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ESTIMATING LIVE FISH CATCHES FROM ARCHAEOLOGICAL BONE FRAGMENTS OF SNAPPER, *Pagrus auratus*

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ESTIMATING LIVE FISH CATCHES FROM ARCHAEOLOGICAL BONE FRAGMENTS OF SNAPPER, *Pagrus auratus*

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ABSTRACT: Five paired cranial bones and the otoliths of a modern sample of 110 New Zealand snapper (*Pagrus auratus*) were weighed and measured and regression analysis performed against live fork length and ungutted weight. A number of regression models and alternative steps in arriving at estimates were examined. Detailed analysis of residuals was used to distinguish between strategies. Fork length could be estimated with a standard error of less than 20 mm, and weight to less than 140 g. For the latter, a two step procedure is suggested, from bone dimension to fork length and from this to live weight, using a sample of 833 fish. Coefficients are provided for 64 equations linking bone size to live characteristics. To reconstruct a size-frequency histogram of a prehistoric fish catch, it is acceptable to measure all bones from a particular species, even though the number of measurements may greatly exceed the MNI (Minimum Number of Individuals) for that species.

INTRODUCTION

The New Zealand snapper, *Pagrus auratus*, is one of the commonest species in archaeological sites, particularly in the North Island and northern parts of the South Island. These fish readily take a baited hook, and in former times, when they were more abundant, could be caught by set and drag nets in shallow inshore waters. Because snapper were prominent in pre-European Māori fish catches, it is desirable to have well developed techniques for reconstructing the nature of live fish catches of this species from bones and

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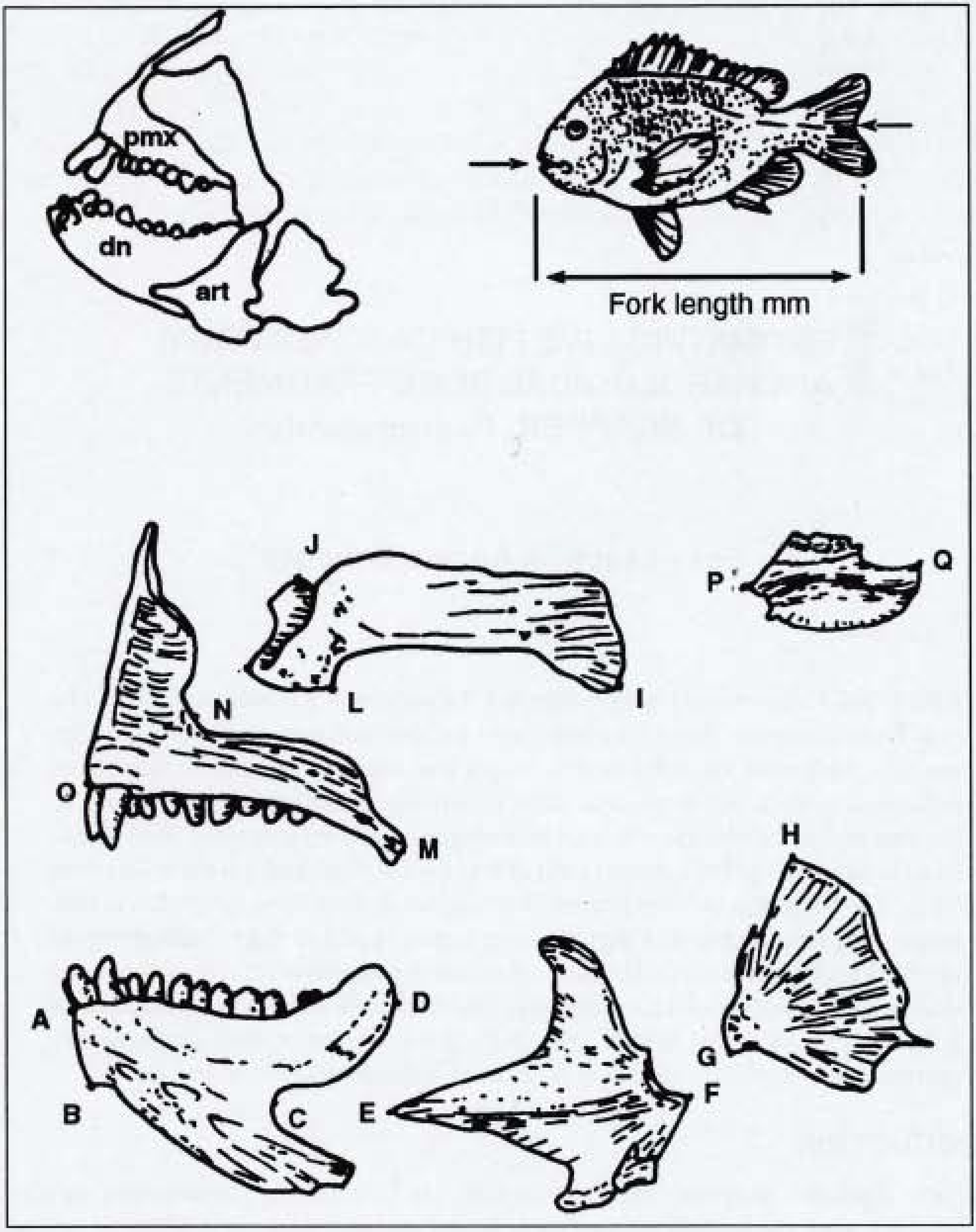

Fig. 1 – Cranial elements of *Pagrus auratus* (snapper) used for measurements. The left bones are illustrated. Measurements are made between landmarks A-D, A-C, and A-B on the dentary; between E-F on the articular; between G-H on the quadrate; between K-I and J-L on the maxilla; between O-M and O-N on the premaxilla; and between P-Q on the otolith.

bone fragments in archaeological sites. There are a number of methodological aspects to this, but the most important is to be able to estimate the size and weight of a fish reliably from its bones. The size-frequency curve of fish catches is basic to examining such issues as the impact of fishermen on inshore fish stocks and changes in fishing technology over time. The weight of fish represented by a catch is primary information for studies of prehistoric economy. Development of reliable methods of length and weight estimation for this species is the focus of this paper.

Several previous studies of the New Zealand snapper have examined the metrical relationship between bone size and live characteristics (Nichol, 1978: 180 ff.; Boocock, 1986; Nichol, 1988: 80 ff.). Unfortunately, these are deficient in several respects. This was the main reason for embarking on a more definitive study of the species. We do not wish to dwell on the weaknesses of earlier research, because it is very labour intensive work, and its contribution should be recognised. However, points to note are small sample sizes, too few specimens of very large individuals, unclear definitions of terms like 'length' (which could refer to fork length or standard length or some other dimension), lack of sophistication with statistical and graphical modelling of metrical relationships, and inadequate examination of systematic errors.

BONE MEASUREMENT METHODOLOGY

The bones measured in this study are five paired cranial bones, which have been used for many years to quantify prehistoric fish catches from archaeological sites in the Pacific and New Zealand (Leach, 1976; Leach and Davidson, 1977; Leach and Ward, 1981; Leach, 1986; Leach and Boocock, 1993), together with otoliths. The five bones (the dentary, articular, quadrate, premaxilla and maxilla) are all relatively strong in snapper and frequently survive intact in archaeological sites. However, it is desirable to carry out measurements which are applicable to broken bones also, and for this reason more than one measurement was made on three of the five bones. Wherever possible the largest dimension was always taken, as this yields the most reliable estimate of the original fish size.

Thus, there is a series of measurements appropriate to whole bones and another series appropriate to various forms of bone fragment. The dimensions chosen follow those previously used by Boocock (1986: 36-37; Leach and Boocock, 1993: 10), and are illustrated in Figure 1. They closely parallel those employed by archaeozoologists on other species (Sternberg, 1992: 8; Rosello-Izquierdo, 1986: 35; Wheeler and Jones, 1989: 139 ff.; Libois and Libois 1988).

In Figure 1 the anatomical landmarks are indicated with a small dot on each bone and given a letter code from A to Q. Each measurement was given a code with three characters; these are listed in Table 1. Thus, LD1 refers to the Left Dentary and the first measurement made on that bone. Where the terminology 'maximum length' is used, the measuring callipers were rotated about the nominated landmarks until a maximum value was obtained. It will be seen in Table 1 that fragment measurements were not taken for the quadrate, articular and otolith. Firstly, the number of these bones identified for any one species is generally considerably lower than for other bones, and in the case of particularly large assemblages the quadrate and articular are sometimes ignored altogether.

