

final report

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Prototype feedlot biometric, gender, and breed identification system

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Executive summary

Effective production of beef cattle requires consistency. Given the diversity of cattle that attend feedlots, there is a need for new tools to assist sorting cattle at arrival, reimplant, or terminus to support profit maximisation. To date, no commercial sorting solution with appropriate embedded intelligence is available to the Australian feedlot industry.

An effective sorting system will require high-quality knowledge of feed intake, carcase growth, and composition of individuals, especially biometric measurements. Advancements in machine vision and learning technologies mean that it ought to be possible to predict growth and carcase composition accurately.

Research into this opportunity is considered vital for Australian lotfeeders as accurate performance predictions may bring value through any one of several modes, namely, profit/loss modelling of cattle of different biological types at different carcase endpoints; categorisation of cattle into homogenous marketing groups (if critical mass of cattle present); optimising days on feed of the sorted group to maximise carcase value over production costs; accurate diet formulation to maximise performance of each pen; and/or most simply, improved eating quality of the produced beef for consumers.

Against these considerations, the current investigation enabled the development and validation of a prototype biometric, gender, and breed identification system suitable for use within a feedlot operation. The system was developed against defined objectives focussed on autonomy, accuracy, precision, and update rate. After achievement of prototyping milestones, including development of an appropriate truthing strategy, performances were evaluated within a commercial feedlot environment.

This report presents outcomes of these validation experiments. We have demonstrated that the prototype system provided very encouraging results, predicting biometric measurements accurately, repeatedly, and quickly. Gender was not assessed during the experiment as only steers were available at the experiment's host site. Breed identification was only moderately accurate; however, this report also considers further improvements that can be explored to further enhance measurement outcomes against this criterion.

We have delivered a very promising prototype autonomous biometric and breed identification system, providing significant potential benefits for the red meat industry. The ability to autonomously generate identifications on a large sample of diverse feedlot cattle should enable future R&D on the value proposition of the data, which in turn ought to represent a high-value outcome for the sector.

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1 Introduction

This final report describes the results of an experiment to evaluate a prototype autonomous system to estimate biometrics of feedlot cattle as they are inducted.

1.1 Project intent

Cattle feeders strive to produce beef that is consistent in cut size, has minimal waste fat, maximal red meat yield, and meets customer expectations (for example, tenderness, taste, and safety). This consistency is often challenging given the diversity of cattle that arrive at the feedlot, so tools are needed to assist sorting cattle for profit maximisation at arrival, reimplant, or terminus.

With modern technologies it is possible that objective information collected on breed content, biometrics, and gender could benefit accurate predictions of growth, carcase composition, and eating quality prediction of individuals. For example, reliable knowledge of the empty body fat content of cattle is necessary to predict mature size and growth of feedlot cattle with the NRC (2016) and Cattle Value Discovery System models. Several recent studies have also reported the potential of manual biometrics to improve the precision of estimation of body fat depots in separate genetic populations of cattle (Fernandes et al. 2010; De Paula et al. 2013; Gomes et al. 2016; Fonseca et al. 2017).

This project has developed a cost-effective autonomous system to generate biometrics on a large sample of diverse feedlot cattle, thereby enabling future R&D on the value proposition of the data.

2 Project objectives

The overall project objective that was agreed in the agreement is as follows,

- 1. Develop a prototype automatic biometric measurement system to predict height at withers, rib depth, body diagonal length, body length, pelvic girdle length, rump depth, rump height, pin bone width, hook bone width, abdomen width, girth circumference, hump height and circumference as well as locations for point of shoulder, withers, hook bones, and pin bones (as per Fernandes et al., 2010).
- 2. Determine the precision, accuracy, and speed of result of the prototype to predict biometric measurements for a sample of independent cattle from three breeds (British, European, and Brahman).
- 3. Determine possible biometrics associated with gender and breed identification.

3 Methodology

Effectiveness of the prototype system was based on core technologies including, though not limited to, artificial intelligence, machine learning, distributed computing, and data generation and presentation to users.

