3 STATISTICAL PROCEDURES

Evaluating sample variation

Univariate statistics were invaluable for the initial evaluation of the variation contained within this skeletal sample. Such commonly reported values as the mean, minimum, maximum and standard deviation are all measures of the amount of variation found within a sample. The coefficient of variance is the result of a calculation that relates the standard deviation to the mean (standard deviation x 100/mean) and is thus a value that effectively summarizes the relative amount (as a percentage) of sample variation for any element dimension.

The coefficient of variance (officially "V" but often designated "CV") was found to be an especially useful statistic for initial assessment of the sample variation. Simpson et.al (1960) point out that taxonomic comparisons are most reliably based on characters that are the least variable within taxa and that the CV is one simple way of establishing the identity of these less variable characters. Average CV values are usually between 5 and 6, with a range of 3-10 (Kurten 1968; Brothwell 1993). Simpson et al. (1960) caution that much lower values may indicate the sample was not large enough to show the true variability. It has been suggested that CV values may be naturally somewhat higher for domestic taxa than for wild ones (due to a higher inherent variability which some suggest may be necessarily associated with domesticates) but this assumption has not yet been demonstrated statistically (Brothwell 1993). Some dimensions (such as the facial region of the cranium) consistently show higher CV values than average while other dimensions are always below average. In general though, especially high values of CV for a particular measurement usually indicate that the sample includes animals of mixed ages, sexes, or different taxonomic categories.

The CV values calculated on combined sex samples, for example, are often higher than for single sex samples (Simpson et.al. 1960). In explaining how CV values relate to sexual variation within a sample, Plavcan (1994: 467) states "with increasing sexual dimorphism, the difference between male and female means increases, causing a proportional increase in the pooled-sex sample standard deviation".

In order to assess the affects of sexual dimorphism on the variation exhibited by the Northwest Coast sample, the calculation of univariate statistics (including minimum & maximum, mean, standard deviation, coefficient of variance) for the sexually dimorphic cranial sample has been calculated and presented here two ways: first for all of the cases together (sexes combined) and then for each of the sexes separately (Table 3-1).

The coefficient of variance calculated for the combined sex sample of cranial measurement #1 (greatest length) in Table 3-1, at 8.9%, suggests that the amount of variation for this dimension is high relative to other mixed-sex wild and domestic canid samples, which average about 4.0% (Table 3-2). The exception shown is from Nowak's (1979) study of a sample of 50 domestic dogs (taken from at least 11 different known modern breeds, which varied in size from an Irish wolfhound to a beagle), and in this case the coefficient of variance is understandably high.

Table 3-3 is a summary of univariate statistics for selected cranial measurements presented by Nowak (1979), Friis (1985), Onodera et.al. (1987), and Gollan (1982) for two samples of modern wolf subspecies and two samples of modern dog breeds. The statistics for each sex have been calculated separately. Note that for all samples, the CV values for greatest cranial length (measurement #1) are below 5% for both sexes, even for the dingo sample which was drawn from a feral population of what is considered to be a very primitive dog type. In contrast, the CV value for the greatest length for females in the Northwest Coast crania sample (from Table 3-1) is above 5% (which may not be statistically significant) but the value for males is almost 8%.

Although the sample sizes are probably too small to give too much credence to these results, this comparison does suggest that the amount of variation both within each sex and for the sample as a whole may be too great to support the hypothesis that these animals came from a single homogeneous population. Although perhaps not statistically significant, there is nonetheless some justification presented by the sample itself (i.e. something other than the ethnohistoric records) for exploring the possibility that two unrecognized groups are contained with the same-sex samples.

Table 3-1. Univariate statistics of the Northwest Coast crania sample, sexes combined (total sample) and sexes recorded separately.