Secondly, these two bones and the otolith are quite robust and adequate measurements can be taken on whole specimens. Three measurements are indicated for the dentary, and two each for the maxilla and premaxilla. In addition to these measurements, the relationship between bone weight and live fish characteristics was examined, although it is appreciated that differential tooth loss and demineralisation increase error margins in the metrical relationships markedly.

The purpose of the three-character code is to permit simple coding of measurements on plastic bags containing identified archaeological fish bones. These are later entered into a database according to archaeological provenance and equations used for live length and weight estimation based on these three character codes.

Mitutoyo digital callipers model 500-322 were used for linear measurements and recorded to ± 0.01 mm precision, and a Sartorius model BA310S balance was used for weight measurements with a precision of ± 0.001 g.

MODERN COMPARATIVE SAMPLE OF *Pagrus auratus*

A sample of 107 fish was obtained by Boocock (1986: 21) from the Hauraki Gulf in May 1986. She had difficulty measuring the fork length, which is the most common length measurement recorded for this species, owing to fragmented caudal fins. Instead, she measured the length from the snout to the base of the body where it joins the caudal fin. Contrary to what is stated by Boocock (1986: 19), this is equivalent to the standard length (Casteel, 1976: 50).

Although the difference between these two length measurements is relatively minor, it is desirable to convert the recorded lengths for these fish into fork lengths to be consistent with other research on snapper. Fortunately this problem has been encountered before by scientists at MAF (Ministry of Agriculture and Fisheries), who provided data on fork length and standard length for 194 fish taken from catches landed in Auckland from both eastern and western waters.

These are graphed out in Figure 2, and the results of linear regression form a suitable basis for estimating one quantity from the other. The regression equations are (dimensions are given in millimetres):

$$\text{STANDARD LENGTH} = 0.921359 * \text{FORK LENGTH} - 4.11 \quad (\pm 6.1)$$

$$\text{FORK LENGTH} = 1.081636 * \text{STANDARD LENGTH} + 5.77 \quad (\pm 6.6)$$

The original sample of fish ranged in fork length from 133 to 586 mm with a mean of 257 mm. Studies of archaeological bones suggest that snapper caught in the prehistoric era were frequently at the large end of this distribution, and sometimes considerably greater in size. The collection was therefore augmented with specimens up to 940 mm fork length. Boocock had prepared and measured cranial bones from the original sample (Boocock, 1986). All bones were remeasured for the present study and bone weights were added to the list of variables. A number of errors of measurement and coding were identified during this re-measurement.

The final sample of 110 fish had records for 37 variables, consisting of standard length, fork length, girth, depth, ungutted body weight, and 32 bone measurements. Some bones were broken, and not all measurements could be taken. The final data matrix of 4070 entries had 47 missing values. These were not estimated in the subsequent analysis, but arrays were concatenated in pairs as appropriate.

LEAST-SQUARES ANALYSIS OF MODERN COMPARATIVE MATERIAL

The main objective of this study was to establish reliable regression relationships between bone dimension and live fork length and ungutted weight which could then be used for archaeological bones. The former involves seeking best fit relationships directly between the bones of individual fish and the live fork length of the same fish.

However, although this same procedure could have been followed for the second objective, we decided to use two steps:

- establish the relationship between a bone dimension and fork length (by using the first equation), and also the relationship between fork length and ungutted weight (using the second equation), and
- estimate the fork length with the first and the weight with the second equation.

An advantage of this two-step procedure is that the length/weight relationship is determined from a much larger sample than the 110 fish in the osteological collection. It was decided to test this alternative method.

Information was available for fork length and weight from trawls made in the early 1960s in the East Northland, Hauraki Gulf and Bay of Plenty areas (N = 790 fish), and a small sample of much larger specimens from Tasman Bay (N = 43). These data were combined (N = 833) for purposes of analysis.

With the data available there were three possible methods by which weight could be determined from bone dimensions, and all three were examined.

METHOD 1: from bone dimension to weight using individual equations worked out from the comparative osteological collection

METHOD 2: from bone dimension to fork length using individual equations worked out from the comparative osteological collection, followed by application of one equation linking fork length to weight established from analysis of the same sample of fish (N = 110).

METHOD 3: from bone dimension to fork length using individual equations worked out from the comparative osteological collection, followed by application of one equation linking fork length to weight established from analysis of the much larger non-osteological sample of fish (N = 833) from the Northland and Tasman Bay areas.

Various types of curve were fitted to the Northland/Tasman Bay data using the least-squares method, and the statistics for these are given in Table 2. The equations for estimating Y from X are as follows (A = constant, B = slope):

LINEAR FIT:

$$Y = A + B * X$$

EXPONENTIAL FIT:

$$Y = A * \exp(B * X)$$

LOGARITHMIC FIT:

$$Y = A + B * \ln(X)$$

POWER CURVE FIT:

$$Y = A * X^B$$

CUBIC FIT:

$$Y = A + B * X^3$$

Only the cubic relationship and power curve fits are satisfactory, and these two are difficult to distinguish. The power curve fit has an exponent of 2.97, very close to cubic, and the two curves are not significantly different. For example, in the case of the two correlation coefficients, if we add their associated standard errors and multiply by 3 we get a confidence range of ± 0.0038.

The two values of R of 0.992 and 0.990 are not significantly different using this yardstick. Similarly, the residuals and SE of estimate of Y are not significantly different either. Although a cubic relationship could be defended on purely theoretical grounds, the slightly better residuals for the power curve fit might be sufficient reason for choosing this as the best fit on pragmatic grounds. However, when the data points are plotted out which are used for the least squares fit in each of these two cases (Figures 3 and 4), it is noticeable that the two models achieve stabilisation of variance at opposite ends of the size range.

In the case of the double log transformation (power curve fit) the variance of very large fish is minimised at the expense of variance for very small fish. The opposite is true when the fork length is cubed. The power curve expression was adopted for weight estimates (weight in grams and length in millimetres):

$$\text{WEIGHT} = 0.00002289 * \text{FORK LENGTH}^{2.973897} \quad (\pm 138)$$

The same analysis was made of the 110 fish in the comparative collection. The best fit was clearly a cubic one with the equation:

$$\text{WEIGHT} = 0.0000203 * \text{FORK LENGTH}^{3} \quad (\pm 113)$$

The next step in the analysis was to examine the metrical relationship between bone dimensions and fork length and live weight using various curve fitting procedures. These are shown in Figure 5, using the example of the right dentary maximum length. The correlation coefficients are 0.99, 0.92, 0.96, 0.99, 0.81 for the fork length curves and 0.92, 0.92, 0.74, 0.99, 0.98 for the weight curves (linear, exponential, logarithmic, power, and cubic fits respectively). These values are all fairly high and one could easily make a poor choice of model if only the numeric statistical results were consulted.

Superimposing the graphical models on top of the data points is useful. This was done for all models and all measurements listed in Table 1 and in cases where it was difficult to decide which choice was best, the standard error of the estimate of Y was used as the arbiter. The final choices are listed in Table 3. In the analysis of each bone dimension, the 95% confidence boundary for the standard error of the estimate for Y on X was also calculated (Schefler, 1969: 155-157; Snedecor and Cochran, 1967: 155).). An example of this is provided in Figure 6.

The results presented in Table 3 indicate that fork length can be estimated from bone measurements with standard errors ranging between ± 9 and ± 18 mm, and the live weight ranging between ± 120 and ± 344 g. The analysis of the fork length and weight data for the sample of fish in the comparative collection gave a standard error of ± 113 g and the Northland/Tasman Bay sample was ± 138 g. These appear to be very satisfactory results.

It is also important to examine residuals, and this should help to decide which of the three methods mentioned above would be best for estimating live weight. This analysis was carried out by examining the differences between observed and expected (the residual) for four quantities:

DIFFERENCE 1: The fork length estimated from a bone measurement - the actual fork length. The fork length is estimated using the appropriate equation listed in Table 3.

DIFFERENCE 2: The weight estimated from a bone measurement - the actual weight. The weight is estimated using the appropriate equation listed in Table 3. This method of estimating the weight is labelled Method 1.

DIFFERENCE 3: The weight estimated from a bone measurement - the actual weight. This is done in two steps. First the fork length is estimated from the bone measurement using the appropriate equation listed in Table 3. Second, the weight is estimated using the cubic equation from the analysis of the osteological collection (N = 110) (Method 2).

DIFFERENCE 4: The weight estimated from a bone measurement - the actual weight. This is done in two steps. First the fork length is estimated from the bone measurement using the appropriate equation listed in Table 3. Second, the weight is estimated using the power curve equation from the analysis of the non-osteological collection (N = 833) (Method 3).

Any one of these differences was expressed as a percentage, that is:

$$(\text{OBSERVED} - \text{EXPECTED}) / \text{EXPECTED} * 100.0.$$

These four differences were examined for the matrix of 3474 bone measurements comprising the osteological collection in several different ways.