Achievement of project objectives benefitted from regular communications with MLA and the host site (Mort & Co's Grassdale Feedlot, Cecil Plains, Qld) so that all stakeholders were always aware of project statuses and milestones. All project engineering and factory testing was completed at our base in Brisbane, Queensland. Field development, data collection, and experiments were undertaken at the host site.

The following sub-sections include a high-level summary of the methodology to achieve the required experimental output.

3.1 Apparatus

In the early stages of the project, we investigated possible sensor and networking technologies and their arrangements. Based on our evaluations, and with project objectives in mind, we opted to provide an array of depth camera sensors (Microsoft Kinect 2.0, WA, USA) for the waiting bay (last bay upstream of crush): two side elevation cameras and one overhead camera for animal plan view.

The cameras were installed on customised robust mounting adapters and were calibrated by exercising a standard protocol; this is freely available in the public domain. The protocol enabled an estimation of a camera scene's structure to be described in Euclidean space and removed factors such as lens distortion, which may have degraded measurement accuracy. In practice the calibration was performed by placing a special printed checkerboard target of known dimensions in each camera's field-of-view, and then detecting corner points in the generated image. Automatically calculated parameters account for intrinsic factors (for example, focal length, skew, distortion, and image centre) and these were unique for each camera. Extrinsic parameters (relative positions and orientations in the world) for the cameras were configured in-situ after commissioning.

On the physical layer, the side panel of the waiting bay on the non-working side was replaced with a custom designed gate to decrease vision-obscuring rails in sensors' fields-of-view. Additional external illumination was provided with directional white-light LED lamps. The cameras' data were networked in a distributed processing arrangement, before being integrated in a centralised processing platform (main processor, Intel i7, 16GB RAM), complete with GPU (NVIDIA GeForce RTX 2080, Santa Clara, CA, USA) enabling parallel-processing optimisations.

The main processor operated two convolutional neural networks (CNN) in parallel: pose estimation and breed identification. We trained each network on a labelled dataset of 400 images of cattle previously collected at the host site; these were based on multiple frames each for approximately 50 cattle. Pose labelling involved manual identification of specific biometric points on each image accurately and consistently. Knowledge was then transferred from a free open-source animal pose model to the small application-specific dataset (400 images) with a view to improve CNN learning; the network was trained on approximately 200k iterations. As the breed dataset was composed of the same 400 images, its network also used transfer learning. Breed labelling required manual identification in each image (within the three nominal categories); personnel from the host site provided all labelling inputs for the breed dataset to improve likelihood of accuracy and consistency. The breed network's training process required approximately only 100 iterations, due to the simplified architecture of the breed selection CNN (that is, selection of only one out of three options).

During the training data collection and load experiment activities, animals were individualised with new slide gates (Thompson Longhorn, Goomburra, Qld) at entry and exit of the second-last bay upstream of the crush. This manual process reduced bunching of target animals in the waiting bay during measurements, and improved calming of animal/s upstream in race. Only steers were available within the three target breeds at the host site during the project's programme, and so it was agreed with stakeholders that the gender identification requirement will be excluded from scope of this project's activities.

3.2 No-load truth validation

With a view to validating accuracy and precision of cameras, outside of normal production, seven rectangular prisms of different sizes were observed in three dimensions in three nominal locations along waiting bay length. Prisms were elevated from bay's floor level via an ad hoc shelf installed across side-panels' horizontal rails. Observations were made with a flexible ruler and recorded digitally in a simple worksheet. Predictions were derived retrospectively back at our base from the recorded depth camera images. The prediction results were generated while blind to the observations and were also recorded digitally.

3.3 Load experiment

The following subsections describe the load experiment protocol.

3.3.1 Biometrics reference schematic

Measurements completed were consistent with Fernandes et al., 2010, and these are reproduced with brief labels in Fig. 1.



Fig. 1: Reproduced from Fernandes et al., 2010. Schematic representation of A) lateral and B) posterior views of a steer showing the relative locations of biometric measurements, including 1) height at withers, 2) rib depth, 3) body diagonal length, 4) body length, 5) pelvic girdle length, 6) rump depth, 7) rump height, 8) pin bone width, 9) hook bone width, and 10) abdomen width. The girth circumference (not shown in panel A) was taken as the smallest circumference just posterior to the anterior legs in the vertical plane. Points a, b, c, and d are relative locations of the point of shoulder, withers, hook bones, and pin bones, respectively.