Statistics *	Measurement code numbers												
	1	2	3	12	13	15	15B	15C	15D	16	17	17A	19
total count	18	17	17	19	15	16	19	19	19	18	15	19	17
total mean	173.8	162.9	154.0	73.7	85.3	56.5	87.4	53.3	42.0	17.5	44.1	40.6	17.7
total std	15.5	10.8	10.3	6.9	6.7	4.8	5.7	2.9	2.3	1.1	4.3	2.4	1.0
total min.	146.3	145.4	135.8	59.3	72.8	47.8	76.0	47.7	37.5	15.6	36.4	35.0	16.4
total max.	203.0	188.4	177.1	87.4	98.2	66.4	99.0	58.8	46.2	19.5	51.9	44.9	19.6
total CV	8.92	6.65	6.67	9.37	7.88	8.57	6.56	5.42	5.40	6.54	9.69	6.02	5.78
female count	5	4	4	5	5	4	5	5	5	5	3	5	4
female mean	158.9	154.5	146.0	68.0	80.4	53.5	83.4	51.5	41.0	18.0	41.7	39.3	17.4
female std	8.1	5.3	5.9	5.0	4.9	3.8	4.1	2.0	1.6	0.3	3.8	1.3	0.7
female min.	146.3	145.4	135.8	59.3	72.8	47.8	76.0	47.8	38.6	17.7	36.4	36.9	16.6
female max.	169.0	158.3	150.0	72.6	85.7	57.0	87.7	54.0	43.4	18.6	44.4	40.9	18.5
female CV	5.13	3.42	4.02	7.32	6.13	7.07	4.88	3.96	3.80	1.85	9.03	3.35	3.96
male count	13	13	13	14	10	12	14	14	14	13	12	14	13
male mean	179.6	165.4	156.5	75.8	87.8	57.5	88.8	53.9	42.4	17.3	44.7	41.1	17.8
male std	13.7	10.8	10.1	6.3	6.1	4.7	5.6	2.9	2.4	1.3	4.2	2.6	1.1
male min.	162.0	148.2	140.7	65.2	78.4	50.8	78.0	47.7	37.5	15.6	39.0	35.0	16.4
male max.	203.0	188.4	177.1	87.4	98.2	66.4	99.0	58.8	46.2	19.5	51.9	44.9	19.6
male CV	7.63	6.53	6.43	8.34	6.96	8.25	6.28	5.38	5.60	7.43	9.36	6.30	6.11

Statistics	Measurement code numbers											
	22A	23	25	25A	27	29	30	31	32	34	35	36
total count	16	17	17	17	17	15	13	16	15	16	17	16
total mean	15.9	63.1	35.2	31.6	18.4	53.1	99.4	34.7	49.9	61.1	33.4	36.9
total std	2.0	4.0	2.9	2.5	1.4	2.5	7.4	2.0	4.5	3.6	4.3	3.2
total min.	12.0	56.0	30.0	27.8	16.0	50.7	87.8	31.0	42.1	56.4	21.0	33.0
total max.	19.3	71.2	40.9	36.8	21.2	58.3	110.6	38.3	57.4	69.0	39.5	44.2
total CV	12.64	6.39	8.10	8.04	7.40	4.67	7.46	5.80	9.10	5.89	12.86	8.69
female count	4	4	4	4	4	5	2	5	3	4	4	4
female mean	14.9	60.7	35.0	31.3	17.9	51.8	95.7	34.2	46.8	59.7	32.9	35.8
female std	1.1	1.2	1.3	0.9	0.8	0.6	6.2	1.7	4.5	1.0	1.0	1.7
female min.	13.4	59.4	33.0	30.0	16.9	50.7	89.4	31.4	42.1	58.5	31.5	34.1
female max.	16.5	62.0	36.5	32.2	19.1	52.4	101.9	36.8	52.8	60.9	34.3	38.5
female CV	7.46	2.04	3.61	2.83	4.46	1.11	6.51	5.03	9.58	1.72	3.04	4.76
male count	12	13	13	13	13	10	11	11	12	12	13	12
male mean	16.2	63.8	35.3	31.6	18.6	53.8	100.1	35.0	50.7	61.6	33.5	37.3
male std	2.1	4.3	3.2	2.9	1.5	2.8	7.4	2.1	4.2	4.0	4.9	3.5
male min.	12.0	56.0	30.0	27.8	16.0	51.0	87.8	31.0	44.5	56.4	21.0	33.0
male max.	19.3	71.2	40.9	36.8	21.2	58.3	110.6	38.3	57.4	69.0	39.5	44.2
male CV	13.15	6.73	9.02	9.02	7.85	5.19	7.41	5.98	8.31	6.50	14.52	9.38

* std = standard deviation; min. = minimum value; max. = maximum value; CV = coefficient of variation

Table 3-2. Univariate statistics of other canid crania samples compared to the total Northwest Coast sample, sexes combined.

