophilus	parryi	2.872							1				
127	Rodentia	Spermophilus	spilosoma	1.948									1		
128	Rodentia	Spermophilus	tridecemlineatus	1.899									1		
129	Rodentia	Spermophilus	franklini	2.651								1			
130	Rodentia	Spermophilus	mexicanus	1.400	1										
131	Rodentia	Spermophilus	richardsonii	2.622								1			
132	Rodentia	Spermophilus	spilosoma	1.949	1	1									
133	Rodentia	Spermophilus	tridecemlineatus	2.206				1	1			1			
134	Rodentia	Spermophilus	variegatus	2.912	1	1									
135	Rodentia	Synaptomys	cooperi	1.432				1		1				1.892	12
136	Rodentia	Tamias	striatus	1.987						1		1			
137	Rodentia	Tamiasciurus	hudsonicus	1.050			1			1	1	1			
138	Rodentia	Thomomys	talpoides	2.343								1			
139	Rodentia	Zapus	princeps	1.447			1					1			
140	Rodentia	Zapus	hudsonicus	1.242				1			1	1			
141		Pedomys	ochrogaster	1.602									1		

3 MAMMALS OF SUBTROPICAL WET FOREST SITES IN CENTRAL AMERICA

No	SITE NAME	REFERENCE
1	Columbia River Forest Reserve	Emmons, L. 1993.
2	Michoacan	Hall, E.R. and B. Villa-R., 1949

No	SCIENTIFIC NAME ORDER	GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTERNATIVE MASS	SITE
1	Artiodactyla	Mazama	americana	4.417	1			
2	Artiodactyla	Odocoileus	virginianus	4.720		1		
3	Artiodactyla	Tayassu	pecari	4.512	1			
4	Artiodactyla	Tayassu	sp	4.090		1		
5	Artiodactyla	Tayassu	tajacu	4.371	1			
6	Carnivora	Bassariscus	sumichrasti	1.724	1			
7	Carnivora	Canis	latrans	4.114		1		
8	Carnivora	Conepatus	mesoleucus	3.303		1		
9	Carnivora	Eira	barbara	3.699	1			
10	Carnivora	Lynx	rufus	4.281		1		
11	Carnivora	Mephitis	macroura	2.882		1		
12	Carnivora	Mustela	frenata	2.072		1		
13	Carnivora	Nasua	narica	3.568	1	1	3.602	2
14	Carnivora	Nasua	nasua	3.602	1			
15	Carnivora	Panthera	onca	4.740	1			
16	Carnivora	Potos	flavus	3.415	1			
17	Carnivora	Procyon	lotor	3.699		1		
18	Carnivora	Spilogale	angustifrons	2.699		1		
19	Carnivora	Urocyon	cinereoargenteus	3.548		1		
20	Insectivora	Cryptotis	parva	0.699		1		
21	Insectivora	Sorex	saussurei	0.778		1		
22	Lagomorpha	Lepus	callotis	3.398		1		
23	Lagomorpha	Sylvilagus	cunicularis	2.845		1		
24	Lagomorpha	Sylvilagus	floridanus	3.130		1		
25	Marsupicarnivora	Didelphis	marsupialis	3.136	1			
26	Marsupicarnivora	Marmosa	mexicana	1.623		1		
27	Marsupicarnivora	Marmosa	canescens	1.600		1		
28	Marsupicarnivora	Philander	opossum	2.633	1			
29	Perissodactyla	Tapirus	bairdii	5.352	1			
30	Primates	Alouatta	pigra	3.813	1			
31	Rodentia	Agouti	paca	3.903	1			
32	Rodentia	Baiomys	musculus	0.928		1		
33	Rodentia	Baiomys	taylori	0.903		1		
34	Rodentia	Dasyprocta	punctata	3.568	1			
35	Rodentia	Heteromys	desmarestianus	1.954	1			
36	Rodentia	Liomys	irroratus	1.623		1		
37	Rodentia	Liomys	pictus	1.602		1		
38	Rodentia	Microtus	mexicanus	1.544		1		

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTERNATIVE MASS	SITE
39	Rodentia	Mus	musculus	1.238		1		
40	Rodentia	Nelsonia	goldmani	1.748		1		
41	Rodentia	Neotoma	latifrons	2.271		1		
42	Rodentia	Neotomodon	alstoni	1.699		1		
43	Rodentia	Orthogeomys	hispidus	2.813	1			
44	Rodentia	Oryzomys	alfaroi	1.470	1			
45	Rodentia	Oryzomys	couesi	1.841		1		
46	Rodentia	Oryzomys	fulvescens	1.094		1		
47	Rodentia	Ototylomys	batti	2.079	1			
48	Rodentia	Pappogeomys	gymnurus	2.602		1		
49	Rodentia	Pappogeomys	tylorhinus	2.627		1		
50	Rodentia	Pappogeomys	varius	2.380		1		
51	Rodentia	Peromyscus	aztecus	1.505		1		
52	Rodentia	Peromyscus	banderanus	1.580		1		
53	Rodentia	Peromyscus	boylii	1.346		1		
54	Rodentia	Peromyscus	maniculatus	1.352		1		
55	Rodentia	Peromyscus	melanophrys	1.771		1		
56	Rodentia	Peromyscus	melanotis	1.513		1		
57	Rodentia	Peromyscus	perfulvus	1.146		1		
58	Rodentia	Peromyscus	truei	1.427		1		
59	Rodentia	Rattus	rattus	2.366		1		
60	Rodentia	Reithrodontomys	chrysopsis	1.114		1		
61	Rodentia	Reithrodontomys	fulvescens	1.322		1		
62	Rodentia	Reithrodontomys	megalotis	1.114		1		
63	Rodentia	Sciurus	aureogaster	2.775		1		
64	Rodentia	Sciurus	deppei	2.312	1			
65	Rodentia	Sigmodon	hispidus	2.192		1		
66	Rodentia	Sigmodon	melanotis	2.301		1		
67	Rodentia	Spermophilus	adocetus	2.404		1		
68	Rodentia	Spermophilus	variegatus	2.874		1		
69	Rodentia	Thomomys	umbrinus	2.220		1		
70	Rodentia	Tylomys	nudicaudus	2.447	1			
71	Rodentia	Zygogeomys	trichopus	2.653		1		
72	Xenarthra	Dasypus	novemcinctus	3.699		1		

4. MAMMALS OF NEOTROPICAL DRY DECIDUOUS FOREST IN CENTRAL AND SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Chamela	Medellin, R.A. 1992.
2	Parque Nacional Machalilla	Emmons, L. and V. Albuja, 1992.

No.	SCIENTIFIC NAME ORDER	GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTERNATIVE MASS	SITE
1	Artiodactyla	Mazama	americana	4.529		1		
2	Artiodactyla	Odocoileus	virginianus	4.602	1	1		
3	Artiodactyla	Tayassu	tajacu	4.371	1	1		
4	Carnivora	Bassariscus	astutus	3.034	1			
5	Carnivora	Canis	latrans	4.114	1			
6	Carnivora	Conepatus	mesoleucus	3.431	1			
7	Carnivora	Dusicyon	sechurae	3.653		1		
8	Carnivora	Eira	barbara	3.699		1		
9	Carnivora	Felis	concolor	4.568	1			
10	Carnivora	Felis	pardalis	4.051	1	1		
11	Carnivora	Felis	tigrina	3.477		1		
12	Carnivora	Felis	wiedii	3.477	1			
13	Carnivora	Felis	yagouaroundi	3.602	1	1	3.699	2
14	Carnivora	Lutra	longicaudis	3.995	1			
15	Carnivora	Mephitis	macroura	3.267	1			
16	Carnivora	Mustela	frenata	2.327	1			
17	Carnivora	Nasua	narica	3.568		1		
18	Carnivora	Nasua	nasua	3.602	1			
19	Carnivora	Panthera	onca	4.975	1	1	4.863	2
20	Carnivora	Potos	flavus	3.415		1		
21	Carnivora	Procyon	cancrivorus	4.000		1		
22	Carnivora	Procyon	lotor	3.658	1			
23	Carnivora	Spilogale	pygmaea	2.371	1			
24	Carnivora	Urocyon	cinereoargent	3.602	1			
25	Lagomorpha	Sylvilagus	brasiliensis	2.914		1		
26	Lagomorpha	Sylvilagus	cuniculari	3.352	1			
27	Marsupicarnivora	Caluromys	derbianus	2.488		1		
28	Marsupicarnivora	Didelphis	marsupialis	3.036		1		
29	Marsupicarnivora	Didelphis	virginiana	3.146	1			
30	Marsupicarnivora	Marmosa	mexicana	1.845	1			
31	Primates	Alouatta	palliata	3.825		1		
32	Rodentia	Agouti	paca	3.903		1		
33	Rodentia	Baiomys	musculus	0.875	1			
34	Rodentia	Coendou	sp.	3.628		1		
35	Rodentia	Dasyprocta	punctata	3.568		1		
36	Rodentia	Liomys	pictus	1.653	1			
37	Rodentia	Neotoma	alleni	2.569	1			

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTER-NATIVE MASS	SITE
38	Rodentia	Nyctomys	sumichrasti	1.720	1			
39	Rodentia	Oryzomys	alfaroi	1.470		1		
40	Rodentia	Oryzomys	melanotis	1.470	1			
41	Rodentia	Oryzomys	palustris	1.778	1			
42	Rodentia	Oryzomys	xantheolus	1.699		1		
43	Rodentia	Pappogeomys	bulleri	2.130	1			
44	Rodentia	Peromyscus	banderanus	1.531	1			
45	Rodentia	Peromyscus	perfulvus	1.512	1			
46	Rodentia	Proechimys	sp	2.431		1		
47	Rodentia	Reithrodontomys	fulvescens	1.061	1			
48	Rodentia	Sciurus	colliaei	2.676	1			
49	Rodentia	Sciurus	granatensis	2.563		1		
50	Rodentia	Sciurus	stramineus	2.477		1		
51	Rodentia	Sigmodon	mascotensis	2.192	1			
52	Rodentia	Xenomys	nelsoni	1.914	1			
53	Xenarthra	Choloepus	hoffmanni	3.954		1		
54	Xenarthra	Dasypus	novemcinctus	3.633	1	1		
55	Xenarthra	Tamandua	mexicana	3.778		1		

5. MAMMALS OF NEOTROPICAL CHACO AND CERRADO SITES IN SOUTH AMERICA

Nº	SITE NAME	REFERENCE
1	Curuyuqui Bolivia	Emmons L. 1993.
2	Perforacion	Emmons L. 1993.
3	Caatinga	Mares M.A. 1985 Dowrung J A and M Silva 1995

Nº	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	ALTERNATIVE MASS	SITE
1	Artiodactyla	Catagonus	wagneri	4.544	1					
2	Artiodactyla	Lama	guanicoe	3.929			1			
3	Artiodactyla	Mazama	gouazoubira	4.279	1		1	1	4.176	5
4	Artiodactyla	Odocoileus	virginianus	4.602		1				
5	Artiodactyla	Ozotoceros	bezoarticus	4.699				1		
6	Artiodactyla	Tayassu	pecari	4.512	1		1			
7	Artiodactyla	Tayassu	tajacu	4.371	1		1			
8	Carnivora	Cerdocyon	thous	3.748	1			1	3.813	5
9	Carnivora	Conepatus	chinga	3.275	1		1			
10	Carnivora	Conepatus	semistriatus	3.079				1		
11	Carnivora	Dusicyon	sp	3.748	1		1			
12	Carnivora	Dusicyon	thous	3.602		2				
13	Carnivora	Eira	barbara	3.699	1		1			
14	Carnivora	Felis	concolor	4.568	1	1	1	1	4.653	5
15	Carnivora	Felis	onca	5.061				1		
16	Carnivora	Felis	pardalis	4.051	1		1			
17	Carnivora	Felis	yaguarondi	3.699	1		1	1		
18	Carnivora	Galictis	vittata	3.243		1		1	3.505	5
19	Carnivora	Lutra	longicaudis	3.995	1					
20	Carnivora	Panthera	onca	4.845	1		1			
21	Carnivora	Procyon	cancrivorus	4.000				1		
22	Edentata	Chlamyphorus	sp	2.114	1		1			
23	Edentata	Tolypeutes	matacus	3.204	1		1			
24	Lagomorpha	Lepus	capensis	3.301	1		1			
25	Lagomorpha	Sylvilagus	brasiliensis	2.916			1	1	3.061	5
26	Marsupicarnivora	Didelphis	albiventris	3.097	1	1	1			
27	Marsupicarnivora	Marmosa	agilis	1.421				1		
28	Marsupicarnivora	Marmosa	cinerea	2.176				1		
29	Marsupicarnivora	Marmosa	karimii	1.845				1		
30	Marsupicarnivora	Monodelphis	americana	1.288				1		
31	Marsupicarnivora	Thylamys	pusilla	1.407			1			
32	Perissodactyla	Tapirus	terrestris	5.352	1		1			
33	Primates	Aotus	trivirgatus	3.006	1		1			
34	Primates	Callicebus	moloch	3.066	1		1			
35	Primates	Callithrix	jacchus	2.491				1		
36	Primates	Cebus	apella	3.462				1		
37	Rodentia	Akodon	arviculoides	1.531				1		
38	Rodentia	Bolomys	lasiurus	1.602				1		

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	 2	 3	 4	ALTER NATIVE MASS	 SITE
39	Rodentia	Calomys	callosus	1.653	1			1	1.176	5
40	Rodentia	Cavia	aperea	2.699		1				
41	Rodentia	Coendou	prehensilis	3.526	1		1			
42	Rodentia	Ctenomys	sp	2.556	1		1			
43	Rodentia	Dasyprocta	azarae	3.364	1					
44	Rodentia	Dasyprocta	prymnolopha	3.477				1		
45	Rodentia	Galea	musteloides	2.362	1					
46	Rodentia	Galea	spixii	2.602				1		
47	Rodentia	Graomys	griseoflavus	1.845			1			
48	Rodentia	Kerodon	rupestris	2.903				1		
49	Rodentia	Lagostomus	maximus	3.709			1			
50	Rodentia	Oryzomys	eliurus	1.613				1		
51	Rodentia	Oryzomys	subflavus	1.920				1		
52	Rodentia	Rhipidomys	mastacalis	1.833				1		
53	Rodentia	Sigmodon	alstoni	1.869		1				
54	Rodentia	Thrichomys	apereoides	2.544				1		
55	Rodentia	Wiedomys	pyrrhorhinos	1.763				1		
56	Rodentia	Zygodontomys	brevicauda	1.792		1				
57	Xenarthra	Chaetophractus	sp	3.255	1					
58	Xenarthra	Dasypus	novemcinctus	3.477				1		
59	Xenarthra	Dasypus	spp	3.544	1					
60	Xenarthra	Euphractus	sexcinctus	3.519				1		
61	Xenarthra	Euphractus	sexcinctus	3.699	1		1			
62	Xenarthra	Myrmecophaga	tridactyla	4.484	1		1			
63	Xenarthra	Priodontes	maximus	4.740	1					
64	Xenarthra	Tamandua	tetradactyla	3.799	1		1	1	3.699	5
65	Xenarthra	Tolypeutes	tricinctus	3.146				1		

6 MAMMALS OF CACTUS SCRUBLAND SITES IN SOUTH AMERICA

No	SITE NAME	REFERENCE
1	Monte Desert, Argentina	Mares, M.A. 1985., Downing, J.A. and M. Silva 1995.

		SCIENTIFIC NAME		Mean Log10 Body Mass	
No	ORDER	GENUS	SPECIES		1
1	Artiodactyla	Lama	guanicoe	4.929	1
2	Artiodactyla	Vicugna	vicugna	4.653	1
3	Carnivora	Conepatus	chinga	3.275	1
4	Carnivora	Conepatus	rex	3.243	1
5	Carnivora	Dusicyon	culpaeus	3.869	1
6	Carnivora	Dusicyon	griseus	3.643	1
7	Carnivora	Dusicyon	gymnocercus	3.752	1
8	Carnivora	Felis	colocolo	3.692	1
9	Carnivora	Felis	concolor	4.681	1
10	Carnivora	Felis	geoffroyi	3.461	1
11	Carnivora	Felis	yagouaroundi	3.602	1
12	Carnivora	Lyncodon	patagonicus	2.352	1
13	Marsupicarnivora	Didelphis	albiventris	3.602	1
14	Marsupicarnivora	Marmosa	pusilla	1.279	1
15	Rodentia	Akodon	andinus	1.362	1
16	Rodentia	Akodon	sp	1.431	1
17	Rodentia	Akodon	varius	1.602	1
18	Rodentia	Andalgalomys	olrogi	1.544	1
19	Rodentia	Calomys	musculinus	1.204	1
20	Rodentia	Ctenomys	frater	1.845	1
21	Rodentia	Ctenomys	fulvus	2.176	1
22	Rodentia	Ctenomys	saltarius	2.231	1
23	Rodentia	Dolichotis	patagonum	3.865	1
24	Rodentia	Eligmodontia	typus	1.279	1
25	Rodentia	Galea	musteloides	2.447	1
26	Rodentia	Graomys	griseoflavus	1.875	1
27	Rodentia	Microcavia	galea	2.447	1
28	Rodentia	Octomys	mimax	2.130	1
29	Rodentia	Phyllotis	darwini	1.699	1
30	Xenarthra	Chaetophractus	vellerosus	3.045	1

7 MAMMALS OF NEOTROPICAL GRASSLAND SITES IN SOUTH AMERICA

No.	SITE NAME	REFERENCE
1	Cerro Mutiles, SW Ecuador	Parker III T A 1992
2	Jauneche, SW Ecuador	Dunning Jr J.B. 1993

	SCIENTIFIC NAME			Mean Log10 Body	Site	
No	ORDER	GENUS	SPECIES	Mass	1	2
1	Artiodactyla	Mazama	americana	4.529		1
2	Artiodactyla	Tayassu	pecari	4.512	1	1
3	Artiodactyla	Tayassu	tajacu	4.371	1	1
4	Carnivora	Eira	barbara	3.699		1
5	Carnivora	Felis	concolor	4.568	1	
6	Carnivora	Felis	pardalis	4.051		1
7	Carnivora	Felis	tigrina	3.477		1
8	Carnivora	Felis	wiedii	3.477		1
9	Carnivora	Felis	yagouaroundi	3.699	1	1
10	Carnivora	Lutra	longicaudis	3.995		1
11	Carnivora	Mustela	frenata	2.327		1
12	Carnivora	Nasua	narica	3.568		1
13	Carnivora	Potos	flavus	3.415		1
14	Carnivora	Procyon	cancrivorus	4.000		1
15	Lagomorpha	Sylvilagus	brasiliensis	2.916		1
16	Marsupicarnivora	Caluromys	derbianus	2.488		1
17	Marsupicarnivora	Chironectes	minimus	2.826		1
18	Marsupicarnivora	Didelphis	marsupialis	3.036		1
19	Marsupicarnivora	Metachirus	nudicaudatus	2.574		1
20	Marsupicarnivora	Philander	opossum	2.633		1
21	Primates	Alouatta	palliata	3.825	1	1
22	Primates	Cebus	albifrons	3.302		1
23	Primates	Cebus	capucinus	3.512	1	
24	Rodentia	Agouti	paca	3.903	1	1
25	Rodentia	Coendou	rothschildi	3.607		1
26	Rodentia	Dasyprocta	punctata	3.568	1	1
27	Rodentia	Heteromys	australis	1.875		1
28	Rodentia	Oryzomys	albigularis	1.740		1
29	Rodentia	Oryzomys	alfaroi	1.470		1
30	Rodentia	Oryzomys	xantheolus	1.699		1
31	Rodentia	Sciurus	granatensis	2.563	1	1
32	Rodentia	Sciurus	stramineus	2.477	1	1
33	Xenarthra	Choloepus	hoffmanni	3.954		1
34	Xenarthra	Cyclopes	didactylus	2.602		1
35	Xenarthra	Dasypus	novemcinctus	3.477	1	1
36	Xenarthra	Tamandua	mexicana	3.778		1

8 MAMMALS OF NEOTROPICAL WET, MONTANE FOREST SITES IN SOUTH AMERICA

No	SITE NAME	REFERENCE
1	Cerro Blanco SW Ecuador	Emmons L. and V Albuja, 1992.
2	Cerro Pata de Pajaro, SW Ecuador	Emmons, L. and V Albuja, 1992.
3	Reserva Natural La Planada, Colombia	Alberico M and J.E. Orejuela 1983

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	ALTER NATIVE MASS	SITE
1	Artiodactyla	Mazama	americana	4.529	1	1	1	4.417	4
2	Artiodactyla	Odocoileus	virginianus	4.602	1				
3	Artiodactyla	Pudu	mephistophiles	3.954			1		
4	Artiodactyla	Tayassu	pecari	4.572	1	1			
5	Artiodactyla	Tayassu	tajacu	4.371	1				
6	Carnivora	Bassaricyon	gabbii	3.097			1		
7	Carnivora	Dusicyon	thous	3.602			1		
8	Carnivora	Eira	barbara	3.699	1	1	1		
9	Carnivora	Felis	concolor	4.568	1				
10	Carnivora	Felis	pardalis	4.061	1	1	1		
11	Carnivora	Felis	tigrina	3.477	1		1		
12	Carnivora	Felis	wiedii	3.477	1				
13	Carnivora	Felis	yagouaroundi	3.699	1	1			
14	Carnivora	Galictis	vittata	3.464	1				
15	Carnivora	Mustela	frenata	2.327	1	1	1		
16	Carnivora	Nasua	narica	3.568	1	1			
17	Carnivora	Panthera	onca	4.845	1				
18	Carnivora	Potos	flavus	3.415	1	1	1		
19	Carnivora	Procyon	cancrivorus	4.000	1	1			
20	Carnivora	Tremarctos	ornatus	5.146			1		
21	Lagomorpha	Sylvilagus	brasiliensis	2.916	1	1	1		
22	Marsupicarnivora	Caluromys	derbianus	2.488		1			
23	Marsupicarnivora	Chironectes	minimus	2.826					
24	Marsupicarnivora	Didelphis	marsupialis	3.036	1	1	1		
25	Marsupicarnivora	Metachirus	nudicaudatus	2.574					
26	Marsupicarnivora	Philander	opossum	2.633	1				
27	Primates	Alouatta	palliata	3.825	1	1	1		
28	Primates	Aotus	trivirgatus	3.006			1		
29	Primates	Ateles	fusciceps	3.778			1		
30	Primates	Cebus	albifrons	3.302	1	1			
31	Primates	Cebus	capucinus	3.512			1		
32	Rodentia	Agouti	paca	3.903	1	1	1		
33	Rodentia	Coendou	rothschildi	3.607	1				
34	Rodentia	Dasyprocta	punctata	3.568	1	1	1		
35	Rodentia	Heteromys	australis	1.875			1		
36	Rodentia	Microsciurus	sp	1.954			1		
37	Rodentia	Oryzomys	caliginosus	1.728	1	1			
38	Rodentia	Oryzomys	capito	1.740	1	1			
39	Rodentia	Oryzomys	xanthoeolus	1.699	1				

