Final report



Fingerprinting

Digital fingerprinting for primals back to carcases

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1.0 Executive summary

This project's intent is to perform initial beef validation on an AI solution that would allow for beef primals to be tracked by Carcass ID, without cumbersome changes to production environments. Traceability after carcass breakdown is a key industry need. Currently, once a carcass is broken down beyond quarters it is not practical to track and trace pieces, as this would require physical labels on every piece, which adds substantial complexity to systems, along with foreign body and quality concerns. This project will focus on Striploin primals and ensuring they can be traced from quarter, when a physical label is still present and could be read, to post trimming.

A target of 95% primals correctly matched to carcass ID was set, with less than 1% false positives.

To gather the relevant data, engineers with smart phones positioned themselves at "DC1" (Data Collection Point 1), before the chiller to capture quarter images, and at "DC2" (Data Collection Point 2), between the trimming and packing areas in the boning hall.

5 batches of data were gathered across 3 production days. A variety of data augmentations and algorithm iterations were tested to optimize the Fingerprinting solution. Following these, all the data was processed and the Fingerprinting AI ran an exhaustive matching process, attempting to match every DC1 image with every DC2 image for that batch. This led to a total of 66,366 DC1/DC2 pairs to be assessed. The table below shows the results, with "Positive Pairs" being pairs where DC1 and DC2 were confirmed to be the same striploin by human visual inspection. Every pair the Fingerprinting AI recognized was correct, with no false positives. The dataset was visually inspected for "Missed Pairs" i.e. DC1 and DC2 are the same striploin, but the Fingerprinting AI did not identify this. No "Missed Pairs" could be found by human visual inspection, but the large dataset means it cannot be definitely said that there were zero. It can be said with confidence that there were approximately zero missed pairs. Batch A was inspected in detail, while other batches were randomly sampled.

Batch	DC1 Images	DC2 Images	Total Number of Pairs	Positive Pairs	False Positives	Missed Pairs
Batch A	88	99	8,712	37	0	~0
Batch B	74	128	9,472	30	0	~0
Batch C	65	114	7,410	41	0	~0
Batch D	157	179	28,103	79	0	~0
Batch E	103	123	12,669	15	0	~0

It can be concluded that the Fingerprinting test resulted in approximately 100% accuracy, certainly well above the targeted 95% outlined in the project objectives. There were 0% false positives, beating the 1% target outlined in the project objectives.

It is recommended that this technology next advance to multiple primal types, and multiple operating sites. It is recommended this technology be installed in production in 2 site types; 1 that is fully conveyed, and 1 with some carting of product, as this effects the sequence of product between DC1 and DC2. Secondary cuts should also be tested to assess feasibility and procedure.

2.0 Introduction

This project's intent is to perform initial beef validation on an AI solution that would allow for beef primals to be tracked by Carcass ID, without cumbersome changes to production environments. Traceability after carcass breakdown is a key industry need. Currently, once a carcass is broken down beyond quarters it is not practical to track and trace pieces, as this would require physical labels on every piece, which adds substantial complexity to systems, along with foreign body and quality concerns.

If a reliable solution can be validated that can trace primals back to their carcass, without substantial infrastructure and procedure change, this unlocks huge value in yield, genetics, quality control, recall efficiency, etc.

This project intends to prove the core technology associated with a solution to this traceability problem, developed by FloVision Solutions. This solution is referred to as "Fingerprinting", where a unique "fingerprint" of each object can be scanned and matched together, analogous to human fingerprint analysis or facial recognition. This project will focus on Striploin primals and ensuring they can be traced from quarter, when a physical label is still present and could be read, to post trimming, when the primal is about to be packaged and a label could easily be printed for further traceability.

3.0 Project objectives

3.1 Objective 1

Work with 1 processor to design and install a system that can take carcass ID and an image at a specified viewing angle as inputs at the time of carcass breaking, and then take a further image at the same viewing angle after trimming has been complete, prior to packing.

3.2 Objective 2

Software developed to enable matching of primals between the 2 data capture locations, and linking that primal to the relevant carcass ID.

3.3 Objective 3

A series of tests and validation studies performed remotely to assess accuracy of the system.

3.4 Objective 4

A target of 95% primals correctly matched to carcass ID, with less than 1% false positives.

4.0 Methodology

- Initial conversations were had with site to understand site specifics and restrictions.
- Following this, initial design decisions were made. 2 approaches were considered, as there was a high degree of uncertainty associated with the site physical space, and a tight timeline to implement a solution.
 - An adjustable mountable camera system was designed and manufactured, using the base FloVision Nano hardware and software, with adjustable camera mounting hardware. One device would be

positioned at "DC1" (Data Collection Point 1), before the chiller. The other device would be positioned at "DC2" (Data Collection Point 2), after striploin primal trimming.