It was found that the residuals varied markedly depending on whether one assumed that the regression equations passed through the origin or not, and also whether bone weight estimators were included in the analysis or not. A cursory examination of Table 3 shows that estimates on the basis of bone weights are generally inferior to those made on the basis of bone length measurements. It was also found that the percentage residuals were sometimes much larger for very small fish, raising the possibility that these might best be excluded from the analysis.

After considerable experimental research, it was concluded that it was essential to assume that the equations passed through the origin (Thomas, 1976: 370 ff.), not only because the residuals were greatly reduced in all cases, but because clustering was observed when the 3474 points were graphed as scatter plots.

Size-frequency histograms of the residuals also showed gross non-normal characteristics. These are clear signs of an inappropriate model. The final results are given in Figures 7-10 and the associated statistics in Table 4.

This analysis reveals that the estimation of fork length from bone dimensions is very satisfactory with residuals having a standard deviation of only 4% around zero. This evaluation is clear when the bone weights and lengths are combined together, so there is no need for separate treatment of these (see Table 4, Difference 1 and Figure 7).

Of the three different methods for estimating live ungutted weight, the first is not very satisfactory (See Table 4, Difference 2 and Figure 8). As mentioned above, bone weight performs poorly alongside bone length, and this is amply illustrated by the bimodal distribution in Figure 8.

In the case of Methods 2 and 3, there is surprisingly little to choose between them. They have very similar distributions and statistics. It is noticeable that both show lower than expected weights in the case of small fishes, that is, fish less than about 300 mm fork length (see lower part of Figures 7 and 8).

Unfortunately, this constitutes the bulk of the modern osteological sample. The main part of the sample was taken in the Hauraki Gulf in May 1986, and had a mean fork length of 257 mm. The more recent addition of large specimens up to 940 mm has not affected the overall bias of the collection towards small specimens, with more than 76% being less than 300 mm. In a detailed study of the condition factor of snapper, fish smaller than 254 mm were discarded (Cassie, 1957: 378), and the conclusions are notably guarded: "the amount of data available is not sufficient to come to any definite conclusion as to the yearly cycle of condition of the snapper" (Cassie, 1957: 386).

Despite these reservations, Cassie's results show a strong increase in body weight in October and a decline during the spawning season of November and December (Cassie, 1957: 386). Unfortunately, over this three-year study, no samples were taken in the months of April, May, June and July. However, there is no reason to expect a second high condition peak after the May low and the rise beginning in August evident in his Weight-Index graph (Cassie, 1957: Figure 3).

The lower than expected weights for small fish indicated in this study may therefore reflect the month of sampling. The boundary between sexually juvenile and mature snapper is not a sharp one, but 250 mm is a reasonable choice (Paul, 1993: pers. comm.). It is possible that the allometric relationship between length and weight is slightly different for juvenile and mature fish. The results of this present study suggest that fish smaller than 250 mm weigh less than expected by about 16-17%. As far as the two methods of estimating weight are concerned, there is so little difference in their residual statistics that this is not helpful in deciding.

As a general rule, it is considered better to opt for a method based on the largest sample, and for this reason Method 3 is chosen, because it is based on a sample of 833 fish, compared with only 110 for Method 2. Moreover, of the two fork length to weight equations, that derived from the larger sample has a larger standard error (± 138 cf. ± 113 g), and this is a more conservative approach. Thus, the method adopted is:

The live ungutted weight is estimated from a bone measurement in two steps:

- First, the fork length is estimated from the bone measurement (bone length or weight) using the appropriate equation listed in Table 3.
- Second, the weight is estimated from this fork length using the power curve equation from the analysis of the non-osteological collection:

$$\text{WEIGHT} = 0.00002289 * \text{FORK LENGTH}^{2.973897} \ (\pm 138)$$

PUTTING THE ALGORITHMS TO WORK

Following the identification of anatomy and species of fish bone collections, wherever possible one of the bone dimensions described in Table 1 is measured. These are then coded into a computer file by provenance, for example:

CROSS CREEK SITE, LAYER 1, SQUARE A

RM1 39.37	RM2 20.24	RM2 16.59	LM2 20.78	LM2 16.46
LM2 16.02	RP1 41.40	RP1 36.73	RP1 33.59	RP2 10.83
RP2 11.25	RP2 17.01	RP2 16.76	RP2 16.78	RP2 11.71
RP2 8.06	RP2 15.08	RP2 12.89	RP2 10.68	RP2 10.99
LP2 14.10	LP2 13.64	LP2 11.63	LP2 17.99	LP2 15.34
LP2 15.31	RD3 10.64	RD3 14.63	RD3 7.59	LD3 11.40
LD3 5.85	LD3 7.83	LD1 45.37	LD1 32.57	LD3 10.12
RD1 45.59	RD1 37.44	RD1 34.56	RD1 32.49	RD1 23.43
RD3 8.59	LDW 1.13	RDW 1.21	RDW 3.38	

A simple computer program is then required to convert these measurements into estimates of fork length and ungutted weight. For example, the first measurement RM1 is the maximum length of a right maxilla. The equation for estimating fork length from this dimension is given in Table 3. It is a linear equation with the following form (again, with weight in grams and length in millimetres):

$$\text{FORK LENGTH} = 10.61411 * \text{RM1} \quad (\pm 12)$$

Since RM1 = 39.37 in the first specimen, the fork length is estimated as 417.88 mm. Next, the ungutted weight is estimated using the equation

$$\text{WEIGHT} = 0.00002289 * \text{FORK LENGTH}^{2.973897} \quad (\pm 138)$$

This yields a weight of 1427 g. These results may be compared with those recorded for the nearest RM1 measurements in the osteological collection:

RM1	FORK (mm)	WEIGHT (g)
33.87	389	1139
38.13	413	1417
39.37	418	1427*
48.19	513	2809

** = this specimen*

The results are perfectly reasonable in this context. By carrying out these estimates for a large assemblage of bone material from an archaeological site, a picture can then be built up of the original fish catch which the bones represent.

There are several stages involved in the treatment of archaeological bone collections, building towards an abundance measure for each species known as the MNI (Minimum Number of Individuals). This concept is explained fully elsewhere (Leach, 1986) and refers to the smallest number of individuals of any one species which can satisfactorily account for all the bones identified as belonging to that species. The original number of individuals is larger than this number.

By strictly adhering to certain rules for the calculation of the MNI, a table is built up for an archaeological site so that the relative abundance of different species is a fair reflection of the relative abundance of the original numbers of individuals. In other words, although the original numbers may have been a great deal larger than the MNIs, the percentage figures of both series should be very similar. Such calculations are basic to the analysis of archaeological fauna.

The present study is aimed at providing the basis of a method for assessing the size-frequency diagram for prehistoric catches, and an important question arises – whether all bones from one species should be measured for this purpose, or just a smaller number of them, perhaps just one part of the anatomy.

If all bones are measured, the number of measurements will be far greater than the MNI for that species. Would a size-frequency diagram and its associated statistics be a proper reflection of the original catch, or would it be biassed? An examination of published literature shows that little attention has been given to this question, and discussions with colleagues revealed that it is commonly assumed that this is not a significant problem. However, although most agree that this is intuitively acceptable, there does not appear to have been any formal examination of the problem published. This matter is explored in Appendix 1, using a simulation algorithm. It is concluded that it is normally acceptable to measure all bones of a species in order to arrive at a size-frequency histogram of the original fish catch. In rare cases where differential survival by bone size is suspected to vary according to different parts of the anatomy, this issue would have to be considered afresh.

CONCLUSIONS

This analysis of modern snapper bones has shown that it is feasible to estimate the live fork length and ungutted weight from cranial bones of snapper in archaeological sites within acceptable margins of error. Fork length can be estimated with a standard error of better than 20 mm and weight to better than 140 g. In seeking to reconstruct a size-frequency histogram of a prehistoric fish catch it is acceptable to measure all bones from a particular species, even though the number of measurements may greatly exceed the MNI for that species.

