final report

Project code: A.MQA.0017

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Date published: April 2016

PUBLISHED BY
Meat and Livestock Australia Limited
Locked Bag 1961
NORTH SYDNEY NSW 2059

DEXA Lamb Eating Quality and Supply Chain Grading

Meat & Livestock Australia acknowledges the matching funds provided by the Australian Government and contributions from the Australian Meat Processor Corporation to support the research and development detailed in this publication

Executive Summary

1. A prototype DEXA system has been installed at the JBS abattoir in Bordertown, SA, mirroring the system installed at the Finegand abattoir, near Balclutha, NZ. Work was undertaken to establish the algorithms to predict carcase composition in lambs.
2. Experiment 1 demonstrated that the prototype DEXA can effectively determine chemical fat % and tissue depth and remove bone-containing tissue from images based upon DEXA R-values.
3. Using the relationships established in Experiment 1, Experiment 2 then tested the DEXA system across an initial group of 48 lamb carcases randomly chosen from one days' production, but selected across a diverse range of weight (17-32kg hot carcase weight) and fatness (5-27mm GR tissue depth). This demonstrated excellent precision for determining carcase fat % using computed tomography (CT) (R2 = 0.84, RMSE = 1.60). However, the association with CT lean% and bone % were less precise (CT lean % R2 = 0.64, RMSE = 1.89; CT bone % R2 = 0.64, RMSE = 0.90).
4. Experiment 3 then tested the DEXA system across a much larger population of lambs. These were from MLA's nucleus flock, with 600 lambs re-located to South Australia, feedlot finished to target slaughter weights, and then killed in groups of about 100 lambs, with each group balanced for sire. This produced a population of lambs that were spread across a diverse range of fatness (2-44mm GR tissue depth), weight (10.9-39.3kg hot carcase weight), and genotype. The final DEXA prediction equation was established within this population, and tested for robustness by transporting the prediction equation between slaughter groups. The precision of these models was very high, with R2 for CT fat %, lean % and bone % of 0.89, 0.74, 0.71, and root mean square error of 1.42, 1.69, and 0.80, which represented 6%, 9%, and 8% of the data range across nucleus flocks 2-6 for CT fat, lean and bone. This precision was maintained when these equations were derived within one slaughter group and transported to the others, and the accuracy for predicting CT fat % was also maintained within 1%.
5. Experiment 4 tested the precision of prediction for CT composition within regions. For fat% and lean% it was reduced when predicted within the fore, saddle and hind sections using DEXA values specific to these regions. Alternatively, when using the whole carcase DEXA value to predict CT composition the precision was diminished by markedly less in the fore and hind quarter, and within the saddle section it was the same or even slightly improved (for bone and lean) compared to the whole carcase predictions of composition.
6. These results demonstrate that this system will provide precise and accurate prediction of carcase composition enabling more accurate valuation of carcasses up and down the supply chain on the basis of lean meat yield.

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1 Background

Saleable meat yield is a function of the weight of muscle relative to the weight of the carcass, and represents a key determinant of carcass value along the supply chain. This includes consumers who demand large and lean cuts of lamb, processors who are required to trim excess fat from carcasses which costs time as well as representing loss of saleable product, and farmers who are attempting to achieve larger slaughter weights without incurring penalties for fatness (Pethick et al.. 2006). For this reason most Australian processors offer price grids that take account of both carcass weight and fatness.

To measure carcass fatness Australian processors palpate the GR site (110mm from the spine over the 12th rib) to “estimate” a fat score which acts as a surrogate marker of whole body fatness and lean meat yield. Yet this is a highly imprecise estimate of lean meat yield (Gardner et al. 2015). This precision can be markedly improved by actually measuring GR tissue depth, however reliance upon a single point measurement is still likely to introduce significant bias in genetically diverse populations. This can be extrapolated from the results of Anderson et al. (2015) who demonstrated marked redistribution of lean to the loin region in lambs that were the progeny of sires with extremes in post-weaning eye muscle depth and fat depth breeding values. Therefore “whole carcass” measurement systems that don’t rely on point measures are required, and they must be easy to implement within the supply chain.

One opportunity identified was to modify an existing lamb robotic boning system (Scott Technology Ltd.) which has the capacity to operate at 3-times the fastest chain speeds (capacity to scan 30 carcases per minute) and makes use of 2D X-ray images to identify cutting lines. An initial project was undertaken at the Finegand plant near Balclutha, New Zealand, to investigate ways of adapting this to a dual energy x-ray absorptiometry (DEXA) system that meets robotic image requirements while also enabling the determination of body composition. Medical DEXA devices have long been used for determining body composition in production animals, including sheep (Pearce et al. 2009). However the way in which these medical devices physically acquire the DEXA images, either through pulsing the X-ray tube or using K-edge filters (Pietrobelli et al. 1996), was not directly transferable to the abattoir scenario due to practical limitations associated with speed, carcass movement, and expense. Therefore we developed a “sandwich” style detector that combines two photodiodes separated by a copper filter. A single emission from an X-ray tube passes through the first photodiode that is more responsive to low energy photons, then through the copper filter which attenuates the low energy photons, and then through the second photodiode that is more responsive to high energy photons, enabling the acquisition of low and high energy images.

This study details the early calibration of this prototype DEXA system which has also been installed at the JBS Bordertown plant in South Australia, with the hypothesis that this system could determine body composition at chain speed.

2 Project Objectives

Outcome 1. Deliver an Australian algorithm for predicting lean in lamb carcasses using DEXA.

This would involve the assembly of a large dataset of lamb carcasses (n=500 to be robust) that represent the full range of weight and fatness evident within the Australian lamb industry. These carcasses will be scanned using both computed tomography (CT) and the Scott Technology DEXA system enabling the generation of a DEXA algorithm that can predict percent CT lean.

Outcome 2. Assess the potential for determining age in lamb carcasses using DEXA.

This would involve the construction of a large dataset of lamb carcasses (n=500) of known ages and genotypes. Experimental work would require no CT scanning of carcasses, significantly reducing costs.

Outcome 3. Assess the potential for determining Intramuscular Fat (IMF) in lamb carcasses using DEXA.

3 Methodology

3.1 Experiment 1. Tissue phantoms

3.1.1 Introduction

Initial proof-of-concept tests were required to determine whether the prototype DEXA system that has been installed at the JBS Bordertown plant in South Australia could determine chemical fat composition within soft tissue. Furthermore, the base relationship between DEXA value from this device and chemical fat composition for tissues of varying thickness needed to be established. These relationships could then be applied to the calculation of chemical fat % within carcase tissues.

3.1.2 Materials and Methods

To establish the base relationship between DEXA value and chemical fat composition, samples of lean and fat tissue were dissected from Merino lamb carcases and used to create mixtures of the following fat:muscle ratios: 0:100, 25:75, 50:50, 75:25, or 100:0. These samples were then ground and homogenised, after which subsamples were taken for the determination of chemical fat percentage, and percent dry matter, as reported in

Table *1* below.

Table 1. Dry matter and chemical fat percentage of mixtures of dissected fat and lean.

Fat:Lean ratio	Percent Dry Matter	Chemical Fat %
100:0	91.4	87.99
75:25	70.1	60.56
50:50	53.4	39.99
25:75	36.4	18.33
0:100	26.6	6.25

Each of these 5 fat:lean mixtures were then used to create calibration blocks of 3 different uniform sizes using custom-built moulds which were 12.5mm, 80mm, or 160mm thick. This process was repeated 3 times, providing triplicates for each fat:lean mixture at each thickness. X-Ray images were then generated using a single emission from a 140kV X-ray tube, with a set of 2 images captured using 2 photodiodes separated by a copper filter. The first photodiode used ZnSe as the scintillant, and the second used CsI as the scintillant. Each calibration block was then scanned 5 times, each time capturing different regions of the block enabling estimation of repeatability.

Prior to carrying out image analysis regions of interest within each calibration block image were selected corresponding to one of the 5 tissue mixtures. The corresponding pixels within the low and high energy images were then used to calculate an R value for these pixels according to the following formula:

$(R = \ln(I_{Low}/Air_{Atten}) / \ln(I_{High}/Air_{Atten}))$;

Where: I_{Low} represents the pixel value in the low energy image (ZnSe Photodiode)
I_{High} represents the pixel value in the high energy image (CsI Photodiode)
Air_{Atten} represents the pixel value corresponding to the un-attenuated photons (I_0) in the white part of each image.

The R values for the pixels of each tissue mixture were then averaged to give a single R-value representing that tissue mixture. In this way 5 R-values were calculated representing the 5 different tissue mixtures in each calibration block. With each block constructed in triplicate at 3 different thicknesses and scanned 5 times this resulted in a total of 225 data-points. A linear mixed effects model (SAS) was used to analyse R-value, with chemical fat % and tissue depth and their interaction included as covariates, and calibration block identification used as a random term to account for the repeated scanning of each block. To assess the potential for predicting tissue depth directly, the log(pixel value) from the low energy (ZnSe Photodiode) image was also analysed using a linear mixed effects model (SAS), with tissue depth and chemical fat % and their interaction used as covariates, and calibration block identification again used as a random term.

Results

There was a negative linear relationship between increasing chemical fat % and the corresponding R-value (Figure 1). Thus in the 12.5mm calibration block increasing chemical fat % from 6.25 up to 88.0% decreased the average R-value by about 0.11 units (from 1.35 down to 1.24). However, the sensitivity of this relationship diminished as the calibration block thickness increased such that for the 160mm calibration block, the R-value only decreased by 0.05 units across the same increasing chemical fat range.

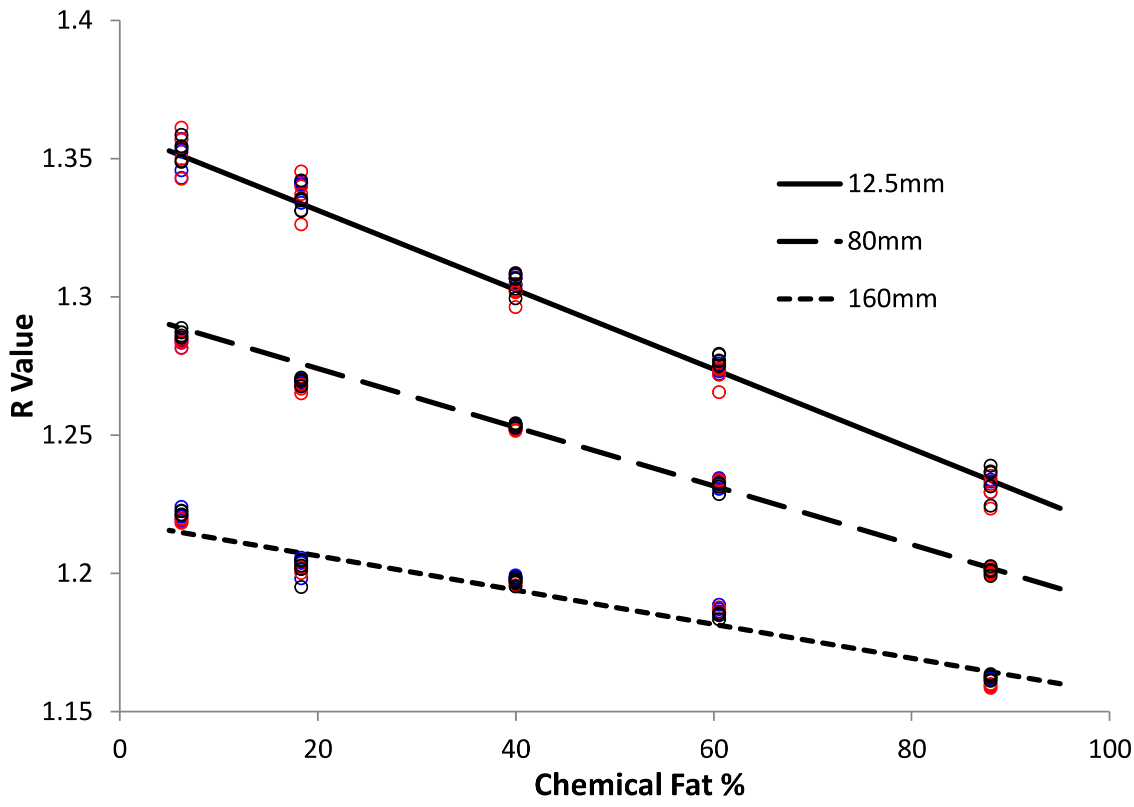


Figure 1. Relationship between R value chemical fat % in calibration blocks of 12.5mm, 80mm, and 160mm thickness.

This relationship was described with a high degree of precision (94.3% of variance described) using a linear mixed effects model, with the coefficients as shown in Table 2. This implies that we can solve for Chemical Fat % but must have knowledge of both R-values and tissue thickness.

Table 2. F-values and coefficients for the prediction of R value using chemical fat % and thickness of calibration blocks.

Parameter	F Value	Coefficient ± SE
Intercept		1.372 ± 0.001
Thickness (mm)	11076*	-0.001 ± 0.000
Chemical Fat (%)	7050*	-0.002 ± 0.000
Thickness (mm)*Chemical Fat (%)	995.4*	$5.55\text{x}10^{-6}$ ± 0.000

*, P<0.01; Thickness = tissue thickness (mm).

There was a linear association (P<0.05) between tissue depth and the log(pixel value) for the low energy image which varied at different levels of chemical fat % (Figure 2). Hence at 6% chemical fat, log pixel values changed by 3.10 when thickness changed from 12.5mm to 160mm, while at 88% chemical fat, log pixel values changed by 2.78.

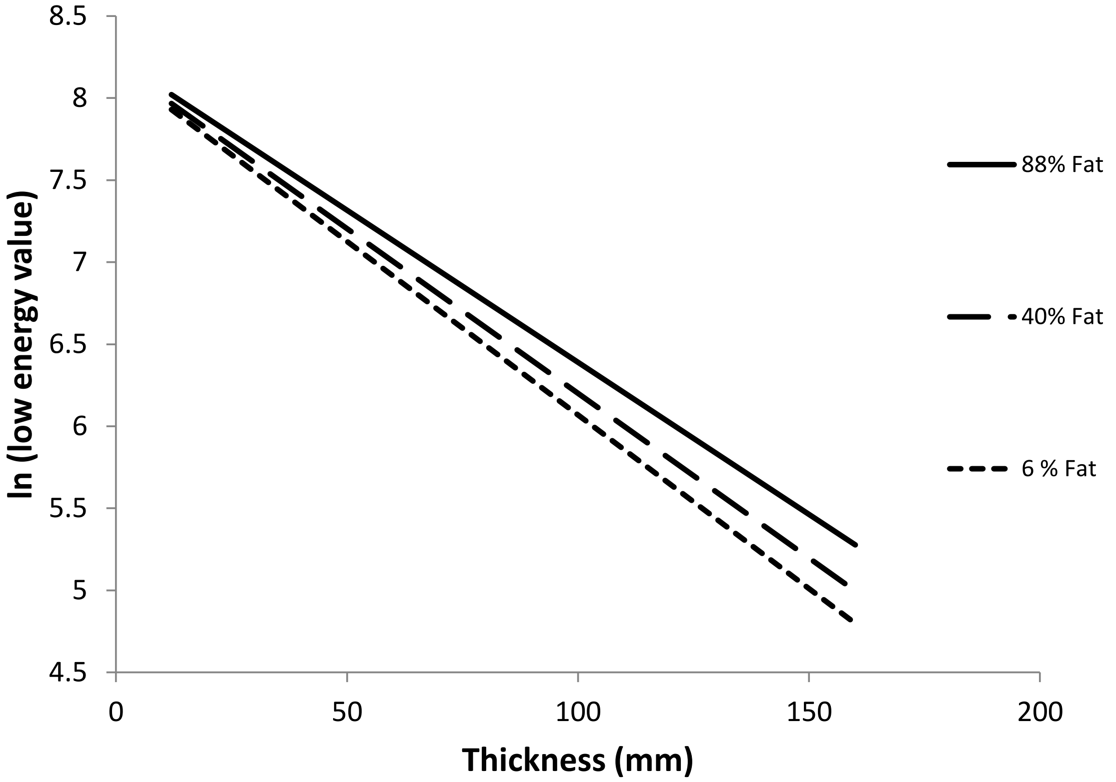


Figure 2. Relationship between tissue depth and the log pixel values for the low energy image at varying levels of chemical fat %. Standard errors are obscured by the response surface, but at most were ±0.011.

Using a linear mixed effects model, this relationship was described with a high degree of precision (98.9% of variance described) using only calibration block thickness as the predictor (Model 1, Table 3). Of course the chemical fat % itself is likely to affect the precision of this thickness estimate, hence it was not surprising that when it was also included in the prediction model (Model 2), it did slightly improve the precision of the estimate (99.8% of variance described). However this effect was particularly small relative to the importance of thickness itself as evidenced by both the F-values in Table 3, and the relationship shown in Figure 2.

Table 3. F-values and coefficients for the prediction of log(pixel value) from the low energy image using only thickness of calibration blocks (Model 1), and thickness of calibration block and Chemical Fat % (Model 2).

Parameter	Model 1		Model 2 – includes Chemical Fat	
	F Value	Estimate ± SE	F Value	Estimate ± SE
Intercept		8.210 ± 0.015		8.179 ± 0.011
Thickness	19447*	-0.020 ± 0.000	35980*	-0.022 ± 0.000
Chemical Fat %			11.01*	$7.35 \times 10^{-4} \pm 2.22 \times 10^{-4}$
Thickness* Chemical Fat %			215.5*	$3.20 \times 10^{-5} \pm 2.18 \times 10^{-6}$

*, P<0.01; Thickness = tissue thickness (mm).

3.1.3 Discussion

As expected, the R-values from the prototype DEXA at Bordertown abattoir demonstrated a strong association with chemical fat % within tissue mixtures of muscle and fat. These were influenced by tissue depth, highlighting the need for depth correction in the calculation of individual pixel R-values when scanning lamb carcases of variable depth. Tissue depth can be estimated through its association with increasing attenuation of X-rays, shown through its relationship with log(pixel values). This estimate is further improved with knowledge of chemical fat %, creating a circular argument given that knowledge of tissue depth improves the estimation of chemical fat %. However, the relative importance of chemical fat % in the model describing log(pixel value) (see Table 3) is much smaller compared to the importance of tissue depth (see Table 2) for describing pixel R-values. On this basis we propose that estimates of pixel depth are made using a fixed value of 56.6 chemical fat % which is based on the estimated fat content of lambs using CT described by Anderson et al (2016).

3.2 Experiment 2. First 48 calibration carcases

3.2.1 Introduction

The next phase of this experiment was to determine the percentage of fat in the non-bone containing pixels of the carcase image, and generate a weighted average of these pixels based upon their tissue depth. This could then be related to our “gold-standard” composition reference - the CT determined composition of bone, muscle, and fat in each carcase.

3.2.2 Materials and Methods

48 lamb carcasses were selected over a 45 minute period across a broad range of fatness (5-27mm GR tissue depth) and carcass weight (17-32kg) immediately following slaughter at a commercial abattoir near Bordertown, SA. These carcasses were then DEXA scanned at 24 hours post-mortem, with the brisket oriented towards the X-ray source. Carcasses were then transported at 2˚C to Murdoch University, WA, where they were scanned using a Picker PQ 5000 spiral computed tomography (CT) scanner using the same scanning protocols detailed in Anderson et al. (2015). Scanning was carried out between 5 and 6 days post mortem after cutting carcases into 3 sections, fore, saddle, and hind section. This enabled the estimation of percent lean (CT lean %), fat (CT fat %), and bone (CT bone %) within each of these 3 sections.

The DEXA hardware consisted of a 140kV X-ray tube with an aluminium filter, and ZnSe and CsI photodiodes separated by a copper filter (Sens-tech, UK). Each time that carcasses were scanned, images were generated using a single emission from the x-ray tube, with a set of 2 images captured on the ZnSe (low energy image) and CsI (high energy image) photodiodes. From these two images, the ratio of the photon attenuation for corresponding pixels within the low and high energy images was then used to calculate an R-value for each pixel (Pietrobelli et al. 1996) according to the following formula:

$(R = \ln(I_{Low}/Air_{Atten}) / \ln(I_{High}/Air_{Atten}))$;

Where: I_{Low} represents the pixel value in the low energy image (ZnSe Photodiode)
I_{High} represents the pixel value in the high energy image (CsI Photodiode)
Air_{Atten} represents the pixel value corresponding to the un-attenuated photons (I_0) in the white part of each image.

The average R-value for all pixels in the carcass image was calculated, setting a threshold value with pixels above this value removed from the image. This eliminates predominantly bone-containing pixels, reducing the image to a two part mixture consisting of fat and lean (see Figure 3). It should be noted that not all bone containing pixels are removed. Pixel R-values were then converted to chemical fat %, weighted based on thickness, and then the mean calculated. In order to align positively with lean meat yield, this value was subtracted from 100 to reflect an average “DEXA value” for all of the pixels in the carcass image. This conversion of R-values for each pixel into the corresponding chemical fat % and

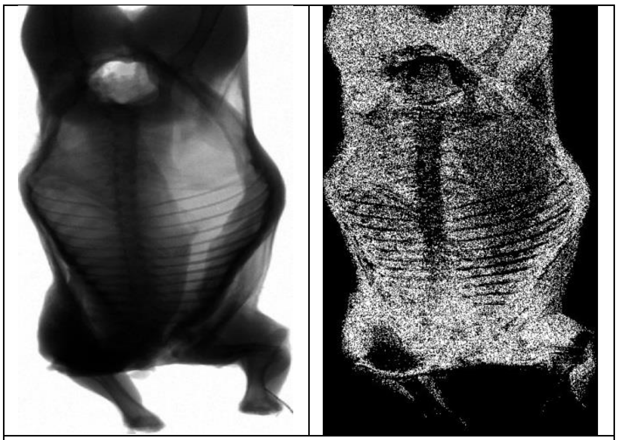


Figure 3. X-ray image from ZnSe photodiode (on left), and after threshold removal of bone-containing pixels (on right).

associated thickness, was based upon the relationships described in Experiment 1 of this report.

General linear models (SAS) were used to predict CT fat%, lean%, and bone%, with DEXA value as the covariate (see Figure 4, Figure 5, Figure 6, and Table 5). These models were then repeated but also incorporating hot carcase weight as a covariate (see Table 5). Covariates were tested as polynomial terms, however were not significant (P>0.05).

To indicate precision the R-square and root mean square error (RMSE) of all associations between DEXA value and the corresponding CT composition are shown in Table 5.

3.2.3 Results

Descriptive carcase statistics are provided in Table 4 below, demonstrating the range in carcase weight and composition for the lambs tested.

Table 4. Descriptive carcase statistics for 48 lamb carcases that were scanned using computed tomography (CT) and on-line dual x-ray absorptiometry at Bordertown in 2015.

	Mean	Standard Deviation	Minimum	Maximum
Hot Carcase Weight (kg)	24.7	4.4	17.4	32.2
GR Tissue Depth (mm)	15	5	5	27
CT lean %	61.30	3.10	51.96	67.84
CT fat %	21.74	3.99	12.70	33.81
CT bone %	16.96	1.48	13.56	21.36

There was a strong relationship (P<0.01) between CT fat% and the DEXA value for each carcase, with a change of 30 units in DEXA value associated with a reduction in CT fat % of about 17 units, and describing about 85% of the variation in CT fat % (see Figure 4). There were also associations with CT lean % (P<0.01) and CT bone % (P<0.01), although weaker, and inverse to that seen for CT fat %. Thus the same change of 30 units in DEXA value was associated with an increase in CT lean % of about 11.8 units, and CT bone % of about 5.5 units, and describing about 64% of the variation in either case (see Figure 5, and Figure 6).

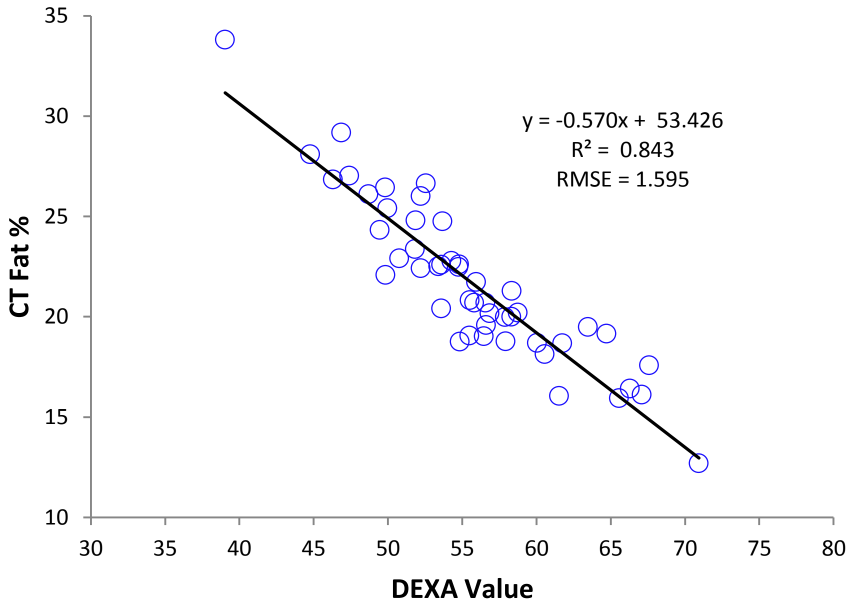


Figure 4. Relationship between CT Fat% and DEXA lean values for 48 lamb carcases selected randomly across a fat and liveweight strata.

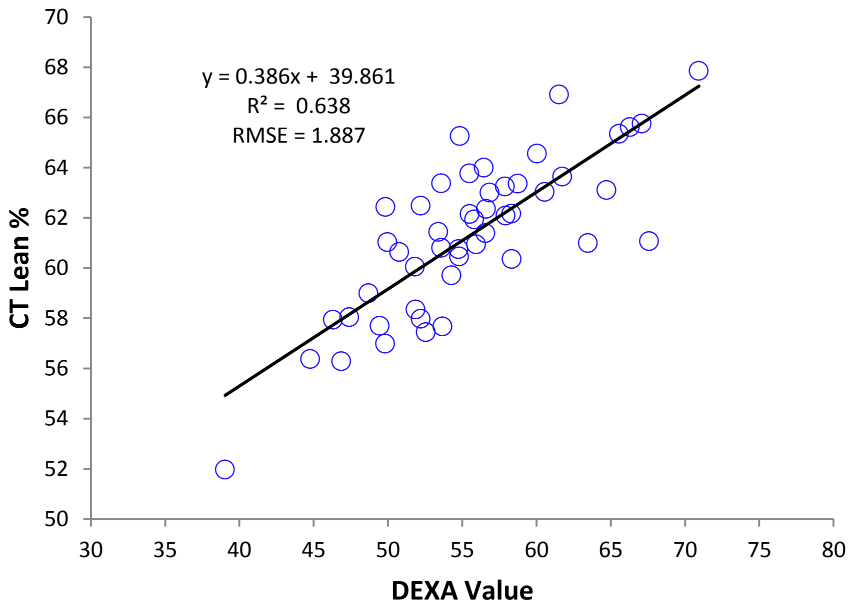


Figure 5. Relationship between CT lean % and DEXA lean values for 48 lamb carcases selected randomly across a fat and liveweight strata.