3.3.2 Target animals

Load experiment measurements were undertaken on 293 randomly selected cattle during normal induction activities over a two-day period at the host site; 469 cattle in total were recorded. The animals were non-consecutive so a diverse range of breed and size compositions could be targeted across the required three broad breed groups: British, European, and Brahman. Animals accepted within the experimental results met the following requirements,

- Timestamp: Cattle were selected within time periods when the system was fully functional, and confidence existed in the output measurements.
- Valid measurements: While the system recorded cattle measurements even when the full set was not complete, we opted to reject individuals when all 10 measurements were not available. This consideration removed 31 cattle (6.6%) from the experiment dataset.
- Tracked time in waiting bay: In general, the longer individuals were retained in the waiting bay, the more time the system had available to detect locating nodes on the live animals, and this in turn provided more accurate measurements. The prototype automatically tracked cattle in the waiting bay, producing measurement start and stop events. Simple machine vision algorithms were employed, however in practice they were susceptible to environmental conditions such as changes in ambient light. On failure events due to changes in lighting, the tracking algorithm was manually recalibrated to the new environmental conditions. It follows that this tracked time aspect was simply implemented on the recorded dataset by only including individuals that had at least 15 seconds within the waiting bay: this removed 145 cattle (31%) from the experiment dataset.
- Breed: The project required 50 individuals from each of the three broad breed categories. On this basis we opted to include as many of each breed as possible during the experiment's duration, especially while also considering the previous three qualifying criteria.

At all stages experiment personnel were mindful of not overly interrupting operations or isolating animals displaying agitation or other aggressive behaviour/s.

3.3.3 Predictions

Data from depth cameras fed forward to the main processor, and this in turn output biometrics measurements and breed autonomously, as determined by the two neural networks. Data were presented live via a bespoke web application and results databased (complete with timestamps) on a local client laptop.

3.3.4 Observations

Back at base, images generated by the depth cameras for each assessed animal were manually postprocessed, and required measurements were recorded in a simple worksheet; this activity was undertaken while blind to predictions.

The host site identified breeds of the assessed animals via simple image annotation. These were directly input to a bespoke web application, consistent with the software arrangement previously provided to the host site to generate dataset to train the breed CNN.

4 Results

The following section describes the statistical analyses employed to assess the outputs of the evaluations, followed by presentation of the experimental results.

4.1 Statistical analyses

Several statistical analyses have been undertaken with a view to assessing the performances of the prototype system objectively.

Observed biometrics have been regressed on predicted measurements output by the prototype system. The coefficient of determination (r^2) has been calculated on the line of regression as a measure of the observed and predicted measurements' relationship strength.

Evaluation of the model's precision has been enabled through employment of several commonly used measures of deviance, including mean absolute error (MAE), mean square prediction error (MSPE), and root mean square error (RMSPE). Shah and Murphy (2006) defined MSPE as: Σ (Oi – Pi)²/n, where n = number of paired observed (O) and predicted (P) measurement values being compared. The MAE is defined as: (Σ |Oi – Pi|)/n.

Furthermore, the MSPE can be decomposed to assess sources of variation, viz, (1) variation in central tendency (mean bias), (2) variation resulting from regression (systematic bias or line bias), and (3) random variation.

Variation resulting from mean bias has been calculated by squaring the mean bias of the prediction. Systematic bias has been calculated as the product of predicted measurements' variance and the square of the deviation from 1 of the regression of observed on predicted gradient. Random variation was calculated as the product of the variance of observed data and the deviation from 1 of the coefficient of determination of the regression of observed on predicted data. Shah and Murphy (2006) noted that mean bias is useful to test the robustness of the model, whereas line bias can be used to test inadequacy in model structure. Mean proportional bias has been calculated as the slope of the regression of the predicted data on observed data with an intercept of 0 (Shah and Murphy, 2006). Over the range of observed values, a value of mean proportional bias less than one (< 1) denotes underprediction, whereas a value more than one (> 1) denotes overprediction.