		SCIENTIFIC NAME		Mean Log10 Body	Site			ALTER NATIVE	
No	ORDER	GENUS	SPECIES	Mass	1	2	3	MASS	SITE
40	Rodentia	Proechimys	decumanus	2.431	1				
41	Rodentia	Proechimys	semispinosus	2.398			1		
42	Rodentia	Proechimys	sp	2.431	1				
43	Rodentia	Sciurus	granatensis	2.563	1	1	1		
44	Rodentia	Sciurus	stramineus	2.477	1				
45	Xenarthra	Bradypus	tridactylus	3.568			1		
46	Xenarthra	Bradypus	variegatus	3.591		1			
47	Xenarthra	Choloepus	hoffmanni	3.954	1				
48	Xenarthra	Cyclopes	didactylus	2.602		1			
49	Xenarthra	Dasypus	novemcinctus	3.477	1	1	1	3.580	4
50	Xenarthra	Myrmecophaga	tridactyla	4.484	1				
51	Xenarthra	Tamandua	mexicana	3.778	1	1			
52	Xenarthra	Tamandua	sp	3.748			1		

9. MAMMALS OF NEOTROPICAL RAINFOREST SITES IN SOUTH AND CENTRAL AMERICA

No.	SITE NAME	REFERENCE
1	Barro Colorado Island, Panama	Medellin, R.A., 1992.
2	Belem, Brazil	Medellin, R.A., 1992.
3	Cusco Amazonico, Peru	Medellin, R.A., 1992.
4	Guatopo, Venezuela (Downing)	Medellin, R.A., 1992.
5	Selva Lacandona, Mexico	Medellin, R.A., 1992.
6	La Selva Biological Station, Costa Rica	McDade, L. A., K. S. Bawa, H. A. Hespenheide, and G. S. Hartshorn, 1994.
7	Manu National Park, Peru	Medellin, R.A. 1992.
8	Alto Madidi Region, NW Bolivia	Emmons, L. 1990.
9	Kanuku Mountain West, Guyana	Emmons, L. 1993.
10	Surinam	Eisenberg, J. 1989. Husson, 1962,1978, Robinson and Redford, 1989
11	Guatopo, Venezuela (Legendre)	Medellin, R.A. 1992.
12	Rio Cenepa, Peru	Patton, J.L., 1982; Downing J.A. and Silva, M. 1995.
13	Rio Santiago, Peru	Patton, J.L., 1982, Downing J.A. and Silva, M., 1995.
14	Sierra de Chama, Guatemala	Hendrichs, H. 1977. Downing J.A. and Silva, M., 1995

		SCIENTIFIC NAME		Mean Log10 Body	Site														ALTER-NATIVE	ALTER-NATIVE
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	6	7	8	9	10	11	12	13	14	MASS	SITE
1	Artiodactyla	Mazama	americana	4.178	I	I	I	I	I	I	I	I	I	I	I	I	I	I	4.309	2,3,4,5,7,10,13
2	Artiodactyla	Mazama	gouazoubira	4.093		I					I		I	I			I		4.279	9
3	Artiodactyla	Odocoileus	virginianus	4.601	I		I		I	I				I				I	4.679	14
4	Artiodactyla	Tayassu	pecari	4.511		I	I		I	I	I			I		I	I	I	4.436	10
5	Artiodactyla	Tayassu	tajacu	4.375		I	I	I	I	I	I	I	I	I	I	I	I	I	4.362	13
6	Carnivora	Atelocynus	microtis	3.889		I	I					I				I	I		3.976	10,11
7	Carnivora	Bassaricyon	alleni	3.302												I				
8	Carnivora	Bassaricyon	gabbii	3.307			I			I	I	I								
9	Carnivora	Cerdocyon	thous	3.748		I								I					3.863	11
10	Carnivora	Conepatus	semistriatus	3.389				I	I	I								I	3.509	14
11	Carnivora	Eira	barbara	3.659	I	I	I	I	I	I	I		I	I		I	I		3.610	10,13
12	Carnivora	Felis	concolor	4.568		I	I	I	I	I	I	I	I	I						
13	Carnivora	Felis	onca	5.061												I				
14	Carnivora	Felis	pardalis	4.051	I	I	I	I	I	I	I	I		I		I			4.080	11
15	Carnivora	Felis	tigrina	3.477										I						
16	Carnivora	Felis	wiedii	3.477		I	I		I	I				I		I			3.500	10
17	Carnivora	Felis	yagouaroundi	3.689	I	I	I	I	I	I	I					I			3.600	1
18	Carnivora	Galictis	vittata	3.464			I			I	I			I		I	I		3.170	10
19	Carnivora	Herpailurus	yagouaroundi	3.808														I		
20	Carnivora	Leopardus	pardalis	4.131														I		
21	Carnivora	Leopardus	tigrinus	3.383														I		
22	Carnivora	Leopardus	wiedii	3.613														I		
23	Carnivora	Lutra	annectens	3.550														I		
24	Carnivora	Lutra	longicaudis	3.999		I	I		I	I	I	I	I	I		I			4.079	11
25	Carnivora	Mustela	africana	2.308		I														
26	Carnivora	Mustela	frenata	2.327						I								I	2.477	11
27	Carnivora	Nasua	narica	2.586														I		
28	Carnivora	Nasua	nasua	3.720	I	I	I			I	I		I	I		I			3.588	5,6,7,9,10
29	Carnivora	Panthera	onca	4.881		I	I	I	I	I	I	I		I				I	4.740	6,7,8,10
30	Carnivora	Potos	flavus	3.415	I	I	I	I	I	I	I	I	I	I		I	I	I	3.386	10
31	Carnivora	Procyon	cancrivorus	4.000		I		I			I			I		I			3.672	4,10
32	Carnivora	Procyon	lotor	3.828					I	I								I	3.988	14
33	Carnivora	Pteronura	brasiliensis	4.464		I	I				I			I					4.679	10
34	Carnivora	Puma	concolor	4.823														I		
35	Carnivora	Speothos	venaticus	3.778		I	I							I		I			3.769	12
36	Carnivora	Tayra	barbara	3.655														I		
37	Carnivora	Tremarctos	ornatus	5.166												I				
38	Carnivora	Urocyon	cinereoargenteus	3.600					I											
39	Carnivora	Urocyon	cinereoargenteus	2.586														I		
40	Edentata	Cabassous	unicinctus	3.580		I	I	I						I	I	I			3.661	4,11,12
41	Edentata	Cabassous	centralis	3.429	I				I	I										
42	Insectivora	Sorex	veraepacis	0.875														I		
43	Lagomorpha	Sylvilagus	brasiliensis	2.916	I	I	I	I	I		I	I		I	I	I	I	I	2.600	4,13,14
44	Lagomorpha	Sylvilagus	floridanus	3.066														I		
45	Marsupicarnivora	Caluromys	derbianus	2.480	I				I	I								I	2.490	14
46	Marsupicarnivora	Caluromys	lanatus	2.556			I				I	I	I			I	I	I	13,14	
47	Marsupicarnivora	Caluromys	philander	2.311		I		I						I	I				3.500	10
48	Marsupicarnivora	Caluromysiops	irrupta	2.586							I									
49	Marsupicarnivora	Chironectes	minimus	2.628	I	I	I	I	I	I				I	I	I			2.576	13,11
50	Marsupicarnivora	Didelphis	marsupialis	2.506	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3.373	11
51	Marsupicarnivora	Didelphis	virginiana	3.165					I											
52	Marsupicarnivora	Lutreolina	crassicaudata	2.699										I						

		SCIENTIFIC NAME		Mean Log10 Body	Site														ALTER-NATIVE	ALTER-NATIVE
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	6	7	8	9	10	11	12	13	14	MASS	SITE
53	Marsupicarnivora	Marmosa	cinerea	1.881										I						
54	Marsupicarnivora	Marmosa	cinerea	2.176											I					
55	Marsupicarnivora	Marmosa	elegans	1.415										I						
56	Marsupicarnivora	Marmosa	bicolor	1.799				I							I				1.778	11
57	Marsupicarnivora	Marmosa	germana	2.526												I	I			
58	Marsupicarnivora	Marmosa	impavida	1.407													I			
59	Marsupicarnivora	Marmosa	lepida	1.544										I						
60	Marsupicarnivora	Marmosa	mexicana	1.663					I	I								I		
61	Marsupicarnivora	Marmosa	murina	1.633		I	I	I				I	I	I	I	I	I		1.712	4,10,11
62	Marsupicarnivora	Marmosa	robinsoni	1.926	I															
63	Marsupicarnivora	Marmosa	rubra	1.799												I				
64	Marsupicarnivora	Marmosops	noctivagus	1.565			I				I	I								
65	Marsupicarnivora	Marmosops	parvidens	1.332		I	I						I							
66	Marsupicarnivora	Metachirus	nudicaudatus	2.575	I	I	I		I		I	I	I	I		I	I		2.653	13
67	Marsupicarnivora	Monodelphis	adusta	1.395			I									I			1.602	12
68	Marsupicarnivora	Monodelphis	americana	1.662		I														
69	Marsupicarnivora	Monodelphis	brevicauda	1.903											I					
70	Marsupicarnivora	Monodelphis	brevicaudata	1.905				I						I						
71	Marsupicarnivora	Philander	andersoni	2.512			I													
72	Marsupicarnivora	Philander	opossum	2.618	I	I			I	I			I	I		I	I	I	2.879	10
73	Perissodactyla	Tapirus	bairdi	5.368														I		
74	Perissodactyla	Tapirus	bicolor	5.381	I					I										
75	Perissodactyla	Tapirus	terrestris	5.577		I	I	I			I	I	I	I	I	I			5.507	6,9
76	Primates	Alouatta	belzebul	3.806		I														
77	Primates	Alouatta	palliata	3.825	I					I										
78	Primates	Alouatta	pigra	3.813																
79	Primates	Alouatta	seniculus	3.778			I	I			I	I	I	I	I	I			3.626	4,11
80	Primates	Alouatta	villosa	3.801														I		
81	Primates	Aotus	lemurinus	3.006						I										
82	Primates	Aotus	nigriceps	3.006			I													
83	Primates	Aotus	trivirgatus	3.006	I	I					I	I				I	I		2.978	12,13
84	Primates	Ateles	belzebuth	3.911				I												
85	Primates	Ateles	belzebuth	3.906											I					
86	Primates	Ateles	geoffroyi	3.892	I				I	I								I	3.766	13
87	Primates	Ateles	paniscus	3.886			I				I	I	I	I						
88	Primates	Callicebus	moloch	3.166			I				I	I				I	I		2.979	10,11
89	Primates	Callimico	goeldii	2.961			I				I									
90	Primates	Cebuella	pygmaea	2.086			I													
91	Primates	Cebus	albifrons	3.393			I				I					I				
92	Primates	Cebus	apella	3.501		I	I				I	I	I	I					3.591	11
93	Primates	Cebus	capucinus	3.512	I					I										
94	Primates	Cebus	nigrivittatus	3.462				I							I				3.415	11
95	Primates	Cebus	olivaceus	3.415				I					I	I						
96	Primates	Chiropotes	satanas	3.475		I								I					3.493	10
97	Primates	Lagothrix	lagothricha	3.805			I				I									
98	Primates	Pithecia	hirsuta	3.175													I			
99	Primates	Pithecia	monachus	3.377			I													
100	Primates	Pithecia	pithecia	3.316									I	I						
101	Primates	Saguinus	fuscicollis	2.586			I				I	I								
102	Primates	Saguinus	imperator	2.716			I				I									
103	Primates	Saguinus	midas	2.732		I								I					2.699	10
104	Primates	Saguinus	oedipus	2.581	I															
105	Primates	Saimiri	boliviensis	2.903			I													
106	Primates	Saimiri	sciureus	2.906		I					I	I	I	I		I			2.908	9,10
107	Rodentia	Agouti	paca	3.900	I	I	I	I	I	I	I	I	I	I						
108	Rodentia	Akodon	urichi	1.344				I							I				1.699	11
109	Rodentia	Baiomys	musculus	0.863														I		
110	Rodentia	Cavia	aperea	2.856									I	I						
111	Rodentia	Coendou	bicolor	3.505							I					I			3.613	10
112	Rodentia	Coendou	mexicanus	3.495														I		
113	Rodentia	Coendou	prehensilis	3.528		I							I	I	I				3.433	11
114	Rodentia	Cuniculus	paca	3.869											I	I	I	I	3.914	10,13,14
115	Rodentia	Dactylomys	dactylinus	2.813			I				I	I								
116	Rodentia	Dasyprocta	azarae	3.640				I					I							
117	Rodentia	Dasyprocta	aguti	3.281											I					
118	Rodentia	Dasyprocta	fuliginosa	3.586												I	I			
119	Rodentia	Dasyprocta	leporina	3.556										I						
120	Rodentia	Dasyprocta	prymnolopha	3.568		I														
121	Rodentia	Dasyprocta	punctata	3.550	I				I	I								I	3.591	14
122	Rodentia	Dasyprocta	variegata	3.431								I								
123	Alouatta	Dinomys	branickii	4.114			I				I					I			4.097	13

		SCIENTIFIC NAME		Mean Log10 Body Mass	Bin														ALTERNATIVE	ALTERNATIVE
No.	ORDER	GENUS	SPECIES		1	2	3	4	5	6	7	8	9	10	11	12	13	14	MASS	SITE
124	Rodentia	Diplomys	labilis	2.556	I															
125	Rodentia	Echimys	armatus	2.602		I								I						
126	Rodentia	Echimys	chrysurus	2.813		I								I						
127	Rodentia	Echimys	semivillosus	2.478				I												
128	Rodentia	Heterogeomys	hispidus	2.813														I		
129	Rodentia	Heteromys	anomalus	1.885				I							I					
130	Rodentia	Heteromys	desmarestianus	1.904	I				I	I								I	3.899	14
131	Rodentia	Holochilus	brasiliensis	2.203		I														
132	Rodentia	Holochilus	guianae	2.212									I							
133	Rodentia	Holochilus	sciureus	2.215										I						
134	Rodentia	Hoplomys	gymnurus	2.600						I										
135	Rodentia	Hydrochaeris	hydrochaeris	4.635	I	I	I				I	I		I		I	I		4.498	8,13
136	Rodentia	Isothrix	bistriata	2.448			I													
137	Rodentia	Isothrix	villosa	2.740													I			
138	Rodentia	Liomys	salvini	1.544														I		
139	Rodentia	Makalata	armatus	2.602												I	I			
140	Rodentia	Mesomys	hispidus	2.243			I				I	I	I							
141	Rodentia	Mesomys	stimulax	2.009										I						
142	Rodentia	Microsciurus	alleni	1.942						I										
143	Rodentia	Microsciurus	flaviventer	2.087												I				
144	Rodentia	Myoprocta	acouchy	2.748									I	I						
145	Rodentia	Myoprocta	pratti	3.087			I				I									
146	Rodentia	Myoprocta	pratti	2.978												I				
147	Rodentia	Neacomys	guianae	1.301									I	I						
148	Rodentia	Neacomys	spinosus	1.236			I									I	I		1.279	10,13
149	Rodentia	Neacomys	tenuipes	1.204			I	I							I				1.255	11
150	Rodentia	Nectomys	squamipes	2.608		I					I		I	I		I	I		2.346	12
151	Rodentia	Nyctomys	sumichrasti	1.770					I	I										
152	Rodentia	Ototylomys	phyllotis	2.037					I											
153	Rodentia	Oecomys	bicolor	1.439	I	I	I	I			I	I								
154	Rodentia	Oligoryzomys	fulvescens	0.999									I							
155	Rodentia	Oligoryzomys	microtis	1.000			I				I	I								
156	Rodentia	Orthogeomys	hispidus	2.813					I											
157	Rodentia	Oryzomys	albigularis	1.740				I							I				1.863	11
158	Rodentia	Oryzomys	alfaroi	1.471					I									I	1.680	14
159	Rodentia	Oryzomys	bicolor	1.699										I	I		I		1.779	13
160	Rodentia	Oryzomys	bombycinus	1.653						I										
161	Rodentia	Oryzomys	caliginosus	1.725						I										
162	Rodentia	Oryzomys	capito	1.653	I	I	I	I			I		I	I	I	I	I		1.499	11
163	Rodentia	Oryzomys	concolor	1.778										I	I	I	I		1.813	11
164	Rodentia	Oryzomys	couesi	1.420					I											
165	Rodentia	Oryzomys	delicatus	1.176										I						
166	Rodentia	Oryzomys	fulvescens	1.000		I			I	I	I									
167	Rodentia	Oryzomys	macconnelli	1.744		I					I			I		I			1.875	12
168	Rodentia	Oryzomys	melanotis	1.479					I											
169	Rodentia	Oryzomys	bicolor	1.740			I				I									
170	Rodentia	Oryzomys	sp.	1.519													I			
171	Rodentia	Oryzomys	yunganus	1.699												I				
172	Rodentia	Ototylomys	phyllotis	1.799														I		
173	Rodentia	Peromyscus	grandis	1.887														I		
174	Rodentia	Peromyscus	guatemalensis	1.872														I		
175	Rodentia	Peromyscus	mexicanus	1.630					I									I	1.580	14
176	Rodentia	Proechimys	brevicauda	2.860			I										I		3.099	10
177	Rodentia	Proechimys	cuvieri	2.647										I						
178	Rodentia	Proechimys	guyannensis	2.678										I					2.497	13
179	Rodentia	Proechimys	bicolor	2.394												I	I			
180	Rodentia	Proechimys	longicaudatus	2.613												I	I			
181	Rodentia	Proechimys	semispinosus	2.398	I			I		I					I		I		2.497	11
182	Rodentia	Proechimys	simonsi	2.398			I				I	I								
183	Rodentia	Proechimys	sp.	2.471									I							
184	Rodentia	Proechimys	steerei	2.398			I				I	I								
185	Rodentia	Rattus	rattus	2.121													I			
186	Rodentia	Reithrodontomys	fulvescens	1.068														I		
187	Rodentia	Reithrodontomys	mexicanus	1.114														I		
188	Rodentia	Reithrodontomys	sumichrasti	1.236			I			I								I		
189	Rodentia	Rhipidomys	fulviventer	1.954										I						
190	Rodentia	Rhipidomys	couesi	2.156			I													
191	Rodentia	Rhipidomys	fulvescens	2.000		I														
192	Rodentia	Rhipidomys	nitela	2.000									I							
193	Rodentia	Rhipidomys	venezuelae	2.100				I							I				1.994	11

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mass Log10 Body Mass	1	2	3	4	5	6	7	8	9	10	11	12	13	14	ALTERNATIVE MASS	ALTER- SITE
194	Rodentia	Sciurillus	pusillus	1.989										I						
195	Rodentia	Sciurus	Rodentia	2.030									I	I						
196	Rodentia	Sciurus	aureogaster	2.749					I									I	2.301	14
197	Rodentia	Sciurus	deppei	2.312					I									I	1.667	14
198	Rodentia	Sciurus	granatensis	2.563	I			I		I					I				2.398	11
199	Rodentia	Sciurus	ignitus	2.366			I				I	I								
200	Rodentia	Sciurus	igniventris	2.610												I				
201	Rodentia	Sciurus	richmondi	2.176							I									
202	Rodentia	Sciurus	spadiceus	2.796			I				I	I				I			2.735	12
203	Rodentia	Sciurus	variegatoides	2.413						I										
204	Rodentia	Sciurus	yucatanensis	3.398					I											
205	Rodentia	Scotinomys	teguina	1.535														I		
206	Rodentia	Sigmodon	alstoni	1.869									I							
207	Rodentia	Sigmodon	hispidus	1.911					I									I	2.041	14
208	Rodentia	Sphiggurus	insidiosus	3.000										I						
209	Rodentia	Sphiggurus	mexicanus	2.903						I										
210	Rodentia	Sphiggurus	rothschildi	3.301	I															
211	Rodentia	Tylomys	nudicaudus	2.647					I											
212	Rodentia	Tylomys	watsoni	2.647						I										
213	Rodentia	Zygodontomys	brevicauda	1.792									I	I					1.896	10
214	Rodentia	Zygodontomys	brunneus	1.726		I														
215	Xenarthra	Bradypus	infuscatus	2.403											I					
216	Xenarthra	Bradypus	tridactylus	2.088									I	I						
217	Xenarthra	Bradypus	variegatus	3.591	I		I			I	I					I	I		3.611	12,13
218	Xenarthra	Choloepus	didactylus	3.602		I				I			I	I					3.638	10
219	Xenarthra	Choloepus	hoffmanni	3.954	I		I				I					I			3.629	10
220	Xenarthra	Cyclopes	didactylus	2.637	I	I	I		I	I	I			I		I	I		2.600	5
221	Xenarthra	Dasypus	kappleri	4.006		I	I							I					2.954	5
222	Xenarthra	Dasypus	novemcinctus	2.080	I	I	I	I	I	I	I		I	I	I	I	I	I	3.605	2,3
223	Xenarthra	Dasypus	septemcinctus	3.212		I														
224	Xenarthra	Euphractus	sexcinctus	3.699		I								I					3.732	13
225	Xenarthra	Myrmecophaga	tridactyla	4.684		I	I				I			I		I	I		4.301	12,13
226	Xenarthra	Priodontes	giganteus	4.398											I					
227	Xenarthra	Priodontes	maximus	4.740			I	I			I		I	I		I			4.600	13
228	Xenarthra	Tamandua	tetradactyla	3.779	I	I	I	I		I	I		I	I	I	I	I	I	3.600	5,11

10. MAMMALS OF GRASSLAND AND DESERT SITES IN AFRICA AND ASIA

No.	SITE NAME	REFERENCE
1	Aghbolagh, Iran	Misonne, X., 1959
2	Amboseli National Park, Kenya	Behrensmeyer, A.K., D. Western, and D.E.D. Boaz, 1979; Downing, J.A. and M. Silva, 1995
3	Region Berbera, Algeria	Kowalski, K.; Downing, J.A. and M. Silva, 1995
4	Donana, Spain	Valverde, J.A., 1964,1976; Downing, J.A. and M. Silva, 1995
5	Golden Gate Highlands NP, South Africa	Rautenbach, I.L., 1976; Downing, J.A. and M. Silva, 1995
6	Ibanda, Rwanda	Misonne, X., 1959; Verschuren, J. 1965; Downing, J.A. and M. Silva, 1995
7	Jebel Marra, Sudan	Happold, D.C.D. 1966,1969; Downing, J.A. and M. Silva, 1995
8	Rwindi-Rutshuru, Zaire	Frechkop, S., 1938,1943; Bourliere, F. and J. Verschuren, 1960; Downing, J.A. and M. Silva, 1995.
9	Transvaal 3, South Africa	Rautenbach, I.L., 1976; Downing, J.A. and M. Silva, 1995
10	Transvaal 7, South Africa	Rautenbach, I.L., 1976; Downing, J.A. and M. Silva, 1995
11	Transvaal 9, South Africa	Rautenbach, I.L., 1976; Downing, J.A. and M. Silva, 1995
12	Transvaal 17, South Africa	Rautenbach, I.L., 1976; Downing, J.A. and M. Silva, 1995