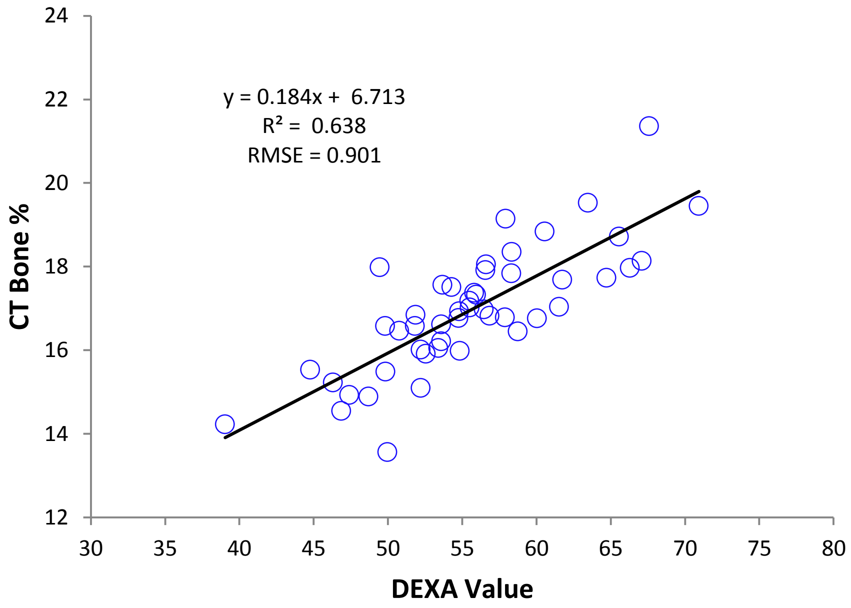


Figure 6. Relationship between CT bone % and DEXA lean values for 48 lamb carcases selected randomly across a fat and liveweight strata.

When hot carcase weight was included in these models it was not significant (P>0.05), with only DEXA value predicting CT composition (see Table 5).

Table 5. F-values, R-square, and root mean square error (RMSE) for models using DEXA value and hot carcase weight (HCWT) as predictors of CT Lean, Bone, and Fat percentage.

Independent Variables	Model with HCWT			Model without HCWT		
	F Value	R-Square	RMSE	F Value	R-Square	RMSE
		CT Lean %			*CT Lean %*	
DEXA Value	**39.67**	0.64	1.894	**81.02**	0.64	1.887
HCWT	0.68					
		CT Fat %			*CT Fat %*	
DEXA Value	**105.44**	0.84	1.607	**247.74**	0.84	1.595
HCWT	0.29					
		CT Bone %			*CT Bone %*	
DEXA Value	**25.57**	0.64	0.905	**81.12**	0.64	0.901
HCWT	0.6					

F-values in bold are significant (P<0.05).

3.2.4 Discussion

These results demonstrate a strong association between DEXA value and CT fat, lean, and bone %, although the precision was substantially better for describing variation in fatness compared to either lean or bone. This was evident through the R-square values, but also the RMSE when assessed as a proportion of the data range, which represented about 7% of the data range for CT fat %, versus 12% for lean and bone. This better prediction of carcase fat % has previously been demonstrated using medical devices. Furthermore, the lack of influence of hot carcase weight within these models indicates that the DEXA value is not simply reflecting weight when determining composition.

3.3 Experiment 3 – nucleus flock calibration.

3.3.1 Introduction

Having established the capacity for the prototype DEXA device to predict composition across a flock consisting of a broad range of weight and fatness, the next phase of experimental work was to assess the performance of this technology across flocks containing a diverse range of genotypes, weights and compositions, and to test the transportability of the resulting prediction equations between these flocks.

3.3.2 Materials and Methods

Experimental design and slaughter details

For this study, lambs from Meat and Livestock Australia's nucleus flock experiment were used, the design of which is detailed elsewhere (Fogarty, Banks, van der Werf, Ball, & Gibson, 2007; van der Werf, Kinghorn, & Banks, 2010). Briefly, about 600 lambs were produced from artificial insemination of Merino or Border Leicester-Merino dams at Kirby NSW, and born between 21 September and 16 October in 2014. The lambs (Merino, Maternal x Merino, Terminal x Merino and Terminal x Border Leicester-Merino) were the progeny of 163 industry sires, representing the major sheep breeds used in the Australian industry. The sires types included Terminal sires (Poll Dorset, Suffolk, Texel, White Suffolk), Maternal sires (Border Leicester, Coopworth, Dohne Merino), and Merino sires (Merino, Poll Merino). After weaning at 90 days of age the lambs were grazed under extensive pasture conditions until being re-located during April 2015 to a feedlot in South Australia, about 100km from the JBS abattoir at Bordertown, SA. All male lambs were castrated.

Slaughter protocol and carcase measurements

These lambs were consigned to 6 slaughter groups on the basis of live weight, with each group killed separately (kill groups) across a period of 4 months to enable a target carcass weight of 21.5 kg to be achieved, except for the final group which aimed for a target weight of 28kg. Within each group, we attempted to represent progeny from each sire, although due to limited numbers of progeny for some sires this was not always possible. Prior to each slaughter, lambs were yarded within 48 hours before slaughter, maintained off-feed for at least 6 hours, and then weighed to determine pre-slaughter live weight. They were then transported for 2 hours via truck to JBS Bordertown abattoir, held in lairage at the abattoir for between 8 and 12 hours, and then slaughtered.

All carcases were electrically stimulated and trimmed according to AUSMEAT standards (Anon, 1992), and hot standard carcase weight (HCWT) was then measured within 40 minutes of slaughter. All lambs were measured and sampled for a wide range of carcase, meat and growth traits including GR tissue depth, which was measured 12 cm from the midline over the 12th rib, and was taken as the total tissue depth above the surface of this rib. These carcases were then DEXA scanned at 24 hours post-mortem, with the brisket oriented towards the X-ray source. The DEXA scanning hardware, image acquisition, and image analysis were the same as described in Experiment 2 above. For nucleus flocks 2-6 a synthetic phantom was also DEXA scanned at the same time as the carcases were DEXA scanned as an internal point of reference (the synthetic phantom scans from the first group were not captured). This synthetic phantom was a single block consisting of sections of nylon and perspex, each 50mm thick. Carcases were then transported at 2˚C to Murdoch University, WA, where they were scanned between 5 and 6 days post-mortem using a Picker PQ 5000 spiral computed tomography (CT) scanner to enable the estimation of percent lean (CT lean %), fat (CT fat %), and bone (CT bone %) using the same scanning protocols detailed in Anderson et al. (2015).

Analysis

A total of 600 lambs were slaughtered, with data from 559 available for analysis after removing animals with missing data. Data was mainly excluded from analysis due to one batch of carcases being oriented incorrectly during DEXA scanning during the first nucleus flock slaughter.

Initially, within each slaughter group general linear models (SAS) were used to predict CT fat%, lean%, and bone%, with DEXA value as the covariate (see Table 6). R-square and root mean square error (RMSE) were used to show precision.

The intercept of these models varied markedly, with much smaller differences in slope. So to reflect these shifts between scanning days within the range of the population the predicted DEXA value at the population mid-point of the range in CT fat % (ie 27.7% CT fat) was determined for each group. This was then plotted against the R-value for the Nylon and Perspex synthetic phantoms which were scanned at the same time as each slaughter group. This process was repeated for CT lean % (DEXA value predicted at 57.6% CT lean) and CT bone % (DEXA value predicted at 14.7% CT bone).

On the basis of the association identified with the nylon synthetic phantom, the DEXA values for the populations from nucleus flocks 2-6 were normalised for the R-value of the nylon phantom scanned with each group. This produced 3 different sets of nylon-normalised DEXA values based on the nylon association with CT lean%, fat% and bone%, which we have termed DEXA lean, DEXA fat, and DEXA bone. Data from these groups were then pooled and analysed using a general linear model. Firstly CT fat % was modelled using DEXA fat value and hot carcase weight as covariates, and identification of nucleus flock group (2-6) used as a fixed effect. Interactions between these terms were tested, but removed due to non-significance (P>0.05). This same process was repeated for CT lean %, but using the normalised DEXA lean value and the covariate, and also for CT bone %, but using the normalised DEXA bone value as the covariate (see Table 11).

Lastly we tested the transportability of the equations for predicting CT fat % (Table 12), lean % (Table 13), and bone % (Table 14) between the different nucleus flock slaughter groups, using the nylon-normalised DEXA data. The equations described above (excluding the term for identification of nucleus flock group) were derived within one nucleus flock group, and then their prediction accuracy and precision tested by transporting them into the other nucleus flock groups. Despite there being no nylon scan at the slaughter of the first nucleus flock group (nucleus flock 1), or for the slaughter of the pre-nucleus flock group which was described in experiment 2 above, these were still normalised on the basis of their "predicted" nylon R-value using the relationships shown in Table 10. In this way they could still be used to test transportability. Also a "combined" group were included which represent all of the data from nucleus flocks 2-6 pooled. To reflect the precision of prediction, R-square, and root mean square error values were reported. To reflect the accuracy of prediction the slope and intercept of the relationship between predicted and actual CT composition was reported, as well as differences between observed minus predicted values calculated at points across the range of CT fat % (20%, 27%, 34%), lean % (52%, 57%, 62%), and bone % (12%, 14.5%, 17%).

3.3.3 Results

Descriptive carcase statistics are provided in Table 7 below, demonstrating the range in carcase weight and composition for the lambs tested.

Table 7. Descriptive statistics for carcases from 6 nucleus flock slaughters that were scanned using computed tomography (CT) and on-line dual x-ray absorptiometry at Bordertown in 2015. Values are Mean ± standard deviation (minimum, maximum).

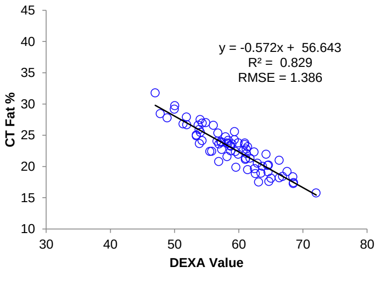
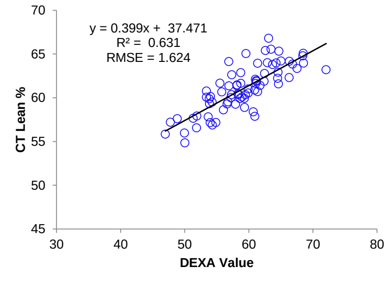
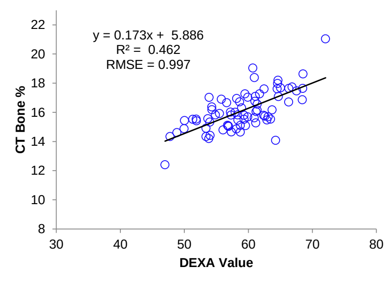
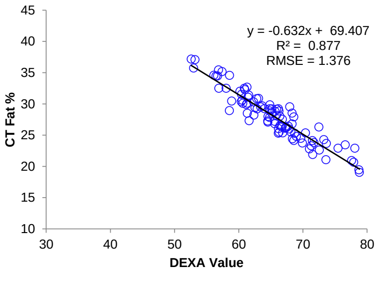
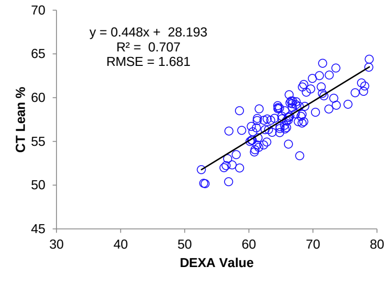
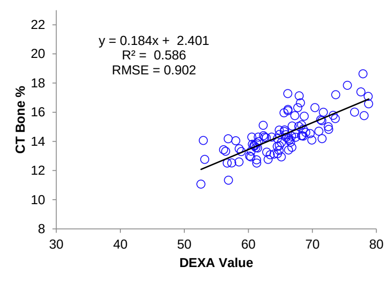
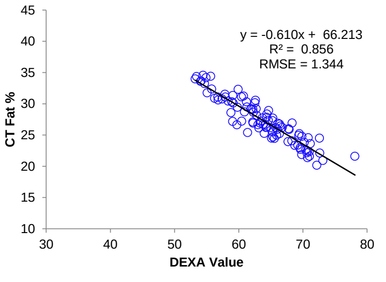
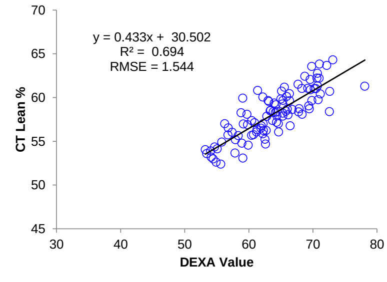
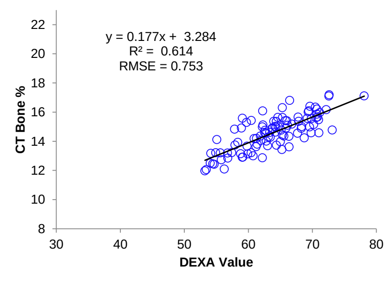
Nucleus Flock (N)	Hot Carcase Weight (kg)	GR Tissue Depth (mm)	CT fat %	CT lean %	CT bone %
1 (74)	19.9±3.1 (13.5 , 29.0)	9.3±3.5 (2 , 17)	22.86±3.33 (15.76 , 31.77)	61.02±2.66 (54.84 , 66.80)	16.12±1.35 (12.40 , 21.04)
2 (95)	23.6±4.8 (13.5 , 35.0)	17.3±5.6 (4 , 30)	27.96±3.91 (19.03 , 37.17)	57.57±3.09 (50.15 , 64.39)	14.47±1.39 (11.07 , 18.63)
3 (98)	23.5±4.6 (13.0 , 34.2)	15.3±5.1 (6 , 28)	27.32±3.52 (20.16 , 34.56)	58.11±2.78 (52.39 , 64.31)	14.57±1.21 (11.97 , 17.18)
4 (98)	21.4±4.9 (12.3 , 33.5)	14.4±5.5 (5 , 30)	26.05±3.98 (18.62 , 36.55)	59.18±3.14 (50.29 , 65.60)	14.78±1.33 (11.86 , 17.86)
5 (100)	22.2±5.4 (10.9 , 37.1)	15.7±6.0 (2 , 36)	27.69±4.20 (17.11 , 36.47)	57.39±3.16 (49.57 , 65.91)	14.91±1.70 (12.05 , 20.91)
6 (94)	26.1±6.1 (13.2 , 39.3)	19.6±7.5 (5 , 44)	29.57±4.54 (18.41 , 39.53)	55.46±3.33 (47.29 , 62.19)	14.96±1.64 (12.28 , 20.17)

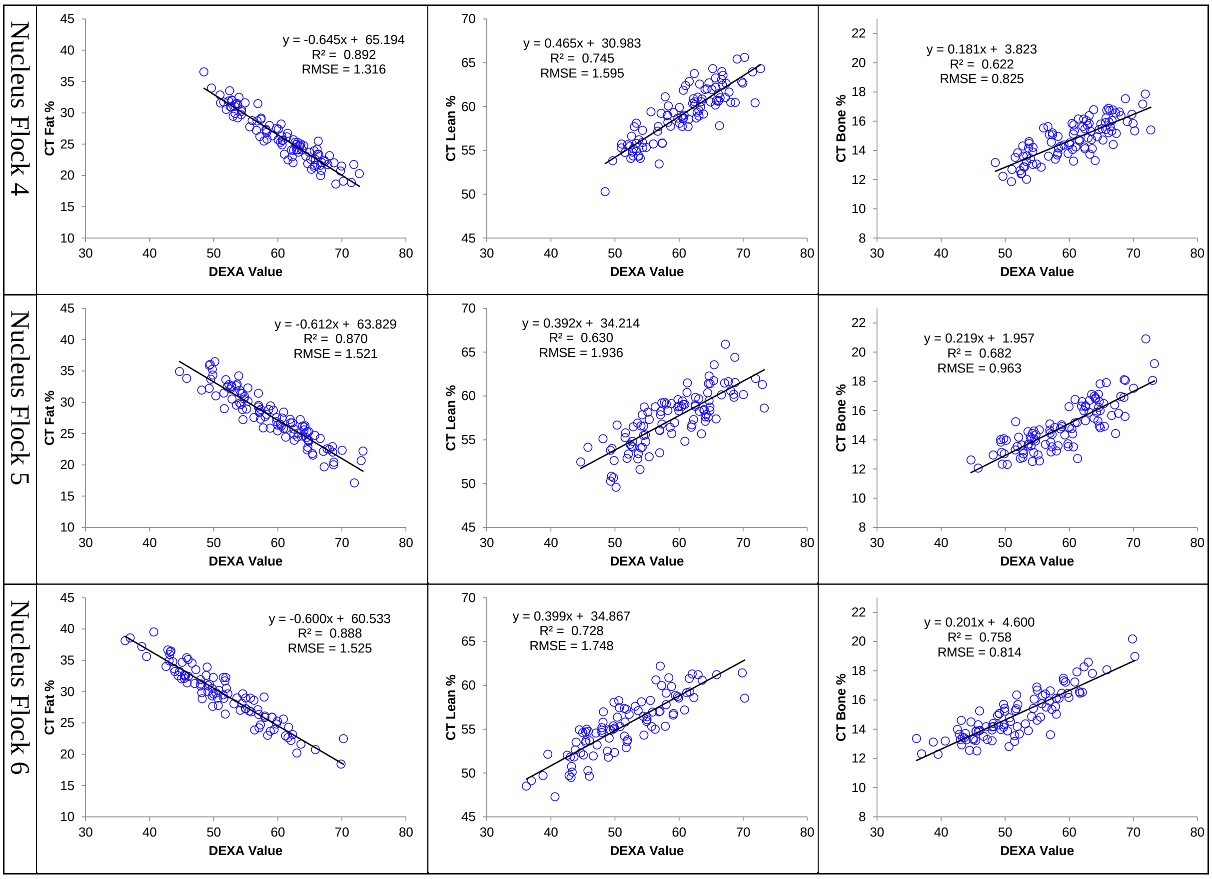
Across 5 of the nucleus flock groups (groups 2-6) there was a strong relationship ($P<0.01$) between CT fat % and the DEXA value for each carcase (see Table 8) describing between 86% – 89% of the variation in CT fat %. The slope of these relationships was relatively consistent, varying between -0.6 and -0.64, however the intercepts varied markedly, ranging between 60 – 69 CT fat % units. The only outlier to this was for the first nucleus flock slaughter, which only described 83% of the variation in CT fat %, had a lesser slope (-0.57) and a smaller intercept value (57) compared to the other groups.

By comparison the association between DEXA value and CT lean % (P<0.01), and DEXA value and CT bone % (P<0.01) was not as strong, describing between 63% -73% of the variation in CT lean % and 58%-76% of the variation in CT bone % across 5 of the nucleus flock groups (groups 2-6). For CT lean % the slopes of this relationship were reasonably consistent, varying between 0.39 – 0.47, while the intercept values varied more markedly by between 28 – 35 CT lean % units. Similarly, for CT bone % the slopes of this relationship were also consistent, varying between 0.18 – 0.22, while the intercept values varied more markedly by between 1.96 – 4.60 CT bone % units.

As was the case for CT fat %, the first nucleus flock group was the outlier to these results. In this group the DEXA value described only 63% of the variation in CT lean % and 46 % of the variation in CT bone %. It also had the lowest slope values (0.40 CT lean %; 0.17 CT bone %) and the highest intercept values (37 CT lean %; 5.89 CT bone %) of all nucleus flock groups.

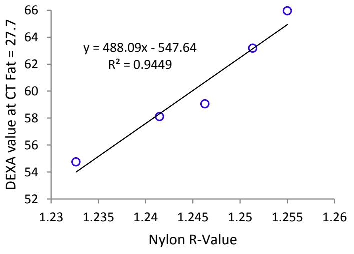
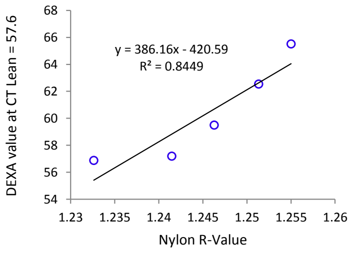
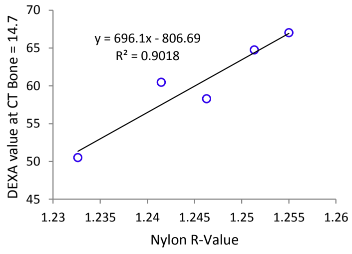
Table 9. Relationship between CT fat, bone, and lean % versus DEXA lean values for 6 nucleus flock slaughters, each consisting of about 100 lamb carcases. Linear equations and R-square values are shown for each graph.

	CT Fat %	CT Lean %	CT Bone %
Nucleus Flock 1			
Nucleus Flock 2			
Nucleus Flock 3			



In order to explore the marked variation in intercept values of these groups, comparisons were made with the synthetic phantoms that were also scanned at the start of each scanning run for each nucleus flock group. To reflect these intercepts within the range of the data an estimate of DEXA value at the population mid-point of the range in CT fat % was determined for each group, and then plotted against the R-value for Nylon and Perspex. This process was repeated for CT lean % and CT bone %. There was little relationship between these population mid-point values and the perspex phantom, however for the nylon phantom there was a strong linear relationship (P<0.01) between its average R-value and the population mid-point values for CT fat %, lean % and bone % (see Table 10). This implies that calibration is required to account for this fixed shift in R-value between slaughter days.

Table 10. Graphs showing the relationship between the average nylon R-value and the population intercept for 5 of the nucleus flock slaughters (nucleus flock 2 – 6).

CT Fat %	CT Lean %	CT Bone %
		

Therefore after adjusting the DEXA value of each data-set to the mean of the nylon R-values, models were generated to predict CT fat %, lean %, and bone % (see Table 11). In all cases hot carcase weight was not significant, DEXA lean value was the most important term, and nucleus flock group were significant although the adjustments between groups were small. The precision of these models was very high, with R2 for CT fat, lean and bone of 0.89, 0.74, 0.71, and root mean square error of 1.42, 1.69, and 0.80, which each represent 6%, 9%, and 8% of the data range across nucleus flocks 2-6 for CT fat, lean and bone.

Table 11. Coefficients, F-values, R-squared, and root mean square error for models using nylon adjusted DEXA values, hot carcase weight, and nucleus flock group as predictors of CT lean, bone, and fat percentage for nucleus flock groups 2 -6.

Variables	*CT Fat %*		*CT Lean %*		*CT Bone %*	
	Coefficient	F Value	Coefficient	F Value	Coefficient	F Value
Intercept	63.79		26.15		8.90	
Adjusted DEXA value	-0.611	**1568**	0.471	**659**	0.139	**260**
Hot Carcase Weight	0.012	0.420	0.078	**12.8**	-0.090	**76.7**
Nucleus Flock Group		**30.6**		**18.9**		**23.5**
2	1.64± 0.215		0.91± 0.250		-0.50± 0.122	
3	0.80± 0.212		1.42± 0.248		-0.52± 0.120	
4	-0.03± 0.215		1.87± 0.255		-1.03± 0.120	
5	-0.51± 0.211		1.89± 0.255		-0.13± 0.127	
6	0		0		0	
R-Square	0.886		0.744		0.712	
Root Mean Square Error	1.419		1.689		0.796	

F-values in bold are significant (P<0.05).

In order to test for robustness when transported, the equations described in Table 11 were derived in one kill group, and then used to predict CT composition in the other kill groups (see Table 12, Table 13, and Table 14). As a general observation, the precision of prediction for determining CT fat % was maintained when determined within the training data set, and then transported to the other 6 data sets. In all cases the precision of prediction within each data set varied little from the precision reported when the prediction equation was derived directly in that data set. Across all tests, the least variation described within any single group was 82.6% and the most was 89.6%. Aligning with this were relatively low root mean square error values, which compared to the data range within each group represented as little as 7.3%, and as much as 9.4% of the data range.

The accuracy of the prediction was also good, with the difference between the actual and predicted CT fat % being relatively small. For the differences calculated at 20%, 27%, and 34% predicted CT fat, two-thirds of the time the inaccuracy was within ±0.92, ±0.74, and ±0.81 observed CT fat %. Across all of the tests, the single worst predictions were an over-prediction by 1.83 CT fat %, and an under-prediction by 2.30 CT fat %.

For CT lean % and CT bone % the precision was generally much lower than CT fat %, although the transportation of the prediction equations was still very robust. This was well demonstrated by the comparison of precision for the data set that it was trained in, compared to the precision of prediction when it was transported into the other data sets. At worst the DEXA/hot carcase weight prediction equation described 52.6% of the variation in CT lean % and 53.1% of the variation in CT bone%, and at best it described 74.6% and 80.5% of the variation. The root mean square error values were also quite variable, and when compared to the data range within each group represented as little as 10.7%, and as much as 13.5% of the data range for CT lean %, and as little as 9.4% and as much as 13.9% for CT bone %.

The accuracy of the prediction for CT lean % and CT bone % was also less compared to CT fat %. The difference between the actual and predicted CT lean % calculated at 52%, 57%, and 62% predicted CT lean was within ±0.97, ±1.03, and ±1.32 observed CT lean % for two-thirds of the transportation tests. Across all of the tests, the single worst predictions were an over-prediction by 3.17 CT lean %, and an under-prediction by 2.69 CT lean %. The difference between the actual and predicted CT bone % calculated at 12%, 14.5%, and 17% predicted CT bone was within ±0.83, ±0.74, and ±0.81 observed CT bone % for two-thirds of the transportation tests. Across all of the tests, the single worst predictions were an over-prediction by 1.51 CT bone %, and an under-prediction by 2.47 CT bone %. All

The final industry algorithm is likely to be based upon test 8, whereby the equation was trained in a combination of data from nucleus flocks 2-6 (also shown in Table 11). Hence its maintained precision after transportation into the group of pre-nucleus flock lambs for CT fat % (R2, 0.84; RMSE, 1.61), CT lean % (R2, 0.64; RMSE, 1.88), and CT bone % (R2, 0.64; RMSE, 0.90) is an excellent result, as these animals were randomly chosen on one production day, and not related to the nucleus flock animals.

