Graph matching with lobsters

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Abstract

The ability to make measurements on lobsters is important in monitoring the size and health of the creatures. This project explores the representation of lobsters as attributed graphs to discover and measure properties such as their size, using an existing dataset of lobster images. Computer vision techniques are applied to detect interest points of different lobster body parts. Probabilistic models and subgraph matching are then used to label and build up the graph representation.

Keypoint detection

Different feature detection algorithms were tried to see which would provide useful keypoints consistently.
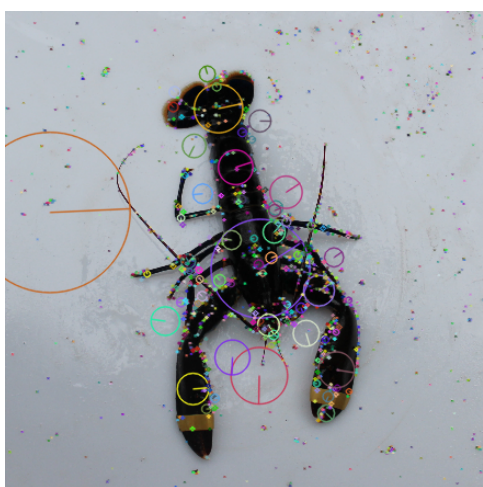

Figure 1: SIFT detector

Figure 2: SURF detector

Keypoint filtering

Multiple methods had to be used to filter out irrelevant keypoints. Octave filtering removed small keypoints and colour histogram filtering removed keypoints not on the lobster.
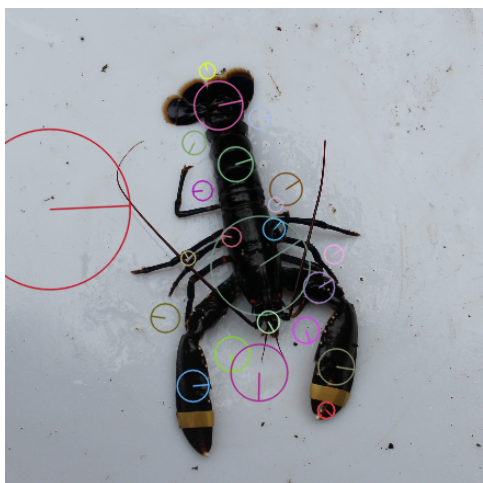

Figure 3: Octave filtering method

Figure 4: Colour histogram filtering method

Matched lobster graph

The probabilistic models with subgraph matching returns the most probable subgraphs found in the image, which are combined into the final graph.
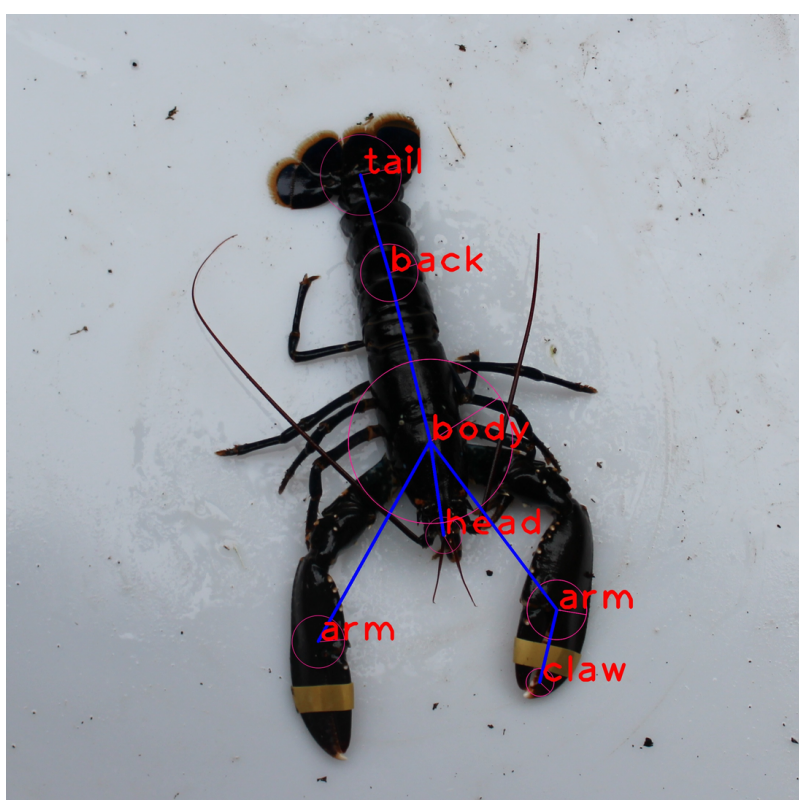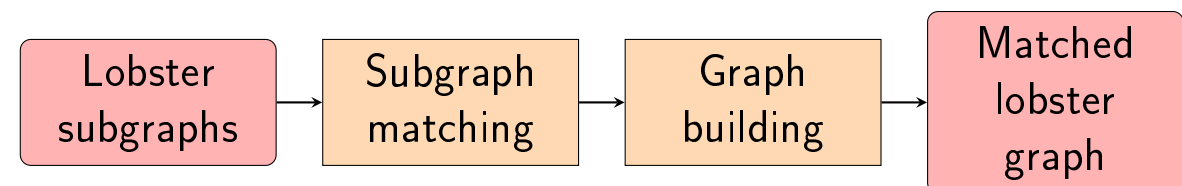

