final report

Project code: P.PSH.0238

Prepared by:

Robotic Technologies Ltd

Date submitted: August 2007

Date published: August 2011

PUBLISHED BY
Meat & Livestock Australia Limited
Locked Bag 991
NORTH SYDNEY NSW 2059

Weight Apportioning System (X-Ray)

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

It has been proved possible to predict the weights of the individual primal sections prior to cutting using RTL's X-Ray system.

Weights have been predicted from images of individual primal sections to a prediction accuracy of — +/- 3.5% of primal weight for 2 S.D. (95.4%) of carcasses analysed (error say — 175g) Where full carcass images were used, and the primal separation plane was at an angle to the x-ray beam, the accuracy was — +/- 6% or — 300g for 2 S.D.

Possibilities exist to improve the accuracy, including:

- Improvement to the cut-plane prediction
- Scaling based on the measured total carcass weight
- Weighing after cutting and predicting the "standard" primal from the cut primal (potentially a different specification). ƒ Accuracy likely to be improved by about 3000%

Contents

1 Project Objectives

- Using the existing RTL Lamb X-Ray Measuring System, determine a relationship between x-ray image intensity and lamb carcass mean density.
- Test the relationship by x-raying samples, weighing the samples, and comparing the measured weight with that predicted using the intensity/density relationship.
- Using the intensity/density relationship and the existing Primal Cutting coordinate analysis, develop and demonstrate a basic system to predict the weight of the three primal sections prior to the separation of the carcass.

2 Overall Status

2.1 Outcomes of the Project

Phase 1

Two significant experiments were conducted:

- Determining the relationship between *weight* and *image intensity x image area* for homogeneous samples
- X-Raying and weighing a sample of primal sections to determine if there is a clear correlation between *x-ray intensity x image area* and *weight* for a real sample

<u>The first experiment</u> showed that there are clear relationships between *image intensity x image area* and *weight* for known material samples (meat, fat or bone). However, there is a different relationship for each different material type.

<u>The second experiment</u> showed that the weight can be predicted from the overall *image intensity x area*, but that there is an error in this method (in 68% - 1 standard deviation - of carcasses, the error was within +/- 10%).

Phase 2

On reassessing the first experiment, it was found that if the thickness of the sample is multiplied by its density (to give mass per unit area), then the relationship is similar for meat, fat and bone (refer graph in 5.3).

- The waviness on the bone graph is assumed to be due to the fact that the bone material sample is in the form of a series of thin laminations. Apart from this waviness, the meat and bone relationships are very similar.
- The fat graph shows a slightly lower absorption of radiation than meat and bone.

Two different exponential relationships were consequently derived – one based on the result for meat, and the other based on both the results for meat and fat, with a weighting between the meat and fat relationships based on typical body composition.

Phase 3

The primal images from the second experiment of Phase 1 were reanalysed using the two new relationships derived in Phase 2, applied to each pixel of the images. This gave rise to the first 2 graphs of 5.2, comparing the measured weight to a prediction value.

It was noted that there was a different trend for each different type of primal. By determining a line of best fit for each primal, a linear weighting was able to be applied to the relationships to get a better fit for the sample.

Using the exponential relationships weighted for the particular primal, the weight of each primal was once again predicted and compared to the measured weights. The histograms of these predictions can be found in 5.2. The X-axis shows the difference between the predicted and the measured weight expressed as a percentage of the measured weight. The Y-axis shows a count of primals.

Phase 4

A further experiment was carried out, whereby 86 carcasses where scanned by the RTL X-Ray system, and subsequently separated into the 3 primal sections which were then weighed. The techniques derived in Phase 3 were then used to predict the weight of each primal section from its whole-carcass image.

In this experiment, the RTL cut-positioning software was used to determine the plane through which the primal sections were to be separated. As this system uses 2 dimensional images, a virtual 2-D cut-line was then generated on one of the images. The position of this virtual cut-line was based on the height of the cut relative to a reference depth plane, and the angle of cut. The images were then separated at these cut-lines to allow the individual primals to be assessed as per Phase 3.

The prediction accuracy was reduced from that of Phase 3 due to the inaccuracy of the primal separation technique as shown in 5.4, but is still potentially accurate enough to be commercially viable. Further improvement to the accuracy may be possible.

2.2 Future Work

Improvements to the system accuracy may be possible by the following means:

- Improved techniques for cut plane prediction (refer 2.1, Phase 4) are likely to reduce this source of error.
- Scaling the predicted primal weights by the measured total carcass weight will reduce the average error.
- Weighing individual primals after cutting will give a significant improvement.
  - Where the cut is a “standard” (for grading purposes) primal cut, the prediction would be bypassed and the weight would be as accurate as the scales.
  - Where the cut is a “non-standard” (for grading purposes) primal cut, the x-ray system would only predict the difference between the real cut and the standard cut.
    - E.g. if a 4-rib is the standard, and a 5-rib cut is made. One rib pitch is say 5% of the forequarter weight. The 2 S.D. error is —3.5% of 5% (— +/- 0.175%) of the forequarter weight, or — +/- 9g.

3 Program Status

This project is complete.
RTL is assessing its options regarding the incorporation of this technology in future machines.