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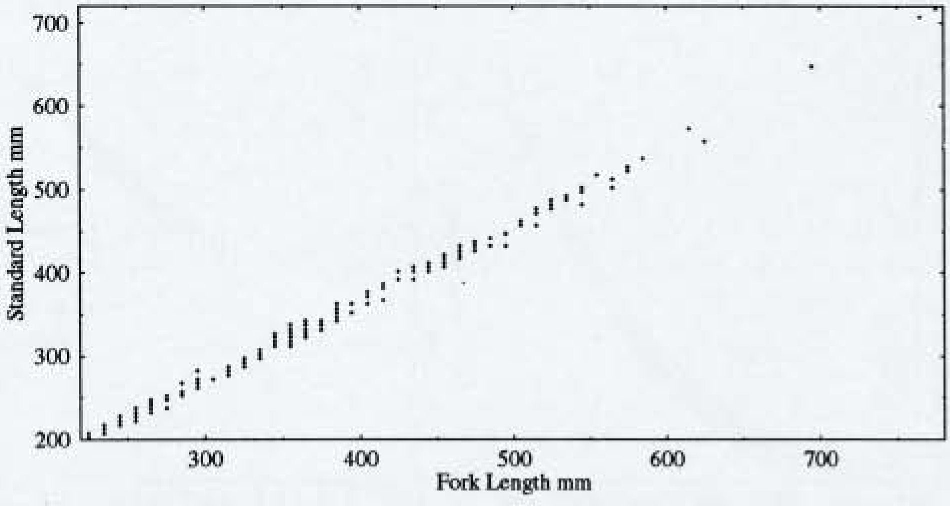

Fig. 2 – A sample of 194 snapper from east and west of Auckland area had both fork length (X) and standard lengths (Y) measured in order to calculate the regression relationship. The correlation coefficient R^2=0.997.

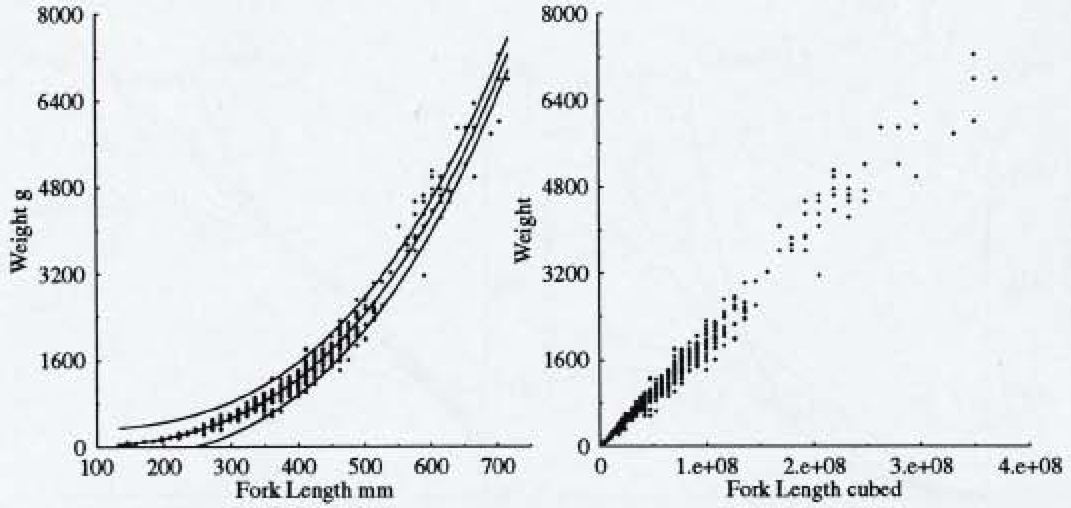

Fig. 3 – Fitting a cubic function to modern snapper fork length against weight (N=833). Note that the variance of very small fish is reduced a great deal more than that of very large fish.

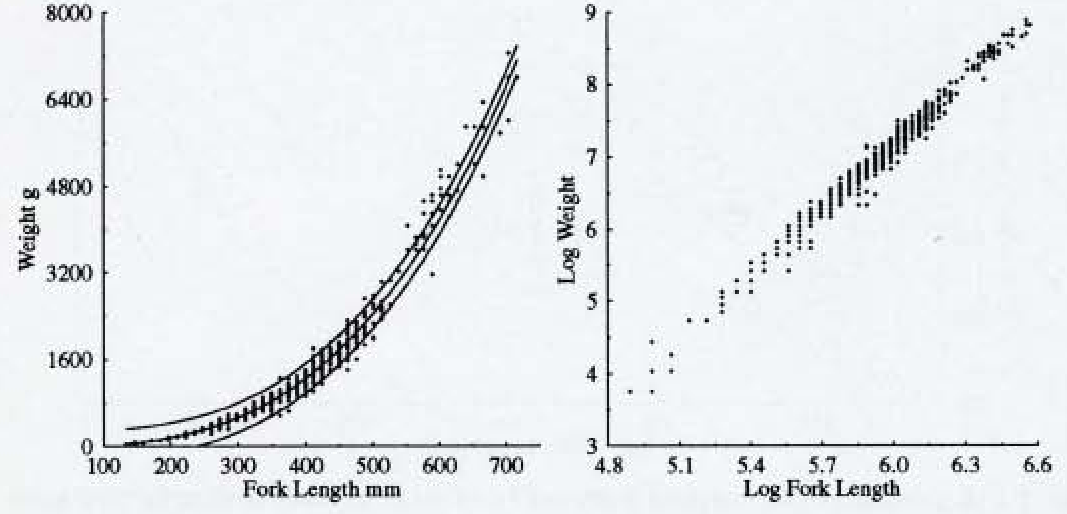

Fig. 4 – Fitting a power curve function to modern snapper fork length against weight (N = 833). Note that the variance of very large fish is reduced a great deal more than that of very small fish.

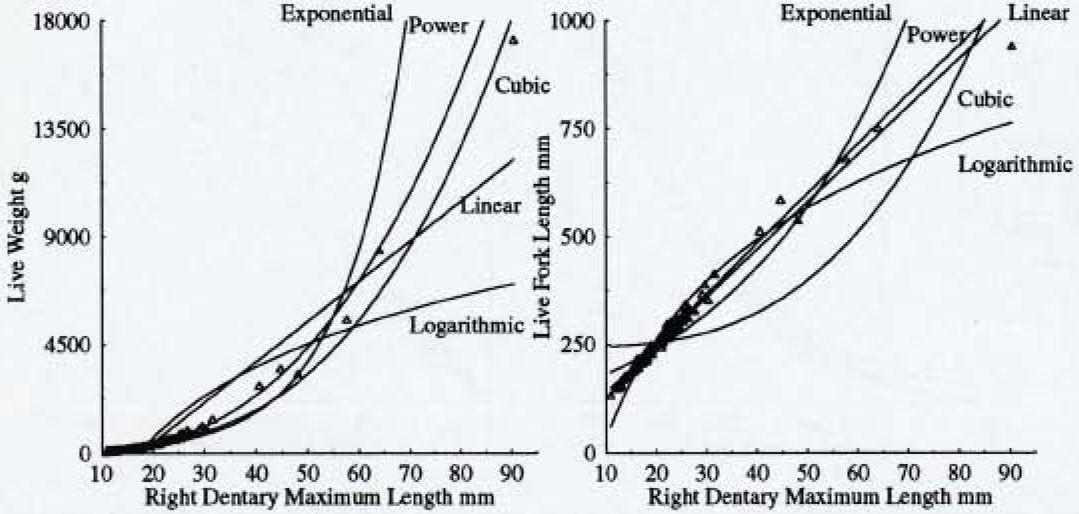

Fig. 5 – Various curve fitting procedures applied to the measurement of right dentary maximum length and live fork length and weight (N = 110). Note that some of the lines of best fit are difficult to distinguish – notably the power curve and cubic in the case of weight estimation, and power curve and linear fit in the case of fork length.

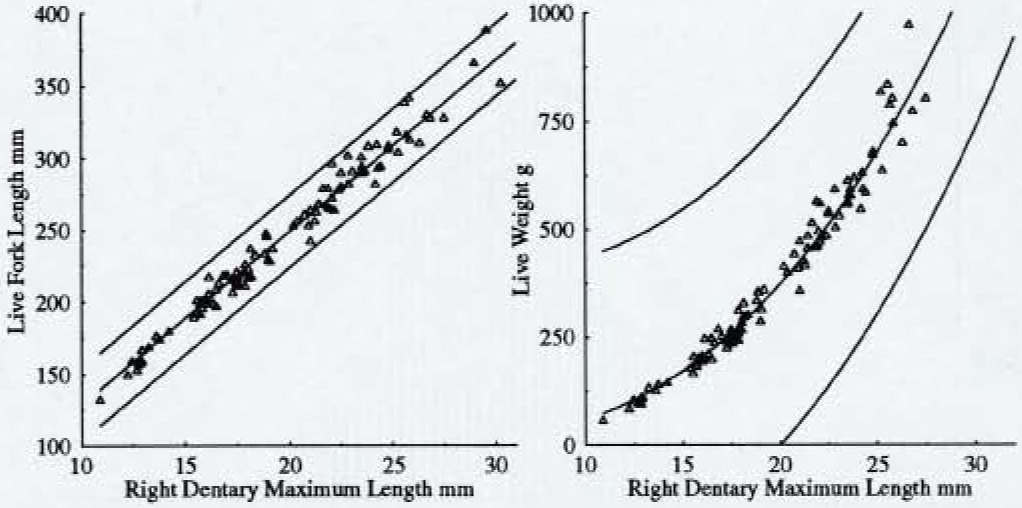

Fig. 6 – Best fit regression lines for estimating live fork length and weight from the right dentary maximum length, showing the 95% confidence boundaries for the standard error of the estimate of Y. In both cases a power curve fit was chosen as the best model for estimating the live characteristics. The standard errors are ± 12 mm and ± 188 g, and the powers 0.96 and 2.69 for fork length and weight, respectively. These powers are close to linear and cubic.

