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Abstract

The accurate detection of bone in a DXA image is crucial to the overall precision and accuracy of its prediction of overall composition, as the non-bone containing pixels are evaluated independent of the bone-containing pixels. Previous algorithms have relied on thresholding bone containing pixels from non-bone containing pixels at the mean R-value of the whole carcass, with those pixels above the mean being classed as bone containing. While this was somewhat effective, as it emulated the fundamental equations used to quantify bone content of bone containing pixels, it was unable to detect bone edges, and as such could not use an accurate R-value for soft tissue. This became problematic for carcasses that did not have bone content close to most of the population, such as certain breeds with naturally higher bone content (Merinos), or sheep with a lower amount of soft tissue – usually mutton or diseased sheep. An improved algorithm was proposed and has been accredited as part of the larger DXA accreditation. This algorithm introduced the evaluation of thickness with the R-value calculation when thresholding for bone content. The implementation of this algorithm sees a very large increase in the precision and accuracy of the prediction of CT bone %, from an $R^2=0.496$ to $R^2=0.925$. There are also modest increases in the precision and accuracy of the predictions of CT fat % and CT lean %. Further improvements on the bone detection algorithm will look to machine learning to detect bone edges and dimensions, a process that is otherwise too slow and difficult at the current chain speed.

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1 Introduction

DXA technology can distinguish 3 components of carcass tissue – fat, lean muscle, and bone. This is achieved in two steps – the separation of bone containing pixels from those with no bone, and the determination of the fat proportion within the soft tissue exclusive of bone. The separation of the pixels containing bone is crucial for precisely and accurately predicting bone content, and the subsequent calculation of composition of the soft tissues.

In previous experimentation, the prediction of CT bone % has been the least precise of the tissue types and has shown to be the cause of small biases in composition prediction between breeds – particularly those that contain more bone. The previous method of bone detection relies on the mean R-value for a carcass to be calculated to be used as a thresholding point, which is susceptible to error in carcasses a greater proportion of bone tissue, as this artificially pushes up the mean R-value of the carcass. This not only underestimates the bone content of those carcasses, but also overestimates lean tissue.

The fundamental method of quantifying bone containing pixels is through the evaluation of each individual pixel, and their closest non-bone containing pixel. For each pixel, the low energy and high energy linear attenuations are individually calculated by the following equation:

$$\text{Attenuation} = \ln(I/I_0)$$

Where I is the pixel value, and I_0 is the value of unattenuated space, set at 4095 in this DXA system. The high energy attenuation is multiplied by the soft tissue R-value, which accounts for the difference in high and low energy absorption, and the low energy attenuation is then subtracted from this value by the following equation:

$$R_S * \ln(I^H/I_0^H) - \ln(I^L/I_0^L)$$

While this technique assists in quantifying the amount of bone in each pixel, it relies on the determination of bone edges, which is a machine specific and proprietary algorithm. Values greater than zero will contain bone, while values less than zero will not contain bone.

2 Experimental Methods

2.1 Previous Technique

The previous algorithm for detecting bone was based on the technique described above, although without the bone edge detection. Without this bone edge detection, the soft tissue R-value was not calculated at the neighbour pixels, but rather over the entire carcass. By rearranging this equation, the mean R-value of all pixels was used

as the new zero, with pixels greater than the mean classified as containing bone, and those less than the mean classified as soft tissue.

As tissue composition is a function of R-value and the thickness of the tissue, this method is prone to error in areas at the extremes of thickness. In general, the R-value of a tissue will decrease with an increase in thickness, despite the same composition. Therefore, very thin areas will have high R-values, and potentially be classified incorrectly as bone, while areas of greater thickness, despite containing bone, may fall under the mean R-value of the entire carcass, and therefore remain classified as not containing bone.

2.2 Accredited technique

The new technique attempts to incorporate tissue thickness, to avoid the incorrect classification of pixels. As there is still no effective bone edge detection technique in such a rapid system, a placeholder threshold is still required for the effective determination of bone containing pixels.

Each tissue-containing pixel is evaluated by calculating the R-value, and a proxy for thickness by the following equation:

$$thickness = \ln (I_L)$$

Where I_L is the attenuation value for the low-energy image.