Selected samples	**Measurement code numbers****				
1. Canis latrans (Rancho La Brea, CA)	**#1**	**#19***	**#30**	**#31**	**#34**
mixed-sex sample (Nowak 1979:147)	1	14	2	9	5
Sample size	n=44	n=43	n=36	n=47	n=21
Mean	205.5	21.1	106.7	36.7	61.2
Minimum	185.0	18.2	90.0	32.9	50.0
Maximum	222.0	23.5	116.0	42.0	67.4
Standard Deviation	9.03	1.29	5.58	2.12	4.31
Coefficient of Variance	4.39	6.14	5.23	5.78	7.05
2. Canis dirus (Rancho La Brea, CA)	**#1**	**#19***	**#30**	**#31**	**#34**
mixed-sex sample, n= 62 (Nowak 1979:149)	1	14	2	9	5
Mean	294.8	31.8	163.3	49.3	96.2
Minimum	258.0	28.7	148.0	43.5	87.7
Maximum	316.0	35.3	177.0	54.4	104.0
Standard Deviation	11.31	1.38	7.15	2.13	3.92
Coefficient of Variance	3.84	4.35	4.38	4.32	4.08
3. Canis familiaris (sample of many breeds)	***#1***	***#19****	***#30***	***#31***	***#34***
mixed-sex sample, n = 50 (Nowak 1979:144)	1	14	2	9	5
Mean	217.2	19.3	112.4	39.2	68.1
Minimum	151.0	14.4	84.0	32.2	51.5
Maximum	285.0	22.7	154.0	44.8	85.5
Standard Deviation	30.88	1.66	12.91	3.17	7.33
Coefficient of Variance	14.27	8.61	11.48	8.08	10.76
4. Canis familiaris (NW Coast sample, two breeds?)	***#1***	***#19***	***#30***	***#31***	***#34***
mixed-sex sample (this study)	#1	#19	#30	#31	#34
Sample size	n=18	n=17	n=13	n=16	n=16
Mean	173.8	17.7	99.4	34.7	61.1
Minimum	146.3	16.4	87.8	31.0	56.4
Maximum	203.0	19.6	110.6	38.3	69.0
Standard Deviation	15.50	1.02	7.42	2.01	3.60
Coefficient of Variance	8.92	5.78	7.46	5.80	5.89
5. Canis familiaris (modern dingo, single primitive breed)	***#1***	***#19****	***#30***	***#31***	***#34***
mixed sex sample, n=60 (Gollan 1982:325-333)	V1	V51	V16	V35	V46
Mean	193.9	19.4	101.5	35.9	56.7
Minimum	176.0	17.0	93.0	31.0	52.0
Maximum	208.0	21.2	112.0	38.0	61.0
Standard Deviation	7.46	0.86	5.01	1.50	2.35
Coefficient of Variance	3:85	4.47	4.94	4.19	4.14

* The measurement for #19 is a tooth measurement in these studies, but is an alveolar measurement of premolar 4 in the Northwest Coast sample

** The column headings on the second line are the measurement numbers used by the original authors

Interpreting sample variation

In terms of a statistical analysis, the critical problem with the dog sample under investigation here is that we must assume that both sexual dimorphism and breed variation are contributing to the total size variation exhibited by the skeletal elements. There are in essence four groups presumed to be represented in the sample: male and female of one type, and male and female of another type.