No.	SCIENTIFIC NAME ORDER	GENUS	SPECIES	Mass Log10 Body Mass	Site 1	2	3	4	5	6	7	8	9	10	11	12	ALTERNATIVE MASS	NOTE	ALTERNATIVE MASS	NOTE
1	Artiodactyla	Adenota	kob	4.887								1								
2	Artiodactyla	Aepyceros	melampus	4.699		1				1				1	1		4.591	6	4.667	10,11
3	Artiodactyla	Alcelaphus	buselaphus	5.146		1			1								5.187	1		
4	Artiodactyla	Antidorcas	marsupialis	4.560					1				1							
5	Artiodactyla	Capra	hircus	4.845	1															
6	Artiodactyla	Cephalophus	natalensis	4.000											1	1				
7	Artiodactyla	Cervus	elaphus	5.195			1	1									5.114	1		
8	Artiodactyla	Connochaetes	gnou	4.250					1											
9	Artiodactyla	Connochaetes	taurinus	5.301		1									1		5.287	1		
10	Artiodactyla	Dama	dama	4.889				1												
11	Artiodactyla	Damaliscus	dorcas	4.903					1											
12	Artiodactyla	Damaliscus	lunatus	5.114								1			1		5.130	1		
13	Artiodactyla	Gazella	cuvieri	4.420			1													
14	Artiodactyla	Gazella	dama	4.543			1													
15	Artiodactyla	Gazella	dorcas	4.393			1													
16	Artiodactyla	Gazella	granti	4.800		1														
17	Artiodactyla	Gazella	leptoceros	4.432			1													
18	Artiodactyla	Gazella	rufifrons	4.431							1									
19	Artiodactyla	Gazella	subgutturosa	4.267	1															
20	Artiodactyla	Gazella	thomsoni	4.035		1														
21	Artiodactyla	Giraffa	camelopardalis	5.903		1									1					
22	Artiodactyla	Hippopotamus	amphibius	6.146		1				1		1			1		6.000	6	6.148	12
23	Artiodactyla	Hippotragus	equinus	5.377									1		1		5.380	11		
24	Artiodactyla	Hippotragus	niger	5.362											1					
25	Artiodactyla	Kobus	defassa	5.262						1										
26	Artiodactyla	Kobus	ellipsiprymnus	5.000		1									1	1	5.090	11,12		
27	Artiodactyla	Litocranius	walleri	4.598		1														
28	Artiodactyla	Madoqua	kirki	3.724		1														
29	Artiodactyla	Neotragus	moschatus	3.778												1				
30	Artiodactyla	Oryx	gazella	5.233		1														
31	Artiodactyla	Ourebia	ourebi	4.166					1	1						1	4.301	5		
32	Artiodactyla	Ovis	orientalis	4.892	1															
33	Artiodactyla	Pelea	capreolus	4.000					1					1	1	1	4.380	5		
34	Artiodactyla	Phacochoerus	aethiopicus	4.845		1			1	1				1	1		4.380	5	4.699	6
35	Artiodactyla	Potamochoerus	porcus	4.898								1		1	1	1				
36	Artiodactyla	Raphicerus	campestris	4.176		1			1				1	1	1		4.000	6	4.045	9,10,11
37	Artiodactyla	Raphicerus	sharpei	4.000											1	1				
38	Artiodactyla	Redunca	arundinum	4.507					1					1	1	1				
39	Artiodactyla	Redunca	fulvorufula	4.447					1						1	1	4.460	10,11		
40	Artiodactyla	Redunca	redunca	4.676		1														
41	Artiodactyla	Sus	scrofa	5.161	1		1	1									4.996	1	4.903	4
42	Artiodactyla	Sylvicapra	grimmia	4.000						1	1			1	1	1	4.107	1	4.307	9,10,11,12
43	Artiodactyla	Syncerus	caffer	5.801		1			1	1		1			1		5.699	1	5.681	6
44	Artiodactyla	Taurotragus	oryx	5.561		1			1	1					1					
45	Artiodactyla	Tragelaphus	angasi	4.861											1					
46	Artiodactyla	Tragelaphus	imberbis	4.845		1														
47	Artiodactyla	Tragelaphus	scriptus	4.477		1						1		1	1	1	4.699	5	4.813	10,11,12
48	Artiodactyla	Tragelaphus	spekei	4.771						1										
49	Artiodactyla	Tragelaphus	strepsiceros	4.980							1			1	1		5.300	10,11		
50	Carnivora	Acinonyx	jubatus	4.685	1	1				1				1	1	1	4.756	2	4.695	6
51	Carnivora	Aonyx	capensis	4.124		1			1	1		1		1	1	1	4.100		4.000	5

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	MEAN LOG 10 WEIGHT	1	2	3	4	5	6	7	8	9	10	11	12	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
52	Carnivora	Aonyx	congica	4.371								1								
53	Carnivora	Atilax	paludinosus	3.591					1	1		1		1	1	1	3.635	6	3.610	8
54	Carnivora	Bdeogale	crassicauda	3.243		1														
55	Carnivora	Canis	adustus	3.813		1				1		1		1	1		3.736	6,8	4.000	10,11
56	Carnivora	Canis	aureus	4.086	1						1						3.613	3	3.950	7
57	Carnivora	Canis	lupus	4.565	1															
58	Carnivora	Canis	mesomelas	3.837					1				1	1	1		3.880	6	3.480	10,11
59	Carnivora	Cercopithecus	albogularis	3.954										1						
60	Carnivora	Crocuta	crocuta	4.747		1				1		1		1	1		4.771	6	4.844	10,11
61	Carnivora	Cuon	alpinus	4.260	1															
62	Carnivora	Cynictis	penicillata	2.919					1				1				2.900	6		
63	Carnivora	Dologale	dybowskii	2.544								1								
64	Carnivora	Felis	aurata	3.362								1								
65	Carnivora	Felis	caracal	3.308	1	1			1					1	1	1	4.109	2	4.047	6
66	Carnivora	Felis	chaus	4.011	1															
67	Carnivora	Felis	libyca	3.740	1				1	1	1			1	1	1				
68	Carnivora	Felis	lynx	3.270	1															
69	Carnivora	Felis	manul	2.544	1															
70	Carnivora	Felis	margarita	3.343	1															
71	Carnivora	Felis	serval	4.197		1				1		1		1	1		4.037	5	3.969	10,11
72	Carnivora	Felis	silvestris	3.585	1	1		1									3.776	3,8		
73	Carnivora	Genetta	genetta	3.176		1		1					1	1	1	1	3.108	6	3.079	9,10,11,12
74	Carnivora	Genetta	rubiginosa	3.388										1	1	1	3.188	11		
75	Carnivora	Genetta	servalina	3.307								1								
76	Carnivora	Genetta	tigrina	3.398		1			1			1					3.291	8		
77	Carnivora	Genetta	victoriae	3.301								1								
78	Carnivora	Helogale	parvula	5.626										1	1	1				
79	Carnivora	Helogale	sp	3.308		1														
80	Carnivora	Herpestes	auropunctatus	2.722	1															
81	Carnivora	Herpestes	edwardsii	3.301	1															
82	Carnivora	Herpestes	ichneumon	3.623		1						1		1	1		3.476	10,11		
83	Carnivora	Herpestes	pulverulentus	3.342					1											
84	Carnivora	Herpestes	sanguineus	2.778						1	1	1		1	1	1				
85	Carnivora	Hyaena	brunnea	4.508									1	1	1	1	4.649	10,11	4.602	12
86	Carnivora	Hyaena	hyaena	4.568							1						4.756	3,7		
87	Carnivora	Ichneumia	albicauda	3.501		1			1	1		1		1	1	1	3.505	6	3.556	10,11,12
88	Carnivora	Ictonyx	striatus	3.243		1			1		1	1		1	1	1	3.081	5	3.085	6
89	Carnivora	Lepus	capensis	3.487																
90	Carnivora	Lutra	lutra	2.778	1															
91	Carnivora	Lutra	maculicollis	3.640					1	1		1		1	1					
92	Carnivora	Lycaon	pictus	4.439		1				1		1		1	1		4.097	8,10,11		
93	Carnivora	Lynx	pardina	4.043				1												
94	Carnivora	Martes	foina	3.300	1															
95	Carnivora	Martes	martes	3.146	1															
96	Carnivora	Meles	meles	4.146	1															
97	Carnivora	Mellivora	capensis	4.000	1	1								1	1	1	3.661	2,10,11,12		
98	Carnivora	Mungos	mungo	3.176		1				1		1		1	1		3.458	2	3.330	10,11
99	Carnivora	Mustela	nivalis	2.301	1															
100	Carnivora	Mystromys	albicaudatus	1.929									1							
101	Carnivora	Nandinia	binotata	3.305		1						1								
102	Carnivora	Oryx	gazella	5.361									1							
103	Carnivora	Otocyon	megalotis	3.490		1							1	1			3.608	9,10		
104	Carnivora	Panthera	leo	5.271	1					1	1	1		1	1	1	5.109	2,6,8	5.279	7
105	Carnivora	Panthera	pardus	4.805	1	1				1	1	1		1	1	1	4.750	2,6,8	4.047	10,11,12
106	Carnivora	Panthera	tigris	5.053	1															
107	Carnivora	Panthera	uncia	4.656	1															
108	Carnivora	Paracynictis	selousi	3.215										1	1	1				
109	Carnivora	Poecilogale	albinucha	3.308		1											2.356	5		
110	Carnivora	Proteles	cristatus	3.934		1			1					1	1	1	3.601	8	3.480	10,11,12
111	Carnivora	Poiana	poensis	3.508				1												
112	Carnivora	Rhynchogale	melleri	3.420										1	1	1				
113	Carnivora	Selenarctos	thibetanus	4.845	1															
114	Carnivora	Suricata	suricatta	3.383									1							
115	Carnivora	Sylvicapra	grimmia	4.207										1						
116	Carnivora	Ursus	arctos	5.303	1															
117	Carnivora	Viverra	civetta	4.097		1				1		1		1	1	1	4.000	6	4.000	10,11,12

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	MEAN LOG 10 WEIGHT	1	2	3	4	5	6	7	8	9	10	11	12	ALTER NATIVE MASS	SITE	ALTER NATIVE MASS	SITE
118	Carnivora	Vormela	peregusna	2.792	1															
119	Carnivora	Vulpes	cana	2.952	1															
120	Carnivora	Vulpes	chama	3.433					1				1				3.487	9		
121	Carnivora	Vulpes	corsac	3.455	1															
122	Carnivora	Vulpes	pallida	3.300							1									
123	Carnivora	Vulpes	rueppelli	3.306	1															
124	Carnivora	Vulpes	vulpes	3.718	1															
125	Chiroptera	Lemniscomys	barbarus	1.477			1													
126	Chiroptera	Lemniscomys	griselda	1.699						1				1	1	1	1.775	10,11,12		
127	Chiroptera	Lemniscomys	striatus	1.756						1	1	1					1.693	7	1.898	8
128	Hyracoidea	Heterohyrax	brucei	3.447						1						1	3.461	12		
129	Hyracoidea	Heterohyrax	syriacus	3.431			1													
130	Hyracoidea	Hylochoerus	meinertzhageni	5.195						1		1								
131	Hyracoidea	Procavia	capensis	3.565					1				1	1	1	1	3.601	10,11,12		
132	Hyracoidea	Procavia	ruficeps	3.491							1									
133	Insectivora	Amblysomus	gunningi	1.449												1				
134	Insectivora	Amblysomus	hottentotus	1.831					1							1				
135	Insectivora	Amblysomus	julianae	1.342											1	1				
136	Insectivora	Chlorotalpa	bicolor	1.512																
137	Insectivora	Chrysospalax	villosus	2.019												1				
138	Insectivora	Crocidura	bicolor	0.803									1	1	1	1				
139	Insectivora	Crocidura	cyanea	0.908					1						1	1	0.959	11,12		
140	Insectivora	Crocidura	dolichura	0.863								1								
141	Insectivora	Crocidura	flavescens	1.447					1							1	1.387	12		
142	Insectivora	Crocidura	hirta	1.130									1		1	1				
143	Insectivora	Crocidura	bicolor	1.000	1															
144	Insectivora	Crocidura	littoralis	1.204								1								
145	Insectivora	Crocidura	mariquensis	1.079											1					
146	Insectivora	Crocidura	maurisca	0.955							1									
147	Insectivora	Crocidura	nanilla	1.146								1								
148	Insectivora	Crocidura	nyansae	1.398							1									
149	Insectivora	Crocidura	occidentalis	1.305								1								
150	Insectivora	Crocidura	russula	0.866			1	1									0.982	4		
151	Insectivora	Crocidura	bicolor	0.778							1									
152	Insectivora	Crocidura	silacea	0.845											1	1				
153	Insectivora	Crocidura	sp.	0.954																
154	Insectivora	Crocidura	whitakeri	1.176			1													
155	Insectivora	Erinaceus	albiventris	2.519		1														
156	Insectivora	Erinaceus	algirus	2.672			1													
157	Insectivora	Erinaceus	europaeus	2.874				1												
158	Insectivora	Erinaceus	frontalis	2.595					1				1							
159	Insectivora	Hemiechinus	auritus	2.399	1															
160	Insectivora	Myosorex	cafer	1.097												1				
161	Insectivora	Myosorex	varius	1.137					1							1	1.091	12		
162	Insectivora	Paraechinus	aethiopicus	2.514			1													
163	Insectivora	Scutisorex	somereni	1.795								1								
164	Insectivora	Suncus	etruscus	0.362			1	1												
165	Insectivora	Suncus	lixus	0.903											1	1				
166	Lagomorpha	Lepus	capensis	3.312		1	1	1	1		1	1	1	1			3.491	3	3.330	4
167	Lagomorpha	Lepus	crawshayi	3.342			1													
168	Lagomorpha	Lepus	europaeus	3.398	1															
169	Lagomorpha	Lepus	saxatilis	3.391					1					1	1	1				
170	Lagomorpha	Oryctolagus	cuniculus	3.176			1	1									3.316	8		
171	Lagomorpha	Pronolagus	crassicaudatus	3.415												1				
172	Lagomorpha	Pronolagus	randensis	3.398										1		1				
173	Lagomorpha	Pronolagus	rupestris	3.380					1											
174	Macroscelidea	Elephantulus	brachyrhynchus	1.643										1	1	1				
175	Macroscelidea	Elephantulus	myurus	1.778									1	1		1				
176	Macroscelidea	Elephantulus	rozeti	1.681			1													
177	Macroscelidea	Elephantulus	rufescens	1.699		1														
178	Macroscelidea	Petrodromus	tetradactyla	2.312		1										1	2.271	10		
179	Perissodactyla	Ceratotherium	simum	6.451											1					
180	Perissodactyla	Diceros	bicornis	6.090		1				1					1		6.054	6,11		
181	Perissodactyla	Equus	burchelli	5.370		1			1						1		5.333	5	5.379	11
182	Pholidota	Manis	temmincki	4.146										1	1					
183	Primates	Cercopithecus	aethiops	3.605		1				1	1	1					3.716	6,7,8		
184	Primates	Cercopithecus	albogularis	3.730												1				

No.	ORDER	SCIENTIFIC NAME		MEAN LOG 10 WEIGHT	1	2	3	4	5	6	7	8	9	10	11	12	ALTERNATIVE		ALTERNATIVE	
		GENUS	SPECIES														MASS	SITE	MASS	SITE
185	Primates	Cercopithecus	aethiops	3.538								I								
186	Primates	Cercopithecus	pygerythrus	3.668						I				I	I	I				
187	Primates	Erythrocebus	patas	4.146							I									
188	Primates	Galago	crassicaudatus	4.090						I					I	I	3.010	11,12		
189	Primates	Galago	senegalensis	1.380		I								I	I	I	2.477	10,11,12		
190	Primates	Macaca	sylvanus	4.047			I													
191	Primates	Papio	cynocephalus	4.080		I														
192	Primates	Papio	doguera	4.415						I	I	I								
193	Primates	Papio	ursinus	4.340					I					I	I	I	4.374	10,11	4.373	12
194	Proboscidea	Loxodonta	africana	6.636		I						I			I		6.477	8	6.326	11
195	Rodentia	Acomys	cahirinus	1.640							I									
196	Rodentia	Acomys	sp.	1.599			I													
197	Rodentia	Acomys	spinosissimus	1.330										I	I					
198	Rodentia	Acomys	subspinosus	1.325		I														
199	Rodentia	Aethomys	chrysophilus	1.930		I			I					I	I	I	1.971	5,10,11,12		
200	Rodentia	Aethomys	namaquensis	1.635					I					I	I	I				
201	Rodentia	Aethomys	nyikae	1.887						I										
202	Rodentia	Allactaga	elater	1.643	I															
203	Rodentia	Allactaga	williamsi	1.655	I															
204	Rodentia	Apodemus	sylvaticus	1.414			I	I									1.410	4		
205	Rodentia	Arvicanthis	abyssinicus	2.062								I								
206	Rodentia	Arvicanthis	dembeensis	1.780	I															
207	Rodentia	Arvicanthis	niloticus	1.283							I									
208	Rodentia	Arvicola	terrestris	1.282	I															
209	Rodentia	Atlantoxerus	getulus	4.800			I													
210	Rodentia	Cricetomys	gambianus	3.017										I		I				
211	Rodentia	Cricetulus	migratorius	1.598	I															
212	Rodentia	Cryptomys	hottentotus	1.813					I					I	I	I	1.889	10,11,12		
213	Rodentia	Ctenodactylus	gundi	2.481			I													
214	Rodentia	Ctenodactylus	sp.	2.228			I													
215	Rodentia	Dasymys	incomtus	2.079								I			I	I	1.975	11,12		
216	Rodentia	Dendromus	insignis	1.176								I								
217	Rodentia	Dendromus	melanotis	0.958					I							I	0.916	12		
218	Rodentia	Dendromus	mesomelas	1.176												I				
219	Rodentia	Dendromus	messorius	0.801								I								
220	Rodentia	Dendromus	mystacalis	1.079					I						I	I	0.900	11,12		
221	Rodentia	Dendromus	nyikae	1.230											I					
222	Rodentia	Dipodillus	lowei	1.602							I									
223	Rodentia	Dipodillus	simoni	1.663			I													
224	Rodentia	Eliomys	lusitanicus	1.857				I												
225	Rodentia	Eliomys	quercinus	1.875			I													
226	Rodentia	Ellobius	fuscocapillus	1.778	I															
227	Rodentia	Gerbillus	campestris	1.350			I													
228	Rodentia	Gerbillus	dunni	1.477							I									
229	Rodentia	Gerbillus	gerbillus	1.468			I													
230	Rodentia	Gerbillus	henleyi	1.068			I													
231	Rodentia	Gerbillus	nanus	1.146			I													
232	Rodentia	Gerbillus	pyramidum	1.785			I													
233	Rodentia	Grammomys	cometes	1.732												I				
234	Rodentia	Grammomys	dolichurus	1.690						I						I	1.716	12		
235	Rodentia	Grammomys	macmillani	1.361							I									
236	Rodentia	Graphiurus	murinus	1.298					I			I		I	I	I	1.609	8	1.398	10,11,12
237	Rodentia	Graphiurus	platyops	1.644												I				
238	Rodentia	Heliosciurus	gambianus	2.332							I									
239	Rodentia	Hystrix	africaeaustralis	4.097					I				I	I	I	I	4.301	9,10,11,12		
240	Rodentia	Hystrix	cristata	4.301		I														
241	Rodentia	Hystrix	sp.	4.279			I				I						4.000	7		
242	Rodentia	Jaculus	jaculus	1.872																
243	Rodentia	Jaculus	orientalis	2.137			I													
244	Rodentia	Lophuromys	aquilus	1.740								I								
245	Rodentia	Lophuromys	flavopunctatus	1.716						I										
246	Rodentia	Malacothrix	typica	1.114					I				I							
247	Rodentia	Mesocricetus	auratus	2.262			I													
248	Rodentia	Mastomys	coucha	1.659								I								
249	Rodentia	Mastomys	kolmei	1.362							I									

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	MEAN LOG 10 WEIGHT	1	2	3	4	5	6	7	8	9	10	11	12	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
250	Rodentia	Mastomys	natalensis	1.627					1	1	1		1	1	1	1	1.699	6	1.699	7
251	Rodentia	Meriones	blackleri	1.620	1															
252	Rodentia	Meriones	crassus	2.130			1													
253	Rodentia	Meriones	libycus	1.954	1		1										2.400	2		
254	Rodentia	Meriones	persicus	2.083	1															
255	Rodentia	Meriones	shawi	2.257			1													
256	Rodentia	Meriones	vinogradovi	2.176	1															
257	Rodentia	Mesocricetus	brandti	1.842	1															
258	Rodentia	Rattus	irani	1.708																
259	Rodentia	Mus	musculus	1.197	1		1	1									1.283	3	1.399	4
260	Rodentia	Mus	spretus	1.182			1													
261	Rodentia	Mylomys	cuninghamei	2.013								1								
262	Rodentia	Mystromys	albicaudatus	1.963					1											
263	Rodentia	Nannomys	minutoides	0.813					1					1	1	1				
264	Rodentia	Nannomys	sp.	0.872								1								
265	Rodentia	Nannomys	tenella	0.778							1									
266	Rodentia	Oenomys	hypoxanthus	1.944								1								
267	Rodentia	Oreotragus	oreotragus	4.061										1	1	1				
268	Rodentia	Otomys	angoniensis	1.930										1	1	1				
269	Rodentia	Otomys	irroratus	2.037					1							1	2.083	10		
270	Rodentia	Otomys	laminatus	2.176												1				
271	Rodentia	Otomys	sloggetti	2.111					1											
272	Rodentia	Otomys	tropicalis	2.114								1								
273	Rodentia	Pachyuromys	duprasi	1.518			1													
274	Rodentia	Paraxerus	cepapi	2.350										1	1	1				
275	Rodentia	Pedetes	capensis	3.544		1			1				1	1	1		3.490	9	3.498	9,10,11
276	Rodentia	Pelomys	fallax	1.987						1										
277	Rodentia	Tatomys	hopkinsoni	1.795						1										
278	Rodentia	Praomys	duodecimmastae	1.380				1												
279	Rodentia	Praomys	fumatus	1.677							1									
280	Rodentia	Praomys	jacksoni	1.620						1										
281	Rodentia	Psammomys	obesus	1.906			1													
282	Rodentia	Rattus	rattus	2.150			1	1				1					2.271	4,5		
283	Rodentia	Rhabdomys	pumilio	1.567					1				1	1		1	1.580	9,10,12		
284	Rodentia	Saccostomus	campestris	1.712										1	1	1				
285	Rodentia	Spermophilus	fulvus	2.895	1															
286	Rodentia	Steatomys	krebsi	1.380									1							
287	Rodentia	Steatomys	parvus	1.455							1									
288	Rodentia	Steatomys	pratensis	2.380										1	1	1				
289	Rodentia	Tachyoryctes	ruandae	2.386								1								
290	Rodentia	Tachyoryctes	splendens	2.362		1														
291	Rodentia	Tatera	brantsi	1.935					1				1	1			1.982	9,10		
292	Rodentia	Tatera	leucogaster	1.848									1	1	1	1				
293	Rodentia	Tatera	nigricauda	1.980								1								
294	Rodentia	Tatera	valida	1.653							1									
295	Rodentia	Taterillus	emini	1.756							1									
296	Rodentia	Thallomys	paedulcus	1.876										1	1	1				
297	Rodentia	Thamnomys	rutilans	1.795								1								
298	Rodentia	Thryonomys	swinderianus	3.698											1	1	3.658	11,12		
299	Rodentia	Xerus	erythropus	2.701		1					1									
300	Rodentia	Xerus	inauris	2.603									1							
301	Rodentia	Zelotomys	hildegardeae	1.771	1															
302	Tubulidentata	Orycteropus	afer	4.803		1				1			1	1	1		4.778	6	3.305	9,10,11