4 Project Risks

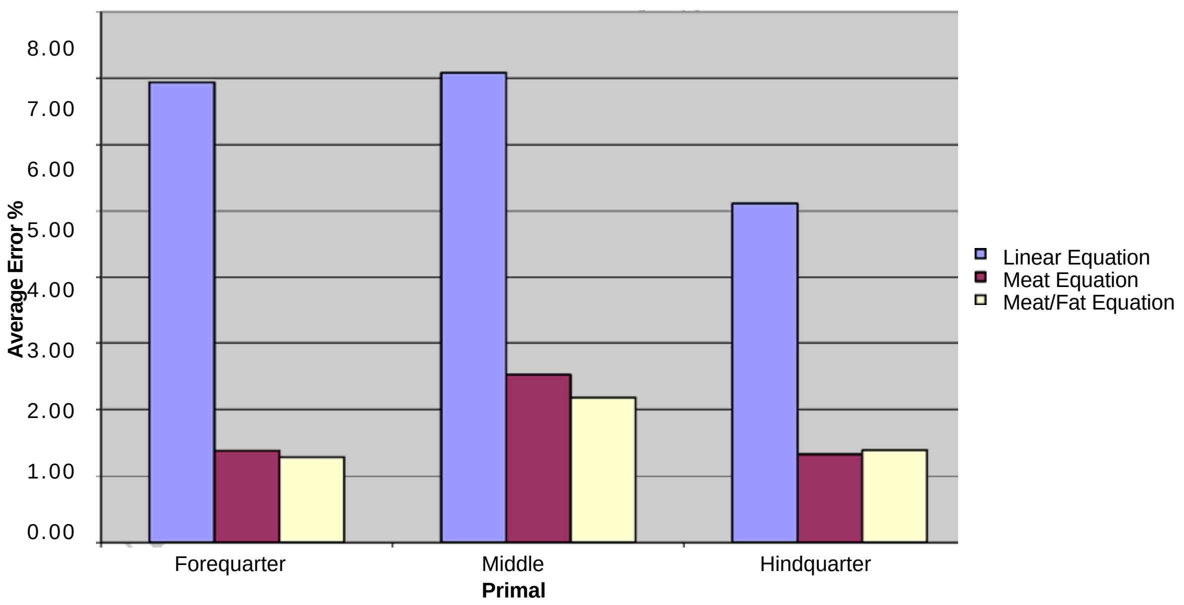
The key risk is the variability of carcasses. The only possible mitigating strategy is to adjust the prediction equations as the sample size increases.

5 Appendix – Experimental Results

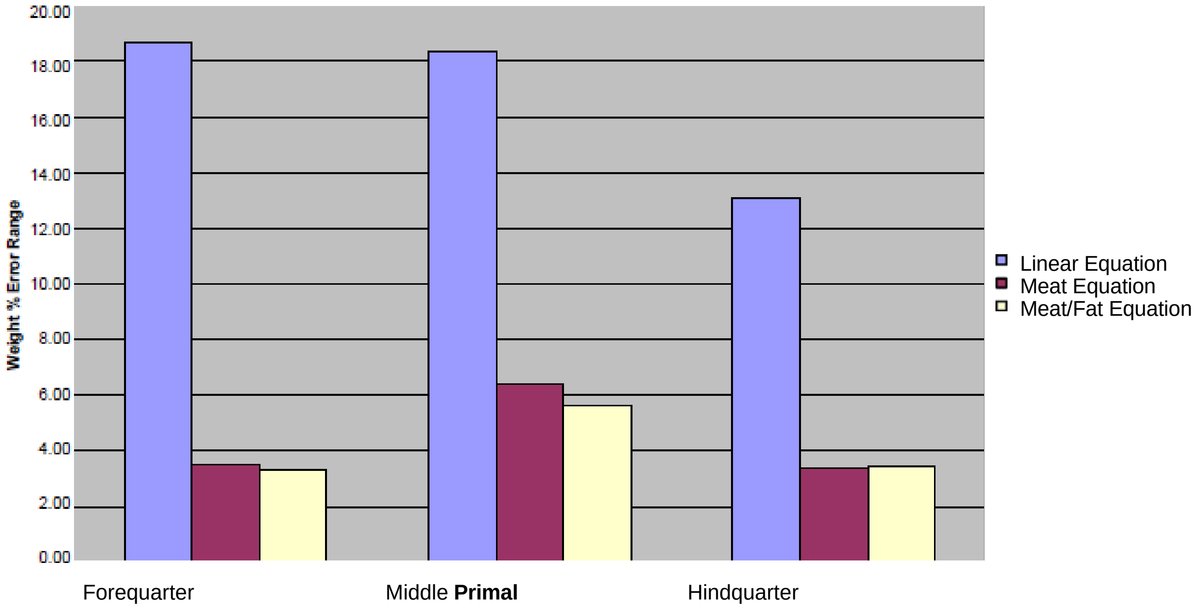
5.1 Primal Weight Prediction Results Summary