One of the significant characteristics that distinguishes the two types of dogs reported in ethnohistoric accounts is their disparity in size. Noticeable disparities in size would encompass traits such as shoulder height, head size and body length differences (Wapnish & Hesse 1993). Thus linear dimensions, such as limb bone element lengths, length of cranium and mandibles, and lengths of the centrum of the vertebrae can be expected to show evidence of both sexual dimorphism and breed variation in size.

Sexual dimorphism in mammals is for the most part size related: males are somewhat larger and more robust than females of the same species or breed and this is reflected in a 2 to 6% difference in their skeletal elements (Benecke 1990; G.R.Clark 1995; Jolicoeur 1959; Klein and Cruz-Uribe 1984; Kurten 1988). As sexual dimorphism is to be expected in any canid sample, in comparing one dog breed to another the amount and nature of the sexual dimorphism is predicted to be very similar within both. For this analysis, I assume that the amount of size variation resulting from sexual dimorphism is probably about the same within populations of both breed types.

Since the primary assumption in this study is that the skeletal differences between the breeds are size related, an analysis method is required which will ignore sex-related size differences so that breed-related size differences can be examined. The statistical method described below appears to satisfy these criteria. This method was originally intended for distinguishing sexes within a single-taxon sample based on size difference, but could in this case be used for distinguishing breeds based on size difference instead (as long as sexual size differences are presumed equal for both populations and ignored).

Plavcan's (1994) review of statistical methods for analyzing the extent of sexual dimorphism present in a small sample (where the sex of the specimens is unknown) used computer modelling on a known skeletal assemblage to assess the accuracy of four methods which had previously been used on fossil and subfossil assemblages of primates, hominoids and hominids. These methods all made the assumption that the variation present within each sample was the result of sexual dimorphism rather than taxonomic difference. Plavcan's study compared the following four methods used for estimating dimorphism in a sample where the sex of individuals is unknown: 1) extrapolation of dimorphism from coefficients of variation (CV); 2) division of a sample into two subsamples about the mean; 3) division of a sample into two subsamples about the median; 4) finite mixture analysis (this last methods involves a somewhat complex computation, the details of which are not relevant to this discussion). The most accurate of these four methods was found to be the division of the sample about the mean into two subsamples, *even when intrasexual variability was high and when sex ratios within the sample were strongly imbalanced*. New means are calculated for the two subsamples that result from splitting the total sample at the mean. One of these subsamples is assumed to contain only females and the other only males.

Using this method (but substituting breed size difference for sexual size difference), the Northwest Coast prehistoric dog samples have been divided into two groups at the mean for the variable that most clearly characterizes size: greatest length of each element. The differences between the means calculated for each subgroup are all highly significant (Table 3-4). This result suggests that the null hypothesis (i.e. that the skeletal sample was drawn from a population of one homogeneous dog type) could be rejected.

After dividing each of the element samples at the mean for the greatest length, the two subsets of measurements thus created should represent two normal distributions that overlap to some extent. When these overlapping distributions are combined to form a single sample, it would be expected to look distinctly bimodal. As both Plavcan (1994), Klein and Cruz-Uribe (1984) and Martin et al. (1994) have noted, however, it is quite possible for a known bimodal distribution to appear normal, especially for samples of less than 100. Martin et al. (1994: 183) depict an idealized histogram that shows combined male and female distributions for a given dimension with various distances between mean values for the two sexes (where n=1000 per

Table 3-3. Univariate statistics of other canid crania samples, sexes recorded separately.

Selected samples	**Measurement code number ****				
1. Canis lupus lycaon (eastern NA group)	**#1**	**#19***	**#30**	**#31**	**#34**
females, n=12 (2) (Nowak 1979:145)***	1	14	2	9	5
Mean	231.4	22.7	125.0	36.9	73.8
Minimum	223.0	21.3	116.0	35.0	69.0
Maximum	241.0	24.2	132.0	42.5	78.3
Standard Deviation	6.64	0.93	4.79	2.21	3.20
Coefficient of Variance	2.87	4.10	3.82	5.99	4.34
males, n= 19 (4)					
Mean	247.1	24.6	134.1	39.8	77.9
Minimum	237.0	22.6	128.0	36.0	74.2
Maximum	255.0	27.5	140.0	44.9	84.3
Standard Deviation	5.96	1.20	3.59	2.77	2.71
Coefficient of Variance	2.41	4.88	2.68	6.95	3.48