11 MAMMALS OF SAVANNA FOREST SITES IN AFRICA

No.	SITE NAME	REFERENCE
1	Gabiro, Rwanda	Misonne, X. 1965; Verschuren, J., 1965; Downing, J.A. and M. Silva. 1995.
2	Lokori, Kenya	Coe, M.J., 1972; Downing, J.A. and M. Silva. 1995
3	Ruaha Valley, Tanzania	Vesey-Fitzgerald, D.F. 1964; Downing, J.A. and M. Silva. 1995
4	Serengeti, Tanzania	Hendrichs, H. 1970; Kingdon, J., 1974a,1974b; Downing, J.A. and M. Silva 1995
5	Zinave, Mozambique	Dalquest, W.W., 1965,1966; Downing, J.A. and M. Silva, 1995

		SCIENTIFIC NAME		Mean Log10 Body	Site					ALTERNATIVE		ALTERNATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	MASS	SITE	MASS	SITE
1	Artiodactyla	Aepyceros	melampus	4.681	1	1	1	1	1	4.699	2 5	4.779	3 4
2	Artiodactyla	Alcelaphus	buselaphus	5.149				1					
3	Artiodactyla	Alcelaphus	lichtensteini	5.158			1		1	5.181	5		
4	Artiodactyla	Cephalophus	sp	4.130			1						
5	Artiodactyla	Connochaetes	taurinus	5.301				1	1	5.267	5		
6	Artiodactyla	Damaliscus	korrigum	5.090			1	1					
7	Artiodactyla	Damaliscus	lunatus	5.061	1								
8	Artiodactyla	Gazella	granti	4.699		1		1		4.602	4		
9	Artiodactyla	Gazella	thomsoni	4.243				1					
10	Artiodactyla	Giraffa	camelopardalis	5.889			1	1	1	6.078	4	6.004	5
11	Artiodactyla	Hippopotamus	amphibius	6.000	1	1	1	1	1	6.149	2	6.341	5
12	Artiodactyla	Hippotragus	equinus	5.301	1		1	1	1	5.389	3 4 5		
13	Artiodactyla	Hippotragus	niger	5.340			1		1	5.255	5		
14	Artiodactyla	Kobus	defassa	5.382	1		1	1					
15	Artiodactyla	Kobus	ellipsiprymnus	5.308					1				
16	Artiodactyla	Kobus	vardoni	4.904			1						
17	Artiodactyla	Madoqua	guentheri	3.741		1							
18	Artiodactyla	Madoqua	kirkii	3.738			1	1		3.740	4		
19	Artiodactyla	Neotragus	moschatus	3.716					1				
20	Artiodactyla	Oryx	gazella	5.114		1		1		5.224	4		
21	Artiodactyla	Ourebia	ourebi	4.097	1	1	1	1	1	4.178	2 3 4	4.134	5
22	Artiodactyla	Phacochoerus	aethiopicus	4.699	1	1	1	1	1	4.845			
23	Artiodactyla	Potamochoerus	porcus	4.888	1		1	1	1	4.785	3,4 5		
24	Artiodactyla	Raphicerus	campestris	4.179			1	1	1	5.080	4	4.041	5
25	Artiodactyla	Redunca	arundinum	4.802			1		1	4.893	5		
26	Artiodactyla	Redunca	fulvorufula	4.477				1					
27	Artiodactyla	Redunca	redunca	4.679	1		1	1					
28	Artiodactyla	Sylvicapra	grimmia	4.000	1		1	1	1	4.292	5		
29	Artiodactyla	Syncerus	caffer	5.881	1		1	1	1	5.699	3 4 5		
30	Artiodactyla	Taurotragus	oryx	5.588	1		1		1				
31	Artiodactyla	Taurotragus	porcus	5.580				1					
32	Artiodactyla	Tragelaphus	angasi	4.939					1				
33	Artiodactyla	Tragelaphus	imberbis	4.845		1							
34	Artiodactyla	Tragelaphus	pantus	5.384				1					
35	Artiodactyla	Tragelaphus	scriptus	4.660			1		1				
36	Artiodactyla	Tragelaphus	spekei	4.771	1		1						
37	Artiodactyla	Tragelaphus	strepsiceros	5.394		1	1		1	5.389	5		
38	Carnivora	Acinonyx	jubatus	4.438	1	1	1	1					
39	Carnivora	Aonyx	capensis	4.100	1	1	1	1		4.266	2	4.124	3 4
40	Carnivora	Atilax	paludinosus	3.352	1	1	1	1	1	3.031	5		
41	Carnivora	Canis	adustus	3.738	1	1	1	1		3.919	3 4		
42	Carnivora	Canis	aureus	3.813				1					
43	Carnivora	Canis	mesomelas	3.837		1		1					
44	Carnivora	Crocuta	crocuta	4.747	1	1	1	1	1				

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	ALTERNATIVE MASS	SITE	ALTERNATIVE MASS	SITE
45	Carnivora	Felis	caracal	4.108		1	1	1					
46	Carnivora	Felis	leo	6.244					1				
47	Carnivora	Felis	libyca	3.740	1				1				
48	Carnivora	Felis	pardus	4.730					1				
49	Carnivora	Felis	serval	4.037	1	1	1	1		4.187	3 4		
50	Carnivora	Felis	silvestris	3.778		1	1	1					
51	Carnivora	Genetta	genetta	3.178		1	1	1					
52	Carnivora	Genetta	rubiginosa	3.301					1				
53	Carnivora	Genetta	tigrina	3.204		1	1	1					
54	Carnivora	Helogale	parvula	2.324					1				
55	Carnivora	Helogale	sp	2.888		1	1	1					
56	Carnivora	Herpestes	ichneumon	3.431		1	1	1	1	3.514	5		
57	Carnivora	Herpestes	sanguineus	2.778	1	1	1	1					
58	Carnivora	Hyaena	hyaena	4.738		1	1	1					
59	Carnivora	Ichneumia	albicauda	3.322	1	1	1	1	1	3.847	5		
60	Carnivora	Ictonyx	striatus	3.243		1	1	1					
61	Carnivora	Lutra	maculicollis	3.032	1	1		1					
62	Carnivora	Lycaon	pictus	4.438	1	1	1	1					
63	Carnivora	Mellivora	capensis	3.841				1	1	3.889	5		
64	Carnivora	Mungos	mungo	3.634	1	1	1	1	1	3.178	2 3 4	3.138	5
65	Carnivora	Nandinia	binotata	3.520	1			1					
66	Carnivora	Otocyon	megalotis	3.460		1		1					
67	Carnivora	Panthera	leo	6.278	1	1	1	1		6.168	2 3 4		
68	Carnivora	Panthera	pardus	4.732	1	1	1	1					
69	Carnivora	Poecilogale	albinucha	2.338			1	1					
70	Carnivora	Proteles	cristatus	3.938		1		1					
71	Carnivora	Rhynchogale	melleri	3.430			1	1					
72	Carnivora	Viverra	civetta	4.027	1		1	1	1	4.026	5		
73	Chiroptera	Lemniscomys	barbarus	1.477				1					
74	Chiroptera	Lemniscomys	griselda	1.869	1				1				
75	Chiroptera	Lemniscomys	striatus	1.756	1		1	1		1.693	4 5		
76	Hyracoidea	Heterohyrax	brucei	3.288	1	1				3.447	2		
77	Hyracoidea	Heterohyrax	syriacus	3.287			1	1					
78	Hyracoidea	Hylochoerus	meinertzhageni	5.105	1								
79	Hyracoidea	Procavia	johnstoni	3.461				1					
80	Hyracoidea	Procavia	sp.	3.477		1							
81	Insectivora	Crocidura	bicolor	0.884		1	1						
82	Insectivora	Crocidura	buttneri	1.204				1					
83	Insectivora	Crocidura	flavescens	1.447				1					
84	Insectivora	Crocidura	hirta	1.230			1	1	1	1.176	5		
85	Insectivora	Crocidura	luna	0.893			1						
86	Insectivora	Crocidura	nanilla	0.778				1					
87	Insectivora	Crocidura	nigricans	1.204			1						
88	Insectivora	Crocidura	occidentalis	1.505			1						
89	Insectivora	Erinaceus	albiventris	2.518		1		1					
90	Insectivora	Suncus	lixus	1.418				1					
91	Lagomorpha	Lepus	capensis	3.312		1	1	1					
92	Lagomorpha	Lepus	nigriscens	3.279					1				
93	Macroscelidea	Elephantulus	brachyrhynchus	1.693			1		1				
94	Macroscelidea	Elephantulus	rufescens	1.698		1		1		1.793	4		
95	Macroscelidea	Elephantulus	rupestris	1.477					1				
96	Macroscelidea	Petrodromus	tetradactyla	2.293					1				
97	Perissodactyla	Diceros	bicornis	6.034	1			1		7.114	4		
98	Perissodactyla	Equus	burchelli	5.380	1		1	1		5.398	3	5.462	4
99	Pholidota	Manis	temmincki	4.148			1	1					

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
100	Primates	Cercopithecus	aethiops	3.724	1	1	1	1	1	3.841	2 3	3.779	4
101	Primates	Cercopithecus	mitis	3.877			1	1	1	3.852	5		
102	Primates	Colobus	abyssinicus	4.255				1					
103	Primates	Colobus	badius	3.945			1						
104	Primates	Erythrocebus	patas	4.148				1					
105	Primates	Galago	crassicaudatus	3.050			1	1	1	3.184	4		
106	Primates	Galago	senegalensis	2.360	1		1	1	1	2.270	4		
107	Primates	Papio	anubis	4.221		1		1		4.230	4		
108	Primates	Papio	cynocephalus	4.284			1						
109	Primates	Papio	doguera	4.415	1								
110	Primates	Papio	ursinus	4.398					1				
111	Proboscidea	Loxodonta	africana	6.230	1	1	1	1	1				
112	Rodentia	Acomys	albigena	1.431				1					
113	Rodentia	Acomys	cahirinus	1.623		1	1		1				
114	Rodentia	Acomys	wilsoni	1.287				1					
115	Rodentia	Aethomys	chrysophilus	1.830			1		1	1.871	5		
116	Rodentia	Aethomys	kaiseri	1.884			1	1					
117	Rodentia	Aethomys	nyikae	1.667	1		1	1					
118	Rodentia	Arvicanthis	abyssinicus	2.061	1			1					
119	Rodentia	Arvicanthis	niloticus	1.828		1	1	1		1.893	3 4		
120	Rodentia	Cricetomys	gambianus	3.083					1				
121	Rodentia	Dasymys	incomtus	2.011	1		1	1		2.189	3 4		
122	Rodentia	Dendromus	nl	1.097	1								
123	Rodentia	Dendromus	melanotis	0.778				1					
124	Rodentia	Dendromus	mesomelas	1.184	1								
125	Rodentia	Gerbillus	diminutus	1.361		1							
126	Rodentia	Gerbillus	gerbillus	1.369		1							
127	Rodentia	Gerbillus	harwoodi	1.431				1					
128	Rodentia	Gerbillus	pusillus	1.078				1					
129	Rodentia	Grammomys	dolichurus	1.658	1	1	1	1		1.716	4		
130	Rodentia	Graphiurus	murinus	1.082	1		1	1		1.301	3 4		
131	Rodentia	Graphiurus	sp	1.366		1							
132	Rodentia	Heliophobius	argenteocinereus	2.204			1						
133	Rodentia	Heliosciurus	gambianus	2.322			1						
134	Rodentia	Hystrix	africaeaustralis	4.098			1		1	4.145	5		
135	Rodentia	Hystrix	cristata	4.301		1							
136	Rodentia	Hystrix	galeata	4.079				1					
137	Rodentia	Lophuromys	flavopunctatus	1.710	1		1	1					
138	Rodentia	Lophuromys	sikapusi	1.899	1								
139	Rodentia	Mastomys	natalensis	1.881	1	1	1	1	1	1.788	5		
140	Rodentia	Mastomys	pernanus	1.980	1			1					
141	Rodentia	Mylomys	dybowskii	1.985	1								
142	Rodentia	Nannomys	cf	0.840	1								
143	Rodentia	Nannomys	minutoides	0.813	1		1	1	1	0.672	3 4	1.017	5
144	Rodentia	Nannomys	tenella	0.845				1					
145	Rodentia	Nannomys	triton	0.863	1		1	1					
146	Rodentia	Oenomys	hypoxanthus	1.844			1						
147	Rodentia	Oreotragus	oreotragus	4.286	1	1	1			4.079	2	4.000	3
148	Rodentia	Otomys	anchietae	2.107			1						
149	Rodentia	Otomys	tropicalis	2.114	1								
150	Rodentia	Paraxerus	cepapi	2.380			1		1	2.259	5		
151	Rodentia	Paraxerus	ochraceus	1.869		1		1					
152	Rodentia	Paraxerus	spenosa	2.843					1				
153	Rodentia	Pedetes	caffer	3.602				1					
154	Rodentia	Pedetes	capensis	3.544		1			1	3.422	5		

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
155	Rodentia	Pelomys	fallax	1 607	1		1	1	1				
156	Rodentia	Pelomys	hopkinsi	1 768	1								
157	Rodentia	Praomys	fumatus	1 477				1					
158	Rodentia	Praomys	jacksoni	1 633			1	1		1 602	4		
159	Rodentia	Rattus	rattus	2 272			1						
160	Rodentia	Rhabdomys	pumilio	1 731			1	1					
161	Rodentia	Saccostomus	campestris	1 672			1	1					
162	Rodentia	Steatomys	pratensis	1 278			1	1					
163	Rodentia	Tachyoryctes	daemon	2 255				1					
164	Rodentia	Tachyoryctes	ruandae	2 343	1								
165	Rodentia	Tachyoryctes	splendens	2 301				1					
166	Rodentia	Tatera	afra	1 862			1		1				
167	Rodentia	Tatera	boehmi	1 635	1		1	1					
168	Rodentia	Tatera	robusta	1 844		1		1		2 011	4		
169	Rodentia	Tatera	valida	2 063			1						
170	Rodentia	Taterillus	nub us	1 778		1							
171	Rodentia	Thallomys	paedulcus	1 826				1					
172	Rodentia	Thryonomys	swinderianus	3 658			1		1				
173	Rodentia	Xerus	rutilus	2 823		1							
174	Rodentia	Zelotomys	hildegardeae	1 775	1			1					
175	Tubulidentata	Orycteropus	afer	4 778	1	1	1	1	1	4 833	2 3 4	4 716	5

12. MAMMALS OF MOIST MONTANE AND WET FOREST SITES IN AFRICA

No.	SITE NAME	REFERENCE
1	Lamto	Bellier, L. et al. 1972. Bourliere, F. et al. 1974 Heim de Balsac, H. 1974. Heim de Balsac, H. and L. Bellier. 1967. Downing, J.A. and M. Silva. 1995
2	Makokou	Emmons, 1979. Emmons, L.H. et al. 1983, Downing, J.A. and M. Silva. 1995,
3	Sangmelina	Perret, J.-L. and V. Aellen, 1984. Downing, J.A. and M. Silva, 1995
4	Tai National Park	Guillaumet, J.-L. and C. Boesch, 1984. Downing, J.A. and M. Silva, 1994

		SCIENTIFIC NAME		Mean Log10 Body	Site				ALTER-NATIVE		ALTER-NATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	MASS	SITE	MASS	SITE
1	Artiodactyla	Alcelaphus	buselaphus	5.176	1							
2	Artiodactyla	Cephalophus	callipygus	4.313		1	1					
3	Artiodactyla	Cephalophus	dorsalis	4.336	1	1	1	1				
4	Artiodactyla	Cephalophus	jentinki	4.813				1				
5	Artiodactyla	Cephalophus	leucogaster	4.104		1						
6	Artiodactyla	Cephalophus	monticola	3.695	1	1	1	1				
7	Artiodactyla	Cephalophus	niger	4.138	1			1	4.097	4		
8	Artiodactyla	Cephalophus	nigrifrons	4.149		1						
9	Artiodactyla	Cephalophus	ogilbyi	4.301				1				
10	Artiodactyla	Cephalophus	rufilatus	4.079	1							
11	Artiodactyla	Cephalophus	sylvicultor	4.832	1	1		1				
12	Artiodactyla	Cephalophus	zebra	4.130				1				
13	Artiodactyla	Choeropsis	liberiensis	5.231				1				
14	Artiodactyla	Hippopotamus	amphibius	6.078	1	1			6.108	2		
15	Artiodactyla	Hyemoschus	aquaticus	4.033		1		1				
16	Artiodactyla	Kobus	defassa	5.362	1							
17	Artiodactyla	Neotragus	batesi	3.423		1	1		3.477	3		
18	Artiodactyla	Neotragus	pygmaeus	3.602	1			1				
19	Artiodactyla	Ourebia	ourebi	4.097	1							
20	Artiodactyla	Phacochoerus	aethiopicus	4.845	1							
21	Artiodactyla	Potamochoerus	porcus	4.868	1	1		1	4.748	4		
22	Artiodactyla	Redunca	redunca	4.607	1							
23	Artiodactyla	Syncerus	caffer	5.688	1	1		1	5.574	2		
24	Artiodactyla	Taurotragus	euryceros	5.301	1	1		1				
25	Artiodactyla	Tragelaphus	scriptus	4.668	1			1				
26	Artiodactyla	Tragelaphus	spekei	4.771		1	1	1	5.000	3		
27	Carnivora	Aonyx	capensis	4.255	1			1				
28	Carnivora	Atilax	paludinosus	3.498	1		1					
29	Carnivora	Bdeogale	nigripes	3.296			1					
30	Carnivora	Crocuta	crocuta	4.695	1							
31	Carnivora	Crossarchus	obscurus	3.097	1							
32	Carnivora	Felis	aurata	4.352	1		1					
33	Carnivora	Genetta	pardina	3.301	1							
34	Carnivora	Genetta	servalina	3.176			1					
35	Carnivora	Genetta	tigrina	3.204	1		1					
36	Carnivora	Genetta	villiersi	0.000	1							
37	Carnivora	Herpestes	naso	3.477			1					

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	ALTER- NATIVE MASS	SITE	ALTER- NATIVE MASS	SITE
38	Carnivora	Herpestes	sanguineus	2 779	1							
39	Carnivora	Ichneumia	albicauda	3 653	1							
40	Carnivora	Lutra	maculicollis	3 602			1	1				
41	Carnivora	Mellivora	capensis	4 079				1				
42	Carnivora	Mungos	gambianus	3 204	1							
43	Carnivora	Nandinia	binotata	3 322	1	1	1	1	3 362	2 3		
44	Carnivora	Panthera	leo	5.230	1							
45	Carnivora	Panthera	pardus	4 680	1							
46	Carnivora	Poiana	richardsoni	2 690	1		1					
47	Carnivora	Viverra	civetta	4 301	1		1					
48	Chiroptera	Lemniscomys	striatus	1 631	1		1		1 708	3		
49	Hyracoidea	Dendrohyrax	arboreus	3.287	1							
50	Hyracoidea	Dendrohyrax	dorsalis	3 544		1	1	1				
51	Hyracoidea	Hylochoerus	meinertzhageni	4 603		1		1				
52	Insectivora	Crocidura	flaniata	1 322		1						
53	Insectivora	Crocidura	dolichura	0 869	1	1						
54	Insectivora	Crocidura	douceti	0 908	1							
55	Insectivora	Crocidura	eburnea	1 217	1							
56	Insectivora	Crocidura	flavescens	1 382	1	1						
57	Insectivora	Crocidura	grassei	1 130		1						
58	Insectivora	Crocidura	groupe	1 287		1						
59	Insectivora	Crocidura	jouvenetae	0 698	1							
60	Insectivora	Crocidura	lamottei	0 698	1							
61	Insectivora	Crocidura	occidentalis	1 505			1					
62	Insectivora	Crocidura	odorata	1 148		1						
63	Insectivora	Crocidura	pasha	1 322	1							
64	Insectivora	Crocidura	poensis	1 223	1		1					
65	Insectivora	Crocidura	theresae	1 248	1							
66	Insectivora	Crocidura	wimmeri	0 903		1						
67	Insectivora	Paracrocidura	schoutedeni	1 041		1						
68	Insectivora	Potamogale	velox	2 820		1	1		2 803	3		
69	Insectivora	Suncus	remyi	0 664		1						
70	Insectivora	Sylvisorex	johnstoni	0 477		1						
71	Insectivora	Sylvisorex	megalura	0 802	1							
72	Insectivora	Sylvisorex	ollula	1.120		1						
73	Lagomorpha	Lepus	crawshayi	3 342	1							
74	Pholidota	Manis	gigantea	4 518	1	1	1	1				
75	Pholidota	Manis	tetradactyla	3 626	1	1		1				
76	Pholidota	Manis	tricuspis	3 346	1	1	1	1				
77	Primates	Arctocebus	calabarensis	2 322		1						
78	Primates	Cercocebus	albigena	3 761		1	1		3 075	3		
79	Primates	Cercocebus	galeritus	3 892		1						
80	Primates	Cercocebus	torquatus	3 783	1			1				
81	Primates	Cercopithecus	aethiops	3 724	1							
82	Primates	Cercopithecus	campbelli	3 613	1			1				
83	Primates	Cercopithecus	cephus	3 648		1	1		3 544	3		
84	Primates	Cercopithecus	diana	3 633	1			1				
85	Primates	Cercopithecus	neglectus	3 740		1	1		3 741	3		
86	Primates	Cercopithecus	nictitans	3 738		1	1	1	3 653	3	3 732	4
87	Primates	Cercopithecus	petaurista	3 255	1			1				
88	Primates	Cercopithecus	pogonias	3 584		1	1		3 588	3		