		Forequarter	Middle	Hindquarter
Linear	Average % Error	6.94	7.08	5.11
	2 Standard Deviations % Error	18.66	18.34	13.08
Meat	Average % Error	1.39	2.52	1.33
	2 Standard Deviations % Error	3.53	6.39	3.39
Meat/Fat	Average % Error	1.29	2.18	1.40
	2 Standard Deviations % Error	3.32	5.62	3.42

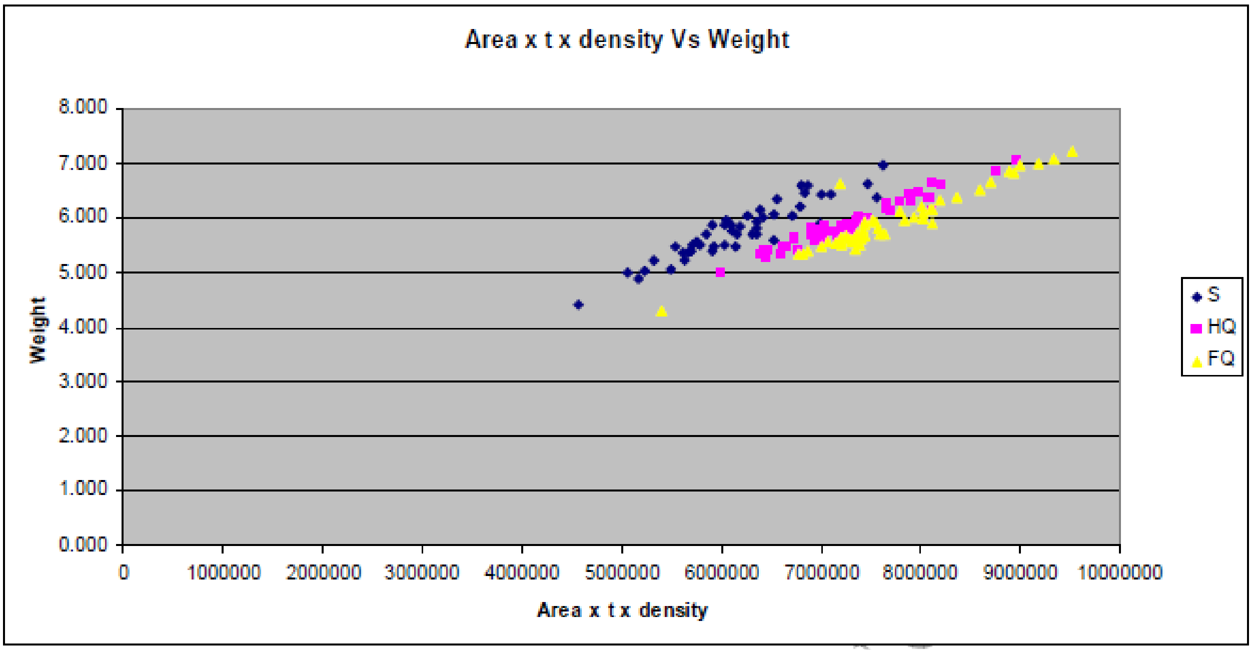
Average Percentage Weight Prediction Error



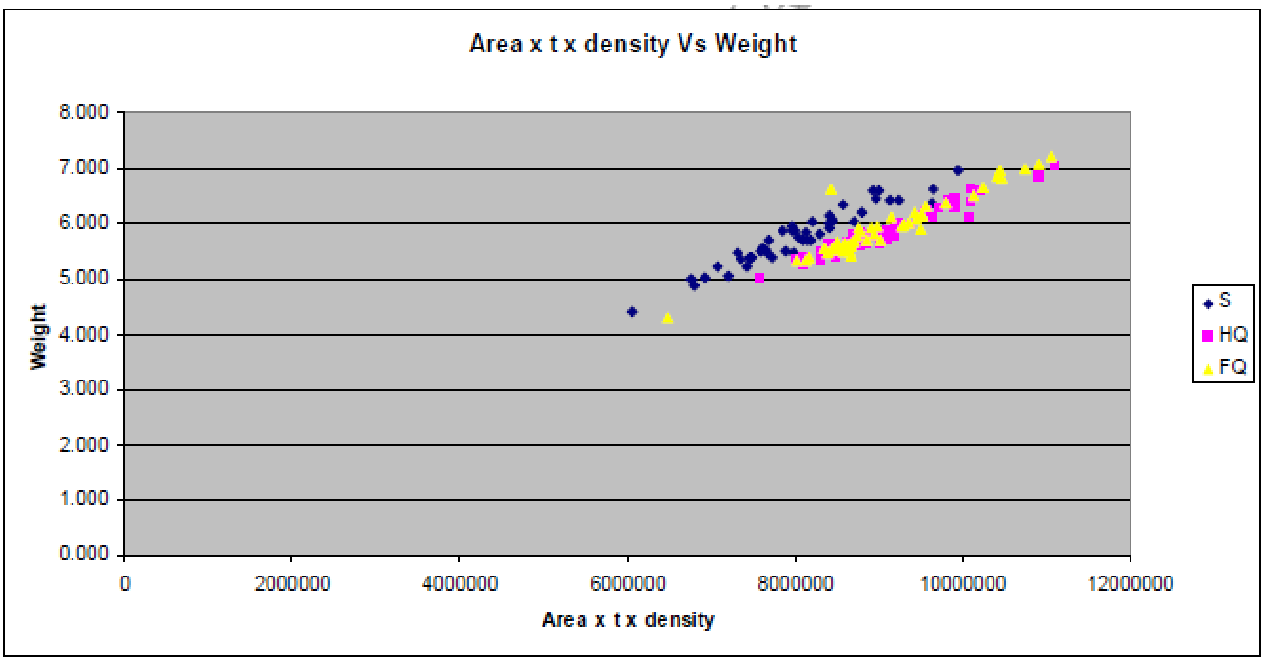
Range of Predicted Weight Error % for Two Standard Deviations (95.4%)