2. Canis lupus crassodon (Vancouver Island, pre-1950)	***#1***	***#19****	***#30***	***#31***	***#34***
females, n=8 (3) (Friis 1985:160)***	1	8	2	15	5
Mean	235.3	25.0	129.9	42.2	76.6
Minimum	225.4	23.7	121.6	38.2	74.3
Maximum	243.1	25.7	135.1	45.0	80.3
Standard Deviation	6.43	0.67	4.20	2.14	2.18
Coefficient of Variance	2.73	2.68	3.23	5.08	2.85
males, n= 9 (2)					
Mean	254.8	25.4	140.5	43.7	81.0
Minimum	245.7	20.8	133.3	37.2	77.9
Maximum	262.2	26.7	143.9	48.1	83.7
Standard Deviation	6.18	1.84	3.44	3.07	2.05
Coefficient of Variance	2.43	7.24	2.45	7.03	2.53

3. Canis familiaris (modern dingo, single primitive breed)	***#1***	***#19****	***#30***	***#31***	***#34***
females, n=30 (Gollan 1982:303-309)	V1	V51	V16	V35	V46
Mean	188.1	18.8	97.6	35.3	54.9
Minimum	176.0	17.0	93.0	31.0	52.0
Maximum	197.0	20.1	104.0	38.0	58.0
Standard Deviation	4.66	0.69	3.20	1.51	1.57
Coefficient of Variance	2.48	3.67	3.28	4.28	2.86
males, n=30					
Mean	199.7	20.0	105.2	36.5	58.6
Minimum	188.0	18.5	99.0	33.0	56.0
Maximum	208.0	21.2	112.0	38.0	61.0
Standard Deviation	4.79	1.01	3.46	1.25	1.32
Coefficient of Variance	2.40	5.05	3.29	3.42	2.25

4. Canis familiaris (modern Japanese shiba breed)	***#1***	***#19****	***#30***	***#31***	***#34***
males, n=45 (Onodera et.al. 1987:29)	1	15	6	11	4
Mean	155.5	17.6	94.8	28.7	59.2
Standard Deviation	6.79	0.78	3.77	2.14	2.45
Coefficient of Variance	4.37	4.43	3.98	7.45	4.14
females, n=42					
Mean	145.3	16.3	88.1	28.2	55.2
Standard Deviation	6.81	0.75	3.81	2.65	2.63
Coefficient of Variance	4.69	4.63	4.33	9.41	4.76

* The measurement for #19 is a tooth measurement in these studies, but is an alveolar measurement of premolar 4 in the Northwest Coast sample.

** The column headings on the second line are the measurement numbers used by the original authors.

*** The numbers in brackets for "n" in Nowak's and Friis' C.lupus samples are those of unknown sex which were assigned to that sex using subjective criteria.

sex, with identical standard deviations). This diagram demonstrates clearly that the distributions will not tend to show evidence of bimodality until the means between the two sexes are separated by three standard deviations, and are not entirely distinct until the means are separated by six standard deviations. Therefore, one should not expect to identify samples that contain significant heterogeneity by visual inspection of measurement distribution patterns alone. Four examples of the distribution patterns of length dimensions frequencies used in this study are illustrated (mandible, ulna, metatarsal II and cervical vertebrae #2; Figures 3-1 through 3-4).

Some overlap between the sample distribution is to be expected and undoubtedly represents especially tall and/or robust specimens of the small type and short and/or gracile specimens of the large type. In addition, some overlap may be due to accidental interbreeding between the two dog types, which would produce individuals of truly intermediate size.

This overlap of the populations can be expressed as a probability that any element classified by this analysis actually belongs to the type to which it has been assigned. Probabilities have been calculated two ways. For selected intact specimens, discriminant function analysis (described below) produced a probability of group membership value, which are included in the main data tables of classification results for each element. Only probabilities of 5% or less are considered significant for the purposes of this study and these are marked as such on the tables.