To extend the range of the R-values that would normally exist over a whole lamb carcass, this value is multiplied by itself, thus improving the sensitivity over this range. This squared R-value is divided by the thickness proxy of the pixel, with the natural log of this result used as the final value, following this equation:

$$\ln \left(\frac{R^2}{thickness} \right)$$

This value is compared to the determined threshold for each DXA system, which at the WAMMCO facility in Katanning is a threshold of 0.074, meaning anything greater than this value is considered bone. The DXA algorithm will classify the pixel accordingly for all pixels and will discard all bone-containing pixels in any soft tissue calculations. The threshold is calculated manually, however further work is being conducted into the automation of this threshold determination through the use of the Scott Automation and Robotics phantom.

The calculation of the predicted bone % is expanded upon from its previous form, using the ratio of bone containing pixels to the total number of carcass pixels, and the mean R-value of the bone containing pixels. This is described in further detail in the technical report for 3.11 – AUSMEAT accredited lamb DXA algorithm performance.

2.3 Trial Details

100 lambs were DXA scanned at WAMMCO, Katanning, and then CT scanned at Murdoch University to validate the DXA predictions of carcass composition.

Two predictions of fat %, lean muscle % and bone % were produced using the previous technique of bone detection and then the improved bone detection algorithm, with the composition of soft tissue in both cases predicted by the updated algorithm for soft tissue as found in Technical Report 3.11 - AUSMEAT accredited lamb DXA algorithm performance.

The predictions of CT fat %, CT lean % and CT Bone % were compared before and after the implementation of the bone detection algorithm.

3 Results and Discussion

The previous bone detection method did a modest job of correctly classifying bone containing pixels, however, was unable to differentiate a low R-value, high thickness tissue section or a high R-value, low thickness tissue section correctly, as the mean R-value of the whole carcass was used as the threshold for bone detection. This can be visualised in Figure 1.

The accredited bone detection algorithm produced an image of greater accuracy when detecting bone containing pixels, and was able to classify the low R-value, high thickness areas and high R-value, low thickness areas correctly. This can be visualised in Figure 2.

The accredited bone detection algorithm saw a modest increase in precision across CT fat and CT lean % predictions, as seen in Table 1. The changes are visualised in figures 3 and 4. The largest increase in precision and accuracy was seen in the CT Bone % prediction (see Table 1), which is best visualised in figure 5.

	R2	RMSE	Slope	Bias
Existing Algorithm				
Fat %	0.896	1.43%	0.97	-4.37
Lean %	0.809	1.36%	0.87	1.4
Bone %	0.925	0.61%	1.25	2.98
Proposed Algorithm				
Fat %	0.938	1.10%	0.97	-1.19
Lean %	0.716	1.66%	0.95	-0.23
Bone %	0.496	1.57%	1.05	1.41

As expected, the prediction of CT bone % saw the largest increase in precision and accuracy, as this algorithm was intended to improve the classification of pixels into

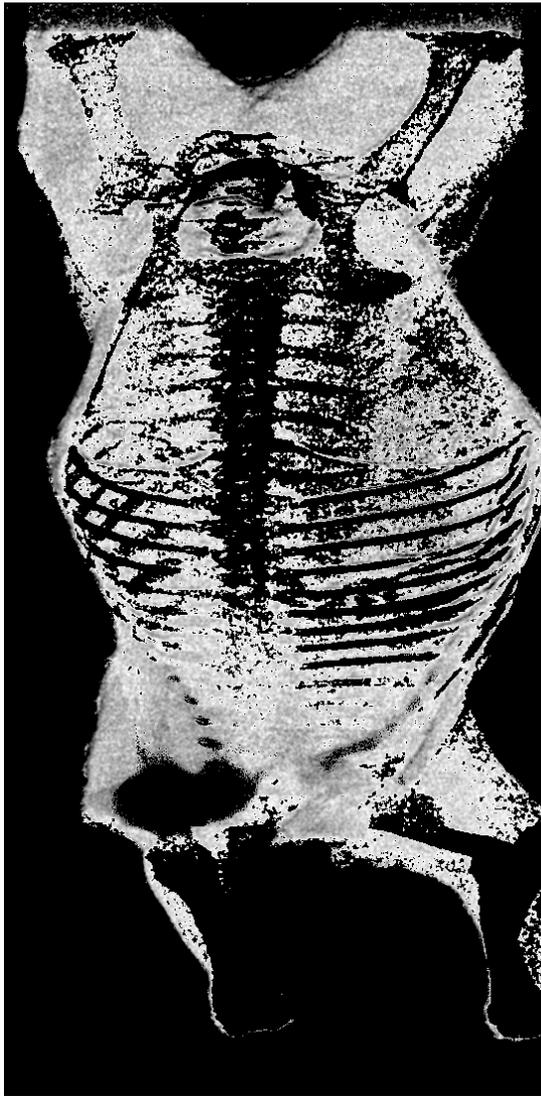


Figure 1 - Lamb carcass radiograph after application of previous bone detection technique. Within carcass boundaries, pixels classified as containing bone appear black