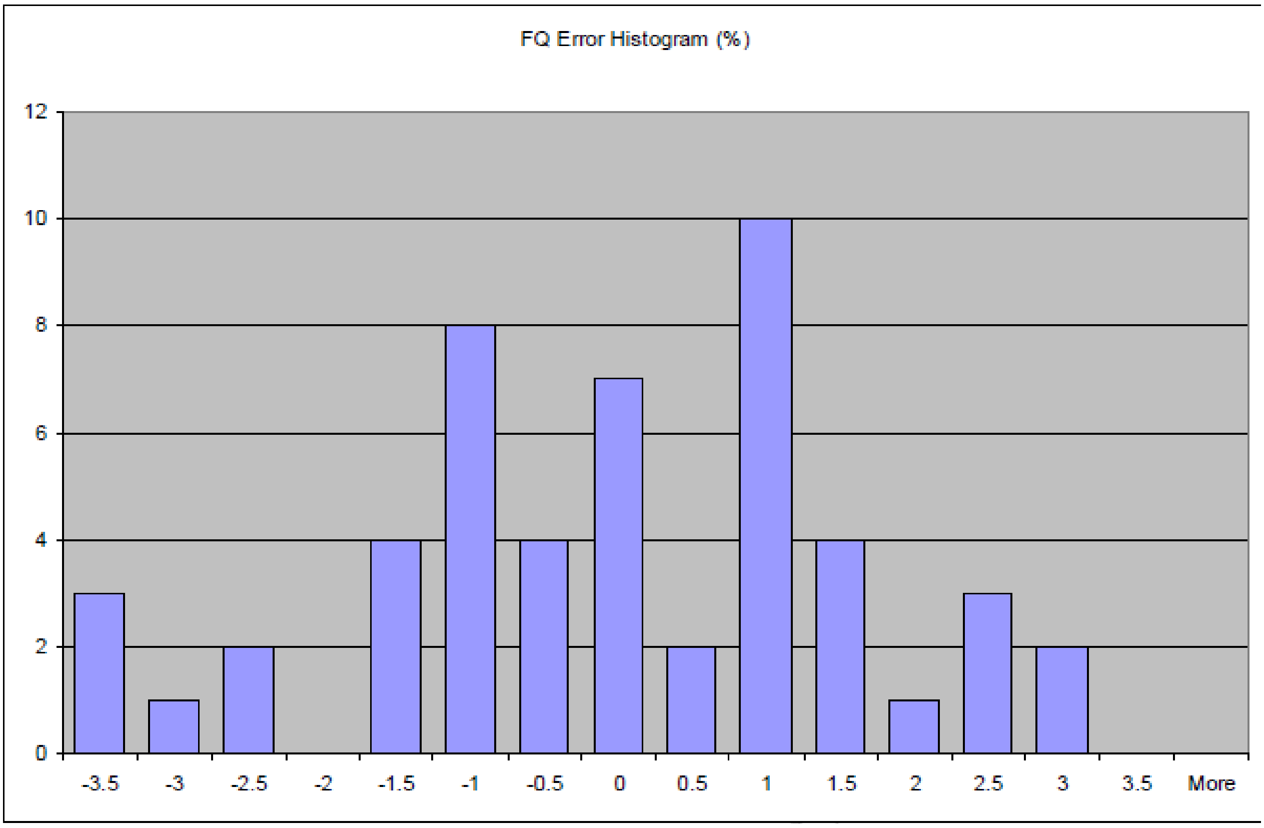
5.2 Primal Weight Prediction Results Detail