Table 12. Precision estimates (R-square and root mean square error), intercept and slope of actual CT fat % versus predicted CT fat %, and accuracy estimates showing difference between observed minus the predicted

at 20% (Diff@20), 27% (Diff@27), and 34% (Diff@34) CT fat using DEXA value (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.844	0.829	0.875	0.852	0.891	0.872	0.888	0.889
	RMSE	1.594	1.387	1.390	1.363	1.324	1.512	1.524	1.532
	Intercept	0.000	0.012	-2.441	-1.902	-4.020	-3.455	-1.218	-1.279
	Slope	1.000	0.993	1.106	1.064	1.133	1.081	1.056	1.042
	Diff@20	0.00	-0.12	-0.32	-0.62	-1.35	-1.83	-0.11	-0.45
	Diff@27	0.00	-0.17	0.42	-0.17	-0.42	-1.27	0.28	-0.16
	Diff@34	0.00	-0.22	1.16	0.28	0.52	-0.70	0.67	0.13
Test 2	R2	0.844	0.829	0.877	0.855	0.892	0.870	0.888	0.891
	RMSE	1.594	1.386	1.380	1.349	1.318	1.518	1.524	1.520
	Intercept	0.043	0.000	-2.336	-1.839	-3.795	-3.082	-1.001	-1.220
	Slope	1.000	1.000	1.108	1.068	1.132	1.075	1.053	1.045
	Diff@20	0.05	0.00	-0.17	-0.48	-1.15	-1.58	0.06	-0.32
	Diff@27	0.05	0.00	0.59	-0.01	-0.23	-1.05	0.43	0.00
	Diff@34	0.05	0.00	1.34	0.46	0.70	-0.52	0.80	0.31
Test 3	R2	0.842	0.827	0.879	0.860	0.892	0.866	0.886	0.893
	RMSE	1.602	1.392	1.367	1.324	1.314	1.544	1.540	1.501
	Intercept	1.930	1.779	0.000	0.332	-1.116	-0.145	1.506	0.854
	Slope	0.900	0.916	1.000	0.967	1.013	0.952	0.938	0.948
	Diff@20	-0.07	0.10	0.00	-0.34	-0.86	-1.11	0.28	-0.19
	Diff@27	-0.77	-0.49	0.00	-0.57	-0.76	-1.45	-0.15	-0.56
	Diff@34	-1.47	-1.07	0.00	-0.81	-0.67	-1.79	-0.59	-0.92
Test 4	R2	0.841	0.826	0.878	0.861	0.891	0.863	0.884	0.893
	RMSE	1.609	1.398	1.370	1.320	1.320	1.561	1.556	1.501
	Intercept	1.504	1.296	-0.313	0.000	-1.298	-0.136	1.347	0.478
	Slope	0.930	0.955	1.033	1.000	1.043	0.975	0.964	0.982
	Diff@20	0.10	0.39	0.36	0.00	-0.44	-0.64	0.63	0.12
	Diff@27	-0.39	0.08	0.59	0.00	-0.14	-0.81	0.38	0.00
	Diff@34	-0.88	-0.24	0.82	0.00	0.16	-0.99	0.14	-0.13
Test 5	R2	0.843	0.828	0.879	0.859	0.893	0.868	0.887	0.893
	RMSE	1.598	1.389	1.369	1.329	1.313	1.534	1.532	1.505
	Intercept	3.089	2.986	1.193	1.507	0.000	0.780	2.536	2.030
	Slope	0.887	0.897	0.984	0.951	1.000	0.943	0.928	0.931
	Diff@20	0.82	0.93	0.88	0.52	0.00	-0.37	1.09	0.65
	Diff@27	0.03	0.20	0.77	0.17	0.00	-0.77	0.58	0.17
	Diff@34	-0.77	-0.52	0.66	-0.17	0.00	-1.17	0.07	-0.31
Test 6	R2	0.842	0.826	0.865	0.836	0.883	0.873	0.885	0.880
	RMSE	1.600	1.398	1.445	1.431	1.367	1.502	1.546	1.593
	Intercept	4.154	4.247	2.011	2.517	0.164	0.000	2.671	2.999
	Slope	0.908	0.881	0.995	0.952	1.032	1.000	0.966	0.934
	Diff@20	2.30	1.87	1.91	1.55	0.79	0.00	1.99	1.67
	Diff@27	1.66	1.04	1.87	1.22	1.01	0.00	1.74	1.20
	Diff@34	1.01	0.21	1.84	0.88	1.24	0.00	1.50	0.74
Test 7	R2	0.844	0.829	0.876	0.853	0.891	0.871	0.888	0.890

	RMSE	1.594	1.387	1.384	1.356	1.320	1.515	1.524	1.526
	Intercept	1.076	1.057	-1.223	-0.748	-2.715	-2.134	0.000	-0.151
	Slope	0.949	0.945	1.050	1.011	1.075	1.023	1.000	0.990
	Diff@20	0.05	-0.04	-0.22	-0.53	-1.23	-1.68	0.00	-0.36
	Diff@27	-0.31	-0.42	0.13	-0.45	-0.70	-1.52	0.00	-0.43
	Diff@34	-0.67	-0.80	0.48	-0.37	-0.18	-1.36	0.00	-0.50
Test 8	R2	0.841	0.826	0.879	0.861	0.892	0.864	0.884	0.893
	RMSE	1.606	1.396	1.369	1.321	1.318	1.555	1.551	1.500
	Intercept	1.500	1.306	-0.368	-0.045	-1.394	-0.278	1.256	0.450
	Slope	0.933	0.955	1.037	1.003	1.047	0.981	0.969	0.985
	Diff@20	0.16	0.42	0.37	0.01	-0.44	-0.66	0.64	0.14
	Diff@27	-0.31	0.10	0.63	0.03	-0.11	-0.80	0.42	0.03
	Diff@34	-0.78	-0.21	0.88	0.06	0.22	-0.93	0.21	-0.07

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Table 13. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % versus predicted CT lean %, and accuracy estimates showing difference between observed minus the predicted at 52% (Diff@52), 57% (Diff@57), and 62% (Diff@62) CT lean using DEXA value (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.641	0.656	0.705	0.683	0.743	0.655	0.742	0.733
	RMSE	1.878	1.569	1.687	1.570	1.599	1.869	1.701	1.824
	Intercept	0.000	0.475	-7.967	-4.470	-10.771	-2.493	-3.836	-2.602
	Slope	1.000	1.007	1.149	1.096	1.213	1.069	1.059	1.058
	Diff@52	0.00	0.84	-0.24	0.54	0.32	1.10	-0.76	0.42
	Diff@57	0.00	0.87	0.50	1.03	1.39	1.44	-0.47	0.72
	Diff@62	0.00	0.91	1.24	1.51	2.45	1.79	-0.17	1.01
Test 2	R2	0.622	0.677	0.635	0.587	0.673	0.678	0.712	0.669
	RMSE	1.928	1.519	1.877	1.792	1.806	1.804	1.800	2.032
	Intercept	-5.496	0.000	-7.697	-1.555	-13.786	-14.262	-9.841	-2.326
	Slope	1.060	1.000	1.122	1.025	1.246	1.261	1.138	1.034
	Diff@52	-2.37	0.00	-1.37	-0.23	-0.97	-0.71	-2.69	-0.57
	Diff@57	-2.07	0.00	-0.76	-0.10	0.26	0.60	-2.00	-0.40
	Diff@62	-1.77	0.00	-0.15	0.02	1.49	1.90	-1.31	-0.23
Test 3	R2	0.640	0.643	0.708	0.692	0.746	0.640	0.736	0.739
	RMSE	1.881	1.599	1.677	1.548	1.590	1.907	1.724	1.805
	Intercept	7.617	7.068	0.000	2.729	-1.701	6.793	4.698	4.417
	Slope	0.863	0.883	1.000	0.962	1.044	0.896	0.902	0.927
	Diff@52	0.51	0.98	0.00	0.73	0.59	1.37	-0.39	0.61
	Diff@57	-0.17	0.40	0.00	0.54	0.81	0.85	-0.88	0.25
	Diff@62	-0.85	-0.19	0.00	0.35	1.03	0.33	-1.37	-0.12
Test 4	R2	0.638	0.632	0.707	0.694	0.745	0.630	0.729	0.739
	RMSE	1.887	1.623	1.681	1.544	1.594	1.934	1.746	1.802

	Intercept	5.657	4.398	-2.618	0.000	-4.046	5.511	3.045	1.710
	Slope	0.892	0.921	1.036	1.000	1.075	0.908	0.923	0.965
	Diff@52	0.07	0.29	-0.73	0.00	-0.17	0.74	-0.96	-0.10
	Diff@57	-0.47	-0.11	-0.55	0.00	0.21	0.28	-1.35	-0.27
	Diff@62	-1.01	-0.50	-0.37	0.00	0.58	-0.17	-1.73	-0.44
Test 5	R2	0.640	0.643	0.708	0.692	0.746	0.641	0.736	0.738
	RMSE	1.881	1.599	1.677	1.548	1.590	1.906	1.723	1.805
	Intercept	9.022	8.519	1.636	4.307	0.000	8.237	6.160	5.938
	Slope	0.827	0.846	0.958	0.921	1.000	0.858	0.864	0.888
	Diff@52	0.02	0.49	-0.56	0.19	0.00	0.86	-0.90	0.09
	Diff@57	-0.84	-0.28	-0.77	-0.21	0.00	0.16	-1.58	-0.47
	Diff@62	-1.71	-1.06	-0.98	-0.60	0.00	-0.55	-2.26	-1.03
Test 6	R2	0.627	0.677	0.649	0.604	0.687	0.679	0.721	0.681
	RMSE	1.916	1.520	1.841	1.755	1.765	1.802	1.770	1.995
	Intercept	6.044	10.351	3.610	8.448	-0.883	0.000	2.347	8.195
	Slope	0.851	0.810	0.914	0.841	1.010	1.000	0.916	0.841
	Diff@52	-1.69	0.46	-0.84	0.20	-0.38	0.00	-2.03	-0.09
	Diff@57	-2.43	-0.49	-1.27	-0.59	-0.34	0.00	-2.46	-0.88
	Diff@62	-3.17	-1.44	-1.70	-1.38	-0.29	0.00	-2.88	-1.68
Test 7	R2	0.641	0.663	0.699	0.673	0.737	0.663	0.744	0.726
	RMSE	1.880	1.552	1.704	1.596	1.617	1.846	1.696	1.847
	Intercept	3.866	5.195	-2.766	0.858	-5.806	0.739	0.000	2.348
	Slope	0.937	0.933	1.067	1.012	1.137	1.023	1.000	0.980
	Diff@52	0.61	1.71	0.70	1.48	1.32	1.94	0.00	1.31
	Diff@57	0.29	1.38	1.04	1.54	2.00	2.06	0.00	1.21
	Diff@62	-0.02	1.04	1.37	1.60	2.69	2.17	0.00	1.11
Test 8	R2	0.640	0.640	0.708	0.693	0.746	0.638	0.734	0.739
	RMSE	1.883	1.606	1.677	1.546	1.591	1.915	1.730	1.804
	Intercept	6.664	5.899	-1.217	1.494	-2.856	6.021	3.810	3.214
	Slope	0.876	0.899	1.016	0.978	1.058	0.904	0.913	0.943
	Diff@52	0.23	0.62	-0.39	0.35	0.18	1.03	-0.72	0.24
	Diff@57	-0.39	0.12	-0.31	0.24	0.47	0.55	-1.15	-0.04
	Diff@62	-1.01	-0.39	-0.23	0.13	0.77	0.07	-1.59	-0.33

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Table 14. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % versus predicted CT bone %, and accuracy estimates showing difference between observed minus the predicted at 12% (Diff@12), 14.5% (Diff@14.5), and 17% (Diff@17) CT bone using DEXA value (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.645	0.531	0.620	0.654	0.644	0.724	0.796	0.664
	RMSE	0.892	0.931	0.863	0.713	0.800	0.898	0.747	0.941
	Intercept	0.000	-1.770	-1.261	-0.630	-0.506	-2.709	-0.986	-0.498
	Slope	1.000	1.060	1.018	0.983	0.966	1.162	1.075	0.995
	Diff@12	0.00	-1.05	-1.04	-0.83	-0.92	-0.76	-0.09	-0.56
	Diff@14.5	0.00	-0.90	-1.00	-0.87	-1.00	-0.36	0.10	-0.57
	Diff@17	0.00	-0.74	-0.95	-0.92	-1.09	0.05	0.29	-0.59
Test 2	R2	0.601	0.630	0.571	0.584	0.596	0.756	0.773	0.591
	RMSE	0.946	0.827	0.917	0.782	0.853	0.843	0.788	1.037
	Intercept	5.414	0.000	4.179	4.965	4.806	2.801	4.830	4.433
	Slope	0.754	1.000	0.711	0.662	0.660	0.833	0.747	0.724
	Diff@12	2.47	0.00	0.71	0.91	0.73	0.80	1.80	1.12
	Diff@14.5	1.85	0.00	-0.02	0.07	-0.12	0.38	1.17	0.43
	Diff@17	1.24	0.00	-0.74	-0.78	-0.97	-0.04	0.54	-0.27
Test 3	R2	0.643	0.566	0.625	0.658	0.645	0.739	0.804	0.663
	RMSE	0.895	0.896	0.857	0.709	0.800	0.872	0.731	0.942
	Intercept	1.384	-1.562	0.000	0.623	0.846	-1.181	0.533	0.635
	Slope	0.985	1.113	1.000	0.963	0.937	1.129	1.044	0.984
	Diff@12	1.21	-0.21	0.00	0.18	0.08	0.37	1.06	0.45
	Diff@14.5	1.17	0.08	0.00	0.09	-0.07	0.69	1.17	0.41
	Diff@17	1.13	0.36	0.00	0.00	-0.23	1.01	1.28	0.37
Test 4	R2	0.644	0.559	0.625	0.659	0.645	0.736	0.804	0.664
	RMSE	0.894	0.902	0.858	0.708	0.799	0.877	0.733	0.941
	Intercept	0.741	-2.039	-0.635	0.000	0.225	-1.903	-0.160	0.032
	Slope	1.021	1.140	1.037	1.000	0.974	1.173	1.085	1.019
	Diff@12	0.99	-0.36	-0.19	0.00	-0.09	0.17	0.86	0.27
	Diff@14.5	1.04	-0.01	-0.09	0.00	-0.16	0.60	1.07	0.31
	Diff@17	1.09	0.34	0.00	0.00	-0.22	1.04	1.29	0.36
Test 5	R2	0.644	0.552	0.624	0.658	0.646	0.733	0.802	0.664
	RMSE	0.893	0.910	0.858	0.709	0.799	0.882	0.735	0.940
	Intercept	0.515	-2.009	-0.840	-0.208	0.000	-2.149	-0.412	-0.145
	Slope	1.045	1.151	1.063	1.025	1.000	1.204	1.114	1.043
	Diff@12	1.05	-0.20	-0.09	0.09	0.00	0.30	0.95	0.37
	Diff@14.5	1.16	0.18	0.07	0.16	0.00	0.81	1.24	0.47
	Diff@17	1.27	0.56	0.23	0.22	0.00	1.32	1.52	0.58
Test 6	R2	0.611	0.628	0.586	0.602	0.608	0.757	0.783	0.609
	RMSE	0.934	0.829	0.902	0.765	0.840	0.842	0.770	1.015
	Intercept	2.781	-3.063	1.588	2.469	2.428	0.000	2.184	1.853
	Slope	0.902	1.176	0.864	0.811	0.801	1.000	0.904	0.876
	Diff@12	1.61	-0.95	-0.04	0.20	0.04	0.00	1.03	0.36
	Diff@14.5	1.36	-0.51	-0.38	-0.27	-0.46	0.00	0.79	0.05
	Diff@17	1.12	-0.07	-0.72	-0.75	-0.96	0.00	0.55	-0.26

Test 7	R2	0.640	0.580	0.624	0.656	0.643	0.744	0.805	0.659
	RMSE	0.898	0.881	0.859	0.711	0.802	0.864	0.729	0.947
	Intercept	0.851	-2.754	-0.563	0.116	0.373	-1.830	0.000	0.023
	Slope	0.951	1.104	0.961	0.923	0.896	1.083	1.000	0.949
	Diff@12	0.26	-1.51	-1.03	-0.81	-0.88	-0.83	0.00	-0.58
	Diff@14.5	0.14	-1.25	-1.13	-1.00	-1.14	-0.63	0.00	-0.71
	Diff@17	0.01	-0.99	-1.23	-1.19	-1.40	-0.42	0.00	-0.84
Test 8	R2	0.640	0.581	0.624	0.656	0.642	0.745	0.805	0.659
	RMSE	0.899	0.880	0.859	0.711	0.802	0.863	0.730	0.948
	Intercept	-0.133	-3.952	-1.557	-0.836	-0.550	-2.954	-1.031	-0.966
	Slope	1.071	1.247	1.082	1.039	1.009	1.220	1.126	1.070
	Diff@12	0.73	-0.99	-0.57	-0.36	-0.45	-0.32	0.48	-0.13
	Diff@14.5	0.90	-0.37	-0.37	-0.26	-0.42	0.23	0.80	0.05
	Diff@17	1.08	0.24	-0.16	-0.17	-0.40	0.78	1.11	0.22

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

3.3.4 Discussion

These results not only demonstrate excellent precision for measuring CT fat % but also demonstrate the robustness of this prediction, both in terms of precision and accuracy, when transported into other data sets. These results are significant given the diverse range of carcase types that this has been tested across, both in terms of weight and fatness, but also genetic diversity.

As was shown in Experiment 2, the precision and accuracy for determining CT lean %, and CT bone % were less, although as was the case with CT fat %, there was no obvious loss in precision when this prediction was transported to other data sets. The functional importance of this reduced precision for CT lean %, and CT bone % is not immediately clear. Valuing carcasses on the basis of lean meat yield to reward producers need only be underpinned by one number – CT fat %. Alternatively, predicting cut weights to enable carcass sorting prior to bone out is likely to be adequately described by carcase weight and CT fat %. Enhancing this prediction further with knowledge of CT lean %, and CT bone % is likely to be subtle, even if these measurements were perfect. This will be explored in future analyses where DEXA estimates of CT lean %, CT bone % and CT fat % are used to predict cut weights.

3.4 Experiment 4 – nucleus flock calibration in quarters

3.4.1 Introduction

The final phase of this work was to assess the precision and accuracy of using DEXA values specific to the fore-section, saddle- section, and hind-section of the carcase for predicting CT composition within these regions. These DEXA values are derived from additional image processing whereby carcase images are divided into sections to approximate these three regions. This image processing mirrors processes that are already in place within the standards Scotts robotic system which identifies the coordinates for robotic cutting into these sections.

3.4.2 Methods

The animals, experimental design, and scanning protocols used for this analysis have already been described in Experiment 3 above. The image processing was the same, except that images for each carcase were divided into fore-section, saddle- section, and hind-section using sectioning algorithms provided by Scott technology that match those currently used within their existing robotic system.

We then derived prediction equations and tested their transportability in exactly the same manner as described in Experiment 3 above, except that in this case DEXA values specific to the fore, saddle, and hind sections were used to predict CT fat %, lean %, and bone % within these same sections. To show the precision and accuracy of prediction, tables similar to Table 12, Table 13, and

Table *14* were generated, resulting in a total of nine additional tables (ie 3 carcase sections x 3 tissue types) which are reported in the appendix (Table 17 - Table 25). However to summarise these results, the precision figures (R-square and root mean square error) from each table have been reported in

Table *15* below.

We have also used general linear models were used to show the simple association between R-value (nylon-normalised) and CT fat%, lean%, and bone% within each of the fore, saddle, and hind sections, and the data distribution around them. These are shown in Table 26 - Table 29 in the appendix.

3.4.3 Results

In general the precision for predicting CT fat %, lean %, and bone % within sections was reduced when using DEXA values specific to that section (

Table *15*). The only section where precision for estimating composition was maintained was for the saddle section, although there was still some loss of precision for predicting CT fat% in this section. In terms of tissue types, the loss of precision was generally greater for predicting CT fat% and lean%, with less loss of precision for predicting CT bone%.

As a point of comparison the CT fat %, lean %, and bone % within sections was also predicted using the single whole carcase DEXA value (Table 16). In this instance the precision of prediction was reduced by far less than when using DEXA values specific to that section. In fact for the saddle region the precision of prediction was actually as good, or better than the precision of prediction of whole carcase composition shown at the top of

Table *15*.

Table 15. Summary of precision estimates R-square, and root mean square error (RMSE) from Table 12 -

Table 14, and from appendix Table 17 - Table 25, showing precision of prediction within different slaughter groups.

Section/tissue		Pre-NF	NF1	NF2	NF3	NF4	NF5	NF6	Combined
Full carcase fat	Ave R^2	0.84	0.83	0.88	0.85	0.89	0.87	0.89	0.89
	Ave RMSE	1.60	1.39	1.38	1.35	1.32	1.53	1.54	1.52
	Data range	21.11	16.12	18.14	14.40	17.93	19.36	21.12	26.82
	RMSE as % of range	7.58	8.63	7.63	9.37	7.39	7.90	7.28	5.67
Full carcase lean	Ave R^2	0.64	0.65	0.69	0.66	0.73	0.65	0.73	0.73
	Ave RMSE	1.89	1.57	1.73	1.61	1.64	1.87	1.74	1.83
	Data range	15.88	11.96	14.24	11.91	15.31	16.33	14.90	20.56
	RMSE as % of range	11.91	13.15	12.13	13.53	10.74	11.46	11.65	8.91
Full carcase bone	Ave R^2	0.63	0.58	0.61	0.64	0.63	0.74	0.80	0.68
	Ave RMSE	0.91	0.88	0.87	0.73	0.81	0.87	0.75	0.91
	Data range	7.79	8.81	7.56	5.22	6.00	8.85	7.89	10.29
	RMSE as % of range	11.63	10.03	11.52	13.91	13.53	9.81	9.44	8.85
Fore-section fat	Ave R^2	0.63	0.39	0.53	0.51	0.53	0.44	0.57	0.63
	Ave RMSE	1.80	2.16	2.33	2.07	2.27	2.69	2.25	2.38
	Data range	16.83	13.03	15.80	13.52	17.17	16.58	15.64	22.65
	RMSE as % of range	10.69	16.60	14.75	15.33	13.20	16.24	14.41	10.51
Fore-section lean	Ave R^2	0.33	0.24	0.27	0.29	0.26	0.13	0.31	0.39
	Ave RMSE	1.96	1.97	2.28	1.97	2.20	2.64	2.02	2.28
	Data range	12.47	11.42	11.91	10.52	12.93	13.44	10.64	16.07
	RMSE as % of range	15.74	17.24	19.17	18.72	17.03	19.64	18.97	14.19
Fore-section bone	Ave R^2	0.49	0.47	0.57	0.56	0.58	0.61	0.69	0.68
	Ave RMSE	0.89	0.90	0.90	0.75	0.90	1.07	0.92	0.96
	Data range	5.69	8.19	9.29	4.81	6.97	8.67	9.01	9.78
	RMSE as % of range	15.60	11.04	9.66	15.66	12.96	12.33	10.23	9.84

Saddle-section fat	Ave R^2	0.89	0.71	0.83	0.82	0.75	0.80	0.81	0.81
	Ave RMSE	2.02	2.95	2.22	2.15	2.80	2.77	2.84	2.82
	Data range	30.03	25.30	25.16	20.52	24.58	30.27	28.90	35.45
	RMSE as % of range	6.73	11.66	8.82	10.48	11.39	9.15	9.82	7.95
Saddle-section lean	Ave R^2	0.85	0.65	0.75	0.74	0.65	0.66	0.73	0.75
	Ave RMSE	1.87	2.56	2.15	2.07	2.70	2.85	2.55	2.61
	Data range	23.97	18.02	21.13	17.78	20.97	23.59	21.59	29.13
	RMSE as % of range	7.79	14.23	10.19	11.66	12.86	12.09	11.83	8.97
Saddle-section bone	Ave R^2	0.63	0.55	0.60	0.65	0.57	0.76	0.75	0.63
	Ave RMSE	1.02	1.18	1.01	0.85	1.03	0.94	0.94	1.10
	Data range	6.87	11.52	8.43	6.56	7.17	11.18	8.45	12.50
	RMSE as % of range	14.88	10.21	11.93	13.02	14.33	8.42	11.08	8.81
Hind-section fat	Ave R^2	0.61	0.42	0.44	0.57	0.65	0.65	0.72	0.67
	Ave RMSE	1.66	1.63	2.04	1.57	1.67	1.64	1.73	1.77
	Data range	12.98	10.90	13.30	9.55	12.67	13.24	14.91	19.33
	RMSE as % of range	12.82	14.98	15.31	16.40	13.20	12.41	11.58	9.17
Hind-section lean	Ave R^2	0.50	0.28	0.29	0.40	0.50	0.38	0.51	0.49
	Ave RMSE	1.60	1.62	1.91	1.49	1.63	1.78	1.73	1.76
	Data range	9.75	8.43	10.25	8.70	11.64	13.20	11.75	14.19
	RMSE as % of range	16.44	19.18	18.62	17.10	13.98	13.50	14.70	12.39
Hind-section bone	Ave R^2	0.39	0.41	0.34	0.38	0.37	0.66	0.59	0.39
	Ave RMSE	0.87	0.93	1.02	0.88	0.89	0.79	0.94	1.08
	Data range	5.35	7.86	8.27	5.32	5.00	8.39	6.83	11.07
	RMSE as % of range	16.27	11.84	12.35	16.58	17.74	9.43	13.71	9.78

Ave R^2, average R-square for all transportation tests within that nucleus flock group; Ave RMSE, average root mean square error for all transportation tests within that nucleus flock group; NF, nucleus flock.

Table 16. Summary of precision estimates R-square, and root mean square error (RMSE) from appendix Table 30 - Table 38, showing precision of prediction within different slaughter groups.

Section/tissue		Pre-NF	NF1	NF2	NF3	NF4	NF5	NF6	Combined
Fore-section fat	Ave R2	0.76	0.62	0.70	0.67	0.76	0.73	0.72	0.79
	Ave RMSE	1.45	1.70	1.81	1.70	1.61	1.88	1.82	1.80
	Data range	16.83	13.03	15.80	13.52	17.17	16.58	15.64	22.65
	RMSE as % of range	8.63	13.08	11.47	12.56	9.36	11.32	11.67	7.97
Fore-section lean	Ave R2	0.52	0.44	0.47	0.45	0.55	0.42	0.52	0.56
	Ave RMSE	1.66	1.70	1.94	1.74	1.72	2.16	1.68	1.94
	Data range	12.47	11.42	11.91	10.52	12.93	13.44	10.64	16.07
	RMSE as % of range	13.32	14.87	16.28	16.57	13.32	16.06	15.82	12.06
Fore-section bone	Ave R2	0.43	0.49	0.51	0.56	0.53	0.64	0.67	0.62
	Ave RMSE	0.93	0.89	0.95	0.76	0.96	1.03	0.95	1.04
	Data range	5.69	8.19	9.29	4.81	6.97	8.67	9.01	9.78
	RMSE as % of range	16.41	10.83	10.25	15.74	13.77	11.87	10.51	10.61
Saddle-section fat	Ave R2	0.86	0.80	0.87	0.85	0.85	0.85	0.88	0.87
	Ave RMSE	2.23	2.45	1.99	1.98	2.17	2.38	2.27	2.37
	Data range	30.03	25.30	25.16	20.52	24.58	30.27	28.90	35.45
	RMSE as % of range	7.44	9.69	7.90	9.64	8.83	7.87	7.85	6.69
Saddle-section lean	Ave R2	0.79	0.69	0.75	0.74	0.74	0.74	0.78	0.77
	Ave RMSE	2.23	2.39	2.17	2.06	2.33	2.51	2.29	2.51
	Data range	23.97	18.02	21.13	17.78	20.97	23.59	21.59	29.13
	RMSE as % of range	9.30	13.25	10.25	11.56	11.13	10.65	10.62	8.60
Saddle-section bone	Ave R2	0.67	0.64	0.67	0.69	0.64	0.78	0.82	0.71
	Ave RMSE	0.96	1.06	0.92	0.80	0.95	0.90	0.80	0.98
	Data range	6.87	11.52	8.43	6.56	7.17	11.18	8.45	12.50
	RMSE as % of range	13.92	9.21	10.87	12.16	13.23	8.07	9.43	7.81
Hind-section fat	Ave R2	0.77	0.72	0.77	0.77	0.79	0.72	0.78	0.81
	Ave RMSE	1.28	1.14	1.32	1.15	1.30	1.46	1.51	1.36

	Data range	12.98	10.90	13.30	9.55	12.67	13.24	14.91	19.33
	RMSE as % of range	9.90	10.46	9.90	12.04	10.29	11.04	10.12	7.01
Hind-section lean	Ave R2	0.48	0.41	0.48	0.51	0.51	0.36	0.53	0.55
	Ave RMSE	1.64	1.46	1.64	1.33	1.61	1.81	1.71	1.65
	Data range	9.75	8.43	10.25	8.70	11.64	13.20	11.75	14.19
	RMSE as % of range	16.86	17.36	16.00	15.34	13.86	13.70	14.52	11.64
Hind-section bone	Ave R2	0.55	0.47	0.48	0.49	0.50	0.68	0.68	0.53
	Ave RMSE	0.75	0.88	0.91	0.80	0.79	0.77	0.82	0.94
	Data range	5.35	7.86	8.27	5.32	5.00	8.39	6.83	11.07
	RMSE as % of range	14.06	11.22	10.97	14.96	15.82	9.21	11.95	8.51

3.4.4 Discussion

The loss of precision for predicting CT composition within regions using regional DEXA values was disappointing, given the greater specificity of these values to the region in question. Alternatively, using the whole carcase DEXA value to predict CT composition with regions was quite successful, retaining levels of precision approaching those of the whole carcase, and in the case of the saddle, exceeding them for CT bone% and lean %. The diminished predictive power of the regional DEXA values, particularly those associated with the hind and fore sections is likely due to the thicker tissues in these regions. This would result in reduced sensitivity for differentiating bone from soft tissue (see Figure 3), and chemical fat % within soft tissue (see Figure 1). This also suggests that at the whole carcase level pixels within the saddle region are likely to be providing the bulk of the predictive power. This assertion is supported by the prediction of composition in the 3 sections using the single whole carcase DEXA value, with the precision of prediction greatest for the saddle region. This has important implications, particularly for predicting composition within animals of diverse genotype, as previous analyses (Anderson et al. 2015; Anderson et al. 2016) have demonstrated that lean, fat, and bone are redistributed between the saddle, fore and hind sections of the carcase in response to carcase breeding values for post-weaning eye muscle depth (PEMD), and post-weaning fat depth (PFAT). A whole carcase DEXA prediction that is more strongly informed by pixels in the saddle region may still result in bias when used in these diverse populations. Future analyses of residuals from these predictions are planned to assess this bias.