The other method of determining the likelihood that an element classified by this analysis actually belongs to the type to which it has been assigned is through the calculation of probabilities associated with standard "Z" scores (Norusis 1981). This method is described in more detail in chapter 9 where it has been used to resolve non-concensus of type classification of several elements belonging to a single individual animal. The "Z" scores and their associated one-tailed probabilities were calculated for all intact elements in the sample for which length measurements could be taken and are available from the author.

Multivariate analysis

Multivariate analysis is a statistical method which allows the relationships between several variables to be examined simultaneously. This type of analysis is especially useful in taxonomic studies and replaces the use of indices (cf Stockard 1941), which were the only practical way of examining more than one variable at a time before the advent of computers. Multivariate discriminant analysis has, for example, been used successfully in other studies to distinguish specific and subspecific differences between extant canid crania (Lawrence and Bossert 1967; Jolicoeur 1975; Nowak 1979; Friis 1985). This approach has also been used on archaeological canid remains to establish the taxonomic status of prehistoric material as dog rather than wild *Canidae* (Benecke 1987; Higham et. al. 1980; Walker & Frison 1982; Morey 1986; Morey & Wiant 1992). Where there are collections of the presumed modern descendants of prehistoric dog populations, such as for the Australian dingo (Gollan 1982) and the Japanese shiba (Shigehara & Onodera 1984; Shigehara 1994), discriminant analysis has been used to compare the two samples.

However, discriminant analysis requires *a priori* definitions of at least one of the groups to be classified (Klecka 1980; Tabachnick & Fidell 1983). It was thus an inappropriate method for the initial classification and characterization portion of this study, as there are no skeletal specimens of known wool or village dogs to which prehistoric specimens could be compared.

Alternative multivariate methods which do not require *a priori* definitions, such as cluster or principal component analysis, were considered

Exploratory cluster analyses of the cranial sample were run three times, using 3, 7 and 11 variables (using 11 variables reduced the sample by 3 specimens, because any missing variables caused the program to remove that specimen from the data set). The results (not shown) confirmed that total cranial length accounted for a very high proportion of the sample variation: 90% when 11 variables were used and 98% when only 3 variables were used. In all of the trial cluster analyses, specimens which had cranial lengths close to the mean of the total sample grouped together, whereas the other samples fell into two clusters that corresponded to the type 1 (small) and type 2 (large) groups as defined below. These results confirm that size rather than shape differences contribute too much to the sample variation for cluster-type analyses to be useful in the classification of ambiguous cases.

Several features of cluster analysis combined to make it a poor choice as an analysis method for

Table 3-4. T-test results for element length measurements (GL or equivalent), using the same specimen subsets as the discriminant analysis.