No.	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
89	Primates	Colobus	abyssinicus	4.285			1					
90	Primates	Colobus	badius	3.938				1				
91	Primates	Colobus	pennanti	3.881	1							
92	Primates	Colobus	polykomos	3.892	1	1		1	3.893	2	3.861	5
93	Primates	Colobus	satanas	3.895		1						
94	Primates	Colobus	verus	3.668	1			1				
95	Primates	Erythrocebus	patas	3.803	1		1					
96	Primates	Galago	alleni	2.418		1	1					
97	Primates	Galago	demidovi	1.803	1	1	1	1	1.808	3		
98	Primates	Galago	elegantulus	2.462		1	1					
99	Primates	Gorilla	gorilla	5.081		1	1					
100	Primates	Pan	troglodytes	4.653	1	1	1	1				
101	Primates	Papio	anubis	4.415	1							
102	Primates	Papio	sphinx	4.255		1						
103	Primates	Perodicticus	potto	3.041	1	1	1	1				
104	Proboscidea	Loxodonta	africana	6.238	1							
105	Proboscidea	Loxodonta	cyclotis	6.461		1		1				
106	Proboscidea	Miopithecus	talapoin	3.078		1	1		3.090	3		
107	Rodentia	Aethosciurus	poensis	2.008	1	1	1					
108	Rodentia	Anomalurops	beecrofti	2.771	1	1	1	1	2.815	4		
109	Rodentia	Anomalurus	beldeni	2.855			1					
110	Rodentia	Anomalurus	derbianus	2.860	1	1		1				
111	Rodentia	Anomalurus	pelii	3.248	1			1				
112	Rodentia	Anomalurus	pusillus	2.805		1						
113	Rodentia	Arvicanthis	niloticus	2.082	1							
114	Rodentia	Atherurus	africanus	3.542	1	1	1	1	3.619	2	3.388	3
115	Rodentia	Cricetomys	emini	3.107	1	1		1	3.114	2		
116	Rodentia	Cricetomys	gambianus	3.041	1		1		2.984	3		
117	Rodentia	Dasymys	incomtus	2.078	1							
118	Rodentia	Dendromus	melanotis	0.778	1							
119	Rodentia	Dendromus	pumilio	0.845		1	1					
120	Rodentia	Deomys	ferrugineus	1.714		1	1		1.718	3		
121	Rodentia	Dephomys	defua	1.807	1							
122	Rodentia	Epixerus	ebii	2.772		1	1	1	2.762	3	2.774	4
123	Rodentia	Funisciurus	anerythrus	2.336		1						
124	Rodentia	Funisciurus	isabella	2.037		1	1		2.041	3		
125	Rodentia	Funisciurus	lemniscatus	2.148		1	1		2.161	4		
126	Rodentia	Funisciurus	mystax	2.338			1					
127	Rodentia	Funisciurus	pyrrhopus	2.473	1	1	1	1	2.464	3	2.477	4
128	Rodentia	Graphiurus	hueti	1.477			1					
129	Rodentia	Graphiurus	lorraineus	1.431			1					
130	Rodentia	Graphiurus	murinus	1.301	1	1						
131	Rodentia	Graphiurus	surdus	1.861			1					
132	Rodentia	Heliosciurus	gambianus	2.322	1							
133	Rodentia	Heliosciurus	rufobrachium	2.660	1	1	1		2.655	2	2.674	3
134	Rodentia	Hybomys	trivirgatus	1.796	1							
135	Rodentia	Hybomys	univittatus	1.778		1	1					
136	Rodentia	Hylomyscus	aeta	1.389		1						
137	Rodentia	Hylomyscus	fumosus	1.238		1						
138	Rodentia	Hylomyscus	parvus	1.161		1						
139	Rodentia	Hylomyscus	simus	1.266	1							

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	ALTER-NATIVE MASS	SITE	ALTER-NATIVE MASS	SITE
140	Rodentia	Hylomyscus	stella	1 322		1						
141	Rodentia	Hystrix	cristata	4 301	1			1				
142	Rodentia	Idiurus	zenkeri	1 477		1						
143	Rodentia	Lophuromys	sikapusi	1 769	1	1	1		1 887	3		
144	Rodentia	Malacomys	edwardsi	1 778	1							
145	Rodentia	Malacomys	longipes	1 881		1	1		1 682	3		
146	Rodentia	Mastomys	sp	1 653	1							
147	Rodentia	Mylomys	dybowskii	2 000	1							
148	Rodentia	Myosciurus	pumilio	1 220		1						
149	Rodentia	Nannomys	minutoides	0 813	1	1						
150	Rodentia	Nannomys	musculoides	1 000			1					
151	Rodentia	Nannomys	setulosus	1 124	1	1	1					
152	Rodentia	Oenomys	hypoxanthus	2.053	1	1	1					
153	Rodentia	Praomys	lukolelae	1 025		1						
154	Rodentia	Praomys	tullbergi	1 825	1	1	1		1 589	3		
155	Rodentia	Protoxerus	stangeri	2 839	1	1		1				
156	Rodentia	Rattus	rattus	2 041	1	1						
157	Rodentia	Steatomys	sp.	1 882	1							
158	Rodentia	Stochomys	longicaudatus	1 956		1	1		1 769	3		
159	Rodentia	Tatera	kempi	2.089	1							
160	Rodentia	Thamnomys	rutilans	1 799	1	1	1		1 710	3		
161	Rodentia	Thryonomys	swinderianus	3 574	1	1	1	1	3 890	2	3 301	3
162	Rodentia	Uranomys	ruddi	1 481	1							
163	Rodentia	Xerus	erythropus	2 613	1							
164	Rodentia	Zenkerella	insignis	2 580		1						
165	Tubulidentata	Orycteropus	afer	4 778	1	1						
166		Miomys	ingoldbyi	1 477	1							
167		Protoxerus	stangeri	2 839			1					

13. MAMMALS OF RAIN FOREST SITES IN AUSTRALIA AND ASIA

No.	SITE NAME	REFERENCE
1	Cape York Peninsula, Australia	Tate G.H.H. 1952, Downing, J.A. and M. Silva, 1995.
2	Malasie (Malaysia)	Harrison, J.L., 1966. Downing, J.A. and M. Silva, 1995.

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	 2
1	Artiodactyla	Bos	gaurus	5.978		1
2	Artiodactyla	Capricornis	sumatraensis	5.000		1
3	Artiodactyla	Cervus	unicolor	5.284		1
4	Artiodactyla	Muntiacus	muntjak	4.097		1
5	Artiodactyla	Sus	scrofa	4.875		1
6	Artiodactyla	Tragulus	javanicus	3.232		1
7	Artiodactyla	Tragulus	napu	3.628		1
8	Carnivora	Aonyx	cinerea	3.607		1
9	Carnivora	Arctictis	binturong	4.061		1
10	Carnivora	Arctogalidia	trivirgata	3.352		1
11	Carnivora	Canis	familiaris	4.301	1	
12	Carnivora	Felis	bengalensis	3.398		1
13	Carnivora	Felis	planiceps	3.267		1
14	Carnivora	Felis	temmincki	4.000		1
15	Carnivora	Lutra	sumatrana	3.740		1
16	Carnivora	Martes	flavigula	3.301		1
17	Carnivora	Mustela	nudipes	2.699		1
18	Carnivora	Paguma	larvata	3.778		1
19	Carnivora	Panthera	pardus	4.602		1
20	Carnivora	Panthera	tigris	5.176		1
21	Carnivora	Paradoxurus	hermaphroditus	3.508		1
22	Carnivora	Prionodon	linsang	2.845		1
23	Carnivora	Tapirus	indicus	5.502		1
24	Carnivora	Viverra	tangalunga	4.000		1
25	Carnivora	Viverra	zibetha	3.929		1
26	Dermoptera	Cynocephalus	variegatus	3.000		1
27	Insectivora	Chimarrogale	platycephala	1.176		1
28	Insectivora	Crocidura	fuliginosa	1.146		1
29	Insectivora	Echinosorex	gymnurus	2.845		1
30	Insectivora	Hylomys	suillus	1.806		1
31	Insectivora	Suncus	etruscus	0.550		1
32	Marsupicarnivora	Acrobates	pygmaeus	1.158	1	
33	Marsupicarnivora	Aepyprymnus	rufescens	3.512	1	
34	Marsupicarnivora	Antechinus	flavipes	1.686	1	
35	Marsupicarnivora	Bettongia	penicillata	3.114	1	

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	MEAN LOG 10 WEIGHT	1	2
36	Marsupicarnivora	Dactylopsila	trivirgata	2.498	1	
37	Marsupicarnivora	Dasyurus	hallucatus	2.786	1	
38	Marsupicarnivora	Dendrolagus	bennettianus	4.114	1	
39	Marsupicarnivora	Dendrolagus	lumholtzi	3.823	1	
40	Marsupicarnivora	Echymipera	rufescens	2.996	1	
41	Marsupicarnivora	Hypsiprymnodon	moschatus	2.716	1	
42	Marsupicarnivora	Isoodon	macrourus	3.106	1	
43	Marsupicarnivora	Isoodon	obesulus	3.114	1	
44	Marsupicarnivora	Macropus	agilis	4.176	1	
45	Marsupicarnivora	Macropus	bicolor	4.000	1	
46	Marsupicarnivora	Macropus	giganteus	4.653	1	
47	Marsupicarnivora	Macropus	parryi	4.130	1	
48	Marsupicarnivora	Macropus	robustus	4.470	1	
49	Marsupicarnivora	Onychogalea	unguifera	3.823	1	
50	Marsupicarnivora	Perameles	nasuta	3.061	1	
51	Marsupicarnivora	Petaurus	australis	2.661	1	
52	Marsupicarnivora	Petaurus	breviceps	2.079	1	
53	Marsupicarnivora	Petrogale	inornata	3.672	1	
54	Marsupicarnivora	Phalanger	maculatus	3.019	1	
55	Marsupicarnivora	Phalanger	orientalis	3.267	1	
56	Marsupicarnivora	Phascolarctos	cinereus	3.736	1	
57	Marsupicarnivora	Pseudocheirus	archeri	3.076	1	
58	Marsupicarnivora	Pseudocheirus	herbertensis	3.029	1	
59	Marsupicarnivora	Pseudocheirus	lanuginosus	2.954	1	
60	Marsupicarnivora	Pseudocheirus	lemuroides	3.114	1	
61	Marsupicarnivora	Pseudocheirus	peregrinus	2.778	1	
62	Marsupicarnivora	Schoinobates	volans	3.130	1	
63	Marsupicarnivora	Sminthopsis	murina	1.312	1	
64	Marsupicarnivora	Sminthopsis	rufigerus	1.000	1	
65	Marsupicarnivora	Thylogale	stigmatica	3.667	1	
66	Marsupicarnivora	Trichosurus	vulpeculus	3.301	1	
67	Monotremata	Ornithorhynchus	anatinus	3.079	1	
68	Monotremata	Tachyglossus	aculeatus	3.602	1	
69	Perissodactyla	Tapirus	indicus	5.302		1
70	Pholidata	Manis	javanica	3.301		1
71	Primates	Hylobates	lar	3.681		1
72	Primates	Macaca	fascicularis	3.477		1
73	Primates	Macaca	nemestrina	3.932		1
74	Primates	Nycticebus	coucang	2.804		1
75	Primates	Presbytis	cristatus	3.477		1
76	Primates	Presbytis	melalophus	3.477		1
77	Primates	Presbytis	obscurus	3.820		1
78	Primates	Symphalangus	syndactylus	4.021		1
79	Proboscidea	Elephas	maximus	6.398		1
80	Rodentia	Aeromys	tephromelas	3.097		1

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	 2
81	Rodentia	Atherurus	macrourus	3.301		1
82	Rodentia	Callosciurus	caniceps	2.477		1
83	Rodentia	Callosciurus	nigrovittatus	2.305		1
84	Rodentia	Callosciurus	notatus	2.398		1
85	Rodentia	Callosciurus	prevostii	2.602		1
86	Rodentia	Chiropodomys	gliroides	1.462		1
87	Rodentia	Dasyurops	maculatus	3.398	1	
88	Rodentia	Hydromys	chrysogaster	2.869	1	
89	Rodentia	Hylopetes	lepidus	1.699		1
90	Rodentia	Hylopetes	spadiceus	1.699		1
91	Rodentia	Hystrix	brachyura	3.903		1
92	Rodentia	Iomys	horsfieldii	2.079		1
93	Rodentia	Lariscus	insignis	2.211		1
94	Rodentia	Leggadina	delicatula	1.176	1	
95	Rodentia	Melomys	cervinipes	1.910	1	
96	Rodentia	Melomys	lutillus	1.930	1	
97	Rodentia	Mesembriomys	gouldii	2.798	1	
98	Rodentia	Petaurista	petaurista	3.306		1
99	Rodentia	Petinomys	sagitta	1.699		1
100	Rodentia	Petinomys	setosus	1.496		1
101	Rodentia	Petinomys	vordermanni	1.602		1
102	Rodentia	Pteromyscus	pulverulentus	2.350		1
103	Rodentia	Rattus	annandalei	2.290		1
104	Rodentia	Rattus	canus	2.079		1
105	Rodentia	Rattus	cremoriventer	1.883		1
106	Rodentia	Rattus	muelleri	2.331		1
107	Rodentia	Rattus	rajah	2.146		1
108	Rodentia	Rattus	sabanus	2.465		1
109	Rodentia	Rattus	surifer	2.323		1
110	Rodentia	Rattus	whiteheadi	1.699		1
111	Rodentia	Ratufa	affinis	3.000		1
112	Rodentia	Ratufa	bicolor	3.000		1
113	Rodentia	Rhinosciurus	laticaudatus	2.398		1
114	Rodentia	Rhizomys	sumatrensis	3.477		1
115	Rodentia	Saccostomus	campestris	1.748		1
116	Rodentia	Sundasciurus	hippurus	2.699		1
117	Rodentia	Sundasciurus	lowii	1.954		1
118	Rodentia	Sundasciurus	tenuis	1.916		1
119	Rodentia	Zyzomys	argurus	1.616	1	
120	Scandentia	Ptilocercus	lowii	1.574		1
121	Scandentia	Tupaia	glis	2.197		1
122	Scandentia	Tupaia	minor	1.796		1
123		Eudromicia	caudatus	1.851	1	

14. MAMMALS OF QUASI BOREAL FOREST SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Kluane	Theberge, J.B. 1976, Kluane National Park Preserve 1984
2	Northern Yukon	Canadian Wildlife Service, Government of Northen Yukon, U.S. Fish and Wildlife, 1989

		SCIENTIFIC NAME		Mean Log10 Body	Site		ALTER-NATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	MASS	SITE
1	Artiodactyla	Alces	alces	5.604		1		
2	Artiodactyla	Antilocapra	americana	4.833		1		
3	Artiodactyla	Bison	bison	5.695		1		
4	Artiodactyla	Cervus	elaphus	5.431		1		
5	Artiodactyla	Odocoileus	hemionus	4.984		1		
6	Artiodactyla	Odocoileus	virginianus	4.876		1		
7	Artiodactyla	Ovibos	moschatus	5.497		1		
8	Artiodactyla	Rangifer	tarandus	4.979		1		
9	Artiodactyla	Sus	scrofa	4.361	1			
10	Carnivora	Alopex	lagopus	3.505		1		
11	Carnivora	Canis	familiaris	4.243	1			
12	Carnivora	Canis	latrans	4.097	1	1	4.121	2
13	Carnivora	Canis	lupus	4.633		1		
14	Carnivora	Felis	catus	3.544	1			
15	Carnivora	Felis	concolor	4.737	1	1		
16	Carnivora	Felis	rufus	3.989	1			
17	Carnivora	Lutra	canadensis	3.788	1	1	3.859	2
18	Carnivora	Lynx	rufus	3.869	1	1	3.914	2
19	Carnivora	Lynx	canadensis	4.079		1		
20	Carnivora	Martes	americana	3.097		1		
21	Carnivora	Martes	pennanti	3.462		1		
22	Carnivora	Mephitis	mephitis	3.033	1	1	3.356	2
23	Carnivora	Mustela	erminea	1.826		1		
24	Carnivora	Mustela	frenata	2.216	1	1		
25	Carnivora	Mustela	nigripes	2.787		1		
26	Carnivora	Mustela	rixosa	1.875		1		
27	Carnivora	Mustela	vison	2.936	1	1		
28	Carnivora	Procyon	lotor	3.643	1	1	3.843	2
29	Carnivora	Spilogale	putorius	2.954	1	1		
30	Carnivora	Taxidea	taxus	3.803		1		
31	Carnivora	Urocyon	cinereoargenteus	3.602	1	1		
32	Carnivora	Ursus	americanus	5.134	1	1		
33	Carnivora	Ursus	arctos	5.311		1		
34	Carnivora	Ursus	maritimus	5.663		1		
35	Carnivora	Vulpes	velox	3.290		1		
36	Carnivora	Vulpes	vulpes	3.675	1	1	3.658	2
37	Chiroptera	Gulo	gulo	4.104		1		
38	Chiroptera	Plecotus	rafinesquii	0.875	1			
39	Insectivora	Blarina	brevicauda	1.286		1		

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTER NATIVE MASS	SITE
40	Insectivora	Blarina	carolinensis	0.987	1			
41	Insectivora	Condylura	cristata	1.444	1	1	1.712	2
42	Insectivora	Cryptotis	parva	0.690	1			
43	Insectivora	Microsorex	hoyi	0.477		1		
44	Insectivora	Scalopus	aquaticus	1.796	1			
45	Insectivora	Sorex	cinereus	0.699		1		
46	Insectivora	Sorex	arcticus	0.911		1		
47	Insectivora	Sorex	fumeus	0.916		1		
48	Insectivora	Sorex	longirostris	0.568	1			
49	Insectivora	Sorex	palustris	1.141		1		
50	Insectivora	Sorex	vagrans	0.845		1		
51	Lagomorpha	Lepus	townsendii	3.464		1		
52	Lagomorpha	Lepus	americanus	3.173		1		
53	Lagomorpha	Lepus	arcticus	3.677		1		
54	Lagomorpha	Sylvilagus	aquaticus	3.286	1			
55	Lagomorpha	Sylvilagus	floridanus	3.057	1	1	3.086	2
56	Lagomorpha	Sylvilagus	palustris	3.125	1			
57	Marsupicarnivora	Didelphis	virginiana	3.279	1			
58	Rodentia	Ammospermophilus	harrisii	2.176		1		
59	Rodentia	Castor	canadensis	4.226	1	1	4.301	2
60	Rodentia	Clethrionomys	gapperi	1.462		1		
61	Rodentia	Clethrionomys	rutilus	1.340		1		
62	Rodentia	Dicrostonyx	torquatus	1.863		1		
63	Rodentia	Erethizon	dorsatum	4.000		1		
64	Rodentia	Eutamias	minimus	1.632		1		
65	Rodentia	Geomys	bursarius	2.395		1		
66	Rodentia	Glaucomys	sabrinus	2.199		1		
67	Rodentia	Glaucomys	volans	1.790	1			
68	Rodentia	Glaucomys	volans saturatus	1.839	1			
69	Rodentia	Lemmus	trimucronatus	1.954		1		
70	Rodentia	Marmota	monax	3.623		1		
71	Rodentia	Microtus	ochrogaster	1.602		1		
72	Rodentia	Microtus	pennsylvanicus	1.519		1		
73	Rodentia	Microtus	pinetorum	1.408	1			
74	Rodentia	Microtus	xanthognathus	2.152		1		
75	Rodentia	Mus	musculus	1.169	1	1		
76	Rodentia	Napaeozapus	insignis			1		
77	Rodentia	Neotoma	floridana	2.291	1			
78	Rodentia	Ochrotomys	nuttalli	1.279	1			
79	Rodentia	Ondatra	zibethicus	3.037	1	1		
80	Rodentia	Onychomys	leucogaster	1.663		1		
81	Rodentia	Oryzomys	palustris	1.723	1			
82	Rodentia	Perognathus	fasciatus	0.973		1		
83	Rodentia	Peromyscus	gossypinus	1.421	1			
84	Rodentia	Peromyscus	leucopus	1.348	1	1	1.301	2
85	Rodentia	Peromyscus	maniculatus	1.373		1		
86	Rodentia	Peromyscus	polionotus	1.130	1			

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	ALTER-NATIVE MASS	SITE
87	Rodentia	Phenacomys	intermedius	1.447		1		
88	Rodentia	Rattus	norvegicus	2.531	1	1		
89	Rodentia	Rattus	rattus	2.362	1			
90	Rodentia	Reithrodontomys	humulis	0.906	1			
91	Rodentia	Reithrodontomys	megalotis	1.176	1	1		
92	Rodentia	Sciurus	carolinensis	2.628	1	1	2.719	2
93	Rodentia	Sciurus	niger	2.953	1			
94	Rodentia	Sigmodon	hispidus	2.015	1			
95	Rodentia	Spermophilus	parryii	2.872		1		
96	Rodentia	Spermophilus	franklinii	2.653		1		
97	Rodentia	Spermophilus	richardsonii	2.622		1		
98	Rodentia	Spermophilus	tridecemlineatus	2.204		1		
99	Rodentia	Synaptomys	borealis	1.519		1		
100	Rodentia	Synaptomys	cooperi	1.452		1		
101	Rodentia	Tamias	striatus	1.987		1		
102	Rodentia	Tamiasciurus	hudsonicus	2.280		1		
103	Rodentia	Thomomys	talpoides	2.141		1		
104	Rodentia	Zapus	princeps	1.447		1		
105	Rodentia	Zapus	hudsonicus	1.242		1		
106	Xenarthra	Dasypus	novemcinctus	3.699	1			
107	Xenarthra	Delphinapterus	leucas	6.134		1		

15. MAMMALS OF BOREAL FOREST SITES IN NORTH AMERICA

No.	SITE NAME	REFERENCE
1	Prince Albert (Duel)	Prince Albert National Park Mammals, 1981
2	Nopiming Provincial Park	Cuthbert, C.W. 1978, Bill Pruitt, personal communication.
3	Taiga Biological Station	Bill Pruitt personal communication.
4	Quetico	Cahn, A.H., 1973 Downing, J.A. and M. Silva, 1983.
5	Whiteshell	

		SCIENTIFIC NAME		Mean Log10						ALTER-	
				Body			Site			NATIVE	
No.	ORDER	GENUS	SPECIES	Mass	1	2	3	4	5	MASS	SITE
1	Artiodactyla	Alces	alces	5.604	1						
2	Artiodactyla	Antilocapra	americana	4.833	1		1				
3	Artiodactyla	Bison	bison	5.695	1		1				
4	Artiodactyla	Cervus	canadensis	5.361				1			
5	Artiodactyla	Cervus	elaphus	5.431	1		1				
6	Artiodactyla	Mazama	americana	4.716				1			
7	Artiodactyla	Odocoileus	hemionus	4.964	1		1				
8	Artiodactyla	Odocoileus	virginianus	4.876	1	1	1	1		4.723	2
9	Artiodactyla	Ovibos	moschatus	5.497	1						
10	Artiodactyla	Ovis	canadensis	4.959			1				
11	Artiodactyla	Rangifer	tarandus	4.979	1			1		4.816	4
12	Artiodactyla	Sus	scrofa	4.361		1					
13	Carnivora	Alopex	lagopus	3.506	1						
14	Carnivora	Canis	familiaris	4.343		1					
15	Carnivora	Canis	latrans	4.121	1	1	1	1		4.097	2
16	Carnivora	Canis	lupus	4.653	1						
17	Carnivora	Euarctos	americanus	5.288				1			
18	Carnivora	Felis	catus	3.544		1					
19	Carnivora	Felis	concolor	4.737	1	1	1				
20	Carnivora	Felis	rufus	3.914			1				
21	Carnivora	Lutra	canadensis	3.970	1	1		1		3.788	2
22	Carnivora	Lynx	canadensis	4.079	1					3.989	4
23	Carnivora	Lynx	rufus	3.914	1	1	1	1		3.860	2
24	Carnivora	Martes	americana	3.097	1			1			
25	Carnivora	Martes	pennanti	3.462	1			1		3.558	4
26	Carnivora	Mephitis	mephitis	3.356	1	1	1	1		3.093	2
27	Carnivora	Mustela	erminea	1.806	1						
28	Carnivora	Mustela	frenata	2.214	1		1				
29	Carnivora	Mustela	nigripes	2.767	1		1				
30	Carnivora	Mustela	nivalis	1.627			1				
31	Carnivora	Mustela	rixosa	1.875				1			
32	Carnivora	Mustela	rixosa	1.875	1						
33	Carnivora	Mustela	vison	2.936	1		1	1			
34	Carnivora	Procyon	lotor	3.845	1	1	1			3.643	2
35	Carnivora	Spilogale	putorius	2.954	1						
36	Carnivora	Taxidea	taxus	3.863	1		1	1			
37	Carnivora	Urocyon	cinereoargenteus	3.602	1	1	1				
38	Carnivora	Ursus	americanus	5.134	1	1					
39	Carnivora	Ursus	arctos	5.311	1						