4 Conclusions/Recommendations

This prototype DEXA will provide a highly precise and accurate measurement of body composition, particularly when compared to the relatively crude system of palpating fat depth currently used within the lamb industry. This will enable more accurate valuation of carcasses up and down the supply chain on the basis of lean meat yield. Importantly this will require extensive support to make sophisticated use of this data, underpinning pricing and feedback systems, but also to potentiate sorting systems that optimise the use of these carcases during fabrication. While beyond the scope of this immediate project, this activity will be essential for adoption of this device going forward.

There are a number of further analytical opportunities that exist within the current data-set. Firstly, we can undertake further analyses of residuals to establish the stability of these DEXA values across the range of breeding values represented by the sires used in this study. Secondly, we need to explore the ability of the DEXA values to predict cut weights. This is possible given that a subset of the lambs within the nucleus flock experiment (groups 2 and 6) having been boned out into a series of commercial cuts. This will involve developing prediction equations to estimate these cut weights using GR tissue depth, CT composition, or DEXA values in combination with hot carcase weight to make these predictions. There are a number of different forms that the DEXA value could take, including whole carcase or section DEXA-specific values, plus varying ways of standardising these values against the nylon phantom that need to be explored for precision and accuracy. All of these tasks are under-way, predominantly funded by projects within the Sheep CRC.

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6 Appendix

Fore CT Fat

Table 17. Precision estimates (R-square and root mean square error), intercept and slope of actual CT Fat % versus predicted CT fat % in the fore quarter, and accuracy estimates showing difference between observed minus the predicted at 20 (Diff@20), 26.5 (Diff@26.5), and 33 (Diff@33) CT Fat % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.643	0.392	0.529	0.505	0.528	0.467	0.587	0.550
	RMSE	1.755	2.158	2.323	2.076	2.266	2.622	2.221	2.632
	Intercept	0.000	7.373	4.325	5.557	5.737	6.789	7.040	3.171
	Slope	1.000	0.778	1.026	0.986	0.913	0.889	0.919	1.043
	Diff@20	0.00	2.94	4.85	5.28	3.99	4.57	5.42	4.03
	Diff@26.5	0.00	1.50	5.02	5.19	3.42	3.86	4.90	4.32
	Diff@33	0.00	0.06	5.19	5.10	2.85	3.14	4.37	4.60
Test 2	R2	0.622	0.400	0.544	0.534	0.541	0.402	0.576	0.544
	RMSE	1.805	2.143	2.285	2.012	2.234	2.779	2.250	2.651
	Intercept	-9.239	0.000	-8.611	-7.559	-6.176	-3.393	-4.395	-9.295
	Slope	1.302	1.000	1.469	1.445	1.314	1.221	1.314	1.463
	Diff@20	-3.19	0.00	0.77	1.34	0.10	1.02	1.88	-0.04
	Diff@26.5	-1.23	0.00	3.82	4.23	2.14	2.46	3.92	2.97
	Diff@33	0.73	0.00	6.87	7.12	4.18	3.89	5.96	5.97
Test 3	R2	0.628	0.400	0.545	0.533	0.541	0.415	0.581	0.548
	RMSE	1.791	2.144	2.284	2.016	2.235	2.748	2.237	2.640
	Intercept	-1.971	5.654	0.000	0.972	1.649	3.621	3.292	-0.777
	Slope	0.899	0.691	1.000	0.981	0.891	0.837	0.894	0.998
	Diff@20	-3.99	-0.54	0.00	0.58	-0.53	0.37	1.17	-0.81
	Diff@26.5	-4.65	-2.55	0.00	0.46	-1.23	-0.69	0.48	-0.83
	Diff@33	-5.31	-4.56	0.00	0.33	-1.94	-1.75	-0.21	-0.84
Test 4	R2	0.619	0.400	0.543	0.535	0.541	0.394	0.573	0.541
	RMSE	1.814	2.143	2.288	2.012	2.234	2.797	2.258	2.658
	Intercept	-2.203	5.358	-0.891	0.000	0.648	3.109	2.516	-1.583
	Slope	0.894	0.686	1.015	1.000	0.910	0.840	0.908	1.010
	Diff@20	-4.33	-0.92	-0.58	0.00	-1.15	-0.09	0.68	-1.39
	Diff@26.5	-5.02	-2.96	-0.48	0.00	-1.73	-1.13	0.08	-1.32
	Diff@33	-5.72	-5.00	-0.38	0.00	-2.32	-2.17	-0.51	-1.26
Test 5	R2	0.622	0.400	0.544	0.535	0.541	0.400	0.575	0.543
	RMSE	1.808	2.143	2.286	2.012	2.234	2.784	2.252	2.653

	Intercept	-3.047	4.744	-1.683	-0.755	0.000	2.386	1.803	-2.390
	Slope	0.989	0.759	1.118	1.099	1.000	0.928	0.999	1.112
	Diff@20	-3.27	-0.07	0.67	1.23	0.00	0.94	1.79	-0.14
	Diff@26.5	-3.35	-1.64	1.43	1.88	0.00	0.47	1.79	0.59
	Diff@33	-3.42	-3.20	2.20	2.53	0.00	0.00	1.78	1.32
Test 6	R2	0.582	0.331	0.434	0.389	0.466	0.501	0.531	0.493
	RMSE	1.899	2.263	2.546	2.306	2.411	2.538	2.367	2.796
	Intercept	-11.175	-2.216	-1.717	0.911	-0.922	0.000	0.846	-4.639
	Slope	1.216	1.007	1.067	0.973	1.006	1.000	0.984	1.148
	Diff@20	-6.85	-2.07	-0.37	0.37	-0.81	0.00	0.52	-1.68
	Diff@26.5	-5.45	-2.03	0.07	0.19	-0.78	0.00	0.42	-0.72
	Diff@33	-4.05	-1.98	0.51	0.01	-0.74	0.00	0.31	0.24
Test 7	R2	0.642	0.396	0.537	0.517	0.534	0.454	0.588	0.552
	RMSE	1.759	2.151	2.303	2.050	2.252	2.655	2.217	2.626
	Intercept	-6.870	2.024	-3.599	-2.233	-1.308	0.123	0.000	-4.690
	Slope	1.061	0.821	1.118	1.082	0.992	0.959	1.000	1.129
	Diff@20	-5.65	-1.56	-1.24	-0.59	-1.46	-0.70	0.00	-2.11
	Diff@26.5	-5.25	-2.72	-0.47	-0.06	-1.51	-0.97	0.00	-1.27
	Diff@33	-4.86	-3.88	0.29	0.48	-1.57	-1.23	0.00	-0.43
Test 8	R2	0.643	0.390	0.525	0.498	0.525	0.472	0.585	0.549
	RMSE	1.756	2.162	2.333	2.089	2.273	2.609	2.225	2.636
	Intercept	-6.454	2.338	-1.922	-0.371	0.162	1.293	1.416	-3.269
	Slope	1.064	0.831	1.079	1.034	0.962	0.940	0.968	1.101
	Diff@20	-5.17	-1.04	-0.33	0.31	-0.61	0.09	0.77	-1.25
	Diff@26.5	-4.75	-2.13	0.18	0.53	-0.86	-0.30	0.56	-0.59
	Diff@33	-4.33	-3.23	0.70	0.75	-1.11	-0.69	0.35	0.06

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Fore CT Lean

Table 18. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % versus predicted CT lean % in the fore quarter, and accuracy estimates showing difference between observed minus the predicted at 51 (Diff@51), 55 (Diff@55), and 59 (Diff@59) CT lean % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.352	0.227	0.266	0.285	0.259	0.156	0.294	0.349
	RMSE	1.927	1.989	2.291	1.978	2.200	2.599	2.037	2.364
	Intercept	0.000	10.274	0.828	-0.545	9.562	17.328	11.174	-2.865
	Slope	1.000	0.815	0.947	0.967	0.816	0.665	0.750	1.016
	Diff@51	0.00	0.82	-1.89	-2.23	0.20	0.26	-1.55	-2.03
	Diff@55	0.00	0.08	-2.11	-2.36	-0.53	-1.08	-2.55	-1.97
	Diff@59	0.00	-0.66	-2.32	-2.50	-1.27	-2.42	-3.55	-1.90

Test 2	R2	0.263	0.267	0.252	0.266	0.237	0.062	0.296	0.276
	RMSE	2.055	1.936	2.313	2.004	2.232	2.740	2.034	2.492
	Intercept	-4.425	0.000	-21.621	-23.164	-13.505	15.691	-13.552	-20.663
	Slope	1.071	1.000	1.328	1.350	1.218	0.695	1.170	1.322
	Diff@51	-0.80	0.00	-4.90	-5.30	-2.41	0.12	-4.89	-4.26
	Diff@55	-0.51	0.00	-3.59	-3.90	-1.54	-1.10	-4.21	-2.97
	Diff@59	-0.23	0.00	-2.28	-2.50	-0.67	-2.32	-3.53	-1.68
Test 3	R2	0.330	0.257	0.289	0.313	0.267	0.128	0.328	0.345
	RMSE	1.959	1.950	2.254	1.938	2.189	2.643	1.987	2.370
	Intercept	7.955	15.682	0.000	-2.438	9.785	19.839	8.552	-0.713
	Slope	0.897	0.757	1.000	1.039	0.850	0.651	0.829	1.021
	Diff@51	2.72	3.28	0.00	-0.47	2.13	2.05	-0.18	0.37
	Diff@55	2.31	2.30	0.00	-0.32	1.53	0.65	-0.87	0.46
	Diff@59	1.89	1.33	0.00	-0.16	0.93	-0.74	-1.56	0.54
Test 4	R2	0.330	0.257	0.289	0.313	0.267	0.128	0.328	0.346
	RMSE	1.959	1.950	2.254	1.938	2.188	2.642	1.987	2.370
	Intercept	10.001	17.424	2.345	0.000	11.785	21.335	10.517	1.664
	Slope	0.865	0.729	0.963	1.000	0.818	0.628	0.798	0.984
	Diff@51	3.12	3.61	0.45	0.00	2.52	2.34	0.19	0.83
	Diff@55	2.58	2.53	0.31	0.00	1.79	0.85	-0.62	0.77
	Diff@59	2.04	1.45	0.16	0.00	1.07	-0.64	-1.43	0.70
Test 5	R2	0.337	0.253	0.288	0.312	0.267	0.135	0.325	0.350
	RMSE	1.949	1.955	2.256	1.939	2.188	2.631	1.992	2.362
	Intercept	-4.176	5.883	-11.652	-14.452	0.000	11.473	-0.550	-13.143
	Slope	1.088	0.909	1.180	1.224	1.000	0.781	0.968	1.214
	Diff@51	0.32	1.24	-2.48	-3.03	0.00	0.32	-2.18	-2.24
	Diff@55	0.67	0.87	-1.76	-2.13	0.00	-0.55	-2.30	-1.38
	Diff@59	1.02	0.51	-1.04	-1.24	0.00	-1.43	-2.43	-0.53
Test 6	R2	0.334	0.180	0.220	0.231	0.237	0.163	0.243	0.319
	RMSE	1.954	2.048	2.361	2.051	2.232	2.589	2.109	2.418
	Intercept	-32.332	-15.180	-18.123	-17.758	-11.154	0.000	-2.996	-28.291
	Slope	1.623	1.302	1.326	1.318	1.219	1.000	1.034	1.513
	Diff@51	-0.56	0.22	-1.50	-1.53	0.01	0.00	-1.26	-2.13
	Diff@55	1.93	1.43	-0.19	-0.26	0.88	0.00	-1.12	-0.08
	Diff@59	4.43	2.64	1.11	1.01	1.76	0.00	-0.99	1.97
Test 7	R2	0.322	0.260	0.288	0.312	0.265	0.119	0.329	0.339
	RMSE	1.972	1.946	2.256	1.940	2.191	2.656	1.986	2.382
	Intercept	0.798	9.155	-9.621	-12.427	1.334	14.446	0.000	-10.085
	Slope	1.044	0.891	1.194	1.240	1.021	0.762	1.000	1.212
	Diff@51	3.07	3.60	0.28	-0.19	2.40	2.31	0.00	0.71
	Diff@55	3.24	3.17	1.05	0.77	2.48	1.36	0.00	1.56
	Diff@59	3.42	2.73	1.83	1.73	2.56	0.41	0.00	2.40
Test 8	R2	0.350	0.237	0.276	0.297	0.263	0.152	0.306	0.352
	RMSE	1.929	1.976	2.276	1.961	2.194	2.606	2.020	2.358
	Intercept	-2.508	8.053	-4.121	-6.023	5.887	14.653	6.845	-7.187
	Slope	1.083	0.887	1.072	1.102	0.915	0.740	0.857	1.134
	Diff@51	1.75	2.31	-0.45	-0.82	1.55	1.40	-0.43	-0.37
	Diff@55	2.08	1.86	-0.16	-0.41	1.21	0.36	-1.00	0.17

	Diff@59	2.42	1.41	0.13	-0.01	0.87	-0.68	-1.57	0.70

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Fore CT Bone

Table 19. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % versus predicted CT bone % in the fore quarter, and accuracy estimates showing difference between observed minus the predicted at 14 (Diff@14), 16.5 (Diff@16.5), and 19 (Diff@19) CT bone % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.508	0.465	0.605	0.593	0.603	0.623	0.707	0.555
	RMSE	0.871	0.907	0.866	0.726	0.882	1.055	0.898	1.132
	Intercept	0.000	-4.070	-8.036	-6.561	-6.460	-9.900	-9.555	-8.313
	Slope	1.000	1.103	1.277	1.195	1.191	1.399	1.387	1.311
	Diff@14	0.00	-2.62	-4.16	-3.83	-3.79	-4.32	-4.14	-3.96
	Diff@16.5	0.00	-2.37	-3.47	-3.34	-3.31	-3.32	-3.18	-3.19
	Diff@19	0.00	-2.11	-2.78	-2.85	-2.83	-2.33	-2.21	-2.41
Test 2	R2	0.449	0.524	0.484	0.468	0.512	0.667	0.715	0.477
	RMSE	0.921	0.855	0.990	0.830	0.978	0.991	0.885	1.228
	Intercept	7.116	0.000	3.652	4.861	3.737	1.428	2.026	3.078
	Slope	0.740	1.000	0.765	0.697	0.757	0.914	0.915	0.827
	Diff@14	3.47	0.00	0.36	0.62	0.33	0.23	0.83	0.66
	Diff@16.5	2.82	0.00	-0.23	-0.14	-0.27	0.01	0.62	0.22
	Diff@19	2.17	0.00	-0.82	-0.90	-0.88	-0.20	0.40	-0.21
Test 3	R2	0.499	0.419	0.621	0.607	0.622	0.558	0.656	0.555
	RMSE	0.879	0.944	0.849	0.714	0.861	1.142	0.973	1.132
	Intercept	7.305	5.140	0.000	0.873	1.007	-0.465	-0.361	0.233
	Slope	0.716	0.738	1.000	0.938	0.936	1.062	1.049	1.008
	Diff@14	3.34	1.47	0.00	0.01	0.12	0.41	0.33	0.34
	Diff@16.5	2.63	0.82	0.00	-0.14	-0.04	0.56	0.45	0.36
	Diff@19	1.92	0.16	0.00	-0.30	-0.20	0.72	0.58	0.38
Test 4	R2	0.501	0.425	0.620	0.607	0.620	0.568	0.664	0.557
	RMSE	0.877	0.939	0.849	0.713	0.863	1.129	0.962	1.130
	Intercept	6.521	4.200	-0.932	0.000	0.157	-1.540	-1.399	-0.742
	Slope	0.771	0.800	1.065	1.000	0.996	1.137	1.123	1.076
	Diff@14	3.32	1.40	-0.02	0.00	0.10	0.37	0.32	0.32
	Diff@16.5	2.74	0.91	0.15	0.00	0.09	0.71	0.63	0.51
	Diff@19	2.17	0.41	0.31	0.00	0.08	1.06	0.93	0.70
Test 5	R2	0.489	0.396	0.617	0.600	0.624	0.515	0.618	0.545
	RMSE	0.888	0.963	0.853	0.720	0.859	1.197	1.024	1.144
	Intercept	7.053	5.348	-0.922	0.027	0.000	-1.082	-1.087	-0.569

	Slope	0.731	0.732	1.057	0.990	1.000	1.103	1.091	1.058
	Diff@14	3.28	1.59	-0.12	-0.11	0.00	0.37	0.18	0.24
	Diff@16.5	2.61	0.92	0.02	-0.14	0.00	0.62	0.41	0.38
	Diff@19	1.94	0.25	0.17	-0.16	0.00	0.88	0.64	0.53
Test 6	R2	0.460	0.524	0.498	0.483	0.522	0.668	0.719	0.487
	RMSE	0.913	0.855	0.976	0.819	0.968	0.990	0.879	1.215
	Intercept	5.997	-1.082	2.301	3.576	2.509	0.000	0.559	1.682
	Slope	0.804	1.065	0.845	0.772	0.830	1.000	1.000	0.909
	Diff@14	3.25	-0.17	0.13	0.39	0.12	0.00	0.56	0.41
	Diff@16.5	2.76	0.00	-0.26	-0.18	-0.30	0.00	0.56	0.19
	Diff@19	2.27	0.16	-0.65	-0.75	-0.73	0.00	0.57	-0.04
Test 7	R2	0.492	0.509	0.550	0.537	0.561	0.661	0.727	0.524
	RMSE	0.885	0.868	0.924	0.775	0.928	1.000	0.866	1.171
	Intercept	5.998	0.567	1.344	2.478	1.971	-0.425	0.000	0.935
	Slope	0.775	0.948	0.878	0.812	0.838	1.002	1.000	0.926
	Diff@14	2.85	-0.17	-0.37	-0.16	-0.30	-0.40	0.00	-0.10
	Diff@16.5	2.29	-0.30	-0.67	-0.63	-0.71	-0.39	0.00	-0.28
	Diff@19	1.72	-0.43	-0.98	-1.10	-1.11	-0.39	0.00	-0.47
Test 8	R2	0.508	0.470	0.600	0.589	0.600	0.629	0.711	0.554
	RMSE	0.871	0.902	0.871	0.730	0.886	1.047	0.891	1.134
	Intercept	5.634	1.952	-0.643	0.384	0.419	-1.886	-1.595	-0.766
	Slope	0.816	0.910	1.029	0.962	0.961	1.132	1.123	1.059
	Diff@14	3.06	0.69	-0.24	-0.14	-0.13	-0.04	0.13	0.06
	Diff@16.5	2.60	0.46	-0.17	-0.24	-0.22	0.29	0.43	0.21
	Diff@19	2.14	0.24	-0.09	-0.33	-0.32	0.62	0.74	0.36

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Fat

Table 20. Precision estimates (R-square and root mean square error), intercept and slope of actual CT fat % versus predicted CT fat % in the hind quarter, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 17 (Diff@17), and 22 (Diff@22) CT fat % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.619	0.416	0.453	0.576	0.662	0.655	0.714	0.629
	RMSE	1.654	1.633	2.017	1.563	1.650	1.636	1.735	1.873
	Intercept	0.000	3.568	4.441	1.190	1.337	1.949	1.610	0.852
	Slope	1.000	0.802	0.883	1.028	1.090	1.011	1.049	1.073
	Diff@12	0.00	1.20	3.03	1.53	2.42	2.08	2.20	1.73
	Diff@17	0.00	0.21	2.44	1.66	2.87	2.13	2.44	2.09
	Diff@22	0.00	-0.78	1.86	1.80	3.32	2.18	2.69	2.46
Test 2	R2	0.611	0.423	0.425	0.584	0.641	0.651	0.730	0.635

	RMSE	1.673	1.623	2.068	1.548	1.702	1.644	1.686	1.859
	Intercept	-4.480	0.000	0.980	-4.430	-4.124	-4.034	-4.398	-4.525
	Slope	1.277	1.000	1.073	1.346	1.396	1.342	1.400	1.379
	Diff@12	-1.16	0.00	1.85	-0.28	0.63	0.07	0.40	0.02
	Diff@17	0.23	0.00	2.22	1.46	2.61	1.79	2.40	1.91
	Diff@22	1.61	0.00	2.58	3.19	4.60	3.50	4.39	3.80
Test 3	R2	0.614	0.399	0.461	0.550	0.663	0.646	0.691	0.608
	RMSE	1.665	1.656	2.004	1.610	1.650	1.657	1.802	1.927
	Intercept	-4.900	-0.295	0.000	-2.727	-3.439	-1.928	-2.588	-3.772
	Slope	1.107	0.899	1.000	1.098	1.198	1.087	1.127	1.173
	Diff@12	-3.62	-1.50	0.00	-1.55	-1.07	-0.88	-1.06	-1.70
	Diff@17	-3.08	-2.01	0.00	-1.05	-0.08	-0.44	-0.43	-0.84
	Diff@22	-2.55	-2.51	0.00	-0.56	0.91	-0.01	0.21	0.03
Test 4	R2	0.614	0.423	0.434	0.585	0.648	0.654	0.728	0.636
	RMSE	1.665	1.623	2.053	1.547	1.684	1.638	1.693	1.856
	Intercept	-0.445	3.165	4.265	0.000	0.407	0.520	0.299	-0.060
	Slope	0.952	0.750	0.811	1.000	1.041	0.991	1.032	1.027
	Diff@12	-1.02	0.17	2.00	0.00	0.90	0.42	0.69	0.27
	Diff@17	-1.26	-1.08	1.05	0.00	1.11	0.37	0.85	0.41
	Diff@22	-1.50	-2.33	0.10	0.00	1.32	0.33	1.01	0.54
Test 5	R2	0.618	0.409	0.459	0.565	0.664	0.651	0.703	0.620
	RMSE	1.657	1.643	2.007	1.584	1.646	1.644	1.767	1.897
	Intercept	-1.474	2.428	3.089	0.166	0.000	0.973	0.504	-0.443
	Slope	0.920	0.744	0.824	0.930	1.000	0.916	0.950	0.982
	Diff@12	-2.43	-0.65	0.97	-0.67	0.00	-0.03	-0.09	-0.66
	Diff@17	-2.83	-1.93	0.09	-1.02	0.00	-0.45	-0.34	-0.75
	Diff@22	-3.23	-3.21	-0.79	-1.36	0.00	-0.87	-0.59	-0.84
Test 6	R2	0.618	0.420	0.447	0.582	0.658	0.656	0.721	0.634
	RMSE	1.656	1.627	2.030	1.552	1.660	1.634	1.714	1.862
	Intercept	-1.516	2.333	3.184	-0.714	-0.515	0.000	-0.341	-0.976
	Slope	0.978	0.779	0.851	1.016	1.068	1.000	1.039	1.052
	Diff@12	-1.79	-0.32	1.40	-0.53	0.30	0.00	0.13	-0.35
	Diff@17	-1.90	-1.43	0.65	-0.45	0.64	0.00	0.33	-0.09
	Diff@22	-2.01	-2.53	-0.09	-0.37	0.98	0.00	0.52	0.17
Test 7	R2	0.603	0.422	0.411	0.579	0.627	0.645	0.731	0.631
	RMSE	1.689	1.624	2.094	1.557	1.734	1.659	1.682	1.869
	Intercept	-0.101	3.423	4.833	-0.017	0.513	0.118	0.000	0.068
	Slope	0.897	0.696	0.738	0.949	0.980	0.957	1.000	0.968
	Diff@12	-1.33	-0.22	1.69	-0.63	0.27	-0.40	0.00	-0.31
	Diff@17	-1.84	-1.74	0.37	-0.89	0.18	-0.62	0.00	-0.47
	Diff@22	-2.36	-3.26	-0.94	-1.14	0.08	-0.84	0.00	-0.63
Test 8	R2	0.619	0.415	0.454	0.575	0.663	0.654	0.713	0.629
	RMSE	1.654	1.634	2.016	1.565	1.649	1.636	1.738	1.876
	Intercept	-2.484	1.579	2.239	-1.309	-1.341	-0.501	-0.944	-1.783
	Slope	1.010	0.811	0.893	1.037	1.101	1.019	1.058	1.084
	Diff@12	-2.36	-0.69	0.96	-0.87	-0.13	-0.27	-0.25	-0.78
	Diff@17	-2.31	-1.63	0.42	-0.68	0.38	-0.18	0.04	-0.36
	Diff@22	-2.26	-2.57	-0.11	-0.50	0.88	-0.08	0.33	0.06