Element	n	SEM (type 1)	SEM (type 2)	Difference between means	SED	Significant difference* (> 2X SED)	Probability > T	Probability >F'
Cranium	16	2.29	3.50	26.07	4.18	*	0.0001	0.25
Mandible	31	1.41	1.57	17.17	2.11	*	0.0001	0.69
Scapula	15	3.30	1.64	18.56	3.69	*	0.0007	0.12
Humerus	26	1.43	1.85	19.28	2.34	*	0.0001	0.39
Radius	21	1.61	1.04	13.90	1.92	*	0.0001	0.17
Ulna	17	2.97	3.58	23.52	4.65	*	0.0002	0.73
Femur	24	1.95	1.31	21.17	2.35	*	0.0001	0.20
Tibia	24	1.89	1.68	15.69	2.53	*	0.0001	0.90
Calcaneus	47	0.32	0.50	5.48	0.59	*	0.0001	0.05
Metacarpal II	30	0.69	0.73	8.93	1.00	*	0.0001	0.64
Metacarpal III	30	0.86	0.96	9.86	1.29	*	0.0001	0.95
Metacarpal IV	32	0.94	0.96	10.57	1.34	*	0.0001	0.93
Metacarpal V	26	0.91	0.74	7.49	1.17	*	0.0001	0.62
Metarsal II	32	0.70	0.64	7.50	0.95	*	0.0001	0.56
Metarsal III	41	0.71	0.46	7.91	0.85	*	0.0001	0.08
Metarsal IV	28	0.80	0.68	8.35	1.05	*	0.0001	0.42
Metarsal V	32	0.67	0.46	6.92	0.81	*	0.0001	0.16
Cervical 01	25	0.13	0.31	2.08	0.34	*	0.0001	0.04
Cervical 02	20	0.63	0.71	5.57	0.95	*	0.0001	0.93
Cervical 03	21	0.39	0.39	3.36	0.55	*	0.0001	0.73
Cervical 04	24	0.32	0.30	2.94	0.44	*	0.0001	0.95
Cervical 05	13	0.31	0.29	2.06	0.42	*	0.0006	0.78
Cervical 06	14	0.27	0.25	2.17	0.37	*	0.0001	0.84
Cervical 07	13	0.32	0.25	1.72	0.41	*	0.0027	0.54
Thoracic 03	10	0.22	0.09	0.75	0.24	*	0.0340	0.17
Thoracic 12	14	0.3	0.18	1.87	0.35	*	0.0007	0.37
Thoracic 13	16	0.37	0.17	2.04	0.41	*	0.0006	0.06
Lumbar 01	17	0.25	0.37	2.48	0.45	*	0.0001	0.40
Lumbar 02	16	0.23	0.47	2.69	0.52	*	0.0013	0.21
Lumbar 03	17	0.37	0.31	2.66	0.48	*	0.0001	0.70
Lumbar 04	13	0.64	0.33	3.58	0.72	*	0.0014	0.18
Lumbar 05	12	1.04	0.25	3.06	1.07	*	0.0590	0.02
Lumbar 06	13	0.35	0.35	2.38	0.49	*	0.0005	0.86
Lumbar 07	19	0.18	0.28	2.61	0.33	*	0.0001	0.25
Sacrum	13	0.48	0.79	4.33	0.92	*	0.0013	0.35

SEM is standard error of the mean **T is an approximate t statistic, assuming unequal variances**
SED is standard error of the difference **F' is the "folded" F statistic, a measure of variance**

*** a difference is significant at the 95% confidence level if the real difference between the sample means is greater than 2X the SED**

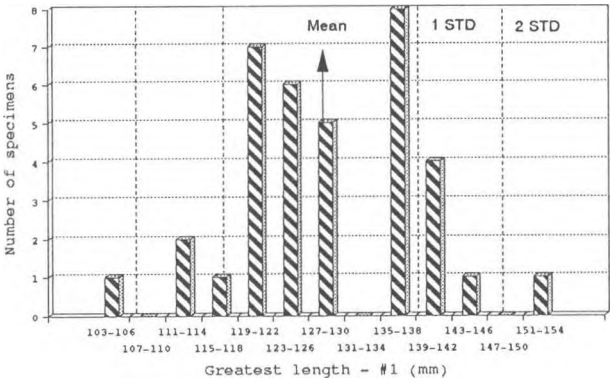

Figure 3-1. Frequency distribution by length of sample of mandibles (n=36) of different lengths.

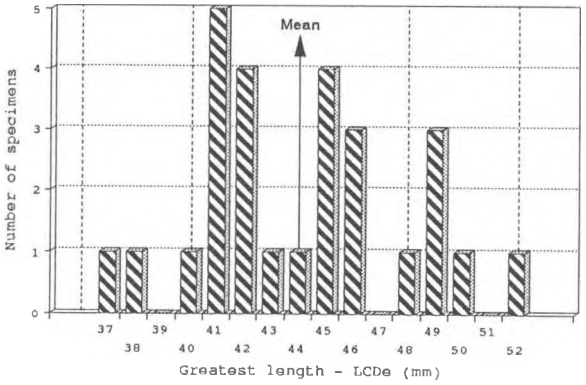

Figure 3-2. Frequency distribution by length of sample of ulnae (n=21) of different lengths.