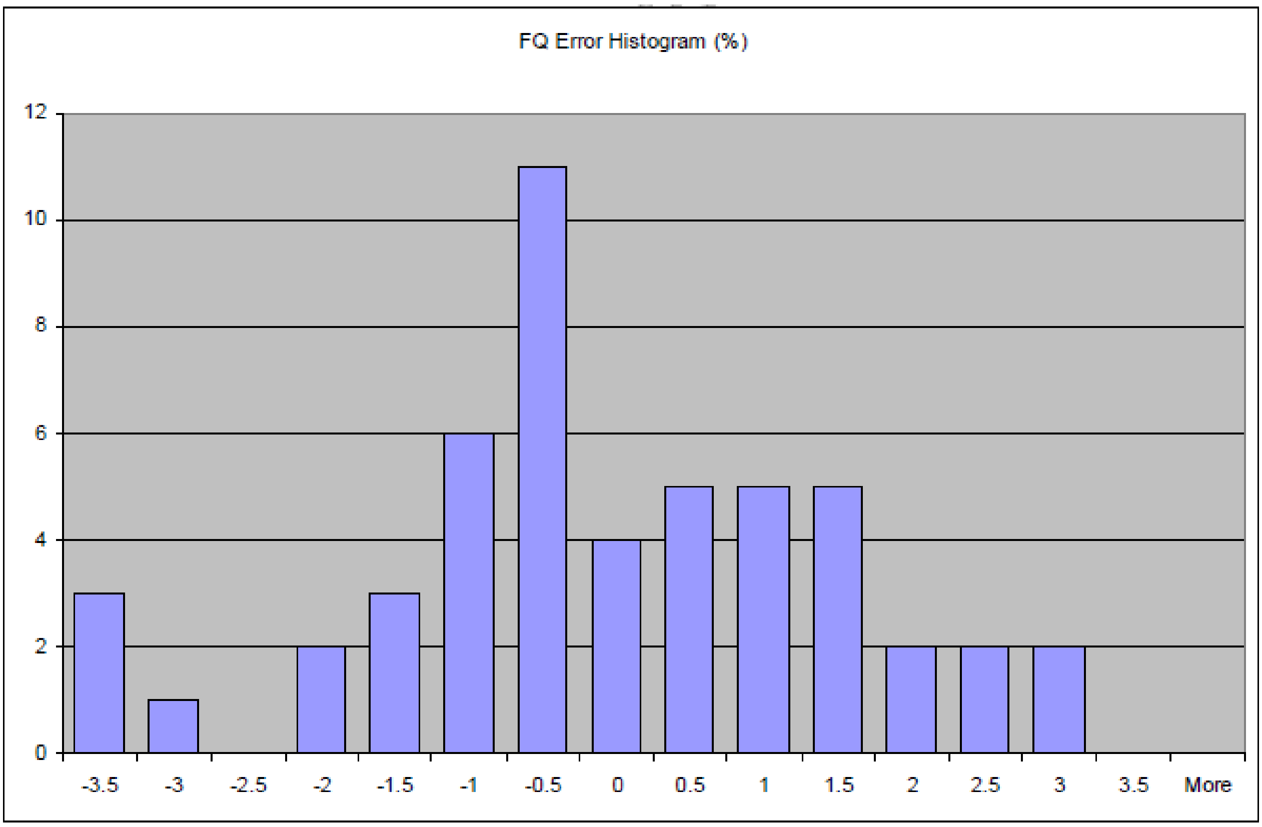
Based on Meat Equation



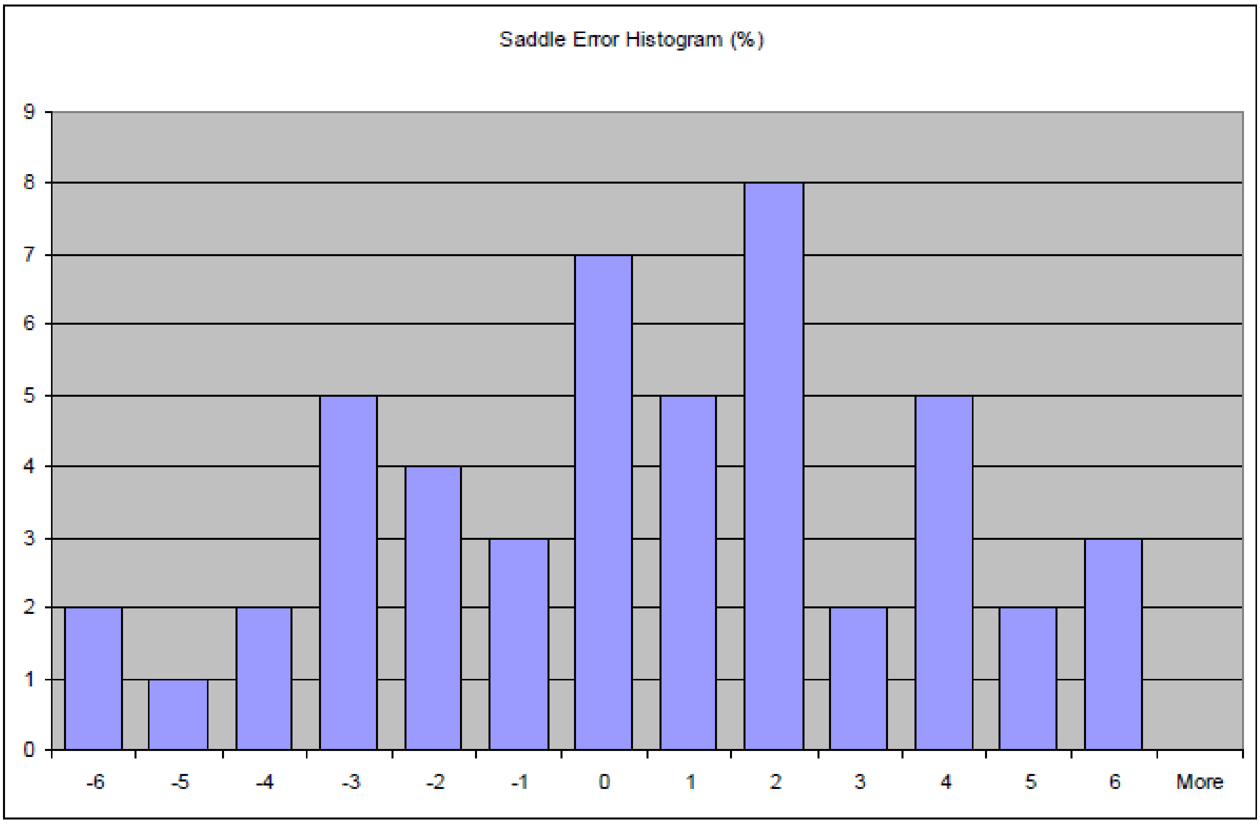
Based of Fat + Meat Equation