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Lean

Table 21. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % versus predicted CT lean % in the hind quarter, and accuracy estimates showing difference between observed minus the predicted at 64 (Diff@64), 67.5 (Diff@67.5), and 71 (Diff@71) CT lean % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.527	0.271	0.317	0.426	0.548	0.389	0.535	0.502
	RMSE	1.560	1.630	1.878	1.451	1.556	1.773	1.691	1.731
	Intercept	0.000	22.584	17.085	5.735	-1.032	8.364	3.047	3.164
	Slope	1.000	0.681	0.741	0.924	1.016	0.875	0.943	0.953
	Diff@64	0.00	2.18	0.53	0.86	-0.03	0.38	-0.61	0.13
	Diff@67.5	0.00	1.06	-0.38	0.59	0.03	-0.06	-0.81	-0.04
	Diff@71	0.00	-0.05	-1.28	0.32	0.08	-0.50	-1.01	-0.20
Test 2	R2	0.361	0.350	0.186	0.250	0.275	0.333	0.401	0.344
	RMSE	1.813	1.540	2.052	1.658	1.970	1.853	1.920	1.989
	Intercept	-17.574	0.000	18.972	5.809	-3.341	-22.335	-24.843	-6.116
	Slope	1.231	1.000	0.703	0.907	1.038	1.314	1.326	1.073
	Diff@64	-2.80	0.00	-0.02	-0.12	-0.88	-2.27	-3.97	-1.45
	Diff@67.5	-1.99	0.00	-1.06	-0.44	-0.74	-1.17	-2.83	-1.20
	Diff@71	-1.18	0.00	-2.10	-0.77	-0.61	-0.07	-1.69	-0.94
Test 3	R2	0.522	0.241	0.322	0.413	0.558	0.361	0.515	0.494
	RMSE	1.568	1.664	1.872	1.467	1.539	1.813	1.726	1.746
	Intercept	-19.257	10.612	0.000	-11.455	-21.820	-4.291	-12.643	-15.962
	Slope	1.296	0.864	1.000	1.185	1.330	1.067	1.182	1.243
	Diff@64	-0.30	1.89	0.00	0.38	-0.69	0.00	-1.00	-0.42
	Diff@67.5	0.73	1.42	0.00	1.02	0.46	0.23	-0.36	0.42
	Diff@71	1.77	0.94	0.00	1.67	1.62	0.47	0.28	1.27
Test 4	R2	0.527	0.280	0.314	0.427	0.542	0.396	0.539	0.502
	RMSE	1.561	1.621	1.883	1.450	1.566	1.762	1.684	1.731
	Intercept	-6.325	18.027	13.211	0.000	-7.041	1.712	-3.591	-2.572
	Slope	1.083	0.742	0.792	1.000	1.095	0.966	1.032	1.029
	Diff@64	-1.01	1.52	-0.12	0.00	-0.94	-0.48	-1.55	-0.74
	Diff@67.5	-0.71	0.62	-0.84	0.00	-0.60	-0.60	-1.43	-0.64
	Diff@71	-0.42	-0.29	-1.57	0.00	-0.27	-0.72	-1.32	-0.54
Test 5	R2	0.520	0.233	0.322	0.408	0.558	0.354	0.510	0.491
	RMSE	1.573	1.673	1.872	1.474	1.539	1.822	1.736	1.752
	Intercept	2.185	25.136	16.108	8.387	0.000	14.038	7.294	4.500
	Slope	0.973	0.644	0.756	0.885	1.000	0.790	0.881	0.933
	Diff@64	0.45	2.38	0.51	1.02	0.00	0.58	-0.34	0.23

	Diff@67.5	0.35	1.13	-0.34	0.62	0.00	-0.16	-0.76	0.00
	Diff@71	0.26	-0.11	-1.19	0.21	0.00	-0.89	-1.18	-0.23
Test 6	R2	0.499	0.323	0.278	0.395	0.474	0.421	0.537	0.475
	RMSE	1.606	1.572	1.932	1.489	1.678	1.725	1.686	1.779
	Intercept	-1.092	20.054	22.072	7.941	1.637	0.000	-2.732	4.654
	Slope	1.007	0.717	0.666	0.889	0.976	1.000	1.024	0.928
	Diff@64	-0.66	1.91	0.70	0.83	0.09	0.00	-1.21	0.06
	Diff@67.5	-0.64	0.92	-0.47	0.44	0.01	0.00	-1.13	-0.19
	Diff@71	-0.61	-0.07	-1.64	0.05	-0.08	0.00	-1.04	-0.44
Test 7	R2	0.519	0.303	0.300	0.419	0.515	0.414	0.545	0.495
	RMSE	1.574	1.594	1.903	1.460	1.611	1.736	1.673	1.745
	Intercept	-0.461	21.357	19.946	6.435	0.341	3.753	0.000	4.009
	Slope	1.016	0.708	0.708	0.925	1.010	0.958	1.000	0.952
	Diff@64	0.55	2.68	1.27	1.66	0.95	1.06	0.00	0.96
	Diff@67.5	0.60	1.66	0.25	1.40	0.99	0.91	0.00	0.80
	Diff@71	0.66	0.64	-0.77	1.14	1.02	0.76	0.00	0.63
Test 8	R2	0.527	0.266	0.319	0.425	0.551	0.385	0.532	0.502
	RMSE	1.560	1.636	1.876	1.452	1.551	1.779	1.696	1.732
	Intercept	-5.583	18.925	12.509	0.570	-6.914	4.087	-1.852	-2.300
	Slope	1.086	0.737	0.811	1.002	1.105	0.940	1.017	1.036
	Diff@64	-0.11	2.09	0.40	0.72	-0.20	0.26	-0.73	-0.02
	Diff@67.5	0.19	1.17	-0.27	0.73	0.17	0.05	-0.67	0.10
	Diff@71	0.49	0.25	-0.93	0.73	0.53	-0.16	-0.61	0.23

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Bone

Table 22. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % versus predicted CT bone % in the hind quarter, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 14.5 (Diff@14.5), and 17 (Diff@17) CT bone % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.410	0.451	0.356	0.357	0.393	0.686	0.572	0.327
	RMSE	0.858	0.901	1.008	0.896	0.873	0.762	0.952	1.135
	Intercept	0.000	-10.787	-2.484	-1.317	-0.585	-8.069	-4.012	-1.581
	Slope	1.000	1.532	1.009	0.939	0.886	1.349	1.159	0.981
	Diff@12	0.00	-4.40	-2.37	-2.05	-1.95	-3.88	-2.11	-1.81
	Diff@14.5	0.00	-3.07	-2.35	-2.20	-2.23	-3.00	-1.71	-1.86
	Diff@17	0.00	-1.74	-2.32	-2.36	-2.52	-2.13	-1.32	-1.90
Test 2	R2	0.410	0.452	0.352	0.344	0.394	0.689	0.560	0.311
	RMSE	0.859	0.899	1.011	0.905	0.872	0.759	0.965	1.149
	Intercept	7.091	0.000	4.745	5.540	5.656	1.392	4.248	5.626

	Slope	0.653	1.000	0.649	0.595	0.578	0.880	0.749	0.620
	Diff@12	2.92	0.00	0.54	0.68	0.59	-0.05	1.24	1.07
	Diff@14.5	2.06	0.00	-0.34	-0.34	-0.46	-0.35	0.61	0.12
	Diff@17	1.19	0.00	-1.22	-1.35	-1.52	-0.65	-0.02	-0.83
Test 3	R2	0.409	0.444	0.357	0.374	0.390	0.681	0.586	0.348
	RMSE	0.859	0.906	1.007	0.884	0.875	0.768	0.936	1.118
	Intercept	2.607	-6.579	0.000	0.682	1.776	-4.459	-1.146	0.478
	Slope	0.974	1.485	1.000	0.952	0.865	1.319	1.145	0.995
	Diff@12	2.30	-0.75	0.00	0.11	0.15	-0.63	0.59	0.42
	Diff@14.5	2.23	0.46	0.00	-0.01	-0.19	0.17	0.95	0.41
	Diff@17	2.17	1.67	0.00	-0.13	-0.53	0.97	1.31	0.40
Test 4	R2	0.353	0.318	0.294	0.429	0.324	0.595	0.624	0.413
	RMSE	0.899	1.003	1.055	0.844	0.921	0.866	0.892	1.060
	Intercept	4.447	-0.593	2.276	0.000	3.743	-2.141	-0.499	0.358
	Slope	0.808	1.070	0.841	1.000	0.724	1.170	1.080	0.993
	Diff@12	2.14	0.25	0.37	0.00	0.43	-0.11	0.46	0.27
	Diff@14.5	1.66	0.42	-0.03	0.00	-0.26	0.32	0.66	0.25
	Diff@17	1.18	0.60	-0.43	0.00	-0.95	0.74	0.86	0.24
Test 5	R2	0.409	0.452	0.351	0.339	0.394	0.689	0.555	0.304
	RMSE	0.859	0.900	1.012	0.908	0.872	0.758	0.970	1.154
	Intercept	0.718	-9.766	-1.526	-0.127	0.000	-7.239	-3.027	-0.257
	Slope	1.130	1.729	1.117	1.018	1.000	1.523	1.292	1.060
	Diff@12	2.28	-1.02	-0.12	0.09	0.00	-0.96	0.48	0.46
	Diff@14.5	2.60	0.81	0.18	0.13	0.00	0.34	1.21	0.61
	Diff@17	2.93	2.63	0.47	0.17	0.00	1.65	1.95	0.76
Test 6	R2	0.407	0.450	0.346	0.327	0.394	0.690	0.544	0.289
	RMSE	0.861	0.901	1.016	0.916	0.872	0.758	0.983	1.167
	Intercept	6.175	-1.417	3.961	4.975	4.791	0.000	3.248	5.113
	Slope	0.741	1.130	0.723	0.651	0.656	1.000	0.842	0.675
	Diff@12	3.07	0.15	0.64	0.79	0.66	0.00	1.35	1.21
	Diff@14.5	2.43	0.48	-0.06	-0.09	-0.20	0.00	0.96	0.40
	Diff@17	1.78	0.80	-0.75	-0.96	-1.06	0.00	0.56	-0.41
Test 7	R2	0.360	0.331	0.303	0.428	0.331	0.605	0.624	0.412
	RMSE	0.894	0.994	1.048	0.845	0.916	0.855	0.892	1.061
	Intercept	4.697	-0.573	2.435	0.492	3.938	-1.725	0.000	0.775
	Slope	0.757	1.020	0.793	0.923	0.678	1.089	1.000	0.922
	Diff@12	1.79	-0.33	-0.05	-0.44	0.08	-0.66	0.00	-0.17
	Diff@14.5	1.18	-0.28	-0.57	-0.63	-0.72	-0.44	0.00	-0.36
	Diff@17	0.57	-0.23	-1.09	-0.82	-1.53	-0.21	0.00	-0.56
Test 8	R2	0.395	0.406	0.346	0.408	0.371	0.656	0.613	0.389
	RMSE	0.869	0.937	1.016	0.859	0.889	0.797	0.905	1.082
	Intercept	2.417	-5.752	-0.340	-0.749	1.731	-4.687	-1.947	-0.892
	Slope	0.959	1.409	1.011	1.040	0.855	1.325	1.179	1.073
	Diff@12	1.92	-0.85	-0.20	-0.27	0.00	-0.79	0.20	-0.01
	Diff@14.5	1.82	0.18	-0.18	-0.17	-0.36	0.02	0.65	0.17
	Diff@17	1.72	1.20	-0.15	-0.07	-0.73	0.84	1.10	0.35

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Fat

Table 23. Precision estimates (R-square and root mean square error), intercept and slope of actual CT fat % versus predicted CT fat % in the saddle, and accuracy estimates showing difference between observed minus the predicted at 28 (Diff@28), 38.5 (Diff@38.5), and 49 (Diff@49) CT fat % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.891	0.706	0.836	0.825	0.749	0.802	0.808	0.834
	RMSE	2.010	2.956	2.192	2.134	2.808	2.758	2.821	2.651
	Intercept	0.000	-1.669	0.454	-1.467	-1.301	3.296	3.872	1.891
	Slope	1.000	1.054	0.979	0.985	0.998	0.916	0.883	0.931
	28	0.00	-0.16	-0.14	-1.88	-1.35	0.96	0.60	-0.03
	38.5	0.00	0.40	-0.36	-2.04	-1.37	0.08	-0.62	-0.75
	49	0.00	0.97	-0.59	-2.19	-1.39	-0.80	-1.85	-1.47
Test 2	R2	0.887	0.716	0.820	0.818	0.762	0.796	0.800	0.830
	RMSE	2.043	2.906	2.291	2.172	2.738	2.795	2.882	2.685
	Intercept	2.297	0.000	4.491	2.394	2.426	6.988	7.875	4.639
	Slope	0.899	1.000	0.867	0.880	0.894	0.817	0.771	0.849
	Diff@28	-0.54	0.00	0.76	-0.96	-0.53	1.87	1.47	0.42
	Diff@38.5	-1.60	0.00	-0.64	-2.22	-1.64	-0.05	-0.94	-1.17
	Diff@49	-2.66	0.00	-2.03	-3.48	-2.75	-1.97	-3.34	-2.75
Test 3	R2	0.890	0.699	0.837	0.820	0.740	0.801	0.808	0.831
	RMSE	2.014	2.994	2.185	2.158	2.862	2.760	2.817	2.672
	Intercept	0.060	-1.159	0.000	-1.735	-1.548	2.811	3.235	1.862
	Slope	1.020	1.050	1.000	1.001	1.014	0.937	0.909	0.942
	Diff@28	0.61	0.25	0.00	-1.71	-1.16	1.03	0.69	0.25
	Diff@38.5	0.82	0.77	0.00	-1.69	-1.02	0.37	-0.26	-0.36
	Diff@49	1.02	1.30	0.00	-1.68	-0.87	-0.30	-1.22	-0.97
Test 4	R2	0.890	0.710	0.833	0.825	0.754	0.801	0.807	0.834
	RMSE	2.012	2.934	2.207	2.129	2.778	2.762	2.830	2.647
	Intercept	1.164	-0.708	2.008	0.000	0.155	4.762	5.404	3.081
	Slope	1.014	1.086	0.990	1.000	1.014	0.928	0.890	0.949
	Diff@28	1.57	1.69	1.73	0.00	0.54	2.74	2.31	1.66
	Diff@38.5	1.72	2.59	1.63	0.00	0.68	1.99	1.15	1.13
	Diff@49	1.87	3.49	1.53	0.00	0.83	1.23	-0.01	0.60
Test 5	R2	0.886	0.716	0.819	0.817	0.762	0.796	0.799	0.829
	RMSE	2.048	2.906	2.303	2.181	2.737	2.800	2.889	2.692
	Intercept	-0.278	-2.904	2.163	0.029	0.000	4.770	5.820	2.269
	Slope	1.006	1.123	0.969	0.984	1.000	0.914	0.861	0.951
	Diff@28	-0.11	0.53	1.28	-0.43	0.00	2.36	1.93	0.89
	Diff@38.5	-0.05	1.82	0.95	-0.60	0.00	1.46	0.47	0.38
	Diff@49	0.01	3.11	0.62	-0.77	0.00	0.56	-0.99	-0.14

Test 6	R2	0.890	0.704	0.836	0.824	0.746	0.802	0.808	0.833
	RMSE	2.010	2.967	2.188	2.139	2.823	2.758	2.819	2.656
	Intercept	-3.404	-5.093	-3.052	-4.936	-4.806	0.000	0.633	-1.305
	Slope	1.090	1.141	1.068	1.073	1.087	1.000	0.966	1.013
	Diff@28	-0.87	-1.15	-1.15	-2.88	-2.36	0.00	-0.32	-0.94
	Diff@38.5	0.08	0.33	-0.43	-2.11	-1.44	0.00	-0.67	-0.80
	Diff@49	1.02	1.81	0.28	-1.34	-0.52	0.00	-1.03	-0.66
Test 7	R2	0.890	0.699	0.837	0.821	0.740	0.801	0.808	0.831
	RMSE	2.014	2.992	2.185	2.156	2.858	2.759	2.817	2.670
	Intercept	-3.613	-4.975	-3.575	-5.327	-5.187	-0.532	0.000	-1.531
	Slope	1.122	1.157	1.100	1.102	1.116	1.030	1.000	1.037
	Diff@28	-0.19	-0.57	-0.76	-2.47	-1.94	0.32	0.00	-0.48
	Diff@38.5	1.09	1.08	0.29	-1.40	-0.72	0.64	0.00	-0.09
	Diff@49	2.37	2.73	1.34	-0.33	0.50	0.96	0.00	0.31
Test 8	R2	0.890	0.708	0.835	0.825	0.752	0.801	0.807	0.834
	RMSE	2.010	2.945	2.198	2.130	2.793	2.760	2.825	2.648
	Intercept	-1.772	-3.690	-1.085	-3.071	-2.939	1.863	2.554	0.280
	Slope	1.066	1.132	1.042	1.051	1.065	0.976	0.938	0.995
	Diff@28	0.08	0.00	0.10	-1.65	-1.12	1.20	0.83	0.15
	Diff@38.5	0.77	1.39	0.54	-1.11	-0.44	0.95	0.18	0.10
	Diff@49	1.46	2.77	0.98	-0.58	0.24	0.69	-0.46	0.05

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Lean

Table 24. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % versus predicted CT lean % in the saddle, and accuracy estimates showing difference between observed minus the predicted at 41 (Diff@41), 48.5 (Diff@48.5), and 56 (Diff@46) CT lean % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.851	0.648	0.750	0.737	0.647	0.660	0.732	0.757
	RMSE	1.858	2.558	2.142	2.076	2.720	2.848	2.538	2.561
	Intercept	0.000	0.528	2.740	4.242	3.167	7.281	7.881	5.964
	Slope	1.000	0.981	0.950	0.949	0.980	0.855	0.846	0.894
	Diff@41	0.00	-0.26	0.68	2.17	2.33	1.34	1.55	1.63
	Diff@48.5	0.00	-0.40	0.30	1.79	2.18	0.25	0.39	0.84
	Diff@56	0.00	-0.55	-0.07	1.41	2.03	-0.84	-0.77	0.04
Test 2	R2	0.851	0.649	0.750	0.740	0.653	0.660	0.731	0.758
	RMSE	1.859	2.557	2.143	2.065	2.697	2.847	2.544	2.554
	Intercept	0.272	0.000	2.802	4.089	2.984	7.355	8.177	5.797
	Slope	1.007	1.000	0.957	0.961	0.991	0.860	0.846	0.906
	Diff@41	0.56	0.00	1.03	2.47	2.63	1.62	1.88	1.93

	Diff@48.5	0.61	0.00	0.70	2.17	2.56	0.57	0.73	1.22
	Diff@56	0.67	0.00	0.38	1.88	2.50	-0.48	-0.43	0.51
Test 3	R2	0.851	0.648	0.750	0.738	0.648	0.660	0.732	0.757
	RMSE	1.858	2.557	2.142	2.073	2.715	2.848	2.539	2.559
	Intercept	-2.833	-2.448	0.000	1.448	0.277	4.822	5.504	3.328
	Slope	1.053	1.036	1.000	1.001	1.033	0.900	0.889	0.943
	Diff@41	-0.67	-0.99	0.00	1.48	1.61	0.72	0.95	0.98
	Diff@48.5	-0.27	-0.72	0.00	1.48	1.86	-0.03	0.12	0.55
	Diff@56	0.12	-0.45	0.00	1.49	2.10	-0.78	-0.72	0.12
Test 4	R2	0.850	0.647	0.747	0.742	0.661	0.660	0.727	0.758
	RMSE	1.867	2.562	2.155	2.056	2.663	2.851	2.561	2.552
	Intercept	-3.311	-5.103	-0.892	0.000	-1.289	4.018	5.347	1.806
	Slope	1.043	1.058	0.989	1.000	1.033	0.888	0.866	0.946
	Diff@41	-1.56	-2.71	-1.34	0.00	0.05	-0.57	-0.16	-0.39
	Diff@48.5	-1.24	-2.27	-1.42	0.00	0.30	-1.41	-1.17	-0.79
	Diff@56	-0.92	-1.83	-1.50	0.00	0.55	-2.25	-2.17	-1.19
Test 5	R2	0.844	0.636	0.734	0.734	0.668	0.654	0.715	0.752
	RMSE	1.905	2.602	2.212	2.088	2.637	2.874	2.616	2.586
	Intercept	-1.127	-5.428	0.927	1.374	0.000	5.402	7.519	2.565
	Slope	1.009	1.060	0.948	0.966	1.000	0.853	0.817	0.927
	Diff@41	-0.77	-2.97	-1.21	-0.02	0.00	-0.61	0.00	-0.42
	Diff@48.5	-0.70	-2.52	-1.61	-0.28	0.00	-1.71	-1.38	-0.97
	Diff@56	-0.64	-2.07	-2.00	-0.54	0.00	-2.81	-2.75	-1.52
Test 6	R2	0.851	0.649	0.750	0.740	0.652	0.660	0.731	0.758
	RMSE	1.859	2.557	2.143	2.065	2.699	2.847	2.543	2.555
	Intercept	-8.355	-8.491	-5.378	-4.103	-5.469	0.000	0.917	-1.924
	Slope	1.171	1.161	1.112	1.116	1.152	1.000	0.985	1.052
	Diff@41	-1.35	-1.87	-0.78	0.66	0.77	0.00	0.28	0.22
	Diff@48.5	-0.07	-0.66	0.07	1.54	1.91	0.00	0.17	0.62
	Diff@56	1.21	0.55	0.91	2.41	3.05	0.00	0.05	1.01
Test 7	R2	0.851	0.646	0.749	0.729	0.634	0.659	0.733	0.753
	RMSE	1.861	2.566	2.149	2.107	2.770	2.853	2.534	2.582
	Intercept	-9.106	-6.742	-5.469	-3.459	-4.730	-0.219	0.000	-1.318
	Slope	1.171	1.122	1.109	1.099	1.134	1.003	1.000	1.035
	Diff@41	-2.10	-1.74	-0.98	0.61	0.76	-0.11	0.00	0.13
	Diff@48.5	-0.82	-0.83	-0.16	1.35	1.76	-0.10	0.00	0.40
	Diff@56	0.46	0.09	0.66	2.10	2.76	-0.08	0.00	0.66
Test 8	R2	0.850	0.648	0.749	0.742	0.659	0.660	0.729	0.759
	RMSE	1.863	2.559	2.149	2.057	2.674	2.849	2.554	2.551
	Intercept	-4.900	-6.163	-2.310	-1.305	-2.617	2.759	3.955	0.634
	Slope	1.088	1.096	1.033	1.042	1.076	0.928	0.907	0.984
	Diff@41	-1.30	-2.23	-0.97	0.41	0.48	-0.21	0.15	0.00
	Diff@48.5	-0.64	-1.51	-0.72	0.72	1.05	-0.76	-0.55	-0.12
	Diff@56	0.02	-0.79	-0.47	1.04	1.62	-1.30	-1.24	-0.24

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Bone

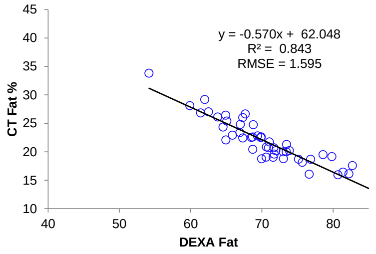
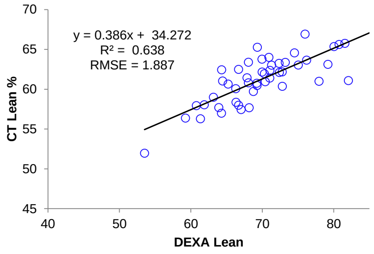
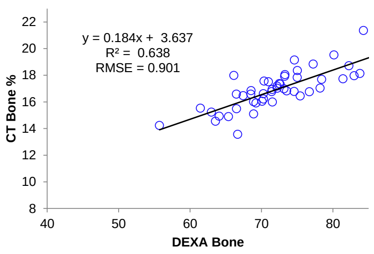
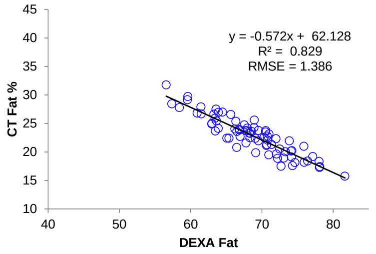
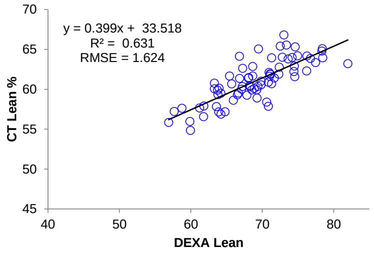
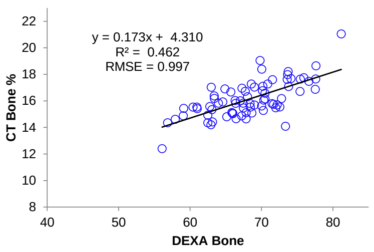
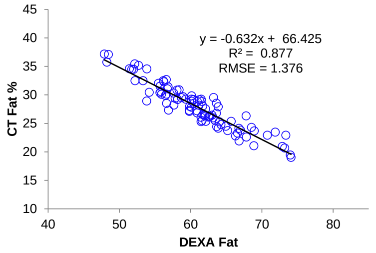
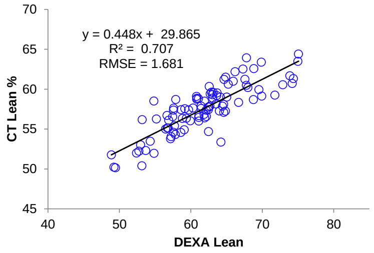
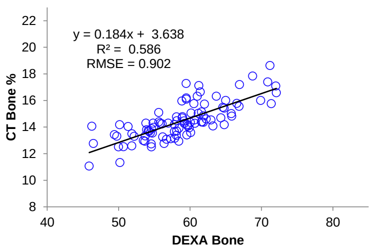
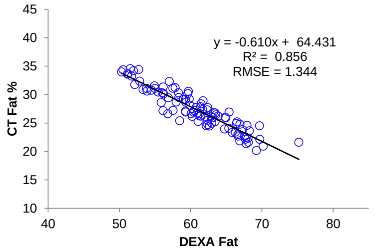
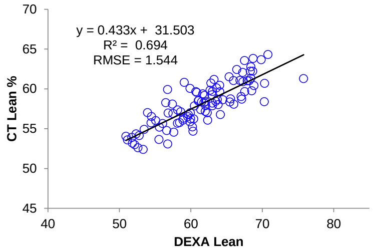
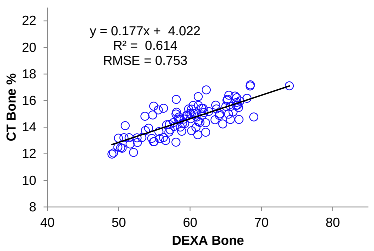
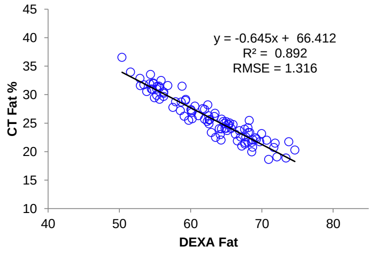
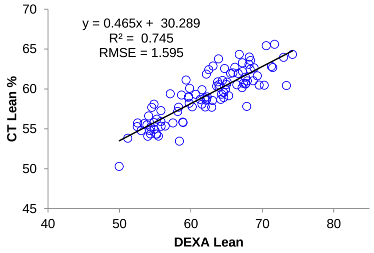
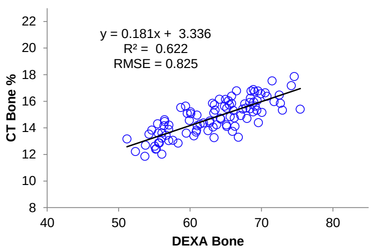
Table 25. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % versus predicted CT bone % in the saddle, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 14.5 (Diff@14.5), and 17 (Diff@17) CT bone % using DEXA (normalised for nylon R-value, based on full carcase) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.630	0.592	0.597	0.639	0.577	0.764	0.758	0.655
	RMSE	1.016	1.124	1.013	0.865	1.021	0.926	0.930	1.067
	Intercept	0.000	-7.049	-0.624	-0.214	-0.606	-2.655	0.446	-0.576
	Slope	1.000	1.500	1.008	0.996	0.979	1.162	0.996	1.022
	12	0.00	-2.55	-0.55	-0.25	-0.80	-1.20	0.41	-0.38
	14.5	0.00	-1.05	-0.52	-0.26	-0.86	-0.71	0.39	-0.31
	17	0.00	0.45	-0.50	-0.27	-0.92	-0.23	0.38	-0.25
Test 2	R2	0.624	0.620	0.554	0.580	0.553	0.758	0.743	0.609
	RMSE	1.024	1.084	1.066	0.932	1.050	0.938	0.957	1.136
	Intercept	5.383	0.000	4.755	5.251	4.774	3.050	5.730	4.773
	Slope	0.647	1.000	0.607	0.587	0.587	0.741	0.615	0.634
	Diff@12	2.21	0.00	1.22	1.53	1.06	0.72	2.27	1.48
	Diff@14.5	1.15	0.00	0.04	0.29	-0.18	-0.06	1.11	0.39
	Diff@17	0.09	0.00	-1.14	-0.95	-1.42	-0.83	-0.04	-0.71
Test 3	R2	0.621	0.490	0.620	0.671	0.570	0.746	0.753	0.661
	RMSE	1.029	1.257	0.984	0.825	1.030	0.961	0.939	1.057
	Intercept	0.622	-2.842	0.000	0.254	-0.122	-1.270	0.866	0.659
	Slope	0.933	1.219	1.000	1.000	0.969	1.097	0.983	0.952
	Diff@12	0.02	-0.88	0.00	0.26	-0.40	-0.40	0.72	0.23
	Diff@14.5	-0.19	-0.22	0.00	0.26	-0.50	-0.10	0.67	0.08
	Diff@17	-0.39	0.44	0.00	0.26	-0.59	0.19	0.62	-0.06
Test 4	R2	0.620	0.487	0.620	0.671	0.569	0.745	0.752	0.660
	RMSE	1.030	1.260	0.984	0.825	1.031	0.963	0.940	1.058
	Intercept	0.381	-3.067	-0.254	0.000	-0.368	-1.539	0.606	0.434
	Slope	0.931	1.212	1.000	1.000	0.968	1.096	0.983	0.950
	Diff@12	-0.24	-1.16	-0.26	0.00	-0.65	-0.68	0.46	-0.02
	Diff@14.5	-0.44	-0.53	-0.26	0.00	-0.75	-0.39	0.41	-0.16
	Diff@17	-0.65	0.11	-0.26	0.00	-0.85	-0.10	0.35	-0.31
Test 5	R2	0.629	0.561	0.610	0.657	0.580	0.761	0.759	0.664
	RMSE	1.018	1.166	0.996	0.842	1.018	0.933	0.927	1.053
	Intercept	0.738	-4.897	0.068	0.389	0.000	-1.561	1.109	0.321
	Slope	0.994	1.433	1.030	1.024	1.000	1.161	1.011	1.022
	Diff@12	0.68	-1.00	0.34	0.61	0.00	-0.11	1.21	0.52
	Diff@14.5	0.66	0.30	0.43	0.68	0.00	0.37	1.24	0.58
	Diff@17	0.64	1.60	0.52	0.75	0.00	0.85	1.27	0.65
Test 6	R2	0.630	0.600	0.592	0.631	0.575	0.764	0.757	0.650
	RMSE	1.016	1.113	1.020	0.874	1.024	0.926	0.932	1.075
	Intercept	2.354	-3.783	1.763	2.172	1.735	0.000	2.801	1.799