Figure 2 - Lamb carcass radiograph after application of accredited bone detection technique. Within carcass boundaries, pixels classified as containing bone appear black

bone and non-bone containing pixels. The modest increase in the CT fat % and CT lean % predictions are likely due to the ability of the accredited algorithm to process the non-bone containing pixels with greater accuracy and impacting upon the subsequent differentiation of the soft tissue into its fat and lean components.

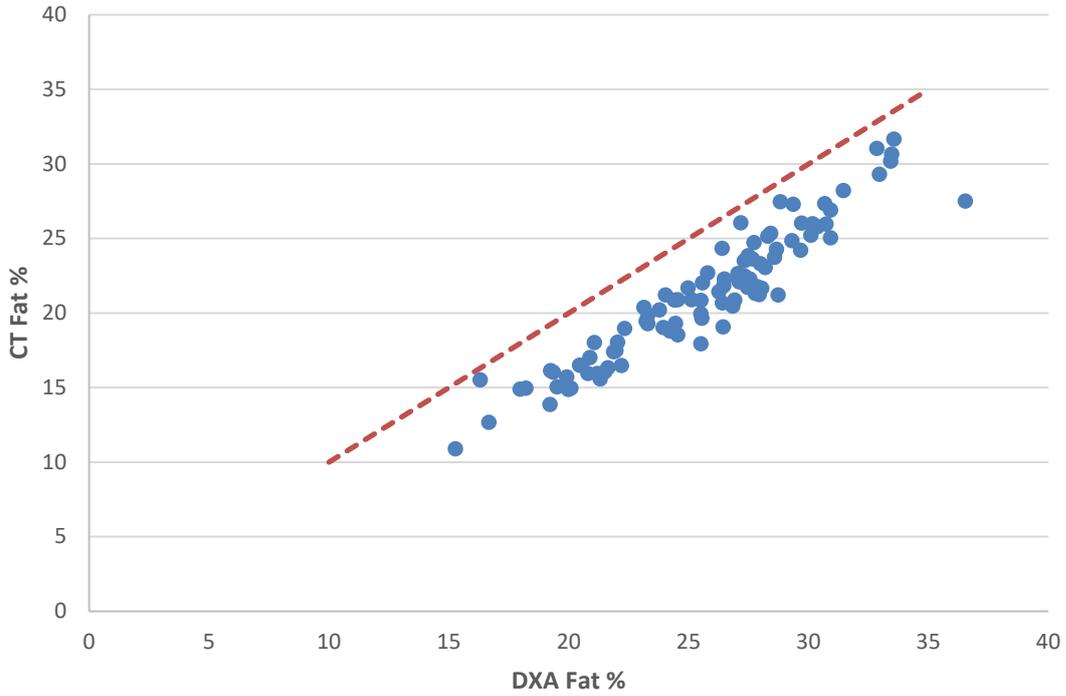


Figure 3 - DXA fat % prediction of CT fat % using the previous bone detection algorithm. Dashed line is line of perfect prediction.