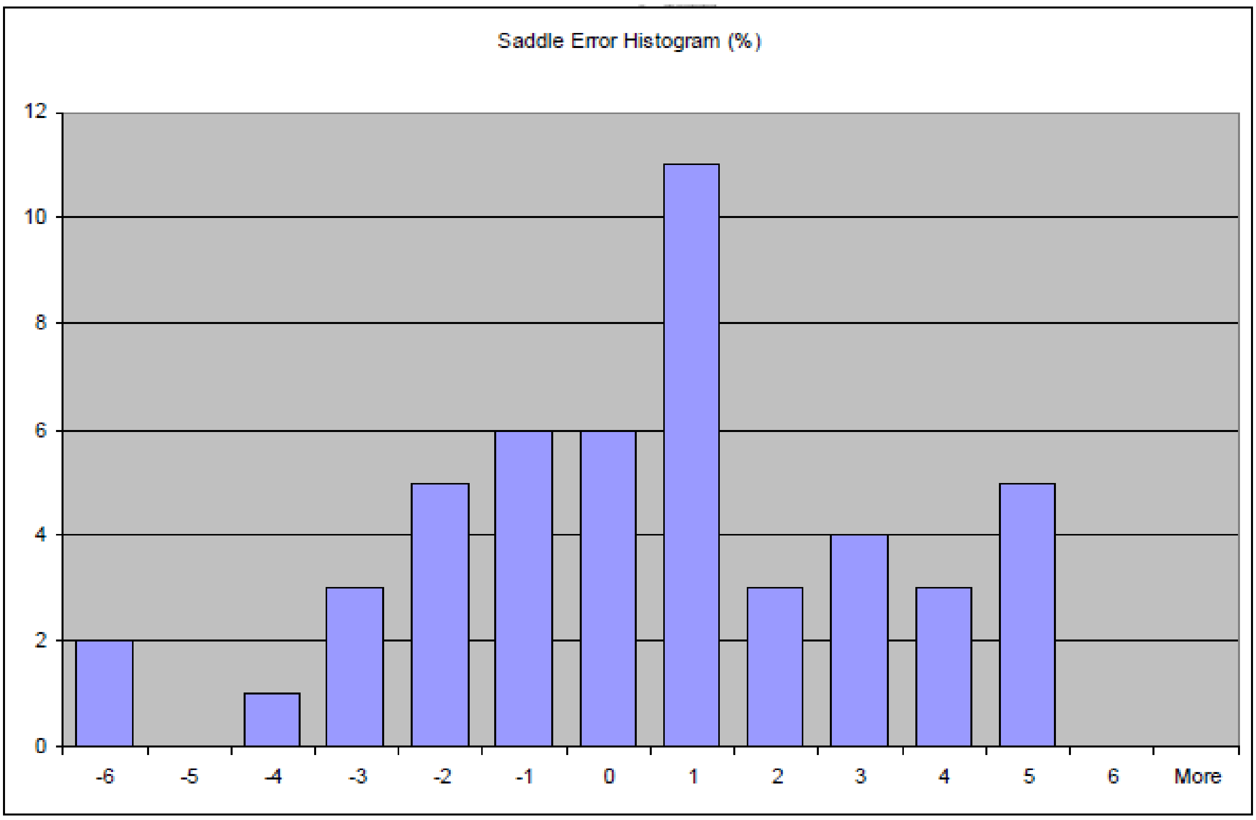
Based on Meat Equation



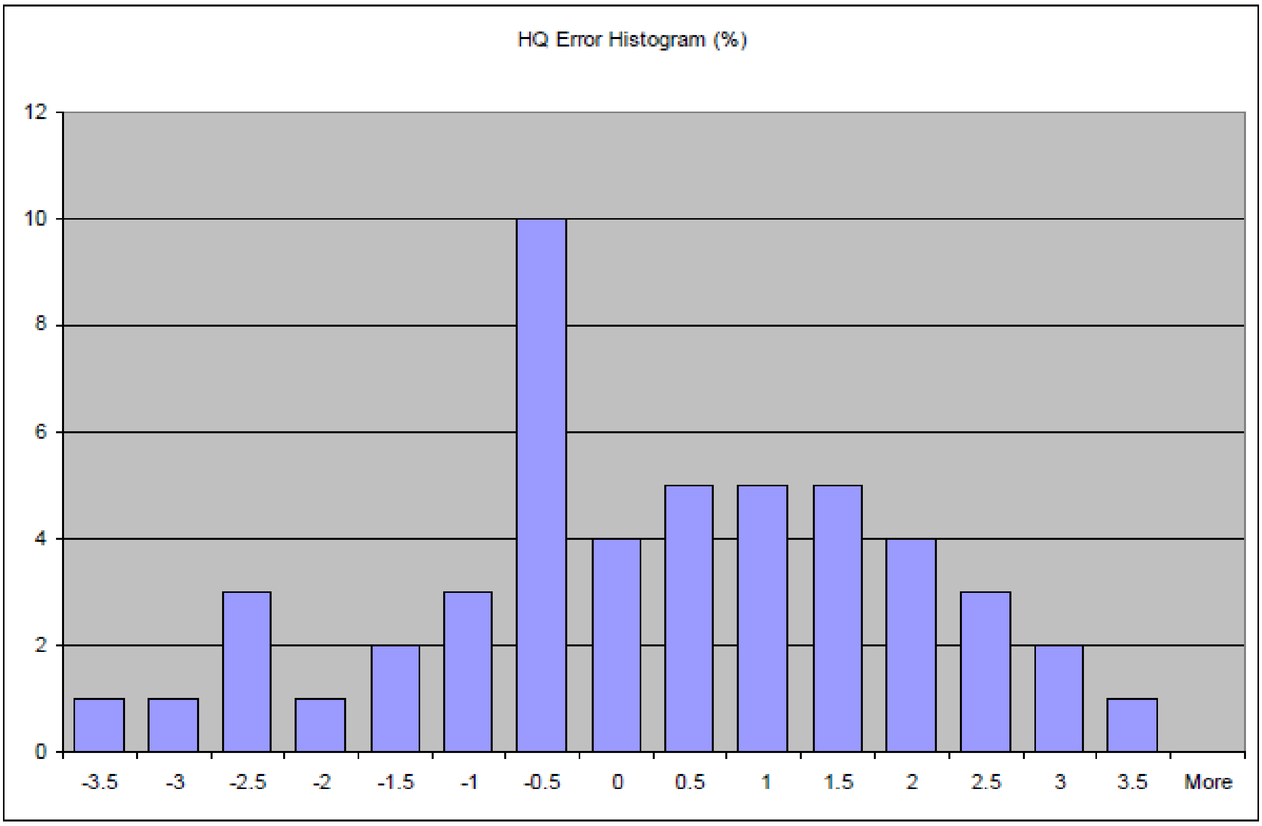
Based on Fat +Meat Equation