In addition, mean and linear biases were calculated by regression of residuals (observed minus predicted measurements) on mean-centred predicted measurements (St-Pierre, 2003). St-Pierre (2003) noted that by centring predictions to the mean value, the intercept of the linear model is estimated at the mean value of the independent variable rather than a value of zero.

The intercept term at the mean value is a measure of the mean prediction bias, and a t-test on the estimate of the intercept has been used to determine the statistical significance of this bias. The slope of this mean-centred regression is an estimate of the linear prediction bias, and a t-test has been used again to test significance. When the linear prediction bias has been found to be significant (P < 0.10), the magnitude of the bias within the range of predicted values was determined by calculating the bias at the minimum and maximum data points of the predicted values (St-Pierre, 2003).

4.2 No-load truth results

The following section contains a summary of no-load experimental data analyses for the prototype system. Graphical charts of the results have also been provided.

4.2.1 Summary of regressions for biometrics measurements

Results of the regression of observed on predicted biometric measurements are shown in Table 1. Mean and linear biases are also reported, determined from the regression of residuals on meancentred predicted measurements. Table 1: No load experiment evaluation statistics of known geometric predictions for prototype system, 63 observations for seven rectangular prisms (HxWxD) in three nominal positions along length of waiting bay. Mean and linear biases calculated using St-Pierre (2003) techniques.

Item	Prototype system			
Mean bias, mm	-1.04			
P-value	< 0.01			
Linear bias	0.00			
P-value	0.11			
r ² regression of observed on predictions	1.00			
RMSPE, mm	2.45			
MSPE, mm ²	5.99			
MAE, mm	1.73			
Mean proportional bias	1.00			
Decomposition of MSPE				
Mean bias, %	15%			
Systematic bias, %	3%			
Random bias, %	82%			
Bias at min. prediction, mm	-			
Bias at max. prediction, mm	-			

Table 1 shows that the prototype system accurately and precisely predicted biometric measurements for the known geometric targets. The prototype system had an insignificant amount of mean bias (P-value <0.01), underpredicting dimensions by 1mm. The system had no linear bias to be tested with statistical significance, and this is reinforced by visual interpretation of its bias being consistent over the full range of measurements. Precision of the prototype was excellent during the experiment ($r^2 = 1.00$). Mean absolute error and RMPSE for the prototype system's measurements were both approximately two millimetres.

4.2.2 Chart results for biometrics measurements

The no-load experiment observed on predicted biometric measurements for the prototype system (machine) are represented graphically in Fig. 2 This figure also shares constituent mean and systemic sources of errors for this experiment; that is, the residuals (errors, observations minus predictions) over mean-centred predictions.



Fig. 2: No load experiment observed on predicted biometric measurements for prototype system (left), and constituent sources of error (right).

Based on these evaluations the prototype system has extremely high accuracy and precision.

4.3 Load experiment results

The following section contains a summary of load experiment data analyses for the prototype system. Graphical charts of the results have also been provided.

4.3.1 Summary of regressions for biometric measurements

Results of the regression of observed on predicted biometric measurements are shown in Table 2. Mean and linear biases are also reported, determined from the regression of residuals on meancentred predicted measurements.

ltan	Biometric measurements by prototype system as per Fernandes et al., 2010*										
Item	1	2	3	4	5	6	7	8	9	10	ALL
Mean bias, mm	47.33	3.13	78.02	17.53	3.68	11.28	20.01	0.12	4.73	12.76	19.86
P-value	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	0.88	< 0.01	< 0.01	< 0.01
Linear bias	0.05	0.01	-0.36	0.03	-0.03	-0.03	-0.03	0.01	-0.06	0.05	-0.07
P-value	0.13	0.50	< 0.01	0.12	0.04	0.13	0.21	0.78	< 0.01	0.05	< 0.01
r ² regression of observed on predictions	0.75	0.91	0.50	0.93	0.94	0.86	0.80	0.59	0.86	0.84	0.99
RMSPE, mm	57.17	14.18	96.09	28.73	14.79	24.08	30.59	13.38	14.07	23.57	40.24
MSPE, mm ²	3,268	201	9,232	825	219	580	936	179	198	556	1,619
MAE, mm	47.96	11.88	81.50	23.88	11.88	19.55	24.96	11.71	11.13	19.20	26.36
Mean proportional bias	0.96	0.99	0.93	0.97	0.99	0.98	0.98	0.99	0.99	0.97	0.97
Decomposition of MSPE											
Mean bias, %	69%	5%	66%	37%	6%	22%	43%	0%	11%	29%	24%
Systematic bias, %	0%	0%	8%	1%	1%	1%	0%	0%	2%	1%	16%
Random bias, %	31%	95%	26%	62%	92%	77%	57%	100%	86%	70%	59%
Bias at min. prediction, mm	-	-	151.18	-	9.29	-	-	-	9.53	7.84	57.96
Bias at max. prediction, mm	-	-	-34.03	-	-5.60	-	-	-	-6.59	27.09	-29.20

