Detection of invariant structures and selection of representative MRI slices of pig lean meat percentage

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Introduction

Tomography techniques are well suited to determine carcass composition. Nevertheless, sometimes some practical constraints appear like: too time consuming, too costly, only joints are available. In these cases scanning some representative slices is a suited alternative.

This study aimed at firstly detecting some invariants to register images and secondly at selecting batches of contiguous slices for assessing the lean meat percentage of slaughterpigs.

Material and Methods

Two datasets were used: a French dataset (n=17) and a Hungarian dataset (n=120), obtained in the framework of the European project EUPIGCLASS. The selection in both included females and castrates from several genotypes.

In the FR dataset the left sides were scanned in a chilled box (5°C) with a 0.2 T Siemens Magnetom Open. 7 or 8 series of 19 images (1 cm each) were needed for each side. For each MRI slice, two gradient-echo MRI images were simultaneously acquired, one with a large carcass vs. background contrast (8 ms echo) and the other with a large muscle vs. fat tissues contrast (19 ms echo). Carcass segmentation was performed on the 8 ms echo images and muscle segmentation on the 19 ms echo images, both using the same threshold for each pig.

In the HU dataset the right sides were scanned with a 1.5 T Siemens Magnetom Vision. Segmentation was performed using a different threshold for each pig and each slice.

Length of sides being different, invariants were found out for images registration. The longitudinal profile of the LMP20 was drawn for each of the 17 FR pigs. LMP20 was the ratio between muscle voxels and side voxels, averaged on 20 contiguous slices.

After images registration LMP20 were the regressors to predict the LMP in the side without head and feet.

Results and Discussion

In the French dataset 3 invariants were found, one in each main part (fore-end, middle, hind part). Using 3 batches, one in each part, the lowest estimation error of LMP was 0.5 %. Using the middle and another part, the error ranged 0.6-0.7 %

In the EU dataset analysis focused on middle and hind part. Unfortunately, only the location in the middle was invariant. The corresponding slice was renumbered 0 and batches of 20 contiguous slices were created.

The curve of the estimation error of LMP showed 3 local minima: one in the middle (RMSE = 1.22 %), another in the separation area between middle and hind part (RMSE = 1.35 %), and the last one in the hind part (RMSE = 1.66 %). Further analysis was limited to the both spatially extreme local minima, assuming they could be more complementary for assessing LMP. This combination reduced substantially the error (RMSE = 0.74 %).

Nevertheless, the RMSE curve showing suboptimal areas around the local minima, it means that in practice there would be a lot of possibilities to choose the exact position of both batches. A practical way could consist in:

1. Locating the junction of the sacrum and the last lumbar vertebra, which is close to the local LMP minima,
2. From the junction, measure about 30 cm towards the head, corresponding to the end of the middle batch,
3. From the junction, measure about 10 cm towards the hind foot, corresponding to the start of the ham batch.

Conclusion

Two batches of 20 cm each, one in the middle and another one in the ham, provided an accurate estimate of LMP. Slices registration can be performed from the following invariant: the local minima LMP at the end of the middle.

Robustness could be increased by investigating suboptimal areas valid for a great variety of pigs. Batches size could be adapted to the characteristics of the imaging device and to the wished acquisition speed. More investigations in the joints seem suited too.