40	Carnivora	Ursus	maritimus	3.663	1						

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	2	3	4	5	ALTER-NATIVE MASS	SITE
41	Carnivora	Vulpes	velox	3.280	1						
42	Carnivora	Vulpes	vulpes	3.658	1	1	1			3.675	2
43	Chiroptera	Gulo	gulo	4.104	1						
44	Insectivora	Blarina	brevicauda	1.284	1				1	1.127	4
45	Insectivora	Blarina	carolinensis	0.987		1					
46	Insectivora	Condylura	cristata	1.712	1			1		1.683	4
47	Insectivora	Cryptotis	parva	0.699		1		1	1	0.633	4
48	Insectivora	Microsorex	hoyi	0.477	1			1		0.602	4
49	Insectivora	Scalopus	aquaticus	1.796		1					
50	Insectivora	Sorex	arcticus	0.911	1						
51	Insectivora	Sorex	cinereus	0.699	1		1	1		0.675	4
52	Insectivora	Sorex	fumeus	0.916	1						
53	Insectivora	Sorex	longirostris	0.568		1					
54	Insectivora	Sorex	palustris	1.141	1			1		1.146	4
55	Insectivora	Sorex	vagrans	0.845	1						
56	Lagomorpha	Lepus	americanus	3.173	1			1		3.173	4
57	Lagomorpha	Lepus	arcticus	3.677	1						
58	Lagomorpha	Lepus	californicus	3.491			1		1		
59	Lagomorpha	Lepus	townsendii	3.464	1		1				
60	Lagomorpha	Sylvilagus	audubonii	2.863			1				
61	Lagomorpha	Sylvilagus	floridanus	3.085	1	1			1	3.097	2
62	Lagomorpha	Sylvilagus	palustris	3.125		1					
63	Marsupicarnivora	Didelphis	marsupialis	3.477		1			1		
64	Marsupicarnivora	Didelphis	virginiana	3.204		1					
65	Rodentia	Ammospermophilus	harrisii	2.175	1						
66	Rodentia	Castor	canadensis	4.301	1	1	1	1		4.226	2
67	Rodentia	Clethrionomys	gapperi	1.462	1			1		1.250	4
68	Rodentia	Clethrionomys	rutilus	1.340	1						
69	Rodentia	Cynomys	ludovicianus	3.097			1				
70	Rodentia	Dicrostonyx	torquatus	1.863	1						
71	Rodentia	Dipodomys	ordii	1.908			1				
72	Rodentia	Erethizon	dorsatum	4.000	1		1	1		3.889	4
73	Rodentia	Eutamias	minimus	1.632	1		1	1		1.602	4
74	Rodentia	Geomys	bursarius	2.395	1		1				
75	Rodentia	Geomys	pinetis	2.217		1					
76	Rodentia	Glaucomys	sabrinus	2.199	1			1		2.140	4
77	Rodentia	Glaucomys	volans querceti	1.814		1					
78	Rodentia	Lemmus	trimucronatus	1.954	1						
79	Rodentia	Marmota	monax	3.623	1			1		3.610	4
80	Rodentia	Microtus	montanus	1.857			1				
81	Rodentia	Microtus	ochrogaster	1.608	1		1		1		
82	Rodentia	Microtus	pennsylvanicus	1.519	1		1	1		1.520	4
83	Rodentia	Microtus	xanthognathus	2.152	1						
84	Rodentia	Mus	musculus	1.149	1		1	1		1.288	4
85	Rodentia	Napaeozapus	insignis	1.351	1						
86	Rodentia	Neofiber	alleni	2.328		1					
87	Rodentia	Neotoma	cinerea	2.477			1				
88	Rodentia	Neotoma	floridana	2.291		1					
89	Rodentia	Ochrotomys	nuttalli	1.279		1					
90	Rodentia	Ondatra	zibethicus	3.097	1		1	1		2.949	4

No	ORDER	SCIENTIFIC NAME GENUS	SPECIES	Mean Log10 Body Mass	Site 1	Site 2	Site 3	Site 4	Site 5	ALTER NATIVE MASS	SITE
91	Rodentia	Onychomys	leucogaster	1.663	1		1				
92	Rodentia	Perognathus	fasciatus	0.973	1		1				
93	Rodentia	Perognathus	hispidus	1.672			1				
94	Rodentia	Peromyscus	floridanus	1.462		1					
95	Rodentia	Peromyscus	gossypinus	1.421		1					
96	Rodentia	Peromyscus	leucopus	1.301	1		1		1		
97	Rodentia	Peromyscus	maniculatus	1.373	1		1	1	1	1.267	4
98	Rodentia	Peromyscus	polionotus	1.130		1					
99	Rodentia	Phenacomys	intermedius	1.447	1						
100	Rodentia	Rattus	norvegicus	2.531	1		1	1		2.472	4
101	Rodentia	Reithrodontomys	megalotis	1.176	1		1				
102	Rodentia	Reithrodontomys	montanus	0.954			1		1		
103	Rodentia	Sciurus	carolinensis	2.719	1	1				2.628	2
104	Rodentia	Sciurus	niger	2.953		1					
105	Rodentia	Sigmodon	hispidus	2.112		1			1		
106	Rodentia	Spermophilus	franklinii	2.653	1						
107	Rodentia	Spermophilus	parryii	2.872	1						
108	Rodentia	Spermophilus	richardsonii	2.622	1						
109	Rodentia	Spermophilus	tridecemlineatus	2.204	1		1		1		
110	Rodentia	Synaptomys	borealis	1.519	1						
111	Rodentia	Synaptomys	cooperi	1.452	1			1		1.453	4
112	Rodentia	Tamias	striatus	1.987	1			1		1.944	4
113	Rodentia	Tamiasciurus	hudsonicus	2.280	1			1		2.283	4
114	Rodentia	Thomomys	talpoides	2.141	1		1				
115	Rodentia	Zapus	hudsonicus	1.242	1		1	1		1.453	4
116	Rodentia	Zapus	princeps	1.447	1						
117	Xenarthra	Dasypus	novemcinctus	3.699		1					
118	Xenarthra	Delphinapterus	leucas	6.134	1						

APPENDIX C
TAXONOMIC AND NICHE CLASSIFICATIONS
FOR 585 MAMMAL GENERA

References

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4 Louise H Emmons 1990 Neotropical Rainforest Animals-A Field Guide
U of Chicago Press Chicago.
5 Ronald M. Novak 1991 Walker's Mammals of the World Vols 1&2, Johns Hopkins
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6 A.W.F Banfield 1974 The Mammals of Canada University of Toronto Press, Toronto
7 Arita et al. 1990 Rarity in neotropic forest mammals and its ecological correlates
Conservation Biology, Vol 4, No 2 pp 181 192

Niche Classes - Substrate

1 Fossorial
2 Semi-fossorial
3 Aquatic
4 semi-aquatic
5 Volant
6 Terrestrial
7 scansorial and semi-arboreal
8 Arboreal

Niche Class - Feeding

1 piscivore & squid-eater
2 carnivore
3 nectarivore
4 gumivore
5 crustacivore & clam-eater
6 myrmecophage
7 aerial insectivore
8 foliage-cleaning insectivore
9 insectivore-omnivore
10 frugivore-omnivore
11 frugivore-granivore
12 frugivore-herbivore
13 herbivore-browser
14 herbivore-grazer
15 planktonivore
16 sanguivore

Order References

1 Artiodactyla
2 Carnivora
3 Chiroptera
4 Cingulata
5 Dermoptera
6 Diprotodonts
7 Hyracoidea
8 Lagomorpha
9 Macroscelidea
10 Marsupicarnivora
11 Monotremata
12 Tubulidentata
13 Paucituberculata
14 Paramelina
15 Perissodactyla
16 Pholidota
17 Pilosa
18 Primates
19 Proboscidea
20 Rodentia
21 Scandentia
22 Insectivora
23 Xenarthra
24 Edentata

Family References

1 Tachyglossidae
2 Ornithorhynchidae
3 Didelphidae
4 Dasyuridae
5 Peramelidae
6 Phascolarctidae
7 Phalangeridae
8 Petauridae
9 Burramyidae
10 Macropodidae
11 Erinaceidae
12 Tenrecidae
13 Chrysochloridae
14 Soricidae
15 Talpidae
16 Macroscelididae
17 Cynocephalidae
18 Pteropodidae
19 Rhinopomatidae
20 Emballonuridae
21 Craseonycteridae
22 Nycteridae
23 Megadermatidae
24 Rhinolophidae
25 Hipposideridae
26 Mormoopidae
27 Noctilionidae
28 Phyllostomidae
29 Natalidae
30 Furipteridae
31 Thyropteridae
32 Vespertilionidae
33 Molossidae
34 Tupaiidae
35 Lorisidae
36 Callitrichidae
37 Cebidae
38 Cercopithecidae
39 Hylobatidae
40 Pongidae
41 Megalonychidae
42 Bradypodidae
43 Myrmecophagidae
44 Dasypodidae
45 Manidae
46 Ochotonidae
47 Leporidae
48 Aplodontidae
49 Sciuridae
50 Geomyidae
51 Heteromyidae
52 Castoridae
53 Anomaluridae
54 Pedetidae
55 Muridae
56 Gliridae
57 Zapodidae
58 Dipodidae
59 Hystricidae
60 Erethizontidae
61 Caviidae
62 Hydrochaeridae
63 Dinomyidae
84 Dasyproctidae
65 Chinchillidae
66 Capromyidae
67 Octodontidae
68 Ctenomyidae
70 Echimyidae
71 Thryonomyidae
72 Bathyergidae
69 Abrocomidae
73 Ctenodactylidae
74 Iniidae
75 Delphinidae
76 Monodontidae
77 Canidae
78 Ursidae
79 Procyonidae
80 Mustelidae
81 Viverridae
82 Hyaenidae
83 Felidae
84 Odobenidae
85 Orycteropodidae
86 Elephantidae
87 Procaviidae
88 Equidae
89 Tapiridae
90 Rhinocerotidae
91 Suidae
92 Tayassuidae
93 Hippopotamidae
94 Camelidae
95 Tragulidae
96 Cervidae
97 Giraffidae
98 Antilocapridae
99 Bovidae

No	Common Name	Genus	Family	Order	Sub-strate	Diet
1	chinchilla rat	Abrocoma	69	20	2	13
2	cheetah	Acinonyx	83	2	6	02
3	Spiny Mice	Acomys	55	20	6	11
4	Pygmy Possums	Acrobates	9	10	8	09
5	Waterbuck, Lechwe, Kob Puku	Adenota = Kobus	99	1	6	14
6	Rat kangaroo	Aepyprymnus	10	10	6	13
7	Impala	Aepyceros	99	1	6	13
8		Aeromys	49	20	8	10
9	Large black flying squirrels	Aethalops	18	3	5	10
10	Bush rats or rock rats	Aethomys	55	20	6	11
11	African bush squirrel	Aethosciurus	49	20	7	11
12	Paca	Agouti	64	20	6	12
13	Giant panda	Ailuropoda	79	2	6	13
14	Lesser panda	Ailurus	79	2	6	14
15	Grass Mouse	Akodon	55	20	6	09
16	Hartebeests	Alcelaphus	99	1	6	14
17	Moose	Alces	96	1	6	13
18	Oil Palm Squirrels= Protoxerus	Allosciurus=sub genus	49	20	8	11
19	Canadian Arctic fox	Alopex	77	2	6	02
20	Red-Handed Howler Monkey	Alouatta	37	18	8	12
21	African Golden Moles	Amblysomus	13	22	1	09
22	Little White-shouldered bat	Ametrida	28	3	5	10
23	Antelope ground squirrel	Ammospermophilus	49	20	2	11
24	barbary sheep	Ammotragus	99	1	6	14
25	— mouse, 2 rare species	Andalgalomys	55	20	6	09
26	1 species, A. beecrofti in history	Anomalurops	53	20	8	10
27	Scaly-tailed Flying Squirrels	Anomalurus	53	20	8	12
28	Tailless Bat	Anoura	28	3	5	03
29		Anourosorex	14	22	1	09
30	Kultarr	Antechinomys	4	10	6	09
31	Broad-footed Marsupia "Mice"	Antechinus	4	10	6	09
32	Springbuck	Antidorcas	99	1	6	14
33	Pronghorn antelope	Antilocapra	99	1	6	14
34		Antilope	99	1	6	14
35	Pallid bat	Antrozous	32	3	5	07
36		Aonyx	80	2	4	05
37	Night Monkey	Aotus	37	18	8	10
38	Mountain beaver	Aplodontia	48	20	2	13
39	Old World Wood and Field Mice	Apodemus	55	20	6	11
40		Arctictis	81	3	8	01
41		Arctictis	81	3	7	10
42	Golden Potto/Angwantibo-primate	Arctocebus	35	18	8	09
43	Southern fur seal	Arctocephalus	84	2	3	01
44	Jamaican fruit-eating bat	Arctogalidia	81	2	7	02

No	Common Name	Genus	Family	Order	Sub-strate	Diet
45	Water voles. Bank voles.	Arctonyx	80	2	2	10
46	Black-handed spider monkey	Artibeus	28	3	5	10
47	Small-eared dog	Arvicanthis	55	20	2	13
48	Brush-tailed Porcupine	Arvicola	55	20	2	12
49		Aselliscus	25	3	5	07
50	Barbary Ground Squirrel	Ateles	37	18	8	12
51	Pigmy mice	Atelocynus	77	2	6	02
52	Thomas sac-winged bat	Atherurus	59	20	6	10
53		Atilax	81	2	4	05
54	Olingo	Atlantoxerus	49	20	2	11
55	Cacomistle, Bassarise	Axis	96	1	6	13
56	Van Gelder's bat	Baiomys	55	20	2	11
57		Balantiopteryx	20	3	5	07
58	Short-nosed "Rat" Kangaroos	Balionycteris	18	3	5	10
59	Bison	Bandicota	55	20	2	10
60	Short-tailed shrew	Bassaricyon	79	2	8	10
61	S.A. Field Mice, Akodon genus	Bassariscus	79	2	8	02
62	Oxen	Bauerus	32	3	5	07
63	Brown-throated 3 toed Sloth	Bdeogale	81	2	6	09
64	Naked-tailed Armadillo	Belomys	49	20	8	10
65	Titi monkey	Berylmys	55	20	6	09
66	Goeldi's Marmoset	Bettongia	10	10	6	13
67	Black-tailed Silvery Marmoset	Bison	99	1	6	16
68	Beutiful and Tricolored Squirrels	Blarina	14	22	2	09
69	Vesper Mice	Bolomys Thomas 1916	55	20	6	11
70	Wooly opossum	Bos	99	1	6	16
71	Black-shouldered opossum	Bradypus	42	23	8	13
72	Coyote	Bubalus	99	23	6	14
73	Goats	Cabassous	44	24	6	06
74	Roe Deer	Callicebus	37	18	8	10
75	Serows Artiodactyla, Bovidae	Callimico	36	18	8	10
76	Silky short-tailed bat	Callithrix	36	18	8	09
77	Beaver	Callosciurus	49	20	8	11
78		Calomys	55	20	6	11
79		Caluromys	3	10	7	10
80	Pygmy marmoset	Caluromysiops	3	10	8	10
81	Brown Pale-fronted Capuchin	Cavia	77	2	6	02
82	Shaggy-haired bat	Cannomys	55	20	2	10
83	Wrinkle-faced bat	Capra	99	1	6	13
84	Duikers- Artiodactyla, Bovidae	Capreolus	96	1	6	13
85	Rhinoceros	Capricornis	99	1	6	13
86	Mangabeys- primates	Carollia	28	3	5	10
87	Guenon	Castor	52	20	6	13
88	Crab-eating fox	Catagonus	92	1	6	13

No.	Common Name	Genus	Family	Order	Sub-strate	Diet
89	Wapiti	Cavia	61	20	2	13
90		Cebuella	36	18	8	04
91		Cebus	37	18	8	10
92	Salvin s white-lined bat	Centronycteris	20	3	5	07
93		Centurio	28	3	5	10
94	Water opossum	Cephalophus	99	1	6	13
95	Pencil tailed tree mice	Ceratotherium	90	15	6	14
96	Brown bearded Saki monkey	Cercocebus	38	18	8	12
97		Cercopithecus	38	18	8	10
98	African golden mole	Cerdocyon	77	2	6	02
99	Godman s bat	Cervus	96	1	6	13
100		Chaetophractus	44	23	2	09
101	Southern Two-toed sloth	Cheiromeles	33	22	5	07
102		Chimarrogale	14	22	4	05
103	Peters false vampire bat	Chiroderma	28	3	5	10
104		Chiromyscus	59	20	7	10
105	Large golden mole	Chimmax	18	3	5	10
106		Chironectes	3	10	4	01
107		Chiropodomys	55	20	8	11
108		Chiropotes	37	18	8	10
109	Red-backed Mice,or Bank Voles	Chlamyphorus	44	24	6	09
110	Mexican porcupine	Chlorotalpa	13	22	1	09
111		Choeroniscus	28	3	5	03
112	African water rat	Choeropsis	93	1	6	12
113	Star-nosed mole	Choloepus	41	23	8	13
114	Striped hog nosed skunk	Chroeomys	55	20	6	09
115	Wildebeest	Chrotopterus	28	3	5	02
116	Wagner's Sac-winged Bat	Chrysochloris	13	22	1	09
117	African giant pouched rat	Chrysospalax	13	22	1	09
118	Common Hamster	Chimarrogale	14	22	4	09
119	White-toothed shrews	Citellus (see Spermop)	49	20		
120		Civettictis	81	2	6	02
121	Common mole-rat	Clethrionomys	55	20	6	09
122	Small-eared shrew	Coelops	25	3	5	07
123	Cuscus	Coendou	60	20	7	12
124	Tuco-tuco	Colobus	38	18	8	12
125	Agouti	Colomys	55	20	2	09
126	Two-toed anteater or Silky anteater	Condylura	15	22	1	09
127		Conepatus	80	2	6	09
128	Colugos, Flying lemurs	Connochaetes	99	1	6	14
129	Prairie dogs	Cormura	20	3	5	07
130		Craseonycteris	21	3	5	08
131		Cricetomys	55	20	6	10
132	Bamboo rat, Coro-coro	Cricetus	55	20	2	11

No	Common Name	Genus	Family	Order	Sub-strate	Diet
133	Striped possum	Crocidura	14	22	2	09
134	Fallow deer	Crocuta	82	2	6	02
135	Sassabies	Cryptomys	72	20	1	11
136	Shaggy swamp rat	Cryptotis	14	22	2	09
137	Mexican agouti	Ctenodactylus	73	20	6	13
138	Nine-banded armadillo	Ctenomys	68	20	1	12
139		Cuniculus	64	20	6	12
140	Beluga or White whale	Cuon	77	2	6	02
141	Tree or bush hyrax	Cyclopes	43	23	8	06
142	Tree kangaroo	Cynictis	81	2	2	06
143	African climbing mice	Cynocephalus	17	5	8	13
144	Congo forest mouse	Cynogale	81	2	4	01
145	Defua rat	Cynomys	49	20	2	14
146		Cynopterus	16	3	5	10
147	Vampire bat	Cyttarops	20	3	5	07
148	White-winged vampire bat	Dactylomys	70	20	8	13
149	Black rhino	Dactylopsila	8	10	8	09
150	Northern ghost bat	Dama	96	1	6	14
151	Collared peccary	Damaliscus	99	1	6	14
152	Collared Lemmings or Varying Lemmus	Dasymys	55	20	6	13
153	Southern opossum	Dasyprocta	64	20	6	12
154	Branick's giant rat or Pacarana	Dasypus	44	23	2	09
155	Hairy-legged vampire bat	Dasyurus	4	10	7	02
156	Soft-furred rat	Delphinapterus	76		3	01
157	Kangaroo Rat	Dendrohyrax	87	7	8	13
158	Patagonia Cavies	Dendrolagus	10	10	8	13
159		Dendromus	55	20	7	09
160		Deomys	55	20	6	09
161		Dephomys	55	20	6	10
162	Arboreal spiny rat	Dermanura	28	3	5	10
163		Desmodus	28	3	5	16
164	Moon rat	Diaemus	28	3	5	16
165	New guinean spiny bandicoot	Dicerorhinus	90	15	6	13
166	White bat	Diceros	90	15	6	13
167	Tayra	Diclidurus	20	3	5	07
168	Long eared elephant shrew	Dicotyles	92	1	6	10
169		Dicrostonyx	55	20	2	13
170		Didelphis	3	10	7	10
171	Garden dormouse	Dinomys	63	20	6	12
172		Diphylla	28	3	5	16
173	Argentine brown bat	Diplomys	70	20	6	12
174		Dipodomys	51	20	6	11
175	North American porcupine	Dolichotis	61	20	6	13
176	Eurasian hedgehog	Dologale	81	2	2	09