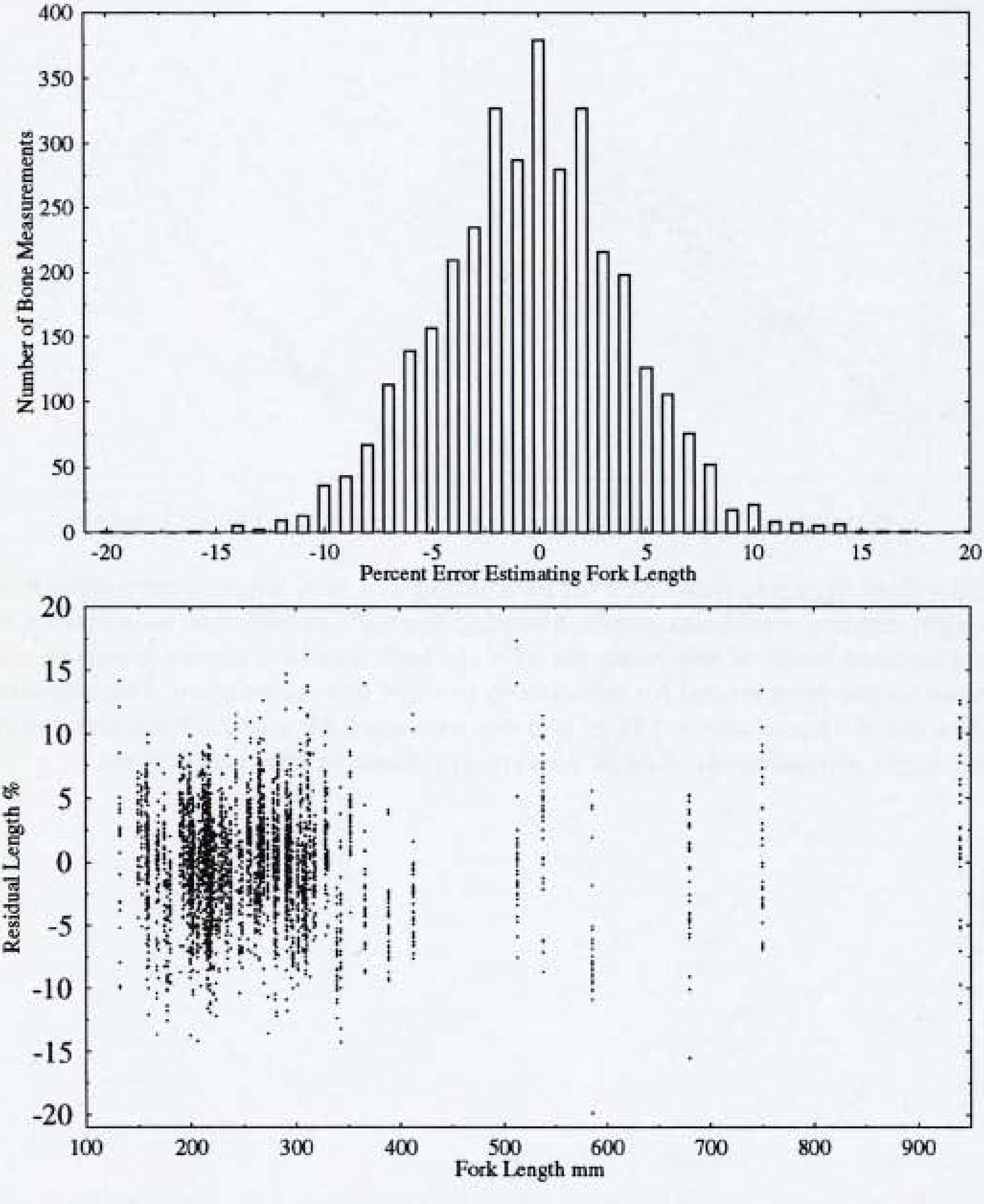

Fig. 7 – Analysis of residuals of Difference 1 (see text, p. 7) for 3474 bone measurements used to estimate fork length. The size-frequency distribution is given above and the scatter plot of all points is shown below. See Table 4 for the distributional statistics. The scatter of points on the far right shows the variation in fork length estimates obtained for the 32 bone measurements made on the largest fish in the comparative osteological collection.

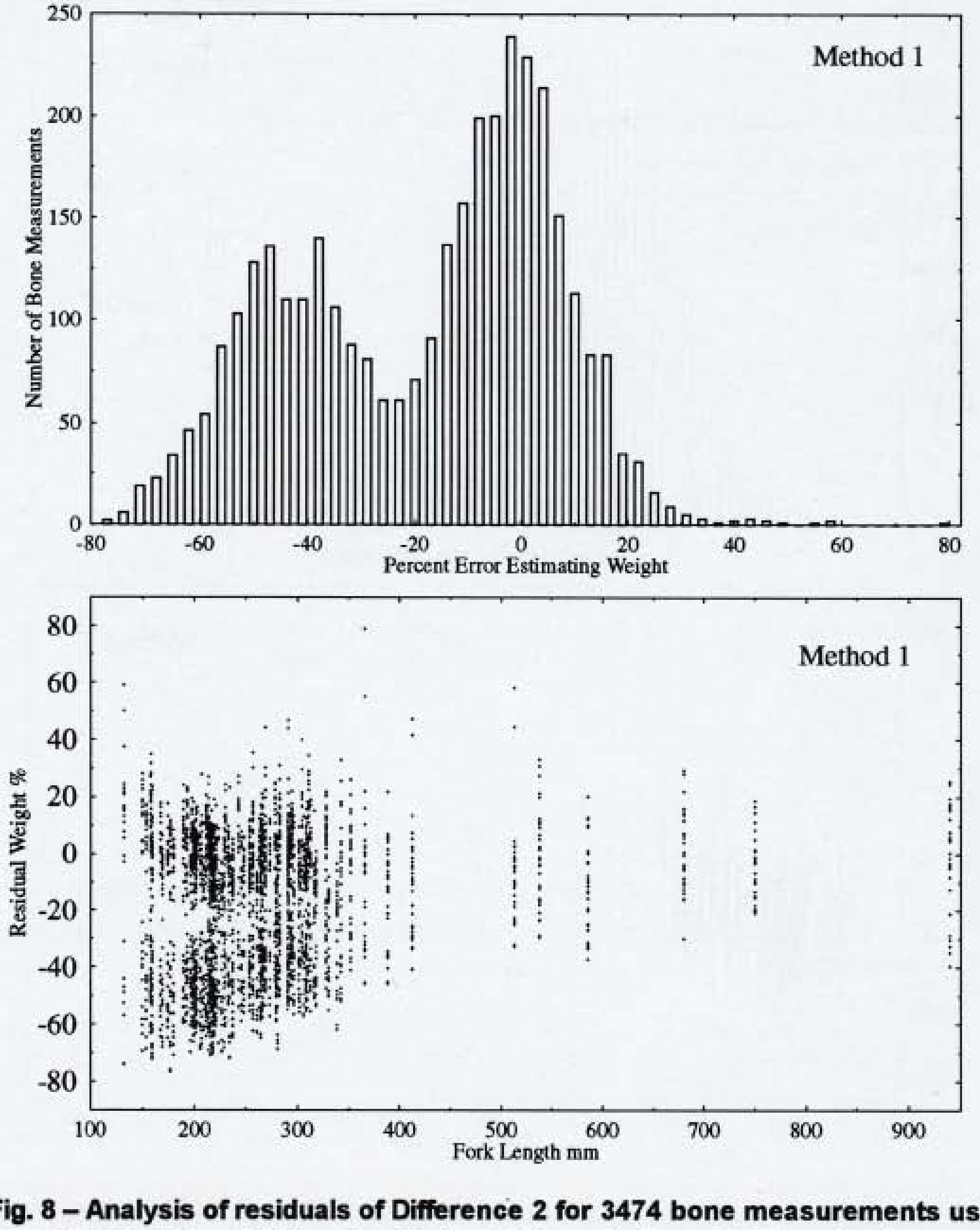

Fig. 8 – Analysis of residuals of Difference 2 for 3474 bone measurements used to estimate live weight using Method 1 (see text, p. 5). The size-frequency distribution is given above and the scatter plot of all points is shown below. See Table 4 for the distributional statistics. The scatter of points on the far right shows the variation in weight estimates obtained for the 32 bone measurements made on the largest fish in the comparative osteological collection. There is clear bimodality in this distribution. The node on the left is almost entirely composed of estimators from bone weight, while that on the right is composed of bone length estimators.