Table 2: Load experiment evaluation statistics of biometric measurement predictions for prototype system, 293 observed cattle across three breed categories. Mean and linear biases calculated using St-Pierre (2003) techniques.

*1) height at withers, 2) rib depth, 3) body diagonal length, 4) body length, 5) pelvic girdle length, 6) rump depth, 7) rump height, 8) pin bone width, 9) hook bone width, and 10) abdomen width.

Table 2 shows that the prototype system accurately and precisely predicted biometric measurements. Overall, the prototype system had a very small amount of mean bias (P-value <0.01), underpredicting measurements by approximately 20mm. The most significant contributors to mean bias were measurements 1 and 3, viz height at withers (47mm) and body diagonal length (78mm) respectively; four of the 10 measurements had a mean bias better than 5mm.

The prototype had minimal linear bias (-0.07 with P-value <0.01), and this is reinforced by visual interpretation of its bias being consistent over the full range of biometric measurements. Minimum and maximum biases have been calculated for all contributing measurements with P-values less than 0.10 including overall experiment result. Precision of the prototype system was excellent during the experiment ($r^2 = 0.99$). Mean absolute error for the prototype was 26mm, and the RMSPE was 40mm.

4.3.2 Chart results for biometric measurements

The load experiment observed on predicted biometric measurements are represented graphically in Fig. 3. This figure also shares constituent mean and systemic sources of errors for this experiment, and it is reinforced that a small mean bias exists (y-offset almost 20mm), with limited linear bias (gradient near zero), and generally low levels of variability (precision).

The observed on predicted chart in Fig. 3 also demonstrates larger variabilities in measurements in the 1,000-2,000mm observed range, and these are attributable to the lower performing measurements previously identified.



Fig. 3: Load experiment observed on predicted biometric measurements for prototype system (left), and constituent sources of error (right).

4.3.3 Speed of result

The pose prediction process recorded measurements approximately seven times per second (7Hz), and these measurements were stored in a buffer and averaged when the animal departed the waiting bay. The breed prediction process recorded classifications approximately 15 times per second (15Hz), and these predictions were stored in a buffer and averaged when the animal departed the waiting bay. In both cases the speed of result was less than normal operating protocols for the induction process, and as aforementioned, had a nominal minimum duration of 15 seconds.

4.3.4 Breed identification

Results of the breed identification function are summarised in Table 3.

Breed category	Count	Correct breed	Correct breed %	
British	95	70	74%	
European	77	26	34%	
Brahman	121	72	60%	
Overall	293	168	57%	

Table 3: Breed identification success by breed category and overall.

Table 3 shows that the prototype system only had moderate accuracies for identifying British and Brahman breeds. Poorer performance when identifying European cattle subsequently also decreased the prototype's overall accuracy.

5 Discussion

The results achieved through this project and summarised in this report should be considered very encouraging. Implementation of two CNNs trained with limited site-specific datasets have yielded extremely high performing biometric measurements across at least eight out of 10 nominal dimensions and all inducted breeds. We expect the two identified dimensions with lower accuracy and precision performances may be improved with additional training.

Moderate performances for breed identifications were achieved, and we expect that this network's deficiencies may be attributed to at least one of several possible input factors. These may include sample size of training dataset, and accuracy of human input training and truth labels, especially given the broad spectrum of crossbreeds received at the experiment's host site.