No	Common Name	Genus	Family	Order	Sub-strate	Diet
177		Dremomys	49	20	7	09
178	Shaw's mastiff bat	Dusicyon	77	2	6	02
179	Wagner's mastiff bat	Dyacopterus	18	3	5	10
180	Six banded armadillo	Echimys	70	20	8	11
181	Western american chipmunk	Echinoprocta	60	20	8	?
182	Mountain lion or Puma	Echinosorex	11	22	6	09
183		Echymipera	5	10	6	09
184		Ectophylla	28	3	5	10
185	Bush baby	Eira	80	2	7	02
186		Elephantulus	16	9	6	09
187	Grison	Elephas	98	19	6	13
188		Eligmodontia	55	20	6	11
189		Eliomys	56	20	7	09
190	Plains pocket gopher	Emballonura	20	3	5	07
191		Eonycteris	18	3	5	03
192		Eothenomys	55	20	2	13
193	Southern flying squirrel	Epixerus	49	20	6	10
194		Eptesicus	32	3	5	07
195		Equus	88	15	6	14
196	Pallas' long-tongued bat	Erethizon	60	20	7	13
197		Erinaceus	11	22	2	09
198		Erythrocebus	38	18	7	10
199		Eumops	33	3	5	07
200		Eumops	33	3	5	07
201	Wolverine	Euphractus	44	23	6	09
202	Crested-tailed deer mouse	Eutamias	49	20	6	11
203		Felis	83	2	6	02
204		Funisciurus	49	20	8	11
205		Furipterus	30	3	5	07
206		Galago	35	18	6	09
207		Galea	61	20	6	12
208		Galictis	80	2	6	02
209	Forest spiny pocket mouse	Gazella	99	1	6	13
210		Genetta	81	2	6	02
211		Geomys	50	20	1	13
212	Roan	Gerbillus	55	20	2	10
213	Allen's wood rat	Giraffa	97	1	6	13
214	Marsh rat or Web-footed rat	Glaucomys	49	20	8	09
215	Armored rat or Thick-spined rat	Glironia	3	20	8	09
216		Glis	56	20	7	10
217	Eastern back-striped mice	Glischropus	32	3	5	07
218	Capybara	Glossophaga	28	3	5	03
219		Gorilla	40	18	6	13
220		Grammomys	55	20	7	10

No.	Common Name	Genus	Family	Order	Sub-strate	Diet
221		Geomys	55	20	7	14
222	Giant forest hog	Graphiurus	56	20	8	11
223		Gulo	80	3	6	02
224		Habromys	55	20	6	10
225	Underwood's long-tongued bat	Hapalomys	55	20	8	13
226		Harpiocephalus	32	3	5	10
227		Heliophobius	72	20	1	12
228		Heliosciurus	49	20	8	11
229		Helogale	81	2	6	09
230		Hemigalus	81	2	6	02
231		Herpestes	81	2	6	09
232	Amazon river dolphin	Heterogeomys	50	20	1	12
233		Heterohyrax	87	7	6	13
234	Short nosed bandicoot	Heteromys	51	20	6	11
235	Toros	Hippopotamus	93	1	4	13
236		Hipposideros	25	3	5	07
237		Hippotragus	99	1	6	14
238	Waterbuck,Kob, Puku	Hodomys	55	20	6	12
239		Holochilus	55	20	4	13
240	Wooly monkey	Hoplomys	70	20	6	10
241		Hyaena	82	2	6	02
242		Hybomys	55	20	6	10
243		Hydrochaeris	62	20	4	13
244	Silver-haired bat	Hydromys	55	20	4	12
245	Red bat	Hyemoschus	95	1	6	12
246		Hylobates	38	18	8	12
247	True lemming	Hylochoerus	91	7	6	14
248		Hylomys	11	22	6	09
249	Saussure's long-nosed bat	Hylomyscus	55	20	8	10
250	Hares or Jack rabbits	Hylonycteris	28	3	5	10
251		Hylopetes	49	20	8	09
252	Forest spiney pocket mouse	Hypsiprimnodon	10	10	6	09
253		Hystrix	59	20	6	10
254		Ia	32	3	5	07
255		Ichneumia	81	2	6	02
256	Tomes' long-eared bat	Ictonyx	80	2	6	02
257		Idiurus	53	20	8	11
258	African elephant	Inia	74		3	01
259	River otter	Iomys	49	20	8	11
260		Isoodon	5	10	6	09
261		Isothrix	70	20	8	10
262		Jaculus	58	20	2	11
263		Kerivoula	32	3	5	07
264	Long-legged bat	Kerodon	61	20	6	13

No	Common Name	Genus	Family	Order	Sub-strate	Diet
265		Kobus	99	1	6	14
266	Waterhouse's leaf-nosed bat	Lagostomus	65	20	2	14
267		Lagothrix	37	18	8	10
268		Lagurus	55	20	2	13
269		Lama	94	1	6	16
270		Lariscus	49	20	6	11
271	Scaly anteater	Lasionycteris	32	3	5	07
272		Lasiurus	32	3	5	07
273		Leggadina	55	20	6	11
274		Lemmus	55	20	2	12
275	American pine marten	Lemniscomys	55	3	2	12
276		Lenothrix	55	20	8	10
272		Leopoldamys	55	20	7	09
278	Red brocket	Leptonycteris	28	3	5	03
279	Thomas's deer mouse	Lepus	67	8	6	14
280		Lichonycteris	28	3	5	03
281	Giant mexican shrew	Liomys	51	20	2	11
282		Lionycteris	28	3	5	10
283		Litocranius	99	1	6	13
284	Striped skunk	Lonchophylla	28	3	5	10
285		Lonchorhina	28	3	5	08
286		Lophuromys	55	20	2	11
287		Loxodonta	86	19	6	13
288		Lutra	80	2	4	02
289	Brown four-eyed opossum	Lutreolina	3	10	6	02
290		Lycaon	77	2	6	02
291		Lynx	83	2	6	02
292	Kangaroo Mouse	Macaca	38	18	8	10
293		Macroglossus	18	3	5	03
294	Brazilian large-eared bat	Macrophyllum	28	3	5	08
295		Macropus	10	10	6	13
296	Neotropical dwarf squirrel	Macrotus	28	3	5	09
297	Pygmy shrew	Madoqua	99	1	6	13
298	Pine vole	Makalata	70	20	8	12
299	Bennett's spear-nosed bat	Malacomys	55	20	6	10
300		Malacothrix	55	20	6	12
301	Broad-faced bat	Manis	45	16	7	06
302	Red mastiff bat	Marmosa	3	10	7	09
303	Three-striped short-tailed opossum	Marmosops	3	10	8	09
304	Peters' ghost-faced bat	Marmota	49	20	2	12
305		Martes	80	2	7	02
306	Muntjacs	Massoutiera	73	20	6	12
307	House mouse	Mastomys	55	20	6	09
308		Maxomys	55	20	6	09

No	Common Name	Genus	Family	Order	Sub-strate	Diet
309	Banana bat or Colima long-nosed bat	Mazama	96	1	6	12
310	Long-tailed weasel	Megaderma	23	3	5	09
311		Megadontomys	55	20	6	12
312	Nutria	Megaerops	16	3	5	10
313		Megasorex	14	22	2	09
314	Acouchi	Mellivora	80	2	6	02
315		Melogale	80	2	2	09
316		Melomys	55	20	8	12
317	Silver-tipped myotis	Menetes	49	20	6	10
318	Giant anteater	Mephitis	80	2	6	09
319		Meriones	55	20	6	09
320		Mesembriomys	55	20	6	12
321		Mesomys	70	20	8	12
322	Woodland jumping mouse	Mesophylla	28	3	5	10
323	Coati	Metachirus	3	10	6	10
324	Mexican funnel-eared bat	Micoureus	3			
325	Spiny rice rat	Microcavia	61	20	6	12
326		Microdipodops	51	20	2	11
327	Nelson s wood rat	Micromys	55	20	7	09
328	Round tailed muskrat or Florida water	Micronycteris	28	3	5	08
329		Micropotamogale	12	22	4	09
330	Eastern wood rat	Microsciurus	49	20	8	09
331	Mexican volcano mouse	Microsorex	14	22	2	09
332	Dwarf Antelope	Microtus	55	20	6	12
333	American Shrew mole	Mimon	28	3	5	08
334	Greater bulldog bat	Miniopterus	32	3	5	07
335	Grey shrew or Desert shrew	Miopithecus	39	19	8	10
336	Northern yellow bat	Molossops	33	3	5	07
337		Molossus	33	3	5	07
338		Monodelphis	3	10	6	09
339	Sumichrast s vesper rat	Mormoops	26	3	5	07
340	Pika	Mungos	81	2	6	09
341	Golden mouse	Muntiacus	96	1	6	14
342		Muntiacus	96	1	6	13
343	Walrus	Murina	32	3	5	07
344	White-tailed deer	Mus	55	20	6	10
345	Rice rat	Muscardinus	56	20	8	10
346		Musonycteris	28	3	5	10
347	Rice rat	Mustela	80	2	6	02
348	Muskrat	Mylomys	55	20	6	13
349		Myocastor	66	20	4	11
350	Grasshopper mice	Myomyscus	55	20	6	10
351	Killer Whale Orca	Myoprocta	64	20	6	11
352	Mountain goat	Myosciurus	49	20	8	11

Nr	Common Name	Genus	Family	Order	Sub-strate	Diet
353		Myosorex	14	22	2	09
354		Myotis	32	3	5	07
355	Taltuza, Hispid pocket gopher	Myrmecophaga	43	23	6	06
356		Mystromys	55	20	2	10
357	aardvark	Naemorhedus	99	1	6	14
358		Nandinia	81	2	6	10
359		Nannomys	35	20	2	10
360		Napaeozapus	57	20	6	10
361	Mchoacan deer mouse	Nasua	79	2	7	10
362		Natalus	29	3	5	07
363		Neacomys	55	20	6	09
364	Yucatan vesper rat	Nectomys	55	20	4	09
365	Big-eared climbing rat	Nelsonia	55	20	6	13
366		Neofiber	55	20	4	12
367	Musk ox	Neomys	14	22	6	09
368	Bighorn sheep	Neotoma	55	20	7	12
369		Neotomodon	55	20	6	13
370		Neotragus	99	1	6	14
371		Neurotrichus	15	22	2	09
372		Niviventer	55	20	8	10
373		Noctilio	27	3	5	01
374	Jaguar	Notiosorex	14	22	2	09
375		Nycteris	22	3	5	07
376		Nycticebus	35	18	8	09
377		Nyctinomops	33	3	5	07
378		Nyctomys	55	20	8	11
379	Hairy-tailed mole	Ochotona	46	8	6	13
380	African bush squirrel	Ochrotomys	55	20	7	11
381		Octomys	67	20	2	13
382		Odobenus	84		3	5
383		Odocoileus	96	1	6	13
384		Oecomys	55	20	8	11
385		Oenomys	55	20	2	13
386		Oligoryzomys	58	20	6	11
387		Ondatra	55	20	4	10
388	Silky pocket mouse	Onychogalea	10	10	6	13
389	White-footed mouse,Deer Mouse	Onychomys	55	20	6	09
390	Greater doglike bat	Orcinus	75		3	02
391		Oreamnos	99	1	6	13
392		Oreotragus	99	1	6	13
393		Ornithorhynchus	2	11	3	02
394		Orthogeomys	50	20	1	13
395	wart hog	Orycteropus	85	12	2	06
396		Oryctolagus	47	8	6	13

No.	Common Name	Genus	Family	Order	Sub-strate	Diet
397		Oryx	99	1	6	14
398	Heather vole	Oryzomys	55	20	6	12
399	Gray Four-eyed opossum	Osgoodomys	55	20	6	12
400	Pale spear-nosed bat	Otocyon	77	2	6	02
401		Otomys	55	20	6	12
402	Eastern pipistrelle	Otonyctomys	55	20	8	11
403	Saki monkey	Ototylomys	55	20	7	12
404		Ourebia	99	1	6	13
405	White-lined bat	Ovibos	99	1	6	13
406	Rafinesque's big-eared bat	Ovis	99	1	6	13
407	Florida mouse	Oxymycterus	55	20	6	09
408		Ozotoceros	96	1	6	14
409		Pachyuromys	55	20	6	09
410		Paguma	81	2	8	02
411	Kinkajou	Pan	40	18	7	10
412	African soft-furred rat	Panthera	83	2	6	02
413		Papio	38	18	7	02
414	Giant armadillo	Pappogeomys	50	20	1	11
415		Paracrocidura	14	22	1	09
416		Paracynictis	81	2	6	09
417		Paradoxurus	81	2	8	02
418	Raccoon	Parascalops	15	22	1	09
419	Spiny rat,Casiragua	Paraxerus	49	20	2	10
420	Thomas' mastiff bat	Paraechinus	11	22	6	02
421		Pedetes	54	20	2	12
422		Pelea	99	1	6	13
423		Pelomys	55	20	6	12
424		Penthetor	18	3	5	10
425		Perameles	5	10	2	06
426		Perodicticus	35	18	8	10
427	Mustached bat	Perognathus	51	20	2	11
428	Giant river otter	Peromyscus	55	20	6	11
429		Peropteryx	20	3	5	07
430		Petaurista	49	20	8	11
431	Caribou,Reindeer	Petaurus	8	10	8	10
432		Petromys	49	20	8	11
433	Brown rat,Norway rat	Petrodromus	16	9	6	09
434		Petrogale	10	10	6	14
435		Phacochoerus	91	1	6	14
436	Slender harvest mouse	Phalanger	7	10	8	10
437		Phascolarctos	6	10	8	13
438	Little Fruit Bat	Phenacomys	55	20	6	12
439	Long-nosed squirrel	Philander	3	10	7	10
440	Climbing rat	Philetor	32	3	5	07

No	Common Name	Genus	Family	Order	Sub-strate	Diet
441	Bamboo rat	Phoniscus	32	3	5	07
442	Central American yellow bat	Phyllostomus	28	3	5	10
443		Phyllotis	55	20	6	12
444	Proboscis bat,Sharp-nosed bat	Pipistrellus	32	3	5	07
445	Volcano Rabbit	Pithecheir	55	3	7	10
446	Walrus	Pithecia	37	18	8	10
447		Pitymys	55	20	2	12
448		Platyrrhinus	28	3	5	10
449	Greater white-lined bat	Plecotus	32	3	5	09
450		Podomys	55	20	2	11
451	Saddle-backed Tamarin	Poecilogale	80	2	2	02
452	Squirrel monkey	Potamochoerus	91	1	6	10
453	Eastern mole	Potamogale	12	22	4	02
454	Western American mole	Potos	79	2	7	10
455		Praomys	55	20	7	10
456	Mexican gray squirrel	Presbytis	38	18	8	13
457	Alston's brown mouse	Priodontes	44	23	2	02
458		Prionodon	81	24	8	02
459	Hispid cotton rat	Prionomys	55	20	2	06
460		Procavia	87	7	6	13
461	Southeastern Shrew	Procyon	79	2	6	10
462		Proechimys	70	20	6	11
463	Bush dog	Promops	33	3	5	07
464	Ground squirrels, Susliks	Pronolagus	47	8	6	13
465	Visored bat	Proteles	82	2	6	09
466	Long-haired prehensile-tailed porcupin	Protoerus	49	20	6	11
467	Spotted skunk	Psammomys	55	20	2	13
468		Pseudocheirus	8	10	7	11
469		Pteromyscus	49	20	8	11
470	Anthony's bat	Pteronotus	26	3	5	07
471		Pteronura	80	2	4	01
472		Pteropus	18	3	5	10
473		Ptilocercus	34	21	8	10
474		Pudu	96	1		
475	Wild boar pig	Rangifer	96	1	6	13
476		Raphicerus	99	1	6	13
477	Forest rabbit,Brazilian Cottontail	Rattus	55	20	6	10
478		Ratufa	49	20	8	10
479	Bog lemmings	Redunca	99	1	6	14
480		Reithrodontomys	55	20	7	11
481	Short-nosed echidna	Rhabdomys	55	20	6	11
482		Rhinoceros	90	15	6	13
483	Broad-tailed bat	Rhinolophus	24	3	5	07
484	Old world mole	Rhinophylla	28	3	5	10

No	Common Name	Genus	Family	Order	Sub-strate	Diet
485	Tamandua,Lesser anteater	Rhinopoma	19	3	5	07
486	Chipmunks	Rhinosciurus	49	20	6	06
487	Red squirrel,Chickaree	Rhipidomys	55	20	8	11
488	Baird s tapir	Rhizomys	55	20	2	13
489		Rhogeessa	32	3	5	07
490		Rhynchogale	81	2	6	09
491		Rhynchonycteris	20	3	5	07
492	American badger	Romerolagus	47	8	2	12
493	Polar bear	Rousettus	18	3	5	10
494		Rupicapra	99	1	6	13
495		Saccopteryx	20	3	5	07
496	Western pocket gopher	Saccostomus	55	20	6	10
497		Saguinus	36	18	8	09
498	Cane rat	Saimiri	37	18	8	10
499		Scalopus	15	22	1	09
500	Pademelon	Scapanus	15	22	1	09
501	Spix s disk winged bat	Sciurillus	49	20	8	11
502	Three banded armadillo	Sciurus	49	20	7	11
503	Spix s round-eared bat	Scotinomys	55	20	6	09
504	Fringe-lipped bat	Scotophilus	32	3	5	06
505		Scutisorex	14	22	2	09
506		Semnopithecus	38	1	8	12
507		Sigmodon	55	20	6	12
508		Sminthopsis	4	10	6	02
509	Brush tailed possum	Sorex	14	22	2	09
510	tree shrew	Soriculus	14	22	6	09
511	Fulvous-bellied climbing rat	Speothos	77	2	6	02
512		Spermophilus	49	20	2	10
513	Grey fox	Sphaeronycteris	28	3	5	10
514	Tent-making bat	Sphiggurus	60	20	8	12
515	Black bear	Spilogale	80	2	6	09
516	Yellow-eared bat	Steatomys	55	20	6	11
517	San Pablo bat Great stripe-faced bat	Stochomys	55	20	6	10
518	White-lined bat	Sturnira	28	3	5	10
519	Linnaeus false vampire bat	Suncus	14	22	2	09
520	Guanaco Llama Alpaca	Sundamys	55		2	09
521		Sundasciurus	49	20	8	10
522	Red fox	Suricata	81	2	2	09
522		Sus	91	1	6	10
524	Magdalena rat	Sylvicapra	99	1	6	13
525		Sylvilagus	47	8	6	13
526	Jumping mice	Sylvisorex	14	22	6	09
527		Synaptomys	55	20	2	12
528	Flightless scaly-tailed squirrel	Syncerus	99	1	6	14

No	Common Name	Genus	Family	Order	Sub-strate	Diet
529	Cane mouse	Tachyglossus	1	11	2	06
530	Tuza	Tachyoryctes	55	20	1	12
531		Tadarida	33	3	5	07
532		Talpa	15	22	1	09
533		Tamandua	43	23	7	06
534		Tamias	49	20	7	11
535		Tamiasciurus	49	20	1	11
536		Tamiops	49	20	8	09
537		Taphozous	20	3	5	07
538		Tapirus	89	13	6	12
539		Tatera	55	20	6	09
540		Taterillus	55	20	2	10
541		Taurotragus	99	1	6	16
542		Taxidea	80	2	2	02
543		Tayassu	92	1	6	10
544		Thalarctos	78	2	6	02
545		Thallomys	55	20	8	04
546		Thamnomys	55	20	8	11
547		Thomomys	50	20	1	12
548		Thrichomys	70	20	7	11
549		Thryonomys	71	20	6	12
550		Thylamys	3	10	7	09
551		Thylogale	18	10	6	16
552		Thyroptera	31	3	5	07
553		Tolypeutes	44	23	2	06
554		Tonatia	28	3	5	09
555		Trachops	28	3	5	02
556		Tragelaphus	99	1	6	13
557		Tragulus	95	1	6	11
558		Tremarctos	78	2	6	10
559		Trichosurus	7	10	7	12
560		Trachys	59	20	2	10
561		Tupaia	34	21	7	09
562		Tylomys	55	20	7	11
563		Tylonycteris	32	3	5	07
564		Uranomys	55	20	6	10
565		Urocyon	77	2	6	02
566		Uroderma	28	3	5	10
567		Ursus	78	2	6	10
568		Vampyressa	28	3	5	10
569		Vampyrodes	28	3	5	10
570		Vampyrops	28	3	5	10
571		Vampyrum	28	3	5	02
572		Vandeleuria	55	20	8	10

No.	Common Name	Genus	Family	Order	Sub-strate	Diet
573		Vicugna	94	1	6	14
574		Viverra	81	2	6	02
575		Viverricula	81	2	6	02
576		Vulpes	77	2	6	02
577		Wiedomys	55	20	6	09
578		Xenomys	55	20	7	12
579		Xerus	49	20	2	11
580		Zapus	57	20	6	10
581		Zelotomys	55	20	6	09
582		Zenkerella	53	20	6	10
583		Zygodontomys	55	20	6	11
584		Zygogeomys	50	20	1	13
585		Zyzomys	55	20	6	12

APPENDIX D
ANIMAL COMMUNITY STUDY SITE DESCRIPTIONS

This appendix tabulates the following descriptors for each study site for which lump analysis was used to study the morphometrics of the animal community: geographical location (latitude, longitude and locator number on continental maps), landcover classifications (Holdridge Life Zone and Biome), landscape structural complexity, and climate data (precipitation and potential evapotranspiration).