	Slope	0.862	1.306	0.861	0.848	0.835	1.000	0.852	0.878
	Diff@12	1.12	-1.03	0.51	0.81	0.25	0.00	1.47	0.70
	Diff@14.5	0.70	-0.11	0.09	0.35	-0.24	0.00	1.03	0.33
	Diff@17	0.29	0.80	-0.32	-0.11	-0.74	0.00	0.59	-0.04
Test 7	R2	0.629	0.564	0.610	0.656	0.580	0.761	0.759	0.663
	RMSE	1.017	1.162	0.997	0.844	1.018	0.932	0.927	1.054
	Intercept	-0.360	-6.590	-1.065	-0.732	-1.095	-2.864	0.000	-0.824
	Slope	0.985	1.426	1.018	1.012	0.989	1.150	1.000	1.012
	Diff@12	-0.50	-2.76	-0.90	-0.62	-1.20	-1.52	0.00	-0.71
	Diff@14.5	-0.54	-1.48	-0.85	-0.58	-1.23	-1.07	0.00	-0.67
	Diff@17	-0.59	-0.20	-0.79	-0.55	-1.26	-0.62	0.00	-0.64
Test 8	R2	0.623	0.507	0.619	0.670	0.574	0.750	0.755	0.664
	RMSE	1.026	1.236	0.985	0.826	1.025	0.953	0.935	1.053
	Intercept	-0.127	-4.366	-0.826	-0.566	-0.919	-2.246	0.109	-0.229
	Slope	0.995	1.332	1.060	1.060	1.028	1.169	1.041	1.019
	Diff@12	-0.18	-1.38	-0.29	-0.03	-0.67	-0.73	0.48	-0.06
	Diff@14.5	-0.19	-0.38	-0.11	0.15	-0.58	-0.22	0.60	0.00
	Diff@17	-0.21	0.62	0.07	0.33	-0.50	0.28	0.72	0.05

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Table 26. Relationship between CT fat, bone, and lean % versus DEXA Fat, lean and bone values for 6 nucleus flock slaughters and 1 pre- nucleus flock slaughter (normalised for nylon R-value). Linear equations, RMSE and R-square values are shown for each graph.

	CT Fat %	CT Lean %	CT Bone %
Pre-Nucleus Flock			
Nucleus Flock 1			
Nucleus Flock 2			
Nucleus Flock 3			
Nucleus Flock 4			

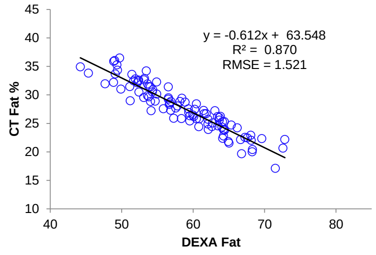
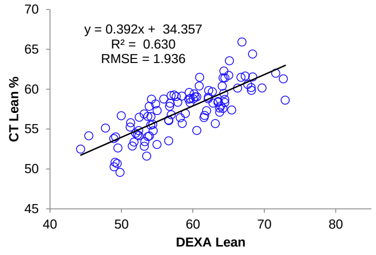
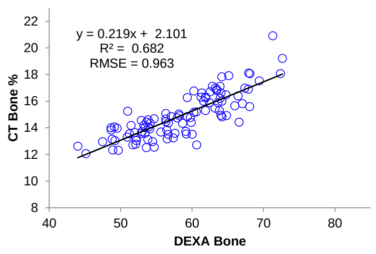
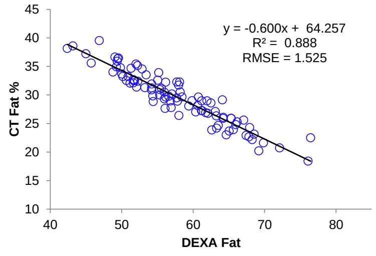
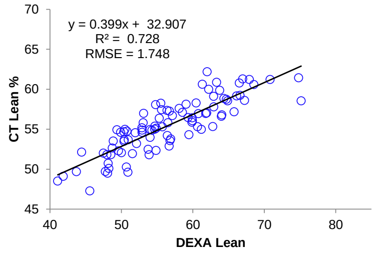
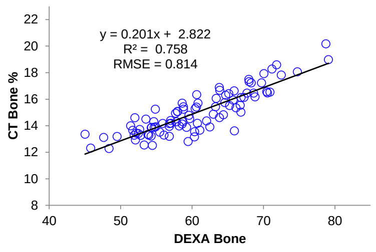
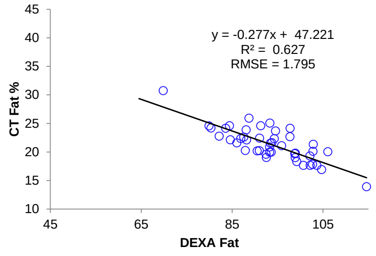
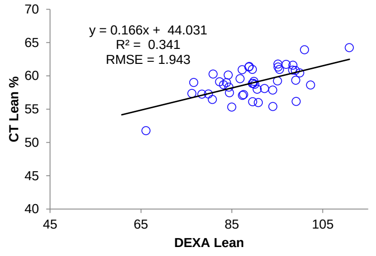
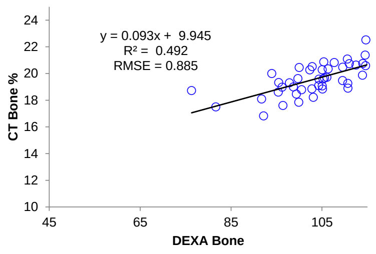
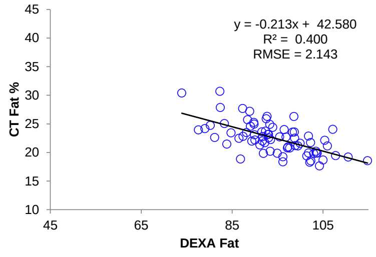
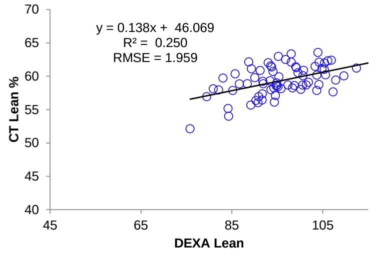
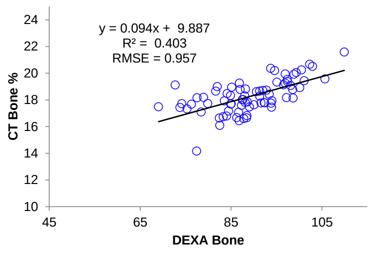
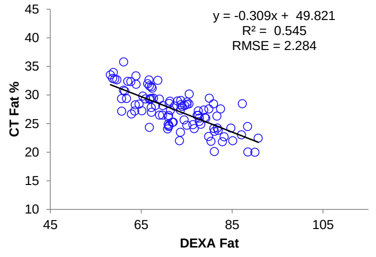
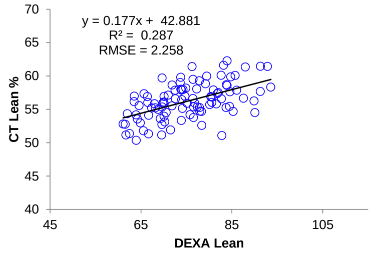
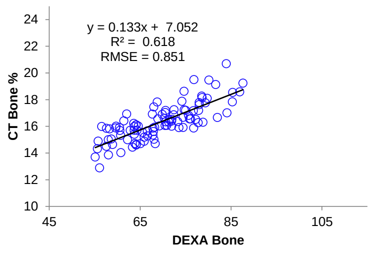
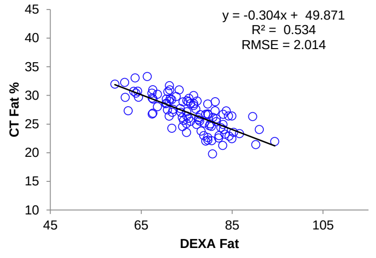
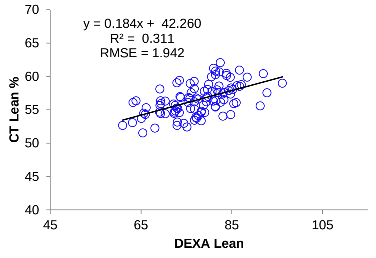
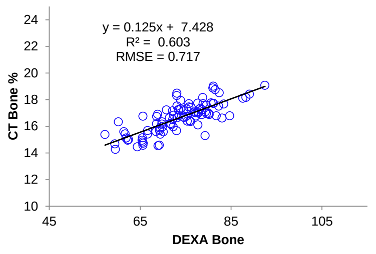
Nucleus Flock 5			
Nucleus Flock 6			

Table 27. Relationship between CT fat, bone, and lean % versus DEXA Fat, lean and bone values for 6 nucleus flock slaughters and 1 pre- nucleus flock slaughter in the fore quarter (normalised for nylon R-value, within the fore quarter). Linear equations, RMSE and R-square values are shown for each graph.

	CT Fat %	CT Lean %	CT Bone %
Pre-Nucleus Flock			
Nucleus Flock 1			
Nucleus Flock 2			
Nucleus Flock 3			

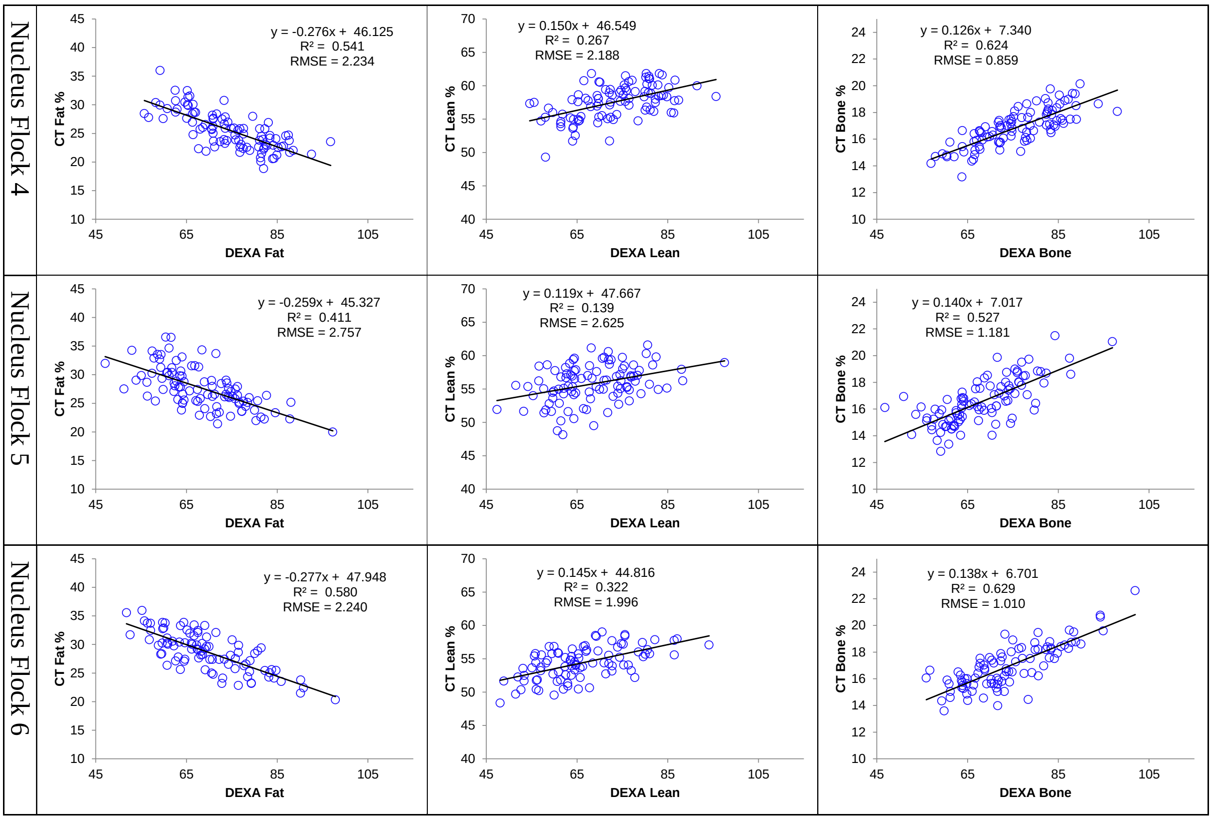
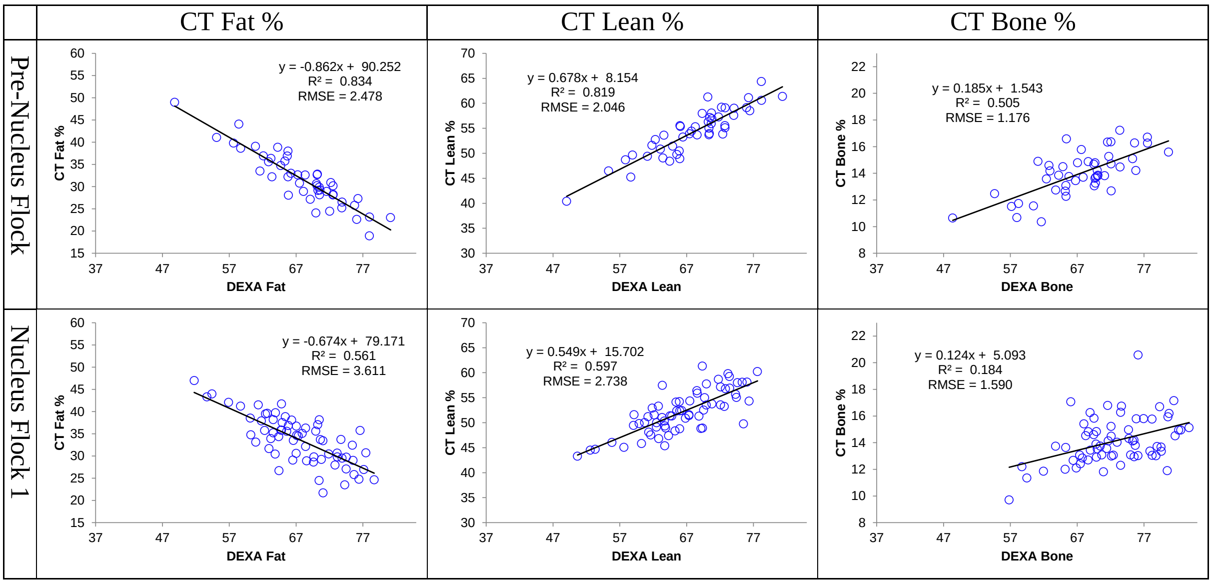


Table 28. Relationship between CT fat, bone, and lean % versus DEXA Fat, lean and bone values for 6 nucleus flock slaughters and 1 pre- nucleus flock slaughter in the saddle region (normalised for nylon R-value, within the saddle). Linear equations, RMSE and R-square values are shown for each graph.



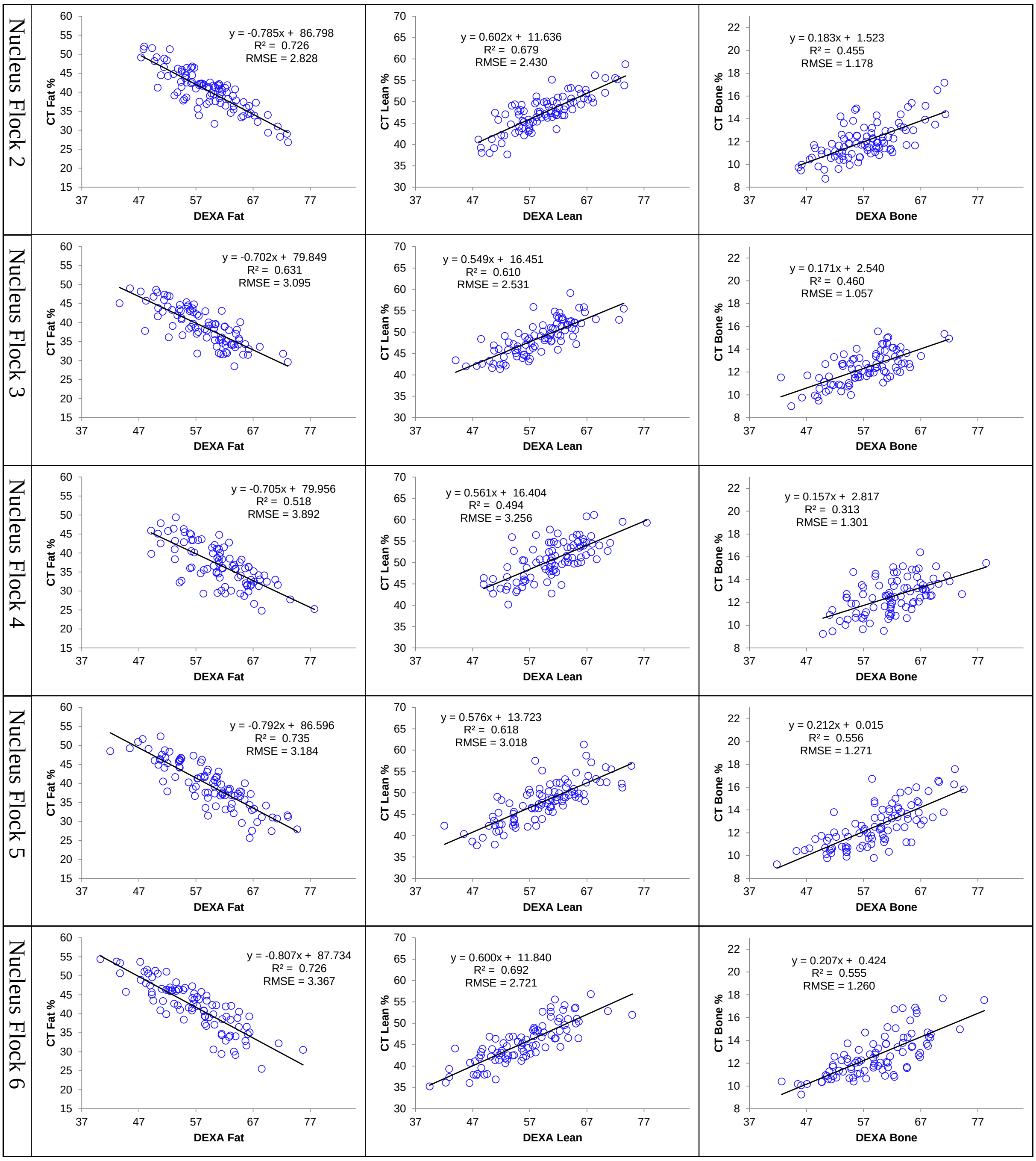
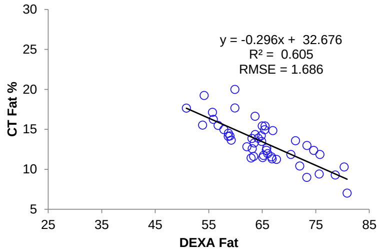
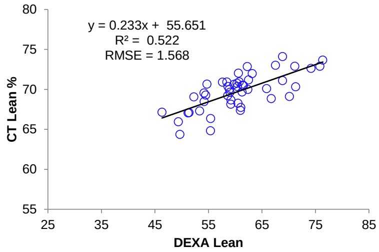
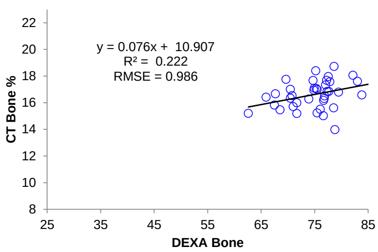
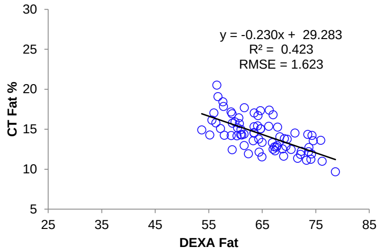
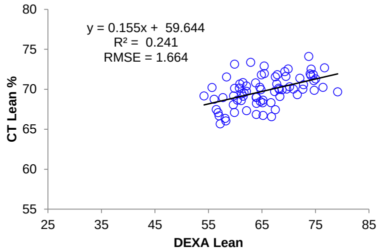
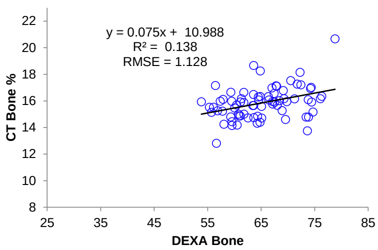
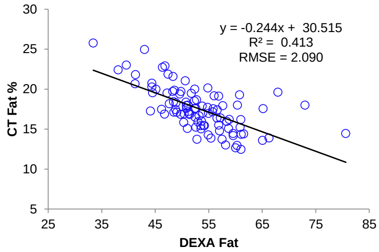
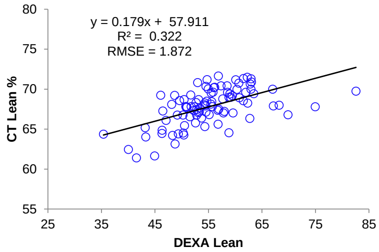
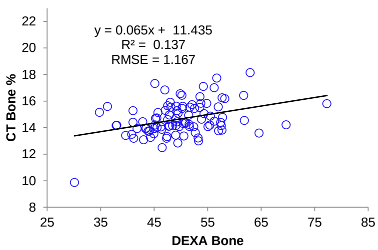
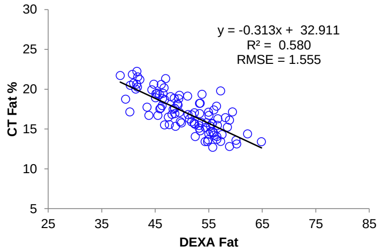
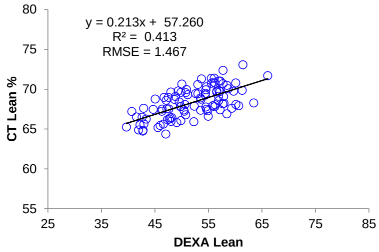
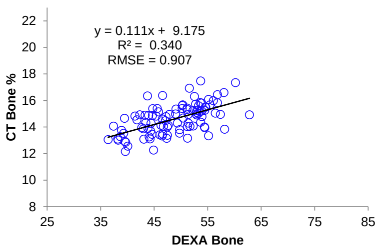
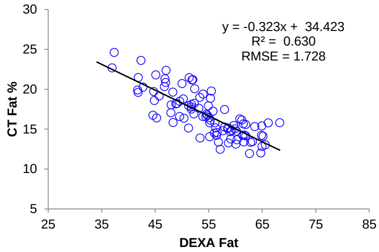
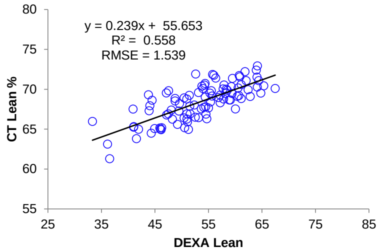
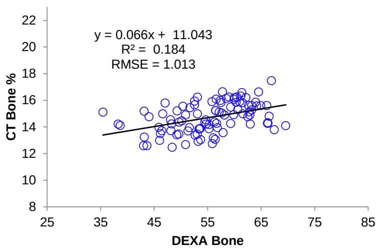
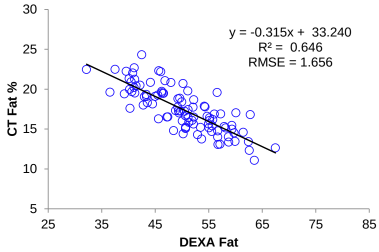
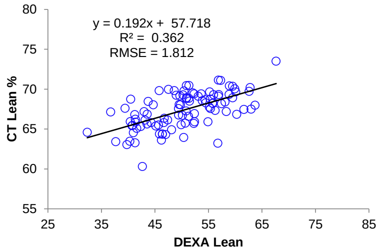
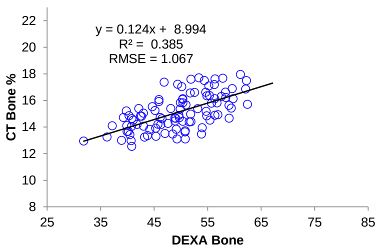
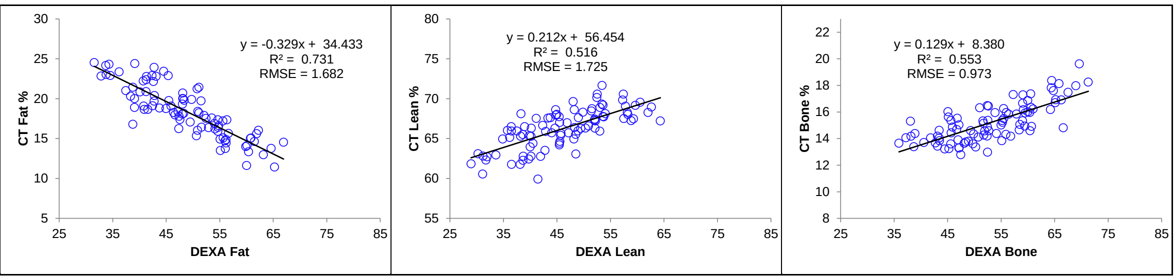

Nucleus Flock 2
y = -0.785x + 86.798
R² = 0.726
RMSE = 2.828
y = 0.602x + 11.636
R² = 0.679
RMSE = 2.430
y = 0.183x + 1.523
R² = 0.455
RMSE = 1.178
Nucleus Flock 3
y = -0.702x + 79.849
R² = 0.631
RMSE = 3.095
y = 0.549x + 16.451
R² = 0.610
RMSE = 2.531
y = 0.171x + 2.540
R² = 0.460
RMSE = 1.057
Nucleus Flock 4
y = -0.705x + 79.956
R² = 0.518
RMSE = 3.892
y = 0.561x + 16.404
R² = 0.494
RMSE = 3.256
y = 0.157x + 2.817
R² = 0.313
RMSE = 1.301
Nucleus Flock 5
y = -0.792x + 86.596
R² = 0.735
RMSE = 3.184
y = 0.576x + 13.723
R² = 0.618
RMSE = 3.018
y = 0.212x + 0.015
R² = 0.556
RMSE = 1.271
Nucleus Flock 6
y = -0.807x + 87.734
R² = 0.726
RMSE = 3.367
y = 0.600x + 11.840
R² = 0.692
RMSE = 2.721
y = 0.207x + 0.424
R² = 0.555
RMSE = 1.260
CT Fat %
CT Lean %
CT Bone %
DEXA Fat
DEXA Lean
DEXA Bone
15
20
25
30
35
40
45
50
55
60
30
35
40
45
50
55
60
65
70
8
10
12
14
16
18
20
22
37
47
57
67
77

Table 29. Relationship between CT fat, bone, and lean % versus DEXA Fat, lean and bone values for 6 nucleus flock slaughters and 1 pre- nucleus flock slaughter in the hind quarter (normalised for nylon R-value, within the hind quarter). Linear equations, RMSE, and R-square values are shown for each graph.