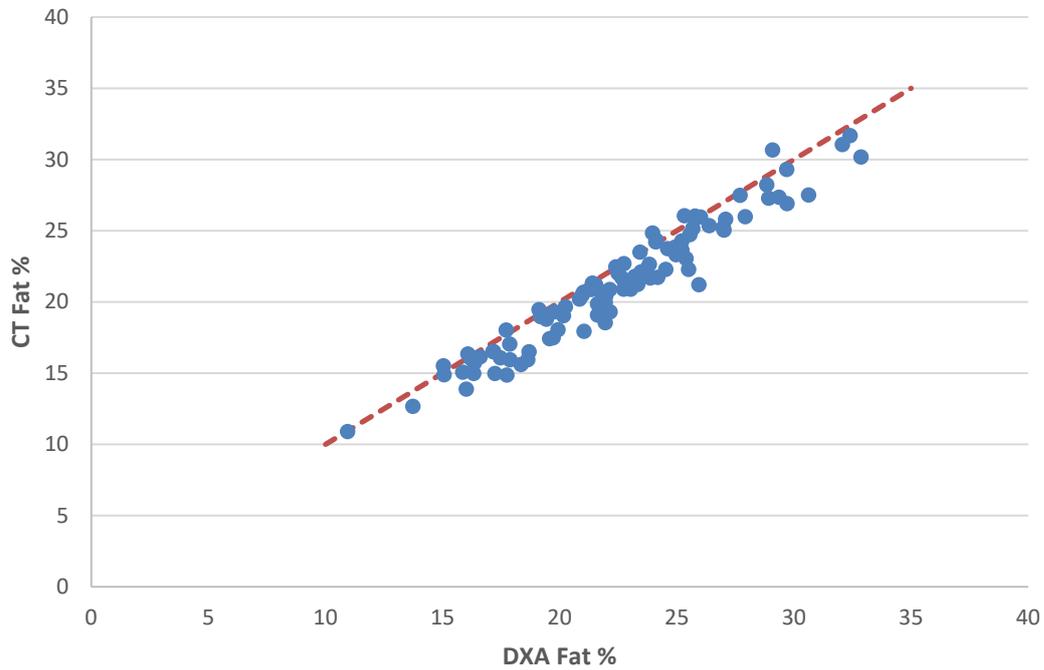


Figure 4 - DXA fat % prediction of CT fat % using the accredited bone detection algorithm. Dashed line is line of perfect prediction.

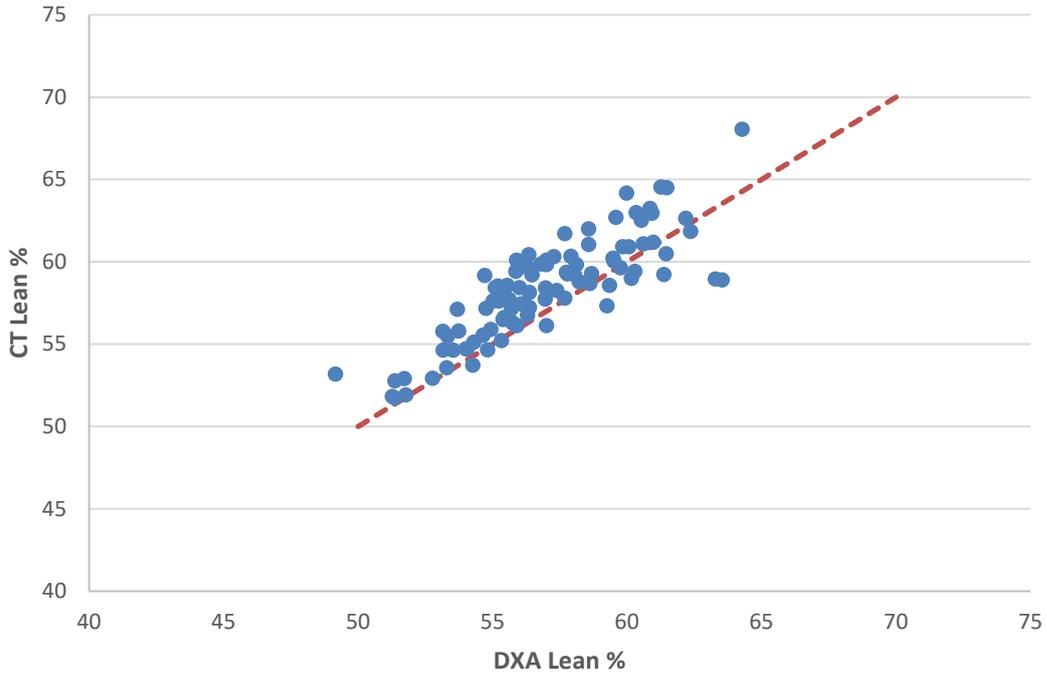


Figure 5 - DXA lean % prediction of CT lean % using the previous bone detection algorithm. Dashed line is line of perfect prediction.