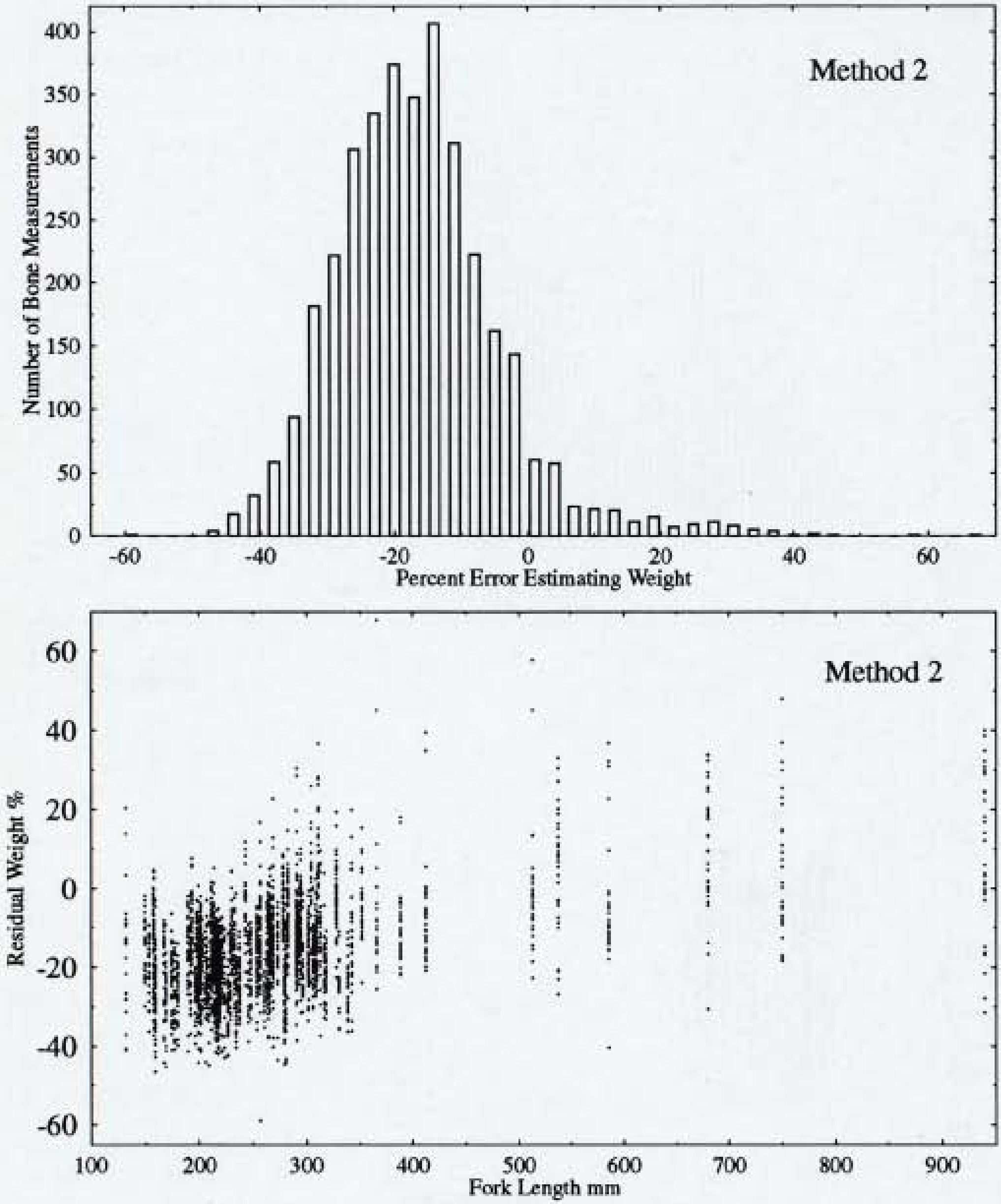

Fig. 9 – Analysis of residuals of Difference 3 for 3474 bone measurements used to estimate live weight using Method 2 (see text, p. 5). The size-frequency distribution is given above and the scatter plot of all points is shown below. See Table 4 for the distributional statistics. The scatter of points on the far right shows the variation in weight estimates obtained for the 32 bone measurements made on the largest fish in the comparative osteological collection. There is slight positive skewness and kurtosis in this distribution, and the estimated weight of small fish is lower than expected.

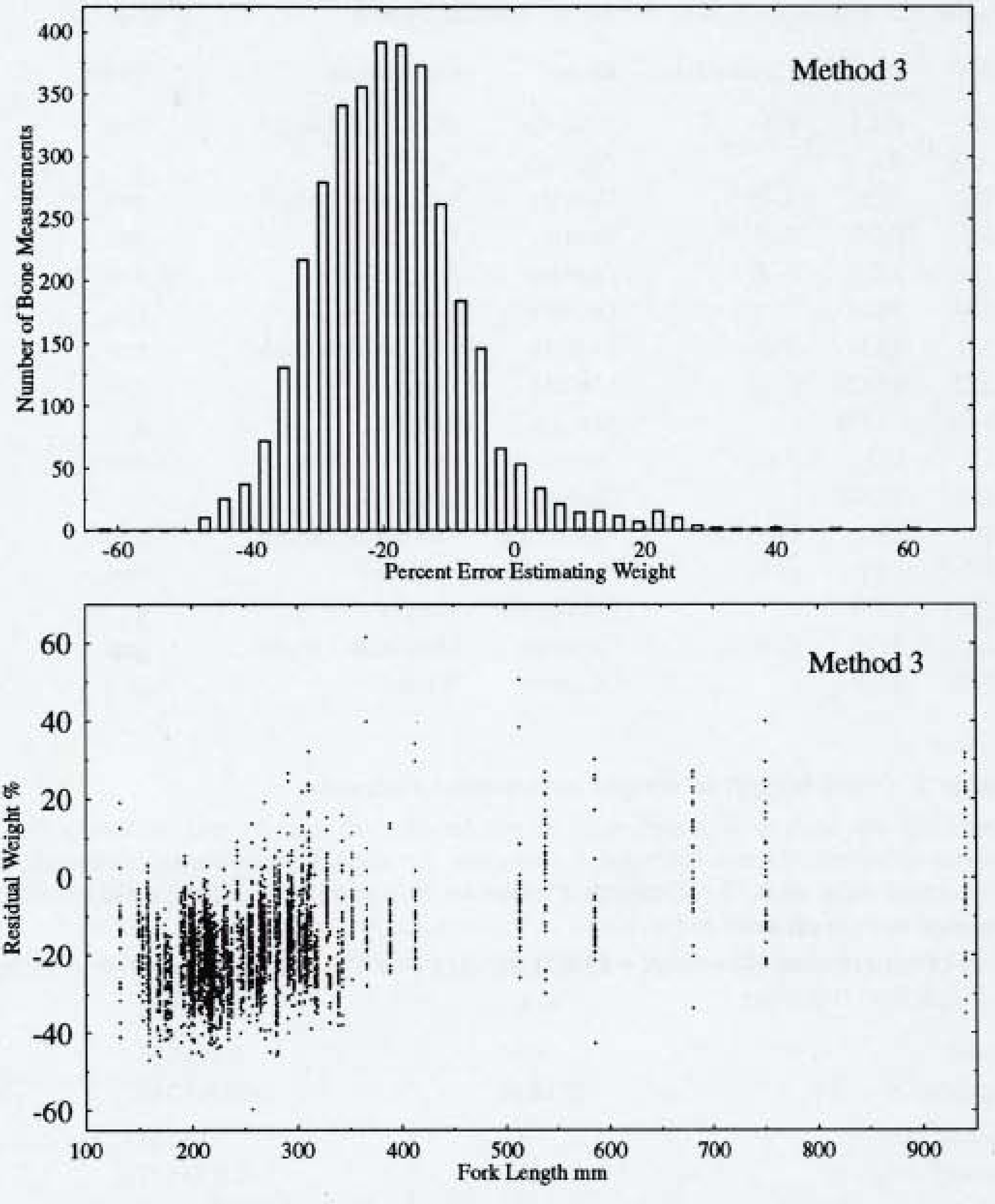

Fig. 10 – Analysis of residuals of Difference 4 for 3474 bone measurements used to estimate live weight using Method 3 (see text, p. 5). The size-frequency distribution is given above and the scatter plot of all points is shown below. See Table 4 for the distributional statistics. The scatter of points on the far right shows the variation in weight estimates obtained for the 32 bone measurements made on the largest fish in the comparative osteological collection. There is slight positive skewness and kurtosis in this distribution, and the estimated weight of small fish is lower than expected.