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION HUMIDITY	ZONE	ALTITUDE	BIOME	LANDSCAPE COMPLEXITY MICRO	MESO	MACRO	TOTAL	TOT ANN PRECIP	POT ET RATIO	Notes
Temperate Desert and Steppe														
Mojave Desert	37	116	8	super arid	subtropical	premontane	desert	6	8	6	20	50	28.8	2
Death Valley	37	-117	5	super arid	subtropical	premontane	desert	7	6	6	22	80	28.8	2
Transvaal 3	27	28	109	per arid	subtropical	premontane	warm wet transitional desert	10	8	4	22	142	8.3	
McKittrick	35	-120	7	per-arid	warm temperate	lower montane	desert	9	8	7	24	328	2.3	
Canyon Lands	38	-110	4	arid	cool temperate	montane	warm-wet transitional desert	10	11	9	30	114	8.3	
Organ Pipe Cactus	32	-113	8	arid	warm temperate	lower montane	desert scrub	nc				172	8.0	
Badlands NP	44	-103	12	arid	tropical		thorne woodland	7	8	6	21	333	4.5	
Transvaal 6	-25	32	111	semi-arid	subtropical	premontane	warm dry dry forest	11	8	6	25	683	2.1	
Berbera	34	3	108	semi-arid	subtropical	premontane	warm wet transitional thorne woodland	nc				559	2.3	
Transvaal 7	-24	29	110	semi arid	warm temperate	lower montane	thorne steppe	11	10	7	28	408	2.5	
Zion	37	-113	10	semi arid	warm temperate	lower montane	thorne steppe					354	2.6	
Jornada	33	-107	18	semi-arid	warm temperate	lower montane	thorne steppe					288	2.8	
Mesa Verde	37	-108	6	sub humid	cool temperate	montane	steppe	8	8	6	22	483	1.1	
Bryce Canyon	38	-112	2	sub-humid	cool temperate	montane	steppe	8	8	8	24	396	1.6	
Capitol Reef	38	-111	3	sub humid	cool temperate	montane	steppe	6	11	7	27	288	1.6	

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION			BIOME	LANDSCAPE COMPLEXITY				TOT ANN PRE CIP	POT ET RATIO	Notes
				HUMIDITY	ZONE	ALTITUDE		MI CRO	ME SO	MA CRO	TO TAL			
CPER	41	-105	18	sub-humid	cool temperate	montane	steppe	7	7	5	18	382	1.2	
Pawnee	41	-105	23	sub-humid	cool temperate	montane	steppe	7	7	5	18	382	1.2	
Cottonwood	44	102	15	sub humid	cool temperate	montane	steppe	6	7	4	17	441	1.2	
Alberta Grasslands	51	-112	53	sub humid	cool temperate	montane	steppe	6	9	5	20	389	1.0	
Matador	50	108	54	sub-humid	cool temperate	montane	steppe	6	9	5	20	346	1.2	
Pantex	36	102	22	sub humid	cool temperate	montane	steppe	nc				408	1.6	6
SW Kansas/NW Oklahoma	38	101	24	sub humid	cool temperate	montane	warm transitional steppe	7	7	5	18	456	1.7	
Donana	37	-7	102	sub-humid	subtropical	premontane	dry forest	12	11	6	29	610	1.6	3
Serengeti	-2	35	113	sub humid	subtropical	premontane	dry forest	nc				866	1.4	
Konza	39	97	18	Transition between steppe moist forest dry forest				11	8	8	26	833	2.3	1
Bridger	46	-111	14	humid	cool temperate	montane	cool wet transitional steppe	8	9	10	28	373	1.1	3
Dickinson	47	102	17	humid	cool temperate	montane	cool wet transitional steppe	nc				486	1.0	
Bison	47	115	13	humid	cool temperate	montane	warm transitional moist forest	6	12	8	26	482	0.8	3
Osage	37	-96	21	humid	warm temperate	lower montane	moist forest	nc				1344	0.8	
Rwindi	1	29	105	humid	subtropical	premontane	moist forest	nc				1276	0.6	

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION HUMIDITY	ZONE	ALTITUDE	BIOME	LANDSCAPE COMPLEXITY MICRO	MESO	MACRO	TOTAL	TOT ANN PRECIP	POT ET RATIO	Notes
Aghbolugh	38	48	100	humid	warm temperate	lower montane	moist forest	7	6	6	19	1417	0 8	
Delta Marsh	50	-97	48	humid	cool temperate	montane	moist forest	9	10	5	24	508	1 0	
Golden Gate State	22	22	103	no precip values available- Holdridge Classification not possible				9	10	11	30	0		10
Chaco and Cerrado														
Caatinga	-10	-40	62	semi arid	subtropical	premontane	cool transitional very dry forest	13	9	4	26	567	2 5	
Cerrado Localitie	-19	-56	63	sub humid	tropical		warm transitional dry forest	13	9	4	26	880	1 8	
Perforacion	-20	-62	61	sub humid	subtropical	premontane	dry forest	11	12	5	26	696	1 4	
Curuyuqui	-18	-62	60	sub humid	tropical		dry forest	12	15	5	32	1349	1 0	
Bolivian Chaco	-18	-63	69	sub humid	tropical		cool wet transitional dry forest					1349	1 0	
Cactus Scrublands														
Monte Desert	-34	-64	65	sub humid	warm temperate	lower montane	dry forest	0	0	0	0	892	1 1	
Savanne with Forest														
Amboseli	-2	37	101	semi arid	subtropical	premontane	warm wet transitional thorne woodland	9	12	4	25	536	2 5	
Masaguaral	8	-67	71	sub humid	subtropical	premontane	dry forest	12	12	3	27	1121	1 5	3

SITE	LAT	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION HUMIDITY	ZONE	ALTITUDE	BIOME	LANDSCAPE COMPLEXITY MI-CRO	MESO	MA-CRO	TO-TAL	TOT ANN PRE-CIP	POT ET RATIO	Notes
Ixiamas Area, Bolivia	-14	-68	66	sub-humid	subtropical	premontane	warm-dry transitional moist forest	10	11	4	25	1228	1.0	
Lower Rio Heath	-14	-68	66	humid	subtropical	premontane	moist forest	13	18	5	36	1226	1.0	
Galilea	-1	30	112	humid	subtropical	premontane	moist forest	10	16	7	33	1276	0.9	
Woodland/Savanna Forest														
Jebel Marra	13	24	104	per-arid	subtropical	premontane	warm-dry transitional desert scrub	11	12	11	34	186	7.4	
Zinave	-23	34	114	arid	subtropical	premontane	warm-dry transitional thorn woodland	13	15	8	36	347	4.3	3
Transvaal 10	-24	30	108	semi-arid	subtropical	premontane	thorn woodland	14	11	8	33	408	2.5	
Concepcion	-16	-62	66	sub-humid	subtropical	premontane	warm-dry transitional moist forest	15	16	5	36	1125	1.1	
Rukwa Valley	-8	33	116	sub-humid	subtropical	premontane	dry forest	11	15	6	32	858	1.1	
Lokari	2	35	118	sub-humid	subtropical	premontane	warm-wet transitional moist forest	11	16	6	33	1045	1.0	
Lamto Ivory Coast	6	5	124	humid	tropical		warm transitional moist forest	0	0	0	0	1608	0.9	
Forest														
N. Yukon NP	69	-140	41	humid	sub polar	alpine	moist tundra	7	7	11	25	158	0.8	3
Chilkat Valley		-136	40	super-humid	boreal	subalpine	rainforest	14	14	9	37	1788	0.1	3

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION HUMIDITY	ZONE	ALTITUDE	BIOME	LANDSCAPE COMPLEXITY MI CRO	ME SO	MA CRO	TO TAL	TOT ANN PRE CIP	POT ET RATIO	Notes
Boreal Forest														
Nopiming Prov Preserve	50	-96	48	sub humid	cool temperate	montane	steppe	13	16	8	37	422	1 1	
Prince Albert	54	-107	51	humid	cool temperate	montane	cool wet transitional steppe	13	20	8	41	414	1.0	
Dore Lake	56	107	44	humid	cool temperate	montane	warm transitional moist forest	nc				466	0 6	
Taiga BS	52	-95	47	humid	cool temperate	montane	moist forest	12	18	7	37	574	0 6	
Whiteshell	50	-95	52	humid	cool temperate	montane	moist forest	12	16	7	37	620	0.7	
Quetico	49	-91	50	humid	cool temperate	montane	moist forest	14	16	5	36	735	0 5	3
Wood Buffalo NP	61	-112	46	humid	warm temperate	lower montane	moist forest	11	17	7	35	1260	0 6	
Rhone Alps	45	6	43	humid	cool temperate	montane	moist forest	14	15	11	40	980	0 6	
Green River	47	-66	45	per-humid	cool temperate	montane	cool wet transitional moist forest	13	15	8	36	860	0.4	
Kluane	61	-139	42	per-humid	boreal	subalpine	wet forest	16	17	7	36	600	0 3	
Temperate Forest														
Turtle Mountain	37	-105	34	semi arid	cool temperate	montane	cool wet transitional moist forest	15	20	8	43	222	1 9	
Glacier NP	49	-117	36	sub humid	cool temperate	montane	steppe	14	17	12	43	446	1 0	

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION			BIOME	LANDSCAPE COMPLEXITY				TOT ANN PRECIP	POT ET RATIO	Notes
				HUMIDITY	ZONE	ALTITUDE		MICRO	MESO	MACRO	TOTAL			
Wind Cave NP	52	-104	36	sub-humid	cool temperate	montane	steppe	12	11	9	32	353	1 6	
Rocky Mountain	32	-106	37	sub humid	montane	montane	warm wet transitional steppe	nc				528	1 2	
Big Bend	29	-103	1	sub-humid	warm temperate	lower montane	dry forest	16	13	10	36	573	1 5	
Katherine Ordway P	47	82	33	sub humid	subtropical	premontane	warm dry transitional moist forest	14	21	5	40	1188	1 0	
Eglin AFB	31	-87	29	humid	subtropical	montane	moist forest	13	15	4	32	1828	0 7	
Arnot Teaching	43	-77	27	humid	cool temperate	montane	moist forest	14	14	7	35	804	0 7	9
Finger Lakes	43	77	28	humid	cool temperate	montane	moist forest	nc				804	0 7	9
Mountain Lake	44	81	32	humid	warm temperate	montane	moist forest	nc				1061	0 7	
Cesky	40	13	34	humid	cool temperate	montane	moist forest	14	14	10	38	898	0 7	
Itasca SP	43	-96	31	humid	cool temperate	montane	moist forest	14	16	8	38	718	0 6	
NW Louisiana	30	93	35	humid	subtropical	premontane	moist forest	15	17	7	38	1270	0 8	
Savannah River Site	33	-82	26	humid	subtropical	premontane	moist forest	14	20	7	41	1217	0 8	
Yellowstone NP	48	-111	25	per-humid	boreal	subalpine	cool-wet transitional moist forest	14	16	10	40	475	0 8	
Hubbard Brook	31	-72	30	per-humid	cool temperate	montane	cool wet transitional moist forest	nc				983	0 5	

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION HUMIDITY	ZONE	ALTITUDE	BIOME	LANDSCAPE COMPLEXITY MICRO	MESO	MACRO	TOTAL	TOT ANN PRECIP	POT ET RATIO	Notes
Dry Deciduous Tropical Forest														
Parque National Machalilla	-2	-81	56	semi-arid	subtropical	premontane	cool transitional very dry forest	14	12	5	31	539	2.0	11
Chamela	20	-105	57	sub-humid	subtropical	premontane	warm dry forest	14	17	6	37	616	1.9	
Rio Machiapo	-15	-68	67	humid	subtropical	premontane	moist forest	ns				1069	1.0	
Subtropical Wet Forest														
Columbia River Forest Res.	17	-89	55	per-humid	tropical		warm transitional wet forest	15	12	6	33	2164	0.7	3
Moist Forest														
Randia	14	17	117	semi-arid	tropical		very dry forest	nc				606	2.8	
Cerro Blanco	-2	-80	75	semi-arid	subtropical	premontane	cool transitional very dry forest	13	13	5	31	631	2.2	11
Cerro Mutiles	1	-79	73	sub humid	cool temperate	montane	steppe	17	13	8	38	424	1.4	
Juanecha	-1	-78	74	humid	tropical		transitional warm moist forest	14	15	5	34	1530	1.0	
Sangmelina	3	12	121	humid	tropical		transitional warm moist forest	0	0	0	0	1768	0.8	3
Brazilian Atlantic Forest	-19	-42	72	humid	subtropical	premontane	moist forest	15	15	7	37	1217	1.0	
Royal Kernali Bardia	28	81	127	humid	subtropical	premontane	moist forest	14	19	8	41	1134	0.6	
Carpanta	4	-73	60	n/a	n/a	n/a	n/a	15	14	9	38	231	21.1	

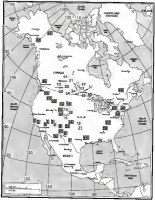
SITE	LAT.	LONG.	MAP	HOLDRIDGE LIFE ZONE CLASSIFICATION			BIOME	LANDSCAPE COMPLEXITY				TOT ANN PRE CIP	POT ET RATIO	Notes
			NO.	HUMIDITY	ZONE	ALTITUDE		MI-CRO	ME SO	MA CRO	TO-TAL			
Wet Forest														
Makokou	13	13	122	semi-arid	subtropical	premontane	warm transitional thorne woodland	15	18	7	41	365	3 5	
Cerro Pata de Pajaro	0	80	76	sub humid	cool temperate	montane	steppe	15	11	6	32	649	1 4	4
Cabaceras de Bilsa	0	-60	77	sub-humid	cool temperate	montane	steppe	18	10	6	34	649	1.4	3, 4
Calabates	15	68	78	humid	subtropical	premontane	moist forest	14	15	8	37	1228	1 0	
Kanuku West	4	-60	91	humid	warm temperate	lower montane	moist forest	15	16	9	40	1571	0 7	
Guatopo	10	-68	90	humid	subtropical	premontane	moist forest	15	17	9	41	1520	0 7	3
Cerro Pirre	8	78	61	humid	warm temperate	lower montane	moist forest	18	17	9	42	2505	0 6	
Park de Tai	6	-6	123	humid	subtropical	premontane	moist forest	15	18	5	38	1413	0 8	
Mt Nimba	8	-6	120	humid	tropical		transitional warm moist forest	15	18	9	42	1613	0 6	
Suriname	4	56	96	humid	subtropical	premontane	warm dry transitional wet forest	nc				2736	0 5	
Belem	-2	48	67	per-humid	subtropical	premontane	wet forest	nc				3037	0 4	
Rainforest														
Archicaya Valley	4	-77		sub humid	subtropical	premontane	dry forest	16	23	7	46	758	1 6	
Cape York	-13	142	125	sub-humid	tropical		moist forest	13	24	11	48	1621	1 5	3
Barro Colorado Island	4	-80	86	humid	tropical		transitional cool-dry moist forest	18	22	5	45	1818	0 9	

SITE	LAT.	LONG.	MAP NO.	HOLDRIDGE LIFE ZONE CLASSIFICATION			BIOME	LANDSCAPE COMPLEXITY				TOT ANN PRECIP	POT ET RATIO	Notes
				HUMIDITY	ZONE	ALTITUDE		MICRO	MESO	MACRO	TOTAL			
La Selva	10	-84	92	humid	tropical		moist forest	18	24	6	48	3427	0.6	3
Alto Madidi Region	-14	-69	65	humid	subtropical	premontane	moist forest	14	24	9	47	1228	1.0	
Manu NP	-12	-71	83	humid	cool temperate	montane	moist forest	16	28	6	50	620	1.0	7
Mont Kivu	-2	29	119	humid	subtropical	premontane	moist forest	16	26	8	50	1301	0.9	
Cocha Cashu	-12	-71	88	humid	cool temperate	montane	moist forest	16	28	6	50	620	1.0	7
Malaysia	4	103	126	humid	tropical		moist forest	15	23	10	48	2408	0.7	
LaPlaneda	1	-78	79	humid	subtropical	premontane	moist forest	15	18	10	43	4437	0.8	
Cuzco/Cuzam	13	72	89	humid	cool temperate	montane	moist forest	17	17	4	38	747	0.8	
Reserva de la Sie	17	-92	94	humid	subtropical	premontane	warm dry transitional wet forest	18	24	7	49	2618	0.5	
French Guiana	4	-52		per-humid	tropical		warm transitional wet forest	18	23	8	49	3760	0.4	
Upper Rio Urucu	-5	65	99	per humid	subtropical	premontane	wet forest	18	23	5	46	2768	0.4	
Rio Cenepa	4	-78	85		n/a			16	24	10	49	438	8.1	5, 6
Rio Santiago	4	78	86		n/a			15	24	10	49	438	8.1	5, 6

Cloud Forest

Marta Real	-2	-79	83	sub humid	cool temperate	montane	steppe	18	22	9	49	368	1.6	
Montaverde	10	-84	84	humid	subtropical	premontane	warm-wet transitional moist forest	18	23	9	50	2363	0.6	3
Lamaboke	4	18	118	humid	tropical		moist forest	0	0	0	0	1870	1.0	


Caribbean Sea
North Atlantic Ocean
VENEZUELA
COLOMBIA
PERU
BRAZIL
BOLIVIA
South Pacific Ocean
CHILE
ARGENTINA
South Atlantic Ocean


Arctic Ocean
GREENLAND (Denmark)
ICELAND
CANADA
U. S. A.
MEXICO
North Pacific Ocean
North Atlantic Ocean
Gulf of Mexico
Caribbean Sea
Salt Lake City
Los Angeles
Chicago
Montreal
Anchorage
60
150
130
110
50
40
140
120
100
90
70
30
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36
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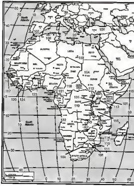
North Atlantic
South Atlantic
Indian Ocean
ALGERIA
LIBYA
EGYPT
MAURITANIA
MALI
NIGER
CHAD
SUDAN
ETHIOPIA
ZAIRE
TANZANIA
KENYA
SOMALIA
ANGOLA
NAMIBIA
SOUTH AFRICA
MADAGASCAR
MOZAMBIQUE
100
101
102
103
104
105
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108
109
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111
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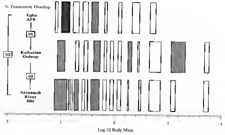
113
114
115
116
117
118
119
120
121
122
123
124
60
50
40
30
20
10
0
10
20
30
40
50
60

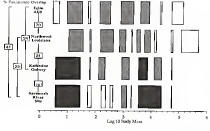
APPENDIX E
STACKED GRAPHICS OF BIOME LUMP STRUCTURES

This appendix contains graphs created by StackClumps software (Paul Marples, unpublished data) which vertically aligns a stack of animal community lump structures all drawn from the same biome so that the lump pattern of each community can be visually compared with those of all other communities of similar landscape structure, i.e. from the same biome

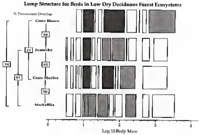
No Biome Lump Structure Page

Lump Structure for Breeding Birds in Southeast Temperate Forest Ecosystems in North America

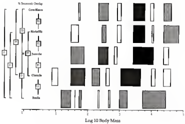


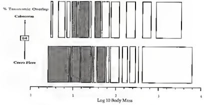


Lump Structure for Breeding Birds
in Southeast Temperate Forest Ecosystems in North America


Lump Structure for Birds in Low Dry Deciduous Forest Ecosystems
% Taxonomic Overlap
Cerro Blanco
88
Juaneche
51
74
65
Cerro Mutiles
81
60
Machalilla
0
1
2
3
4
Log 10 Body Mass

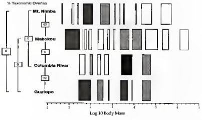
Lump Structure for Mammals in Tropical Dry Deciduous Forest Ecosystems



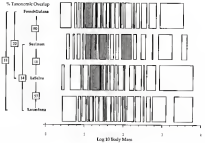


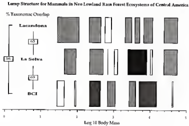
Lump Structure for Breeding Birds in
Low Wet Forest Ecosystems in South America

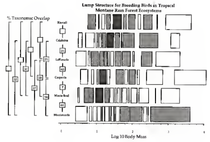
Lump Structure for Mammals in Tropical Wet Forest Ecosystems in Africa and Central and South America



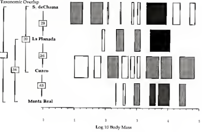
Lump Structure for Birds in Low Rain Forest Ecosystems in Central and South America



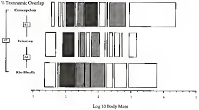

Lump Structure for Mammals in Neo Lowland Rain Forest Ecosystems of Central America
% Taxonomic Overlap
Lacandona
65
56
La Selva
69
BCI
0
1
2
3
4
5
Log 10 Body Mass


Lump Structure for Breeding Birds in Tropical Montane Rain Forest Ecosystems
% Taxonomic Overlap
Kamall
Calabatea
31
LaPlanada
42
Carpanta
7
Monte Real
44
Monteverde
22
30
27
38
25
14
0
1
2
3
4
Log 10 Body Mass

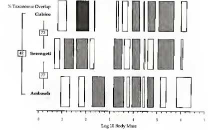
Lump Structure for Mammals in Neotropical Montane Rain Forest Ecosystems on the Andean Side of South America



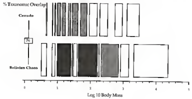
Lump Structure for Breeding Birds in Savannah with Forest Ecosystems
on the Andean Side of South America



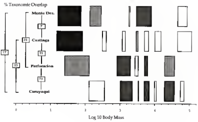
Lump Structure for Mammals in Savannah with Forest Ecosystems in Kenya and Rwanda



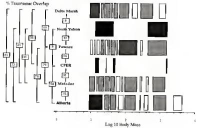
Lump Structure for Breeding Birds in Scrublands Ecosystems in Western South America



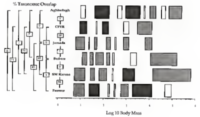
Lump Structure for Mammals in Scrubland Ecosystems in South America



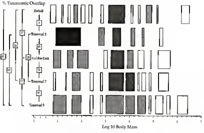
Lump Structure for Breeding Birds in Short Grass Ecosystems of North America



Lump Structure for Mammals in Short Grass Ecosystems in North America



Lump Structure for Mammals in Grassland Ecosystems in Africa



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BIOGRAPHICAL SKETCH

I was born in Waterbury, Connecticut on September 20, 1950 My fascination with the nexus between the natural and human domains has grown out of a life living on the seams between alternate worlds. nineteenth century European households in 1950's New England and segregated Florida, an easterner in the midwest, an American in Africa, Asia and Europe, and an ecologist among engineers This perspective exposed how fragile our reliance is on any person, place or belief and how pivotal is the web of exchanges which joins them.

A reverence for living creatures goes back to my earliest memories of my parents, Tadeusz and Bertha, and their fondness for walking in the outdoors and appreciating both the health and the beauty we gain thereby I found a passion for biology in high school when I met Frank Trevor, who taught me that the 'life' in biology extends to all that makes life possible politics, economics, religion, philosophy, literature as well as the Krebs cycle. What a delicious surprise to find how many creatures live in a mowed lawn or a pile of leaves in the eddy of a stream!

The momentum of this questioning attitude increased with the wild fluctuations of the 1960's, burning riots at home and plundering colonial wars abroad Years later I recognized the fever pitch of those times when, for several hours, it appeared that the Three Mile Island nuclear power station might explosively cover our region with deadly radiation. The surreal discussion of how to evacuate our families, perhaps forever, to another continent would have fit easily into the 1960's. So after completing a B A in biology at Hiram College and a Master's of Arts in Teaching biology at Rhode Island College, I dropped all the trappings of family and profession and lived as a Buddhist monk in Korea This useful pilgrimage showed me that earnest questioning occurs everywhere and is not confined to religion or any of its embellishments

In 1980 I came to Florida to study with H.T Odum how nature and society Interact I applied his systems ideas in measuring the total web of energy needed to produce mussels in the OsterSchelde estuery in Zeeland, Netherlands. I am deeply indebted to him for his enthusiastic encouragement to hold the spaghetti-web of ecological relationships in view and dare to measure what most shyly leave by default to money the significance of contributions by nature to human and non-human organisms. I worked for several years thereafter as a wetlands ecologist in Florida, only to be disillusioned by the fact that the law I upheld in professional practice only provided a state sanction for short-sighted development

In 1990 I returned to the University of Florida to deepen my understanding of how ecosystems and human institutions co-evolve in large scale systems By good fortune C.S "Buzz" Holling had recently arrived with an approach which, by transcending the "stodgy encrustations" of conceptual fiefdoms be they political, social or academic, best appreciates the supple way in which systems adapt and change over time Working with Buzz has shown me that the interface between worlds may be lonely, but it's richer than the perspective one must accept with membership in any clan. The vital edge between theory and practice hums with exchanges which nurture both sides. After years of his gentle encouragement I can truly say that "the scales have dropped from my eyes" and a trans-scalar world is evident.

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philospohy

Joseph Delfino, Chair
Professor of
Environmental Engineering
Sciences

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philospohy

C S Holling

C.S. Holling,
Eminent Scholar of Zoology

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philospohy

Scot Smith
Associate Professor of Civil
Engineering

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philospohy

MABrown

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Environmental Engineering
Sciences

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philospohy

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This dissertation was submitted to the Graduate Faculty of the College of Engineering and to the Graduate School and was accepted as partial fulfillment of the requirements for the degree of Doctor of Philospohy

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