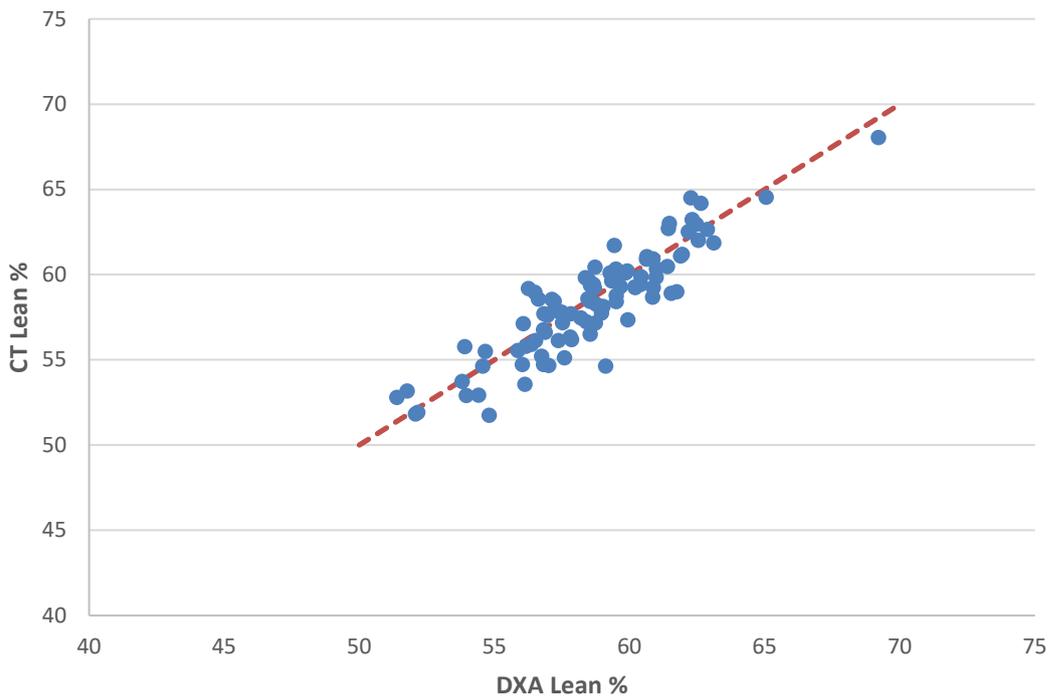


Figure 6 - DXA lean % prediction of CT lean % using the accredited bone detection algorithm. Dashed line is line of perfect prediction.

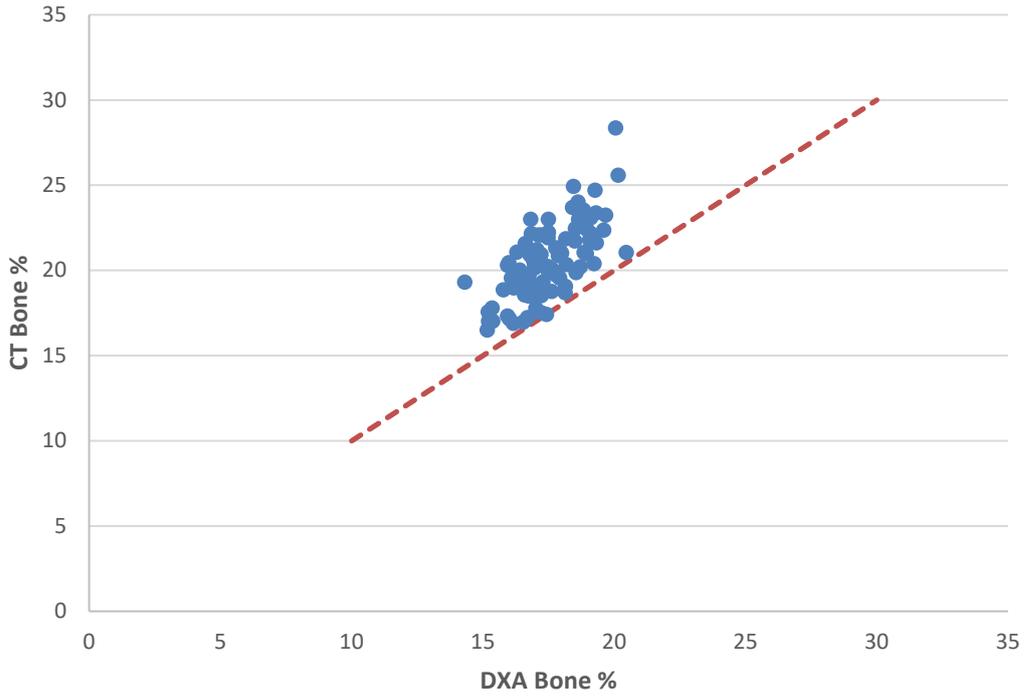


Figure 7 - DXA bone % prediction of CT bone % using the previous bone detection algorithm. Dashed line is line of perfect prediction.