Table 1 – Measurements made on cranial bones.

Left	Right	Landmarks	Bone	Dimension	Units
LA1	RA1	E-F	Articular	Maximum Length	mm
LAW	RAW	-	Articular	Weight	g
LD1	RD1	A-D	Dentary	Maximum Length	mm
LD2	RD2	A-C	Dentary	Fragment 1	mm
LD3	RD3	A-B	Dentary	Fragment 2	mm
LDW	RDW	-	Dentary	Weight	g
LM1	RM1	K-I	Maxilla	Maximum Length	mm
LM2	RM2	J-L	Maxilla	Fragment	mm
LMW	RMW	-	Maxilla	Weight	g
LO1	RO1	P-Q	Otolith	Maximum Length	mm
LOW	ROW	-	Otolith	Weight	g
LP1	RP1	O-M	Premaxilla	Maximum Length	mm
LP2	RP2	O-N	Premaxilla	Fragment	mm
LPW	RPW	-	Premaxilla	Weight	g
LQ1	RQ1	G-H	Quadrate	Maximum Length	mm
LQW	RQW	-	Quadrate	Weight	g

Table 2 – Fork length to weight conversion statistics.

Least squares analysis was performed on the data described in the text, assuming that the various curves pass through the origin. A = constant, B = slope, R = correlation coefficient, SER = standard error of R, T = Student's *t* value for R, Residuals = self-explanatory, SEE_Y = standard error of estimate of Y.

NON-OSTEOLOGICAL SAMPLE (N = 833). THE VALUE OF T HAS 831 DEGREES OF FREEDOM.

	A	B
Linear	0.0	3.708652
Exponential	48.0656	0.00791246
Logarithmic	0.0	210.5952
Power Curve	0.00002289	2.973897
Cubic	0.0	0.00001966

	R	SEE_Y	SER	T	Residuals
Linear	0.926	406.8	0.00494	70.7	425670
Exponential	0.97	261.4	0.00204	115.2	72849
Logarithmic	0.84	584.9	0.01021	44.6	823432
Power Curve	0.992	137.9	0.00057	223.4	9508
Cubic	0.99	150.9	0.00068	203.8	9579

Osteological sample (N=110). The value of T has 108 degrees of freedom.

	A	B
Linear	0.0	4.58007
Exponential	53.3919	0.00743344
Logarithmic	0.0	151.839
Power Curve	0.00007469	2.795207
Cubic	0.0	0.0000202977

	R	SEE_Y	SER	T	Residuals
Linear	.880	898.0	0.02153	19.2	198524
Exponential	.951	584.1	0.00911	32.0	103426
Logarithmic	.717	1317.3	0.04634	10.7	146250
Power Curve	.998	132.7	0.00047	147.6	577
Cubic	.998	113.4	0.00034	172.8	1302

Table 3 – Best fit coefficients for length and weight estimates from bone fragments.

Least squares analysis was performed on the data described in the text, assuming that the various curves pass through the origin. The coefficients are given for the best method of fitting a line to the data based on the smallest Standard Error of the Estimate of Y. Note: SEE_Y truncated to 1 mm in the case of length and 1 g in the case of weight

Estimation of Live Length

Fit	Bone	Constant	Slope	SEE_Y
Power	RA1	13.80103	0.9773467	12
Power	RAW	446.5577	0.295852	14
Power	RD1	14.09165	0.9586253	12
Power	RD2	21.13147	0.9330199	11
Linear	RD3	0.0	41.06181	13
Power	RDW	369.1795	0.2825529	15
Linear	RM1	0.0	10.61411	12
Power	RM2	27.40638	1.003567	14
Power	RMW	402.0101	0.2802992	16
Exponential	RO1	65.99903	0.1306629	18
Power	ROW	792.4077	0.5257831	15
Power	RP1	14.40536	0.9450058	14
Linear	RP2	0.0	31.58893	14
Power	RPW	380.9623	0.2963483	16
Linear	RQ1	0.0	19.43539	9

Power	RQW	526.7075	0.2942389	13
Power	LA1	13.91409	0.9744805	13
Power	LAW	447.4905	0.2979121	14
Power	LD1	13.87569	0.9625565	13
Power	LD2	21.21984	0.934607	11
Linear	LD3	0.0	41.18091	17
Power	LDW	369.4671	0.2836398	15
Power	LM1	12.70081	0.951515	11
Linear	LM2	0.0	27.45226	15
Power	LMW	403.7527	0.2811538	15
Exponential	LO1	69.69265	0.1246624	17
Power	LOW	803.3652	0.5312765	17
Power	LP1	14.40358	0.9448532	14
Linear	LP2	0.0	31.49918	14
Power	LPW	381.7722	0.2952002	16
Linear	LQ1	0.0	19.56692	11
Power	LQW	532.0613	0.2971619	14

Estimation of Live Weight

Fit	Bone	Constant	Slope	SEE_Y
Cubic	RA1	0.0	0.03426734	175
Linear	RAW	0.0	1398.418	221
Power	RD1	0.1180857	2.689188	188
Power	RD2	0.3689695	2.616361	176
Cubic	RD3	0.0	1.260308	200
Power	RDW	1123.725	0.792345	237
Cubic	RM1	0.0	0.01883688	146
Power	RM2	0.7584531	2.818122	203
Linear	RMW	0.0	886.9081	221
Exponential	RO1	9.002427	0.3664282	344
Power	ROW	9702.497	1.48024	250
Cubic	RP1	0.0	0.02459463	191
Cubic	RP2	0.0	0.5624871	120
Linear	RPW	0.0	786.3806	224
Power	RQ1	0.6330411	2.534482	205
Linear	RQW	0.0	2770.362	194
Power	LA1	0.1162242	2.727413	208
Power	LAW	1924.196	0.8340339	224
Power	LD1	0.1131065	2.700203	194

Power	LD2	0.3737832	2.620416	183
Power	LD3	3.614111	2.606831	295
Power	LDW	1125.96	0.7950807	240
Cubic	LM1	0.0	0.01886223	145
Power	LM2	0.833904	2.776671	237
Linear	LMW	0.0	897.8414	233
Exponential	LO1	10.66675	0.347932	321
Power	LOW	9967.362	1.490491	272
Power	LP1	0.1281555	2.644111	223
Cubic	LP2	0.0	0.5981321	177
Linear	LPW	0.0	740.0462	244
Power	LQ1	0.6107132	2.550867	237
Linear	LQW	0.0	2995.969	134

Table 4 – Distributional statistics from analysis of residuals.

Residuals were calculated as percentage statistics: (observed-expected)/expected * 100.0. Results below use equations which pass through the origin. All bone measurements were included in the analysis (N = 3474), excluding 47 missing values. See the text for an explanation of the meaning of Differences 1 to 4. The ± figures are standard errors. The skewness and kurtosis statistics g1 and g2 were calculated according to Geary (1947) and Geary and Pearson (1938) and the normal deviates w1 and w2 are given by Rao (1952: 219).

Difference 1: Observed and Estimated Fork Length

Range of Values	=	-21.7	to	19.7
Mean	=	-0.36	±	0.08
Standard Deviation	=	4.39	±	0.05
Skewness g1/w1	=	0.007	and	2.0
Kurtosis g2/w2	=	3.5	and	6.3

Difference 2: Observed and Estimated Weight Method 1

Range of Values	=	-76.9	to	78.8
Mean	=	-17.00	±	0.41
Standard Deviation	=	24.19	±	0.29
Skewness g1/w1	=	-0.3	and	12.5
Kurtosis g2/w2	=	2.1	and	10.3

Difference 3: Observed and Estimated Weight Method 2

Range of Values	=	-59.0	to	67.8
Mean	=	-15.75	±	0.21
Standard Deviation	=	12.39	±	0.15
Skewness g1/w1	=	1.0	and	24.1
Kurtosis g2/w2	=	6.0	and	36.2

Difference 4: Observed and Estimated Weight Method 3

Range of Values	=	-59.7	to	61.5
Mean	=	-17.84	±	0.20
Standard Deviation	=	11.65	±	0.14
Skewness g1/w1	=	0.9	and	22.9
Kurtosis g2/w2	=	5.7	and	32.6

APPENDIX 1: OBTAINING A RELIABLE SIZE-FREQUENCY HISTOGRAM OF PREHISTORIC FISH CATCHES

The dispersion statistics of an ancient fish catch provide the key to answering a number of questions about prehistoric fishing. The mean fish weight for example, can be multiplied by the MNI (Minimum Number of Individuals) to yield the MMW (Minimum Meat Weight) for a particular site. This information is important when assessing the relative dietary role of different parts of the food web in ancient diets.