Figure 5: Final matched graph drawn on top of lobster image

Method pipeline

(a) Initial process of creating labelled subgraphs for matching.

(b) Process of taking the labelled subgraphs to creating a full lobster graph.

Figure 6: Flow chart of the whole matching process from getting keypoints to creation of the lobster graphs. The yellow steps in the pipeline represent processes and red steps represent inputs and outputs.

Probabilistic models

A Naïve Bayes probability model was used to calculate the probability of a matched graph with n nodes and m edges for both the subgraph creation and graph building stages.

$$P(\text{subgraph}) = \prod_{i=0}^{n} P(\text{node}_i) \cdot \prod_{j=0}^{m} P(\text{edge}_j) \tag{1}$$

$$P(\text{node}) = P(\text{node.label} \mid \text{node.size}) \tag{2}$$

$$P(\text{edge}) = P(\text{edge.length} \mid n_1 \wedge n_2)$$
$$= \frac{P(n_1 \wedge n_2 \mid \text{edge.length}) \cdot P(\text{edge.length})}{P(n_1) \cdot P(n_2)} \tag{3}$$

F1 score

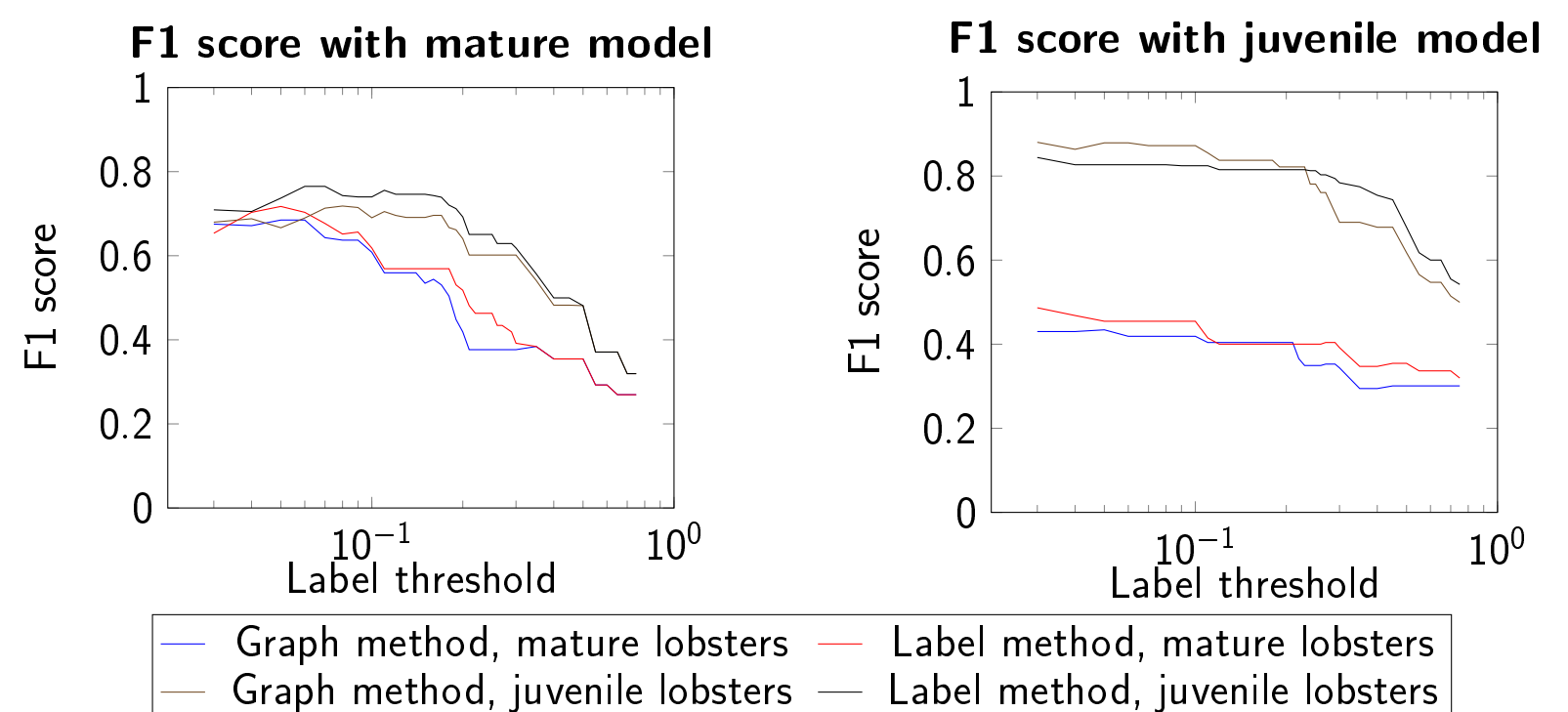The F1 score of the method was used to determine optimal thresholds.