	CT Fat %	CT Lean %	CT Bone %
Pre-Nucleus Flock			
Nucleus Flock 1			
Nucleus Flock 2			
Nucleus Flock 3			
Nucleus Flock 4			
Nucleus Flock 5			

Nucleus Flock 6



Fore CT Fat (DEXA full as independent variable)

Table 30. Precision estimates (R-square and root mean square error), intercept and slope of actual CT Fat % in the fore quarter versus predicted CT fat % the full carcase, and accuracy estimates showing difference between observed minus the predicted at 20 (Diff@20), 26.5 (Diff@26.5), and 33 (Diff@33) CT Fat % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.763	0.624	0.686	0.653	0.766	0.714	0.698	0.774
	RMSE	1.430	1.697	1.851	1.743	1.597	1.922	1.900	1.859
	Intercept	0.000	0.496	-3.103	-1.617	-7.155	-7.111	1.085	-4.166
	Slope	1.000	0.961	1.178	1.102	1.289	1.294	1.027	1.195
	Diff@20	0.00	-0.29	0.46	0.43	-1.37	-1.23	1.62	-0.26
	Diff@26.5	0.00	-0.55	1.62	1.09	0.51	0.68	1.80	1.01
	Diff@33	0.00	-0.80	2.78	1.76	2.39	2.59	1.97	2.28
Test 2	R2	0.762	0.624	0.694	0.663	0.768	0.722	0.709	0.782
	RMSE	1.432	1.696	1.827	1.718	1.588	1.893	1.864	1.827
	Intercept	-0.417	0.000	-3.679	-2.287	-7.310	-6.995	0.643	-4.660
	Slope	1.029	1.000	1.221	1.148	1.319	1.314	1.060	1.235
	Diff@20	0.16	0.00	0.74	0.67	-0.92	-0.72	1.84	0.05
	Diff@26.5	0.35	0.00	2.17	1.63	1.16	1.32	2.23	1.58
	Diff@33	0.54	0.00	3.61	2.59	3.23	3.36	2.62	3.11
Test 3	R2	0.755	0.620	0.704	0.677	0.763	0.732	0.728	0.792
	RMSE	1.455	1.705	1.798	1.682	1.604	1.860	1.803	1.786
	Intercept	2.540	2.705	0.000	0.924	-2.298	-1.321	3.948	-0.849
	Slope	0.836	0.839	1.000	0.950	1.048	1.020	0.861	1.010
	Diff@20	-0.74	-0.51	0.00	-0.07	-1.33	-0.92	1.17	-0.65
	Diff@26.5	-1.81	-1.55	0.00	-0.39	-1.02	-0.79	0.26	-0.59
	Diff@33	-2.88	-2.60	0.00	-0.72	-0.70	-0.66	-0.64	-0.52
Test 4	R2	0.753	0.619	0.704	0.677	0.761	0.732	0.729	0.792
	RMSE	1.461	1.707	1.799	1.681	1.611	1.861	1.798	1.786
	Intercept	1.695	1.827	-0.942	0.000	-3.142	-2.033	3.150	-1.805
	Slope	0.879	0.887	1.051	1.000	1.097	1.064	0.904	1.062
	Diff@20	-0.73	-0.44	0.08	0.00	-1.20	-0.76	1.23	-0.57
	Diff@26.5	-1.52	-1.18	0.41	0.00	-0.57	-0.34	0.61	-0.17
	Diff@33	-2.31	-1.91	0.74	0.00	0.07	0.07	-0.02	0.23
Test 5	R2	0.762	0.624	0.698	0.668	0.769	0.726	0.715	0.785
	RMSE	1.435	1.696	1.816	1.705	1.587	1.881	1.846	1.813
	Intercept	5.106	5.348	2.879	3.822	0.000	0.417	6.359	2.009
	Slope	0.783	0.766	0.932	0.878	1.000	0.991	0.807	0.942

	Diff@20	0.76	0.67	1.52	1.39	0.00	0.23	2.51	0.85
	Diff@26.5	-0.65	-0.84	1.07	0.60	0.00	0.17	1.26	0.48
	Diff@33	-2.06	-2.36	0.63	-0.19	0.00	0.11	0.00	0.10
Test 6	R2	0.754	0.620	0.704	0.677	0.763	0.732	0.728	0.792
	RMSE	1.457	1.706	1.798	1.681	1.607	1.860	1.801	1.786
	Intercept	3.536	3.698	1.214	2.068	-0.978	0.000	4.997	0.376
	Slope	0.822	0.827	0.983	0.935	1.029	1.000	0.846	0.993
	Diff@20	-0.03	0.23	0.88	0.76	-0.40	0.00	1.92	0.23
	Diff@26.5	-1.19	-0.90	0.76	0.34	-0.21	0.00	0.92	0.19
	Diff@33	-2.35	-2.03	0.65	-0.09	-0.02	0.00	-0.08	0.14
Test 7	R2	0.746	0.614	0.701	0.675	0.753	0.730	0.731	0.790
	RMSE	1.481	1.718	1.808	1.687	1.639	1.868	1.793	1.794
	Intercept	-1.629	-1.655	-4.646	-3.600	-6.586	-5.035	0.000	-5.592
	Slope	0.976	1.000	1.165	1.112	1.203	1.155	1.000	1.179
	Diff@20	-2.10	-1.66	-1.34	-1.36	-2.52	-1.93	0.00	-2.01
	Diff@26.5	-2.26	-1.66	-0.27	-0.63	-1.20	-0.92	0.00	-0.84
	Diff@33	-2.41	-1.67	0.81	0.10	0.12	0.09	0.00	0.32
Test 8	R2	0.750	0.617	0.703	0.677	0.758	0.731	0.730	0.791
	RMSE	1.469	1.712	1.802	1.682	1.623	1.863	1.795	1.788
	Intercept	2.287	2.393	-0.128	0.743	-2.122	-0.910	3.864	-0.995
	Slope	0.854	0.867	1.021	0.973	1.060	1.024	0.877	1.032
	Diff@20	-0.63	-0.26	0.29	0.20	-0.91	-0.44	1.41	-0.36
	Diff@26.5	-1.58	-1.12	0.42	0.02	-0.52	-0.28	0.61	-0.15
	Diff@33	-2.53	-1.98	0.56	-0.16	-0.13	-0.13	-0.19	0.06

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Fore CT Lean (DEXA full as independent variable)

Table 31. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % in the fore quarter versus predicted CT lean % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 51 (Diff@51), 55 (Diff@55), and 59 (Diff@59) CT lean % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.522	0.440	0.470	0.451	0.553	0.427	0.525	0.565
	RMSE	1.654	1.692	1.931	1.741	1.708	2.142	1.671	1.932
	Intercept	0.000	4.716	-8.807	-3.329	-14.110	-11.576	3.300	-6.380
	Slope	1.000	0.943	1.156	1.065	1.278	1.219	0.930	1.122
	Diff@51	0.00	1.80	-0.86	0.00	0.06	-0.40	-0.28	-0.18
	Diff@55	0.00	1.57	-0.24	0.27	1.17	0.48	-0.56	0.31
	Diff@59	0.00	1.34	0.38	0.53	2.29	1.35	-0.84	0.79

Test 2	R2	0.510	0.448	0.424	0.385	0.518	0.399	0.494	0.510
	RMSE	1.676	1.680	2.013	1.843	1.774	2.194	1.725	2.050
	Intercept	-7.659	0.000	-12.196	-3.427	-22.825	-24.342	-2.581	-11.099
	Slope	1.096	1.000	1.178	1.034	1.393	1.404	1.000	1.169
	Diff@51	-2.76	0.00	-3.13	-1.69	-2.80	-3.72	-2.59	-2.49
	Diff@55	-2.38	0.00	-2.42	-1.55	-1.23	-2.10	-2.59	-1.82
	Diff@59	-1.99	0.00	-1.70	-1.42	0.34	-0.49	-2.59	-1.14
Test 3	R2	0.520	0.431	0.475	0.466	0.550	0.419	0.521	0.575
	RMSE	1.659	1.706	1.921	1.716	1.714	2.157	1.678	1.909
	Intercept	8.422	11.520	0.000	3.729	-2.688	1.385	11.477	2.240
	Slope	0.854	0.820	1.000	0.940	1.073	0.987	0.785	0.969
	Diff@51	0.96	2.34	0.00	0.68	1.05	0.72	0.52	0.63
	Diff@55	0.38	1.62	0.00	0.44	1.34	0.67	-0.34	0.51
	Diff@59	-0.21	0.90	0.00	0.20	1.64	0.62	-1.20	0.38
Test 4	R2	0.514	0.421	0.472	0.471	0.540	0.406	0.509	0.576
	RMSE	1.669	1.722	1.928	1.710	1.734	2.181	1.698	1.906
	Intercept	6.003	8.157	-3.084	0.000	-4.718	1.256	9.899	-0.945
	Slope	0.894	0.873	1.048	1.000	1.101	0.981	0.808	1.018
	Diff@51	0.59	1.66	-0.62	0.00	0.42	0.28	0.10	-0.01
	Diff@55	0.16	1.15	-0.42	0.00	0.82	0.21	-0.66	0.06
	Diff@59	-0.26	0.64	-0.23	0.00	1.22	0.13	-1.43	0.14
Test 5	R2	0.522	0.439	0.472	0.455	0.553	0.426	0.525	0.568
	RMSE	1.655	1.695	1.927	1.734	1.708	2.143	1.671	1.926
	Intercept	10.976	14.836	3.634	7.916	0.000	2.306	13.538	5.732
	Slope	0.785	0.743	0.910	0.843	1.000	0.947	0.728	0.883
	Diff@51	-0.01	1.71	-0.93	-0.09	0.00	-0.41	-0.31	-0.25
	Diff@55	-0.87	0.68	-1.29	-0.72	0.00	-0.62	-1.40	-0.72
	Diff@59	-1.73	-0.35	-1.65	-1.35	0.00	-0.84	-2.48	-1.19
Test 6	R2	0.522	0.442	0.468	0.446	0.552	0.427	0.524	0.561
	RMSE	1.655	1.690	1.936	1.749	1.710	2.141	1.672	1.940
	Intercept	9.899	14.281	2.922	7.717	-1.519	0.000	12.491	4.947
	Slope	0.812	0.763	0.934	0.857	1.040	1.000	0.756	0.908
	Diff@51	0.32	2.18	-0.43	0.43	0.53	0.00	0.03	0.24
	Diff@55	-0.43	1.23	-0.69	-0.14	0.69	0.00	-0.94	-0.13
	Diff@59	-1.18	0.28	-0.96	-0.71	0.85	0.00	-1.92	-0.50
Test 7	R2	0.522	0.440	0.471	0.454	0.553	0.427	0.525	0.566
	RMSE	1.654	1.693	1.929	1.737	1.708	2.142	1.671	1.928
	Intercept	-3.579	1.176	-13.132	-7.490	-18.609	-15.540	0.000	-10.544
	Slope	1.076	1.017	1.247	1.153	1.373	1.304	1.000	1.209
	Diff@51	0.32	2.05	-0.53	0.29	0.44	-0.02	0.00	0.14
	Diff@55	0.62	2.12	0.46	0.90	1.93	1.20	0.00	0.98
	Diff@59	0.93	2.19	1.44	1.51	3.42	2.42	0.00	1.82
Test 8	R2	0.518	0.428	0.475	0.469	0.547	0.415	0.517	0.576
	RMSE	1.662	1.712	1.922	1.712	1.720	2.165	1.685	1.906
	Intercept	7.354	10.102	-1.406	2.080	-3.689	1.142	10.706	0.831
	Slope	0.867	0.838	1.017	0.962	1.082	0.983	0.793	0.986
	Diff@51	0.57	1.84	-0.53	0.15	0.50	0.27	0.14	0.11
	Diff@55	0.04	1.20	-0.46	-0.01	0.83	0.20	-0.69	0.05

Diff@59	-0.49	0.55	-0.39	-0.16	1.15	0.13	-1.52	0.00

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Fore CT Bone (DEXA full as independent variable)

Table 32. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % in the fore quarter versus predicted CT bone % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 14 (Diff@14), 16.5 (Diff@16.5), and 19 (Diff@19) CT bone % using DEXA (normalised for nylon R-value, within the forequarter) and hot carcase weight as predictors

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.458	0.416	0.517	0.566	0.541	0.588	0.594	0.647
	RMSE	0.914	0.947	0.942	0.751	0.948	1.103	1.057	1.004
	Intercept	0.000	-3.299	-5.984	-4.889	-7.696	-10.764	-7.112	-8.331
	Slope	1.000	1.125	1.247	1.196	1.327	1.529	1.325	1.386
	Diff@14	0.00	-1.55	-2.52	-2.14	-3.11	-3.36	-2.56	-2.92
	Diff@16.5	0.00	-1.24	-1.90	-1.65	-2.29	-2.04	-1.75	-1.96
	Diff@19	0.00	-0.92	-1.29	-1.16	-1.48	-0.71	-0.93	-0.99
Test 2	R2	0.393	0.533	0.460	0.501	0.494	0.664	0.708	0.559
	RMSE	0.968	0.847	0.995	0.805	0.995	0.996	0.895	1.123
	Intercept	8.518	0.000	4.718	5.361	4.115	2.622	3.219	3.157
	Slope	0.633	1.000	0.713	0.686	0.740	0.850	0.851	0.829
	Diff@14	3.37	0.00	0.71	0.97	0.47	0.52	1.14	0.77
	Diff@16.5	2.46	0.00	-0.01	0.18	-0.18	0.14	0.77	0.34
	Diff@19	1.54	0.00	-0.73	-0.60	-0.83	-0.23	0.39	-0.08
Test 3	R2	0.453	0.464	0.530	0.586	0.549	0.633	0.658	0.654
	RMSE	0.918	0.907	0.929	0.733	0.941	1.041	0.969	0.995
	Intercept	4.994	0.242	0.000	0.642	-0.877	-2.773	-1.039	-1.773
	Slope	0.803	1.003	1.000	0.971	1.037	1.183	1.088	1.119
	Diff@14	2.24	0.29	0.00	0.24	-0.36	-0.21	0.19	-0.11
	Diff@16.5	1.75	0.30	0.00	0.17	-0.27	0.25	0.41	0.19
	Diff@19	1.26	0.31	0.00	0.10	-0.18	0.71	0.63	0.49
Test 4	R2	0.452	0.469	0.530	0.587	0.548	0.636	0.663	0.653
	RMSE	0.919	0.903	0.929	0.733	0.941	1.036	0.962	0.996
	Intercept	4.475	-0.625	-0.648	0.000	-1.517	-3.494	-1.778	-2.514
	Slope	0.828	1.044	1.029	1.000	1.064	1.214	1.122	1.152
	Diff@14	2.06	-0.01	-0.25	0.00	-0.61	-0.50	-0.07	-0.38
	Diff@16.5	1.63	0.10	-0.18	0.00	-0.45	0.04	0.24	0.00
	Diff@19	1.20	0.21	-0.10	0.00	-0.29	0.57	0.54	0.38
Test 5	R2	0.454	0.459	0.530	0.586	0.549	0.629	0.652	0.655

	RMSE	0.917	0.912	0.929	0.733	0.940	1.047	0.979	0.994
	Intercept	5.697	1.383	0.887	1.519	0.000	-1.783	-0.037	-0.763
	Slope	0.772	0.951	0.962	0.934	1.000	1.142	1.044	1.075
	Diff@14	2.50	0.70	0.36	0.59	0.00	0.21	0.57	0.29
	Diff@16.5	1.93	0.58	0.26	0.43	0.00	0.57	0.68	0.48
	Diff@19	1.36	0.46	0.17	0.26	0.00	0.92	0.79	0.67
Test 6	R2	0.407	0.531	0.479	0.525	0.508	0.665	0.710	0.583
	RMSE	0.956	0.849	0.978	0.786	0.982	0.995	0.893	1.092
	Intercept	6.560	-2.290	2.350	3.008	1.726	0.000	0.644	0.473
	Slope	0.737	1.129	0.849	0.821	0.875	1.000	0.995	0.981
	Diff@14	2.88	-0.48	0.23	0.50	-0.03	0.00	0.57	0.21
	Diff@16.5	2.22	-0.16	-0.14	0.05	-0.34	0.00	0.56	0.16
	Diff@19	1.56	0.16	-0.52	-0.40	-0.65	0.00	0.54	0.11
Test 7	R2	0.408	0.530	0.480	0.526	0.509	0.665	0.710	0.585
	RMSE	0.956	0.849	0.977	0.784	0.981	0.995	0.893	1.090
	Intercept	6.081	-2.971	1.787	2.459	1.149	-0.652	0.000	-0.173
	Slope	0.741	1.133	0.854	0.826	0.880	1.006	1.000	0.987
	Diff@14	2.45	-1.12	-0.25	0.03	-0.53	-0.57	0.00	-0.36
	Diff@16.5	1.80	-0.78	-0.61	-0.41	-0.83	-0.55	0.00	-0.39
	Diff@19	1.15	-0.45	-0.98	-0.84	-1.13	-0.54	0.00	-0.42
Test 8	R2	0.444	0.491	0.525	0.582	0.544	0.650	0.685	0.645
	RMSE	0.926	0.884	0.934	0.737	0.946	1.016	0.930	1.008
	Intercept	5.197	-0.903	0.284	0.871	-0.421	-2.228	-0.958	-1.571
	Slope	0.795	1.059	0.976	0.951	1.002	1.140	1.081	1.101
	Diff@14	2.33	-0.08	-0.06	0.18	-0.39	-0.27	0.17	-0.16
	Diff@16.5	1.82	0.07	-0.12	0.06	-0.38	0.08	0.37	0.09
	Diff@19	1.30	0.22	-0.18	-0.06	-0.37	0.44	0.58	0.34

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Fat (DEXA full as independent variable)

Table 33. Precision estimates (R-square and root mean square error), intercept and slope of actual CT fat % in the hind quarter versus predicted CT fat % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 17 (Diff@17), and 22 (Diff@22) CT fat % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.772	0.718	0.769	0.769	0.789	0.726	0.785	0.807
	RMSE	1.281	1.135	1.311	1.146	1.304	1.457	1.503	1.351

	Intercept	0.000	1.516	-1.131	-0.652	-2.054	0.099	-0.887	-0.209
	Slope	1.000	0.914	1.102	1.045	1.161	0.979	1.070	1.028
	Diff@12	0.00	0.49	0.09	-0.11	-0.12	-0.15	-0.05	0.13
	Diff@17	0.00	0.06	0.60	0.12	0.69	-0.25	0.30	0.27
	Diff@22	0.00	-0.37	1.10	0.35	1.49	-0.36	0.65	0.41
Test 2	R2	0.771	0.718	0.767	0.765	0.784	0.728	0.784	0.805
	RMSE	1.282	1.134	1.316	1.156	1.320	1.452	1.506	1.358
	Intercept	-1.729	0.000	-3.095	-2.470	-4.235	-1.955	-2.944	-1.990
	Slope	1.105	1.000	1.213	1.149	1.284	1.093	1.188	1.129
	Diff@12	-0.47	0.00	-0.54	-0.69	-0.83	-0.84	-0.69	-0.44
	Diff@17	0.06	0.00	0.53	0.06	0.59	-0.37	0.25	0.21
	Diff@22	0.58	0.00	1.59	0.80	2.01	0.10	1.19	0.85
Test 3	R2	0.772	0.717	0.769	0.771	0.791	0.725	0.785	0.808
	RMSE	1.281	1.137	1.310	1.143	1.297	1.459	1.503	1.349
	Intercept	0.985	2.398	0.000	0.403	-0.814	1.238	0.272	0.820
	Slope	0.906	0.833	1.000	0.950	1.052	0.883	0.967	0.935
	Diff@12	-0.14	0.40	0.00	-0.20	-0.19	-0.16	-0.12	0.04
	Diff@17	-0.61	-0.44	0.00	-0.45	0.07	-0.75	-0.29	-0.29
	Diff@22	-1.07	-1.27	0.00	-0.70	0.33	-1.33	-0.45	-0.62
Test 4	R2	0.771	0.715	0.769	0.772	0.794	0.723	0.785	0.808
	RMSE	1.284	1.141	1.313	1.141	1.288	1.466	1.506	1.349
	Intercept	0.538	1.951	-0.391	0.000	-1.139	1.134	0.004	0.395
	Slope	0.951	0.882	1.051	1.000	1.101	0.917	1.009	0.986
	Diff@12	-0.06	0.54	0.22	0.00	0.08	0.14	0.11	0.22
	Diff@17	-0.30	-0.05	0.47	0.00	0.59	-0.27	0.16	0.15
	Diff@22	-0.55	-0.64	0.73	0.00	1.09	-0.69	0.20	0.08
Test 5	R2	0.767	0.709	0.764	0.769	0.796	0.717	0.781	0.805
	RMSE	1.293	1.153	1.326	1.147	1.282	1.481	1.518	1.360
	Intercept	1.225	2.553	0.584	0.892	0.000	2.313	1.085	1.199
	Slope	0.866	0.817	0.959	0.914	1.000	0.824	0.912	0.905
	Diff@12	-0.38	0.35	0.09	-0.14	0.00	0.20	0.02	0.06
	Diff@17	-1.05	-0.56	-0.11	-0.56	0.00	-0.69	-0.42	-0.41
	Diff@22	-1.71	-1.48	-0.31	-0.99	0.00	-1.57	-0.86	-0.89
Test 6	R2	0.769	0.717	0.761	0.755	0.772	0.729	0.780	0.799
	RMSE	1.290	1.137	1.333	1.181	1.355	1.450	1.521	1.379
	Intercept	0.812	2.371	-0.373	0.184	-1.526	0.000	-0.508	0.596
	Slope	0.994	0.884	1.082	1.021	1.154	1.000	1.076	1.005
	Diff@12	0.74	0.98	0.61	0.43	0.32	0.00	0.40	0.65
	Diff@17	0.71	0.40	1.03	0.54	1.09	0.00	0.78	0.68
	Diff@22	0.68	-0.18	1.44	0.64	1.86	0.00	1.15	0.70
Test 7	R2	0.772	0.717	0.769	0.770	0.790	0.726	0.785	0.807
	RMSE	1.281	1.136	1.311	1.144	1.300	1.458	1.503	1.350
	Intercept	0.769	2.208	-0.256	0.166	-1.103	0.960	0.000	0.591
	Slope	0.936	0.859	1.032	0.980	1.087	0.914	1.000	0.964
	Diff@12	0.01	0.51	0.13	-0.07	-0.06	-0.07	0.00	0.16
	Diff@17	-0.31	-0.19	0.29	-0.17	0.37	-0.50	0.00	-0.01
	Diff@22	-0.63	-0.90	0.46	-0.26	0.81	-0.93	0.00	-0.19
Test 8	R2	0.771	0.714	0.768	0.772	0.794	0.722	0.784	0.807

	RMSE	1.284	1.142	1.313	1.141	1.287	1.467	1.506	1.350
	Intercept	0.176	1.611	-0.779	-0.372	-1.537	0.818	-0.358	0.024
	Slope	0.962	0.894	1.063	1.012	1.114	0.927	1.020	0.998
	Diff@12	-0.28	0.34	-0.02	-0.23	-0.17	-0.06	-0.11	0.00
	Diff@17	-0.47	-0.19	0.30	-0.17	0.40	-0.42	-0.01	-0.02
	Diff@22	-0.67	-0.73	0.62	-0.11	0.97	-0.79	0.09	-0.03

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Lean (DEXA full as independent variable)

Table 34. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % in the hind quarter versus predicted CT lean % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 64 (Diff@64), 67.5 (Diff@67.5), and 71 (Diff@71) CT lean % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.495	0.394	0.500	0.543	0.562	0.348	0.547	0.569
	RMSE	1.612	1.487	1.607	1.293	1.531	1.831	1.670	1.613
	Intercept	0.000	10.454	-4.926	-0.414	-12.009	11.228	-0.408	1.811
	Slope	1.000	0.856	1.078	1.020	1.191	0.843	1.008	0.981
	Diff@64	0.00	1.22	0.04	0.84	0.22	1.18	0.09	0.61
	Diff@67.5	0.00	0.71	0.31	0.91	0.89	0.63	0.12	0.54
	Diff@71	0.00	0.21	0.58	0.98	1.56	0.08	0.15	0.47
Test 2	R2	0.400	0.463	0.399	0.401	0.333	0.398	0.442	0.465
	RMSE	1.758	1.400	1.763	1.480	1.890	1.759	1.852	1.795
	Intercept	-12.036	0.000	-6.579	2.932	-10.382	-24.048	-14.205	-1.840
	Slope	1.154	1.000	1.089	0.958	1.158	1.361	1.194	1.023
	Diff@64	-2.19	0.00	-0.90	0.24	-0.30	-0.94	-1.78	-0.34
	Diff@67.5	-1.65	0.00	-0.59	0.09	0.26	0.32	-1.10	-0.26
	Diff@71	-1.12	0.00	-0.28	-0.06	0.81	1.58	-0.42	-0.18
Test 3	R2	0.494	0.409	0.502	0.542	0.552	0.361	0.550	0.568
	RMSE	1.614	1.468	1.604	1.294	1.549	1.812	1.664	1.614
	Intercept	4.041	14.087	0.000	4.588	-6.741	12.737	3.149	6.613
	Slope	0.934	0.798	1.000	0.941	1.109	0.818	0.951	0.906
	Diff@64	-0.20	1.15	0.00	0.82	0.21	1.10	0.01	0.59
	Diff@67.5	-0.43	0.45	0.00	0.62	0.59	0.47	-0.17	0.26
	Diff@71	-0.66	-0.26	0.00	0.41	0.97	-0.17	-0.34	-0.07
Test 4	R2	0.495	0.399	0.501	0.543	0.559	0.352	0.548	0.569
	RMSE	1.613	1.481	1.605	1.293	1.536	1.825	1.667	1.613
	Intercept	0.141	10.627	-4.604	0.000	-11.715	10.702	-0.453	2.232