The mean size is particularly useful in documenting the historical effects of human predation on marine resources. However, mean size is not the only dispersion statistic which is useful for archaeologists.

The degree of variation about the mean size, for example, can be a guide as to whether people were using gill mesh nets of a certain size. If there is low variation about the mean size, then this could be the explanation. On the other hand, a great deal of variation about the mean size of a certain fish type could indicate the use of drag nets or seine nets with a small mesh. The study of the full range of dispersion characteristics of size-frequency histograms of ancient fish catches is in its infancy in archaeology, and there is little disciplined interpretation at this stage. It can be expected to be an important area of study in the future.

A rather unusual problem arises when trying to obtain a reliable estimate of the size-frequency histogram and the associated dispersion statistics of ancient fish catches. To illustrate the problem, we will use the results of studying the remains of the family Scaridae from Layer 15 at the archaeological site of Mochong on the island of Rota (Leach *et al.*, 1988). The MNI for different parts of the anatomy was found to be as follows:

Anatomy	Mid-line	Left	Right
Inferior pharyngeal cluster	121		
Dentary		115	113
Premaxilla		88	92
Superior pharyngeal cluster		77	76
Maxilla		32	28
Articular		22	23
Quadrate		15	18
MNI	**121**		

Leaving aside for a moment the matter of bone fragments, let us imagine that all of these bones were complete, and that we have sufficient modern comparative material to reconstruct the original live length and weight of the fish from which each bone derives. Which bones should we use to assess the dispersion statistics of the original fish catch ?

Should we use every single bone, or just some of them ? There may be several bones present which originally belonged to the same individual fish specimen, in addition to those bones belonging to different individuals.

A conservative procedure might measure only those bones which yielded the largest MNI – this way we can be certain that we are actually measuring different individual fish specimens. However, there is a disadvantage in this procedure. The MNI is a minimum value and may not be a very large size, a significant sampling problem in working out reliable dispersion statistics. If at all possible, this approach should be avoided.

Measuring all the bones present also has a potential danger. If the MNIs were the same for each part of the anatomy, and there were no problems of differential survival – all bones from all fish specimens were actually represented in the collection – then their measurement would give the same dispersion statistics as those based on measurement of only one part of the anatomy. The standard errors, however, would be smaller in the case of the full set of measurements, because of the larger sample size.

As can be seen from the table above, however, the MNI is anything but uniform from one part of the anatomy to another, so the question arises whether bias could be introduced by pooling all bone measurements ? There certainly could be bias if the processes of differential survival were non random by size for different parts of the anatomy. For example, if small quadrates had a lower survival rate than small dentaries. If we can assume that the survival rate by size is random, then assessing the dispersion statistics with the pooled bones would not be biassed. This assumption probably does not present a serious problem.

There is also a problem of the ability of the archaeologist accurately to identify the bones in the first place – unfortunately this is certainly biassed by anatomy, and also by size. In the case of Scaridae bones, the identification of very small dentaries, premaxillas and pharyngeal clusters (referred to as the toothed bones) presents few difficulties; in the case of the maxillas, articulars and quadrates, we suspect that small ones may not attract the same degree of attention. These three bones are more difficult to identify generally, and the problem is compounded by small size. It might be considered unwise to include these bones in an assessment.

So, we are left with the dentaries, premaxillas, and pharyngeal clusters. We see no reason to suspect that problems of differential survival and differential ability to identify will be biassed by size in a manner which is different from one of these bones to another. Therefore, pooling the measurements for these three bones should lead to more reliable dispersion statistics than measurement of only one of these parts of the anatomy.

This conclusion should not be understood to refer directly to the dispersion statistics of the original fish catch, which of course is what we are actually interested in. The dispersion statistics of these select bones which have survived and been identified may not be the same as those of the original fish catch. Any processes of differential survival according to size would certainly affect these statistics – small dentaries might have less chance of survival than large ones in some archaeological sites. The main point is whether these processes could vary according to anatomy, notably amongst the dentaries, premaxillas and pharyngeal clusters? This seems intuitively rather doubtful, but fortunately is testable. That is the purpose of this appendix.

In order to examine this problem, it was decided to write a simulation program and see what effect different types of samples had on dispersion statistics. The program was written in Fortran-77 and is presented in full in Fleming (1986: Appendix 2). The algorithm follows the following argument:

1: A suitable real sample of Scaridae fish consisted of the modern specimens collected for a study by Fleming (1986). This was used as an example of a prehistoric catch. The lengths of the fish had been recorded, so this data was used to assess the dispersion statistics of the catch. The results for N = 115 (in millimetres) are:

Mean:	σ 72.43
SE Mean:	SE σ 4.78
G1 0.59	W1 3.46
G2 2.53	W2 0.98

The question we address is whether we can we use various kinds of samples of the original bone collection and obtain the same statistical pictures as given above ?

2: There are 115 actual fish which were caught, and there are 13 bones in each which we can routinely identify on archaeological specimens and then use for estimating the original fish lengths. This makes a total of 1495 bones in the collection.

3: Let us imagine that a bulldozer runs over the dentaries and randomly destroys some number of them between 0 and 115, say $n1$. The bulldozer represents the vagaries of archaeological survival, recovery, and identification.

4: Let us now imagine that the same bulldozer randomly destroys some number of the articulars between 0 and 115, say $n2$.

5: Let us further imagine this same procedure is repeated for all the 13 bones, giving us a final series of bone numbers remaining of:

$$n1, n2, n3, n4, n5, \dots, n13$$

These bones from our archaeological site are the ones which have ended up in plastic bags, and which we can use to measure and estimate the original lengths of the fish they came from.

6: When we do this, we thus end up with a series of fish lengths as follows:

$n1$ fish lengths, $n2$ fish lengths, $n3$ fish lengths ... $n13$ fish lengths

7: Now we can calculate the dispersion statistics of the total number of fish lengths in this series. This total will be some number between 0 and 1495 'fish'.

8: The all-important question is, will these results be found to be statistically indistinguishable from those calculated in Step 1 above ?

The simulation program using these assumptions was recursively run 10 times to evaluate the dispersion statistics. The results are given in Appendix Table 1.

Simple inspection of that table reveals that the dispersion statistics are not significantly different to the original ones ($p = 0.05$). That is, the mean, standard deviation, skewness and kurtosis figures are within 95% confidence limits. The only values significantly different are the standard errors of the mean and standard deviation, and the values of W1 and W2, which are the normalised deviates of the skewness and kurtosis figures G1 and G2. These differences are to be expected from the greater sample sizes (113 in the original sample, and up to 917 in the simulations).

This is a very satisfactory conclusion. It indicates that so long as it is safe to assume that the processes of destruction are randomly distributed by anatomy, it will be reasonable to measure ALL bones for which it is possible to estimate the original fish size, without fear of introducing bias into the results.

It is suggested that if there is any doubt about this assumption, and the archaeological collection is large enough to warrant it, then the 'toothed' bones (dentaries, premaxillas and pharyngeal clusters) could be used alone to produce the most reliable statistics.

Appendix Table 1: Dispersion Statistics for the Simulated Archaeological Assemblages

N	Mean	SE Mean	σ	SE σ	G1	W1	G2	W2
617	285.12	2.98	74.18	2.11	0.51	7.32	2.422	2.91
810	275.24	2.41	68.68	1.70	0.60	9.08	2.615	2.21
917	282.76	2.32	70.52	1.64	0.63	9.84	2.674	1.99
858	280.49	2.40	70.34	1.69	0.63	9.54	2.589	2.43
727	277.29	2.64	71.40	1.87	0.64	8.86	2.578	2.30
886	279.76	2.35	69.94	1.66	0.61	9.57	2.618	2.29
684	287.15	2.72	71.29	1.92	0.43	7.08	2.330	3.57
754	282.70	2.74	75.28	1.93	0.63	8.95	2.485	2.87
708	282.71	2.72	72.41	1.92	0.57	8.29	2.368	3.42
917	278.05	2.38	72.06	1.68	0.64	9.94	2.601	2.44

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