Figure 7: Comparison of F1 score for mature and juvenile models on all lobsters with a histogram filter threshold of 0.5
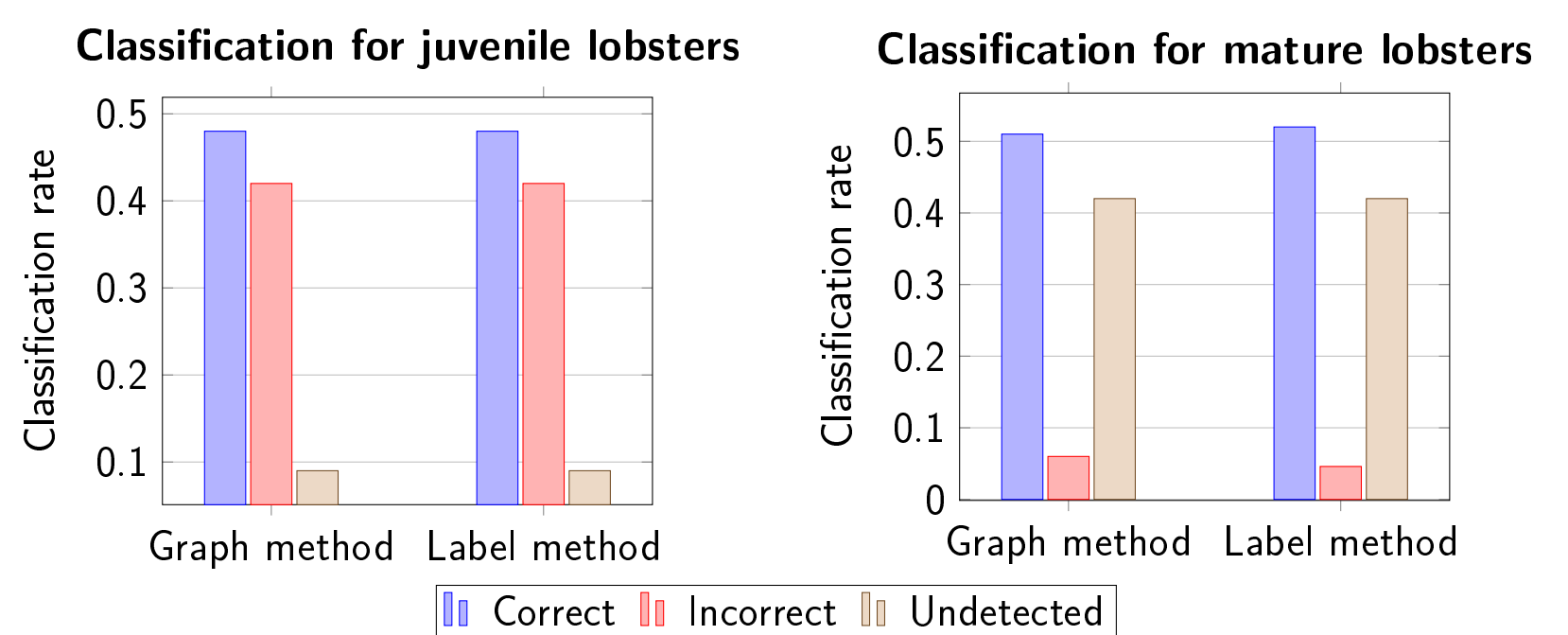
Classification results

Figure 8: Detailed classification results on the specific lobster categories