To continue this thought process, an important feature of neural networks is that they are only as good as the data input for them to learn, so it follows that poor labelling will lead to poor accuracy and overall performance of outputs. Neural networks also generalise their environmental factors. This means that a change in environment, for example a different area within the host feedlot, or another feedlot all together, may require training on an extended dataset to allow the network to learn the features of the new environment.

In future implementations, new training activities will be undertaken during commissioning. This in turn creates performance improvement opportunities, as each subsequent implementation of the training process increases the size of the input dataset, so every network will inherit improved handling of new environments; improvements will be most likely because the network's learning should focus on the cattle inputs rather than the less-important surrounding environment. Extending the dataset also increases the accuracy and robustness of each network, especially when dealing with unique inputs to which the network has not previously been exposed, such as cattle of different colours, shapes, or patterns.

The deficiencies tracking individuals in the waiting bay may also be improved with automatic ambient light calibration routines or algorithmic upgrades. The latter may be possible via a deep learning-based object tracker which will be able to track targets independent of changes in environmental conditions.

Likely future improvements for the breed identification network would probably involve a custom neural network that does not focus on transfer learning, especially if the goal is to determine individual percentages of crossbred content in cattle. Instead, we would suggest a training set of 10k+ images of truth breeds may be appropriate to produce a network with extremely high accuracy for crossbreeds.

6 Conclusions/recommendations

Against the results presented in this report, the prototype system provided highly accurate and repeatable (precise) biometric predictions during the validation experiment in a commercial feedlot environment under normal operating conditions. A statistical methodology has been exercised with a view to assess predictions provided by the prototype system, and the methodology has provided clear and objective support for measurement performances.

Gender identification was not possible at the nominated host feedlot within the breeds available, and so this aspect was excluded from activities.

Breed identification had mixed performances, with moderate accuracies identifying British and Brahman breeds, though poorer accuracy with European cattle.

Our discussion section has introduced likely inputs which may have influenced prototype system performance. Most importantly, the results of the demonstrable system should be considered very favourably, and execution of the corrective actions ought to yield significant system improvements.

7 Key messages

We are excited about the potential benefits that the red meat industry should garner through our technology solutions partnership. We have been pleased with the relationship between ourselves and MLA, and our ability to respond effectively to this opportunity through the supply and validation of the working prototype system.

With MLA's support, we have delivered a prototype autonomous biometric and breed identification system that has demonstrated significant potential benefit to the red meat industry. Based on the successful outcomes of this project, we suggest that a research platform should be available in the near term with a view to further value proposition explorations.

8 Bibliography

The following literature was cited in this report.

De Paula, NF, Tedeschi, LO, Paulino, MF, Fernandes, HJ & Fonseca, MA 2013, Predicting carcass and body fat composition using biometric measurements of grazing beef cattle, Journal of Animal Science, Volume 91, Issue 7, July 2013, Pages 3341–3351.

Fernandes, HJ, Tedeschi, LO, Paulino, MF & Paiva, LM 2010, 'Determination of carcass and body fat compositions of grazing crossbred bulls using body measurements', Journal of Animal Science, vol. 88, pp. 1442–1453.

Fonseca MA., Tedeschi LO, Filho, Valadares, SC, De Paula, NF, Silva, LD & Sathler, DFT 2016, Evaluation of equations to estimate body composition in beef cattle using live, linear and standingrib cut measurements. Animal Production Science 57, 378-390.

Gomes, RA, Monteiro, GR, Assis, GJF, Busato, KC, Ladeira, MM & Chizzotti, ML 2016, Technical note: Estimating body weight and body composition of beef cattle trough digital image analysis, Journal of Animal Science, Volume 94, Issue 12, December 2016, Pages 5414–5422.

Shah, M. A., and M. R. Murphy. 2006. Development and evaluation of models to predict the feed intake of dairy cows in early lactation. J. Dairy Sci. 89:294–306.

St-Pierre, N. R. 2003. Reassessment of biases in predicted nitrogen flows to the duodenum by NRC 2001. J. Dairy Sci. 86:344–350.