- A system was devised to collect data using 2x smart phone cameras. One smart phone would be positioned at "DC1" (Data Collection Point 1), before the chiller, being operated by a FloVision Engineer. The other device would be positioned at "DC2" (Data Collection Point 2), after striploin primal trimming, being operated by a FloVision Engineer.
- Upon arrival, the locations and specifics around DC1 and DC2 were analysed. It was decided by site, and FloVision Engineers, that the smart phone camera system would be more feasible for this project, to allow for quick and easy data collection, with minimal interference with production.
- Data was collected using this system across 3 days, with data being uploaded to Google Drive at the end of each production day. These batches of data could then be downloaded anywhere and reviewed visually.
- All data from DC1 and DC2 had to be the same orientation for the fingerprinting AI model. Data was
 manually reviewed, and relevant images were rotated 90, 180, or 270 degrees. All images were set to be
 "Fat Up", although the selected orientation does not matter as long as it is consistent.
- Small quantities of data were then tested from each batch to allow for quick iteration. 2 sets of pairs were identified by eye for each batch of data to be "Ground Truth" positive pairs (i.e. matches) for model testing and iterating, along with 5 negative pairs (i.e. not matches).
- With these small testing datasets, parameters could be tested to optimize the model for the image environment. The Fingerprinting AI model is sampling the images and comparing the sampled areas to determine if they are "similar". If a sampled area is determined similar – that is 1 keypoint match (an area that appears similar between the 2 images in question). A threshold of keypoint matches is needed to define what is a positive pair of images (e.g. if 10 or greater keypoint matches, the images are of the same primal).
- A number of iteration cycles were carried out to find good confidence levels, number of keypoint matches, and other model parameters. During these iterations it was decided to crop the images to focus on the primal in question, removing other primals or carcasses in the image, to reduce noise and the possibility of false positives. Examples of positive and negative pairs can be found in the Appendix.
- Each batch was run exhaustively checking every possible combination. This "1 to many" approach meant that every DC1 primal was compared to every DC2 primal in sequence for that batch. Each batch took 3-6 hours of compute time, run on cloud GPUs depending on batch size to run this full analysis.
- Following this, all positive pairs (matches) were validated by visual inspection of the images.
- Following this, a large sampling of the 300,000+ non-matching pairs of images were reviewed, including the entirety of Batch A and random images from the other Batches.

5.0 Project outcomes

Batch	DC1 Images	DC2 Images	Total Number of Pairs	Positive Pairs	False Positives	Missed Pairs
Batch A	88	99	8,712	37	0	~0
Batch B	74	128	9,472	30	0	~0
Batch C	65	114	7,410	41	0	~0
Batch D	157	179	28,103	79	0	~0
Batch E	103	123	12,669	15	0	~0

5 batches of striploin data were analysed. Batch information is shown in the below table.

From visual inspection of the primal image results, it was confirmed that all the matches found by the fingerprinting algorithm appeared to be positive pair matches, with no false positives. From visual inspection of the primals not matched, missed pairs could not be easily identified. It cannot be stated with certainty that there are 0 missed pairs, but none where found. Therefore, the number of missed pairs is either 0 or near 0 across the 66,366 pairings within the 5 batches. The most likely reason for missed pairs would be data capture errors (lighting changes, angles, missing the full wing face, blur, etc) associated with the temporary data collection setup.

Appendix 1 shows some example images of Positive Pairs, and non-matching pairs.

6.0 Discussion

It can be concluded that the Fingerprinting test resulted in approximately 100% accuracy, certainly well above the targeted 95% outlined in the project objectives. There were 0% false positives, beating the 1% target outlined in the project objectives.

Every batch had between 15% and 63% of the DC1 (Data Collection Point 1) primals matching. Upon reviewing Batch 1 in detail to try understanding the reason why, it was found that most of the matches occurred in the first half of DC1 primals captured (35 of the 37 positive pairs were contained in the first 42 DC1 primal scans). This indicates that most of the second half of the batch was not captured at DC2, likely due to production reasons (e.g. batch split for different aging spec or other processing) or data capture running between 2 batches. Alternatively, some data was likely missed during batches that would lead to less matches, as FloVision Engineers where not aware of exact times of batch start/end (production did not make batch start and end clear and sometimes did not inform FloVision Engineers on site).

For future projects, a blind validation test outside of production would be beneficial, where an AMPC facilitator feeds primals to a defined program, for example 30 primals through DC1 device and then 30 primals through DC2 device. The matches (positive pairs, decoys, etc) and results would be known to AMPC, but FloVision would be blind and produce results to validate.

7.0 Conclusions / recommendations

This project successfully validated the core technology of FloVision Fingerprinting for Striploin primals, with an approximate success rate of 100%.

It is recommended that this technology next advance to multiple primal types, and multiple operating sites. It is recommended this technology be installed in production in 2 site types; 1 that is fully conveyed, and 1 with some carting of product, as this effects the sequence of product between DC1 and DC2. Secondary cuts should also be tested to assess feasibility and procedure.

A significant amount of development effort is needed to optimize procedures to reduce impact on existing production workload. Mechanical, digital, and operational procedures will need to be developed to ensure correct meat orientation, controlled environment (lighting, blurriness, etc), label reading/scanning, and quick data capture. These factors, that impact data collection, will have the largest impact on fingerprinting accuracy in production settings.

8.0 Appendices

8.1 Appendix 1: Example Images





See alter / Jayer, 20 million

Image 1: Example of strong Positive Pair matching







Image 2: Fingerprinting model performing well on a primal that has gone through substaintial trimming between DC1 and DC2



Image 3: Fingerprinting model performing well on a primal that has gone through significant transformation including significant trimming of the main eye muscle





Image 4: Fingerprinting model correctly not matching different primals (no green lines showing matching keypoints)