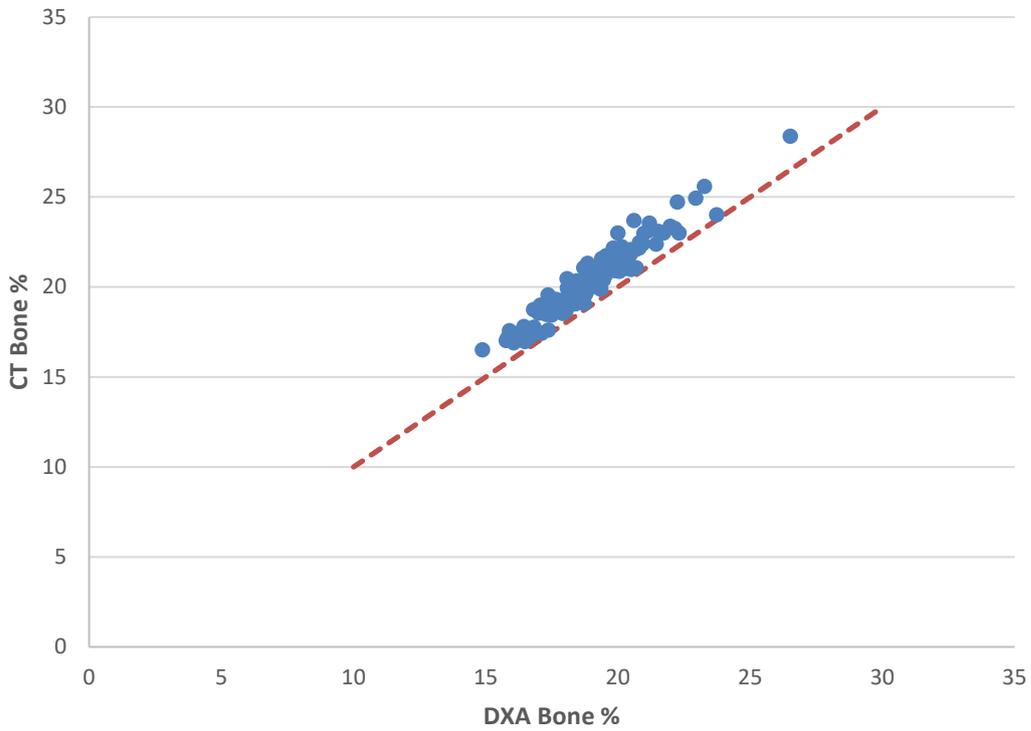


Figure 8 - DXA bone % prediction of CT bone % using the accredited bone detection algorithm. Dashed line is line of perfect prediction.

4 Further Work

Further exploration of bone detection is underway, with the next leap in precision and accuracy likely to come in the form of adequate bone edge detection. This process is difficult to achieve with the existing image processing software and would prove too time consuming and high in computational requirements to achieve at chain speed. This improvement would require the implementation of machine learning, with the focus primarily on calculating bone dimensions and positions. This would allow for the accurate detection of bone edges, resulting in two very important improvements:

1. Fewer events of incorrectly identifying soft tissue as bone, leaving more soft tissue pixels to be included in the larger accredited algorithm, and;
2. The accurate evaluation of neighbour soft tissue R-values, which would enable better quantification of bone containing pixels, including
 - a. Bone mineral content predictions
 - b. Weight of bone within the pixel, and the weight of soft tissue surrounding it

As the precision and accuracy of the soft tissue predictions are already high, there would once again be modest increases in their prediction performance. Further to the improved predictions and additional bone information, the machine learning process would also allow give information regarding the position and dimensions of the bones, potentially providing more accurate skeletal coordinates for automation, as well as assisting geneticists with ongoing work related to bone length and pelvic widths.