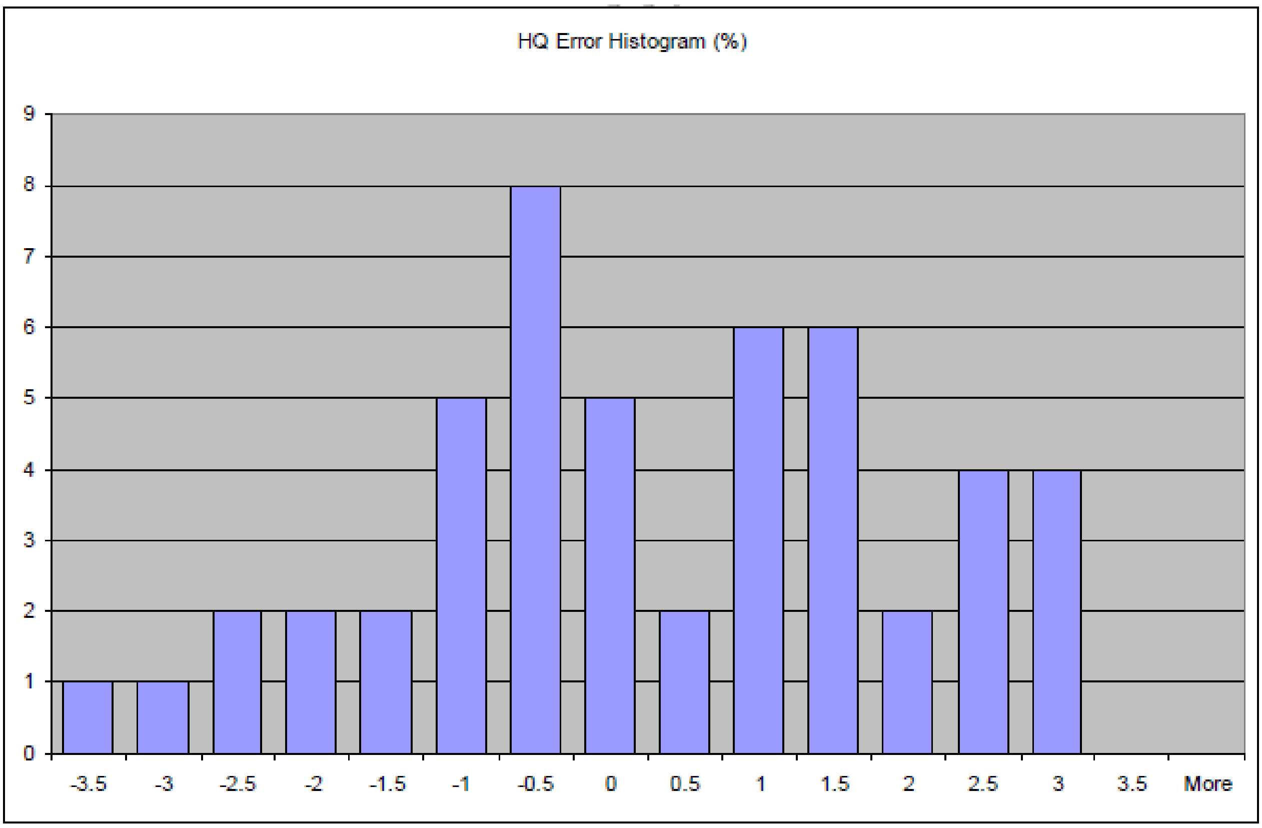
Based on Meat Equation



Based on Fat + Meat Equation

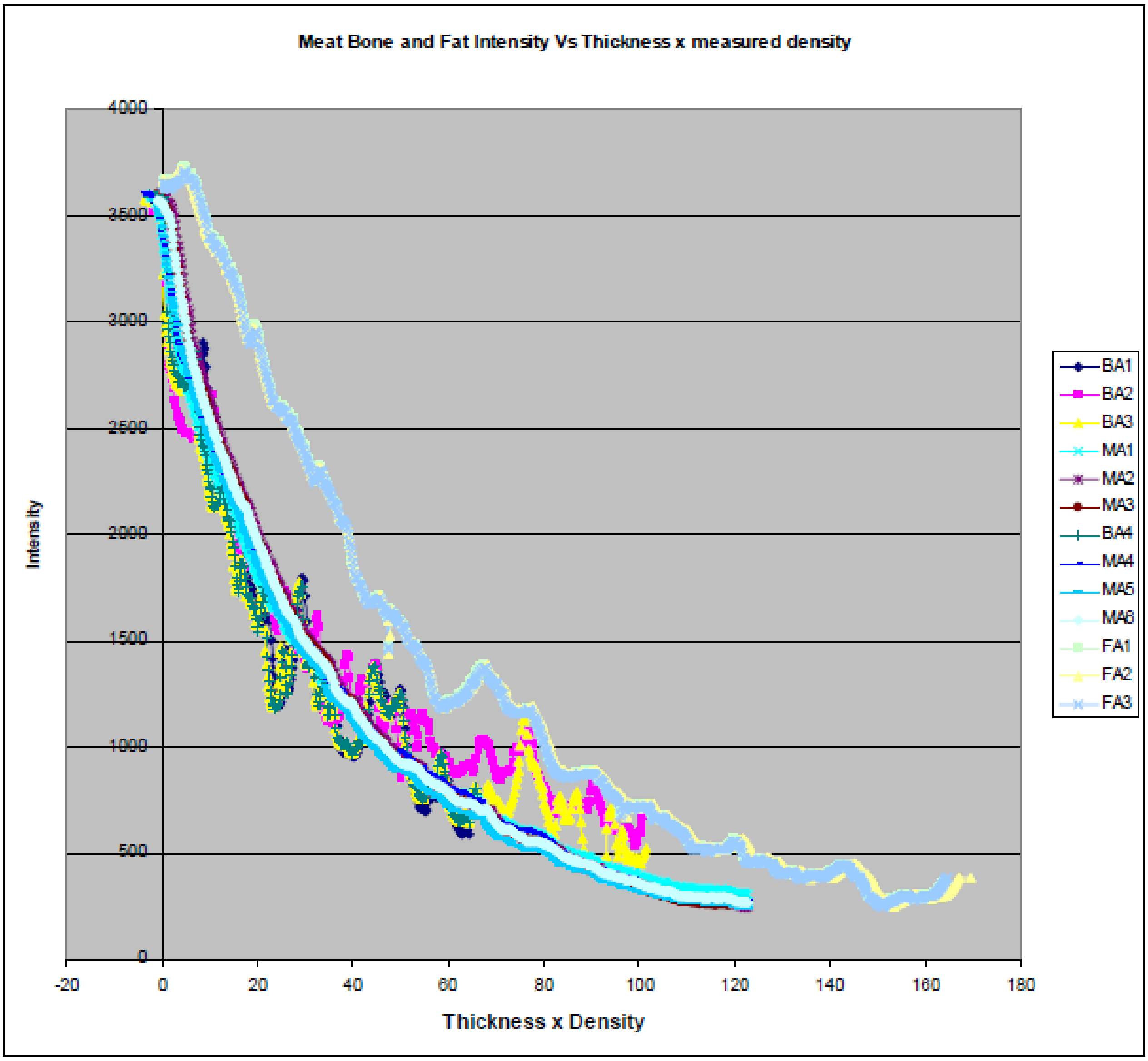


Based on Meat Equation



Based on Fat + Meat Equation

5.3 Intensity Vs Weight per Unit Area



5.4 Forequarter Weight Prediction from Full Carcass Image