	Slope	0.984	0.842	1.059	1.000	1.171	0.840	0.995	0.962
	Diff@64	-0.89	0.49	-0.86	0.00	-0.76	0.46	-0.76	-0.20
	Diff@67.5	-0.94	-0.06	-0.65	0.00	-0.16	-0.10	-0.78	-0.33
	Diff@71	-1.00	-0.62	-0.45	0.00	0.44	-0.66	-0.80	-0.47
Test 5	R2	0.491	0.358	0.485	0.530	0.570	0.321	0.532	0.561
	RMSE	1.619	1.531	1.631	1.311	1.518	1.869	1.696	1.626
	Intercept	10.320	19.193	5.770	9.320	0.000	22.790	10.960	10.612
	Slope	0.841	0.718	0.908	0.865	1.000	0.661	0.829	0.841
	Diff@64	0.16	1.18	-0.09	0.69	0.00	1.12	0.01	0.42
	Diff@67.5	-0.40	0.19	-0.41	0.22	0.00	-0.07	-0.58	-0.14
	Diff@71	-0.95	-0.79	-0.74	-0.25	0.00	-1.25	-1.18	-0.70
Test 6	R2	0.439	0.459	0.442	0.453	0.408	0.407	0.493	0.505
	RMSE	1.700	1.404	1.699	1.414	1.781	1.747	1.766	1.727
	Intercept	4.402	14.984	6.504	13.389	1.406	0.000	2.262	11.634
	Slope	0.908	0.774	0.891	0.800	0.978	1.000	0.949	0.820
	Diff@64	-1.51	0.55	-0.46	0.56	-0.02	0.00	-1.03	0.14
	Diff@67.5	-1.83	-0.24	-0.84	-0.14	-0.09	0.00	-1.21	-0.48
	Diff@71	-2.15	-1.03	-1.22	-0.84	-0.17	0.00	-1.39	-1.11
Test 7	R2	0.493	0.415	0.502	0.540	0.547	0.366	0.550	0.566
	RMSE	1.616	1.461	1.604	1.297	1.558	1.805	1.664	1.617
	Intercept	1.134	11.682	-2.834	2.074	-9.951	9.402	0.000	4.129
	Slope	0.979	0.836	1.045	0.981	1.159	0.870	1.000	0.945
	Diff@64	-0.24	1.16	0.02	0.85	0.24	1.10	0.00	0.61
	Diff@67.5	-0.31	0.58	0.17	0.78	0.80	0.64	0.00	0.42
	Diff@71	-0.39	0.00	0.33	0.71	1.36	0.19	0.00	0.23
Test 8	R2	0.495	0.405	0.502	0.543	0.556	0.357	0.549	0.568
	RMSE	1.613	1.474	1.604	1.293	1.543	1.818	1.665	1.613
	Intercept	2.754	12.926	-1.585	2.978	-8.440	12.236	1.999	5.092
	Slope	0.949	0.811	1.018	0.960	1.128	0.821	0.963	0.924
	Diff@64	-0.53	0.83	-0.41	0.43	-0.26	0.79	-0.37	0.21
	Diff@67.5	-0.71	0.17	-0.35	0.29	0.19	0.16	-0.50	-0.06
	Diff@71	-0.89	-0.49	-0.28	0.15	0.64	-0.46	-0.62	-0.32

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Hind CT Bone (DEXA full as independent variable)

Table 35. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % in the hind quarter versus predicted CT bone % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 14.5 (Diff@14.5), and 17 (Diff@17) CT bone % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

Kill Groups

		Pre-NF	NF 1	NF 2	NF 3	NF 4	NF 5	NF 6	Combined
Test 1	R2	0.563	0.430	0.484	0.501	0.513	0.655	0.695	0.564
	RMSE	0.739	0.917	0.902	0.787	0.782	0.799	0.803	0.913
	Intercept	0.000	-4.762	-2.983	-2.727	-1.207	-3.882	-3.602	-2.708
	Slope	1.000	1.238	1.132	1.107	0.988	1.218	1.207	1.121
	Diff@12	0.00	-1.90	-1.40	-1.44	-1.35	-1.27	-1.12	-1.25
	Diff@14.5	0.00	-1.31	-1.07	-1.17	-1.38	-0.73	-0.60	-0.95
	Diff@17	0.00	-0.71	-0.74	-0.91	-1.41	-0.18	-0.08	-0.65
Test 2	R2	0.514	0.524	0.453	0.456	0.476	0.702	0.658	0.474
	RMSE	0.779	0.838	0.929	0.822	0.811	0.742	0.851	1.003
	Intercept	6.722	0.000	4.163	4.675	5.423	2.936	4.315	4.380
	Slope	0.657	1.000	0.712	0.672	0.604	0.814	0.759	0.716
	Diff@12	2.61	0.00	0.70	0.74	0.68	0.70	1.43	0.97
	Diff@14.5	1.75	0.00	-0.02	-0.08	-0.31	0.23	0.83	0.26
	Diff@17	0.90	0.00	-0.74	-0.90	-1.30	-0.23	0.22	-0.45
Test 3	R2	0.559	0.470	0.489	0.505	0.512	0.675	0.696	0.557
	RMSE	0.742	0.885	0.897	0.784	0.783	0.775	0.802	0.921
	Intercept	2.839	-2.717	0.000	0.291	1.652	-0.686	-0.145	0.174
	Slope	0.884	1.177	1.000	0.972	0.857	1.073	1.054	0.998
	Diff@12	1.44	-0.60	0.00	-0.04	-0.06	0.20	0.50	0.15
	Diff@14.5	1.15	-0.15	0.00	-0.11	-0.41	0.38	0.63	0.14
	Diff@17	0.86	0.29	0.00	-0.18	-0.77	0.56	0.76	0.14
Test 4	R2	0.560	0.462	0.489	0.505	0.513	0.671	0.697	0.559
	RMSE	0.741	0.891	0.898	0.784	0.782	0.780	0.801	0.918
	Intercept	2.563	-2.768	-0.273	0.000	1.370	-0.958	-0.480	-0.083
	Slope	0.907	1.190	1.027	1.000	0.883	1.102	1.084	1.023
	Diff@12	1.45	-0.49	0.05	0.00	-0.03	0.26	0.53	0.20
	Diff@14.5	1.21	-0.02	0.12	0.00	-0.32	0.52	0.74	0.25
	Diff@17	0.98	0.46	0.19	0.00	-0.61	0.77	0.95	0.31
Test 5	R2	0.562	0.446	0.487	0.504	0.514	0.664	0.697	0.562
	RMSE	0.740	0.904	0.899	0.785	0.782	0.789	0.801	0.915
	Intercept	1.192	-3.929	-1.740	-1.474	0.000	-2.520	-2.140	-1.511
	Slope	1.019	1.300	1.155	1.127	1.000	1.239	1.224	1.147
	Diff@12	1.42	-0.33	0.12	0.05	0.00	0.35	0.55	0.25
	Diff@14.5	1.47	0.42	0.51	0.37	0.00	0.95	1.11	0.62
	Diff@17	1.52	1.17	0.89	0.69	0.00	1.55	1.67	0.99
Test 6	R2	0.497	0.521	0.436	0.437	0.462	0.703	0.642	0.444
	RMSE	0.793	0.841	0.943	0.836	0.822	0.741	0.871	1.031
	Intercept	4.641	-3.537	1.964	2.700	3.525	0.000	1.856	2.254
	Slope	0.799	1.232	0.851	0.798	0.727	1.000	0.919	0.853
	Diff@12	2.23	-0.75	0.18	0.28	0.25	0.00	0.88	0.49
	Diff@14.5	1.73	-0.17	-0.19	-0.23	-0.43	0.00	0.68	0.13
	Diff@17	1.23	0.41	-0.56	-0.74	-1.12	0.00	0.48	-0.24
Test 7	R2	0.561	0.456	0.489	0.505	0.513	0.668	0.697	0.561
	RMSE	0.741	0.896	0.898	0.784	0.782	0.783	0.801	0.917
	Intercept	2.968	-2.025	0.215	0.459	1.756	-0.426	0.000	0.414
	Slope	0.835	1.084	0.946	0.922	0.816	1.015	1.000	0.942
	Diff@12	0.99	-1.01	-0.43	-0.48	-0.46	-0.25	0.00	-0.29

	Diff@14.5	0.58	-0.80	-0.57	-0.67	-0.92	-0.21	0.00	-0.43
	Diff@17	0.16	-0.59	-0.70	-0.87	-1.38	-0.18	0.00	-0.58
Test 8	R2	0.559	0.470	0.489	0.505	0.512	0.675	0.696	0.556
	RMSE	0.742	0.884	0.897	0.784	0.783	0.775	0.802	0.921
	Intercept	1.644	-4.338	-1.355	-1.023	0.495	-2.143	-1.569	-1.180
	Slope	0.960	1.280	1.086	1.056	0.931	1.166	1.144	1.084
	Diff@12	1.17	-0.98	-0.32	-0.35	-0.33	-0.15	0.16	-0.17
	Diff@14.5	1.07	-0.27	-0.10	-0.21	-0.50	0.27	0.52	0.04
	Diff@17	0.97	0.43	0.11	-0.07	-0.67	0.68	0.88	0.25

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Fat (DEXA full as independent variable)

Table 36. Precision estimates (R-square and root mean square error), intercept and slope of actual CT fat % in the saddle versus predicted CT fat % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 28 (Diff@28), 38.5 (Diff@38.5), and 49 (Diff@49) CT fat % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.870	0.788	0.862	0.846	0.840	0.841	0.866	0.867
	RMSE	2.187	2.510	2.019	1.998	2.242	2.472	2.359	2.371
	Intercept	0.000	0.236	2.897	2.466	1.210	1.309	4.900	2.607
	Slope	1.000	1.052	0.966	0.952	0.969	0.955	0.892	0.946
	Diff@28	0.00	1.70	1.96	1.12	0.34	0.04	1.89	1.09
	Diff@38.5	0.00	2.24	1.60	0.62	0.01	-0.43	0.76	0.53
	Diff@49	0.00	2.79	1.25	0.11	-0.31	-0.91	-0.38	-0.04
Test 2	R2	0.863	0.801	0.867	0.850	0.853	0.855	0.879	0.867
	RMSE	2.246	2.435	1.978	1.975	2.150	2.354	2.241	2.373
	Intercept	-0.560	0.000	0.858	0.499	-1.856	-2.409	1.727	1.572
	Slope	0.993	1.000	0.962	0.946	0.986	0.975	0.923	0.919
	Diff@28	-0.76	0.00	-0.20	-1.01	-2.24	-3.11	-0.44	-0.69
	Diff@38.5	-0.84	0.00	-0.60	-1.57	-2.38	-3.37	-1.25	-1.54
	Diff@49	-0.91	0.00	-0.99	-2.13	-2.52	-3.63	-2.06	-2.39
Test 3	R2	0.867	0.799	0.869	0.853	0.852	0.852	0.877	0.870
	RMSE	2.213	2.443	1.964	1.952	2.159	2.381	2.260	2.343
	Intercept	-1.845	-1.487	0.000	-0.401	-2.350	-2.600	1.412	0.455
	Slope	1.030	1.054	1.000	0.985	1.017	1.002	0.945	0.962
	Diff@28	-1.00	0.04	0.00	-0.82	-1.88	-2.53	-0.12	-0.60
	Diff@38.5	-0.68	0.61	0.00	-0.98	-1.70	-2.51	-0.70	-0.99
	Diff@49	-0.37	1.18	0.00	-1.13	-1.53	-2.48	-1.28	-1.39

Test 4	R2	0.868	0.799	0.869	0.853	0.851	0.851	0.876	0.871
	RMSE	2.207	2.448	1.965	1.951	2.164	2.390	2.267	2.340
	Intercept	-1.533	-1.205	0.414	0.000	-1.842	-2.037	1.914	0.778
	Slope	1.046	1.074	1.015	1.000	1.030	1.015	0.956	0.979
	Diff@28	-0.26	0.87	0.83	0.00	-1.00	-1.62	0.69	0.18
	Diff@38.5	0.22	1.65	0.99	0.00	-0.68	-1.46	0.23	-0.04
	Diff@49	0.70	2.42	1.15	0.00	-0.37	-1.30	-0.23	-0.27
Test 5	R2	0.864	0.801	0.868	0.851	0.853	0.855	0.879	0.868
	RMSE	2.240	2.435	1.974	1.969	2.150	2.358	2.242	2.366
	Intercept	1.190	1.737	2.610	2.210	0.000	-0.523	3.486	3.203
	Slope	1.007	1.017	0.977	0.961	1.000	0.988	0.934	0.934
	Diff@28	1.40	2.23	1.96	1.12	0.00	-0.86	1.65	1.36
	Diff@38.5	1.48	2.41	1.72	0.71	0.00	-0.99	0.96	0.67
	Diff@49	1.56	2.59	1.47	0.30	0.00	-1.11	0.27	-0.02
Test 6	R2	0.856	0.798	0.859	0.838	0.849	0.857	0.878	0.858
	RMSE	2.307	2.448	2.038	2.048	2.176	2.341	2.252	2.452
	Intercept	3.232	4.015	4.180	3.884	1.052	0.000	4.249	5.042
	Slope	1.006	0.991	0.970	0.950	1.005	1.000	0.949	0.918
	Diff@28	3.41	3.77	3.33	2.49	1.20	0.00	2.84	2.75
	Diff@38.5	3.48	3.68	3.01	1.96	1.25	0.00	2.30	1.90
	Diff@49	3.55	3.59	2.70	1.44	1.31	0.00	1.77	1.04
Test 7	R2	0.862	0.800	0.866	0.848	0.853	0.856	0.879	0.865
	RMSE	2.258	2.436	1.988	1.987	2.153	2.349	2.240	2.387
	Intercept	-2.144	-1.529	-0.770	-1.077	-3.648	-4.283	0.000	0.101
	Slope	1.072	1.075	1.038	1.020	1.067	1.056	1.000	0.990
	Diff@28	-0.12	0.56	0.30	-0.51	-1.78	-2.72	0.00	-0.19
	Diff@38.5	0.64	1.34	0.70	-0.30	-1.07	-2.13	0.00	-0.30
	Diff@49	1.39	2.13	1.10	-0.09	-0.37	-1.55	0.00	-0.41
Test 8	R2	0.869	0.798	0.869	0.853	0.850	0.850	0.875	0.871
	RMSE	2.202	2.453	1.967	1.952	2.171	2.399	2.277	2.339
	Intercept	-1.629	-1.340	0.442	0.022	-1.727	-1.864	2.051	0.724
	Slope	1.050	1.083	1.019	1.005	1.033	1.017	0.957	0.985
	Diff@28	-0.22	0.98	0.98	0.15	-0.81	-1.38	0.86	0.30
	Diff@38.5	0.31	1.85	1.19	0.20	-0.47	-1.20	0.41	0.15
	Diff@49	0.84	2.72	1.39	0.25	-0.13	-1.02	-0.04	-0.01

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Lean (DEXA full as independent variable)

Table 37. Precision estimates (R-square and root mean square error), intercept and slope of actual CT lean % in the saddle versus predicted CT lean % in the full carcass, and accuracy estimates showing difference between

observed minus the predicted at 41 (Diff@41), 48.5 (Diff@48.5), and 56 (Diff@46) CT lean % using DEXA (normalised for nylon R-value) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.798	0.663	0.752	0.747	0.733	0.715	0.768	0.771
	RMSE	2.167	2.505	2.148	2.038	2.366	2.610	2.360	2.487
	Intercept	0.000	-1.846	0.806	2.025	1.479	4.527	6.077	3.055
	Slope	1.000	0.990	0.943	0.938	0.978	0.904	0.851	0.922
	Diff@41	0.00	-2.26	-1.53	-0.54	0.57	0.60	-0.03	-0.16
	Diff@48.5	0.00	-2.33	-1.95	-1.00	0.41	-0.12	-1.15	-0.74
	Diff@56	0.00	-2.41	-2.38	-1.47	0.24	-0.83	-2.26	-1.33
Test 2	R2	0.762	0.711	0.719	0.709	0.727	0.748	0.778	0.745
	RMSE	2.349	2.318	2.284	2.184	2.393	2.451	2.311	2.622
	Intercept	-4.067	0.000	0.474	2.520	-1.431	0.112	0.590	4.342
	Slope	1.091	1.000	0.995	0.974	1.099	1.071	1.013	0.941
	Diff@41	-0.32	0.00	0.26	1.45	2.63	3.01	1.12	1.93
	Diff@48.5	0.37	0.00	0.22	1.26	3.38	3.54	1.22	1.49
	Diff@56	1.05	0.00	0.18	1.06	4.12	4.07	1.32	1.05
Test 3	R2	0.795	0.688	0.758	0.756	0.745	0.731	0.783	0.776
	RMSE	2.182	2.410	2.119	2.002	2.309	2.532	2.286	2.458
	Intercept	-1.362	-1.784	0.000	1.226	-0.003	3.160	4.256	2.962
	Slope	1.058	1.030	1.000	0.995	1.054	0.980	0.928	0.964
	Diff@41	1.01	-0.57	0.00	1.01	2.21	2.34	1.30	1.47
	Diff@48.5	1.45	-0.34	0.00	0.98	2.62	2.19	0.76	1.19
	Diff@56	1.88	-0.12	0.00	0.94	3.03	2.04	0.22	0.92
Test 4	R2	0.794	0.688	0.758	0.756	0.746	0.732	0.783	0.776
	RMSE	2.184	2.407	2.119	2.002	2.308	2.530	2.284	2.458
	Intercept	-2.694	-3.028	-1.236	0.000	-1.329	1.921	3.066	1.792
	Slope	1.064	1.035	1.005	1.000	1.060	0.986	0.934	0.968
	Diff@41	-0.09	-1.61	-1.02	0.00	1.14	1.35	0.35	0.49
	Diff@48.5	0.39	-1.35	-0.98	0.00	1.59	1.24	-0.15	0.25
	Diff@56	0.87	-1.10	-0.94	0.00	2.04	1.14	-0.64	0.01
Test 5	R2	0.790	0.698	0.756	0.753	0.748	0.739	0.787	0.774
	RMSE	2.207	2.368	2.130	2.014	2.299	2.495	2.261	2.469
	Intercept	-1.455	-0.867	0.428	1.755	0.000	2.983	3.807	3.719
	Slope	0.996	0.957	0.938	0.932	1.000	0.936	0.889	0.898
	Diff@41	-1.62	-2.65	-2.11	-1.05	0.00	0.37	-0.76	-0.48
	Diff@48.5	-1.65	-2.97	-2.57	-1.56	0.00	-0.11	-1.60	-1.25
	Diff@56	-1.68	-3.30	-3.04	-2.07	0.00	-0.58	-2.44	-2.02
Test 6	R2	0.766	0.711	0.725	0.716	0.731	0.748	0.781	0.750
	RMSE	2.330	2.319	2.260	2.158	2.375	2.451	2.296	2.599
	Intercept	-4.230	-0.505	0.006	1.961	-1.787	0.000	0.504	3.873
	Slope	1.024	0.943	0.938	0.920	1.032	1.000	0.947	0.888
	Diff@41	-3.26	-2.85	-2.55	-1.32	-0.47	0.00	-1.66	-0.74
	Diff@48.5	-3.08	-3.28	-3.02	-1.92	-0.23	0.00	-2.06	-1.58
	Diff@56	-2.90	-3.71	-3.49	-2.52	0.01	0.00	-2.46	-2.43
Test 7	R2	0.785	0.704	0.751	0.747	0.746	0.743	0.788	0.770

	RMSE	2.234	2.346	2.153	2.039	2.305	2.474	2.255	2.492
	Intercept	-5.398	-3.808	-2.771	-1.288	-3.800	-0.836	0.000	0.884
	Slope	1.108	1.052	1.038	1.028	1.116	1.053	1.000	0.989
	Diff@41	-0.97	-1.66	-1.21	-0.12	0.97	1.34	0.00	0.43
	Diff@48.5	-0.16	-1.27	-0.93	0.09	1.85	1.74	0.00	0.35
	Diff@56	0.65	-0.88	-0.64	0.31	2.72	2.13	0.00	0.27
Test 8	R2	0.796	0.684	0.758	0.755	0.744	0.728	0.780	0.776
	RMSE	2.177	2.426	2.120	2.004	2.316	2.546	2.297	2.459
	Intercept	-3.473	-4.148	-2.126	-0.907	-2.100	1.241	2.538	0.785
	Slope	1.075	1.050	1.016	1.011	1.067	0.991	0.937	0.981
	Diff@41	-0.42	-2.10	-1.47	-0.46	0.66	0.86	-0.04	0.02
	Diff@48.5	0.14	-1.73	-1.35	-0.37	1.17	0.79	-0.51	-0.11
	Diff@56	0.70	-1.36	-1.23	-0.29	1.67	0.72	-0.98	-0.25

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.

Saddle CT Bone (DEXA full as independent variable)

Table 38. Precision estimates (R-square and root mean square error), intercept and slope of actual CT bone % in the saddle versus predicted CT bone % in the full carcase, and accuracy estimates showing difference between observed minus the predicted at 12 (Diff@12), 14.5 (Diff@14.5), and 17 (Diff@17) CT bone % using DEXA (normalised for nylon R-value, within the saddle) and hot carcase weight as predictors.

		Kill Groups							
		Pre-NF	**NF 1**	**NF 2**	**NF 3**	**NF 4**	**NF 5**	**NF 6**	**Combined**
Test 1	R2	0.675	0.648	0.677	0.696	0.638	0.781	0.825	0.719
	RMSE	0.952	1.044	0.912	0.792	0.945	0.893	0.790	0.963
	Intercept	0.000	-4.336	-0.462	0.224	0.139	-1.469	0.288	0.055
	Slope	1.000	1.329	1.037	0.990	0.952	1.154	1.026	1.006
	Diff@12	0.00	-1.37	-0.13	0.13	-0.29	-0.08	0.53	0.11
	Diff@14.5	0.00	-0.39	-0.02	0.10	-0.43	0.38	0.60	0.12
	Diff@17	0.00	0.60	0.10	0.07	-0.58	0.84	0.68	0.14
Test 2	R2	0.665	0.677	0.629	0.643	0.604	0.778	0.801	0.684
	RMSE	0.967	1.001	0.977	0.859	0.988	0.898	0.842	1.022
	Intercept	4.532	0.000	3.960	4.559	4.365	2.932	4.917	4.073
	Slope	0.695	1.000	0.683	0.646	0.625	0.790	0.677	0.696
	Diff@12	1.79	0.00	1.10	1.37	0.99	1.04	2.01	1.34
	Diff@14.5	0.87	0.00	0.15	0.31	-0.14	0.41	1.04	0.43
	Diff@17	-0.04	0.00	-0.80	-0.75	-1.26	-0.22	0.07	-0.49
Test 3	R2	0.672	0.613	0.684	0.704	0.643	0.772	0.826	0.714
	RMSE	0.956	1.094	0.901	0.783	0.938	0.911	0.788	0.972
	Intercept	0.235	-2.632	0.000	0.631	0.386	-0.800	0.426	0.817
	Slope	0.952	1.189	1.000	0.955	0.928	1.107	1.003	0.939
	Diff@12	-0.20	-0.93	0.00	0.23	-0.27	0.16	0.45	0.27

	Diff@14.5	-0.35	-0.36	0.00	0.09	-0.48	0.49	0.46	0.09
	Diff@17	-0.49	0.21	0.00	-0.04	-0.70	0.81	0.46	-0.10
Test 4	R2	0.673	0.616	0.684	0.704	0.643	0.773	0.826	0.715
	RMSE	0.956	1.090	0.901	0.783	0.938	0.909	0.788	0.970
	Intercept	-0.373	-3.511	-0.662	0.000	-0.211	-1.539	-0.206	0.167
	Slope	0.997	1.253	1.047	1.000	0.970	1.159	1.048	0.986
	Diff@12	-0.40	-1.24	-0.24	0.00	-0.48	-0.11	0.23	0.04
	Diff@14.5	-0.41	-0.48	-0.10	0.00	-0.57	0.37	0.37	0.00
	Diff@17	-0.42	0.28	0.04	0.00	-0.66	0.85	0.52	-0.05
Test 5	R2	0.672	0.612	0.684	0.704	0.643	0.771	0.826	0.714
	RMSE	0.957	1.096	0.901	0.783	0.938	0.912	0.789	0.973
	Intercept	-0.163	-3.078	-0.408	0.241	0.000	-1.249	0.003	0.445
	Slope	1.025	1.278	1.078	1.029	1.000	1.193	1.081	1.011
	Diff@12	0.06	-0.57	0.29	0.50	0.00	0.49	0.73	0.54
	Diff@14.5	0.14	0.26	0.52	0.59	0.00	1.07	0.98	0.58
	Diff@17	0.22	1.10	0.76	0.68	0.00	1.65	1.22	0.61
Test 6	R2	0.674	0.666	0.663	0.681	0.628	0.783	0.819	0.712
	RMSE	0.954	1.018	0.931	0.812	0.958	0.889	0.804	0.975
	Intercept	1.537	-3.173	1.037	1.700	1.607	0.000	1.919	1.321
	Slope	0.872	1.203	0.889	0.847	0.813	1.000	0.877	0.881
	Diff@12	0.39	-1.34	0.04	0.32	-0.07	0.00	0.81	0.25
	Diff@14.5	0.00	-0.73	-0.29	-0.14	-0.63	0.00	0.44	-0.10
	Diff@17	-0.38	-0.12	-0.62	-0.60	-1.19	0.00	0.08	-0.46
Test 7	R2	0.674	0.630	0.683	0.703	0.642	0.777	0.827	0.718
	RMSE	0.953	1.071	0.903	0.784	0.939	0.902	0.786	0.965
	Intercept	-0.216	-3.831	-0.585	0.083	-0.069	-1.496	0.000	0.120
	Slope	0.960	1.234	1.004	0.959	0.927	1.113	1.000	0.957
	Diff@12	-0.58	-1.72	-0.54	-0.28	-0.73	-0.48	0.00	-0.27
	Diff@14.5	-0.70	-1.02	-0.53	-0.41	-0.95	-0.14	0.00	-0.40
	Diff@17	-0.82	-0.32	-0.52	-0.53	-1.17	0.19	0.00	-0.53
Test 8	R2	0.674	0.628	0.683	0.703	0.642	0.776	0.827	0.718
	RMSE	0.954	1.074	0.903	0.784	0.939	0.903	0.786	0.965
	Intercept	-0.435	-4.029	-0.802	-0.126	-0.281	-1.729	-0.236	-0.068
	Slope	1.008	1.292	1.056	1.008	0.975	1.169	1.052	1.004
	Diff@12	-0.36	-1.40	-0.30	-0.05	-0.51	-0.20	0.23	-0.03
	Diff@14.5	-0.34	-0.53	-0.13	-0.02	-0.58	0.31	0.39	-0.02
	Diff@17	-0.31	0.34	0.04	0.00	-0.66	0.81	0.55	-0.01

RMSE, root mean square error. NF, nucleus flock. Combined, represents a combination of data from nucleus flock 2 – 6. Within a test row, the values highlighted in yellow represent the training data set, while the values adjacent to these represent the precision when this trained equation is transported into the other data sets.