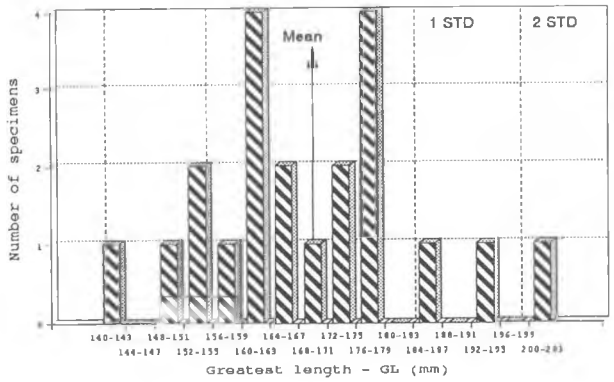

Figure 3-3. Frequency distribution by length of sample of metatarsal II elements (n=32) of different lengths.

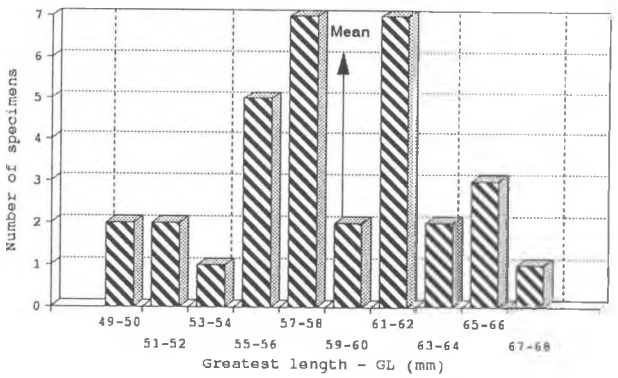

Figure 3-4. Frequency distribution by length of sample of cervical vertebra #2 elements (n=27) of different lengths.

this study. Cluster analyses of all kinds have the disadvantage of requiring an additional computational step to depict data graphically for interpretation. In addition, the algorithm must be re-run to assess each new case. As cluster analysis did not appear to add to the accuracy of the classification of this sample and since using it would mean that any additional specimens could not be assessed without re-computing the values, it was rejected as a classification tool.

I determined that the best analysis approach for this particular sample was to use the simplest method available to define the two types, that of dividing the sample into two subsamples about the mean described earlier in this chapter. This method readily accepts new cases without complex re-calculation of data and specimens with intermediate values are easily identified. Discriminant function analysis was then used to evaluate the relationship between length and breadth dimensions, rather than as a method of testing the statistical validity of the original classification method. This is not the way that discriminant function analysis is traditionally used, but it was a useful analysis procedure for this study.

Discriminant function analysis in the SAS program (SAS Institute Inc., release 6.03, 1988) has a "crossvalidation" option. Crossvalidation is a jack-knife type method that checks which samples may have been statistically misclassified according to the original definition, when more than one criterion is considered. The cross validation function repeatedly uses randomly- selected n-1 samples to create the classification and then tries to place the last sample correctly into that classification. This procedure (and other similar ones) is a test of how well the classification will predict group membership for new cases (Tabachnick & Fidell 1983; Morey 1986). Samples are labelled "misclassified" by the program if their probability of group membership value is below 50%, although I have considered only those values of 5% or less to be truly significant for the purposes of this study. "Misclassification" was interpreted as indicating that breadth dimensions were below or above average compared to length in those specimens. The "probability of membership" values generated were interpreted as indicating particularly robust or gracile individuals.

Very low probabilities of group membership (5% or less) were taken to indicate that specimens were truly intermediate in size and may not have been accurately classified. In other words, the discriminant function analysis identified robust or gracile individuals in each of the subsamples and indicated which specimens probably had values too close to the mean to be confidently classified. Only six specimens fell into this category, and these are indicated on the classification tables for each element

Unfortunately, not all specimens used in the original analysis could be used for the multivariate procedures, as some specimens lacked required dimensions. Multivariate analysis included the length measurement along with as many others as was possible without reducing the size of the data set appreciably.