Estimating landmarks on 2D images of beetle mandibles

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ABSTRACT

Studying links between phenotype/genotype and agricultural practices is one of the main topics in agronomy research. Phenotypes can be characterized by informations like age, sex of animals/plants and more and more often with the help of image analysis of their morphology. From now, getting good quality of images for numerous individuals is easy but that leads to design automatic procedures to replace manual exploration of such amount of images. Several bottlenecks have been identified to analyze automatically images. One of them is segmentation of selected area and/or shapes, and another well-known one is setting automatically morphometric landmarks. Landmarks are points on the object which can be used to identify or to classify the objects.

It exists a lot of methods to experiment landmarks setting, depending on the image contents. This work has been initiated by using the article of Palaniswamy et al. *"Automatic identification of landmarks in digital images"*[4]. They proposed a method based on calculus of a probabilistic Hough transform coupling to a template matching algorithm. They applied their method to the Drosophilia wings. In our study, we have gotten a set of 291 beetles . For each one 2D images of 5 different parts of their anatomy have been taken: mandibles left and right, head, pronotum and elytra. The first part of the project was to test how the Palaniswamy's method could be used to analyze them. We have implemented all the required algorithms to compute positions of mandibles landmarks and compared the obtained results to landmarks which have been manually set by biologists. We will see that even positions automatically obtained are not fully precised, if we used centroid size to characterize mandibles, the size computed from automatic landmarks is closed to this one computed from the manual ones. Future works will focus on definition of a semi-landmarks procedure which would add some features as the measure of the curve between two landmarks.

Keywords
Landmarks identification, probabilistic Hough transform, morphometry of beetle mandible.

1 INTRODUCTION

Morphology analysis is a way to characterize biological shape variations. In the aim to study potential links between these variations and agricultural ecosystems, a set of 291 beetles has been collected. Informations as sex, place where they were found and agricultural practices in this field were set. To grow richer phenotype data, morphometric operations could be done. To do that, a set of landmarks has been defined. Morphometric landmarks are points that can be defined in all specimens and located precisely [6]. Landmarks are widely used in many biological studying and analysis

of geometric characteristics are currently included into classification procedures.

(a) Right mandible   (b) Left mandible
Figure 1: The mandibles of beetle

In this paper, we focus on a method which addresses automatic identification of landmarks in digital images. Palaniswamy et al. [4] have proposed a method to set landmarks on images of Drosophila wings. We have investigated how this method can be implemented to work on images of beetle mandibles (figure 1). The method contains four stages: a features extraction of

mandible structure (segmentation stage), a recording of the features using pairwise geometric histogram (PGH), an estimation of the landmarks positions using Probabilistic Hough Transform (PHT) and finally a refinement of the estimated landmarks by cross-correlation.

2 METHODS

For each mandible image, a set of 18 landmarks have been manually set by biologists corresponding to morphological points of interest (see figure 2). It will constitute our ground truth.

The automatic procedure to estimate these positions extracts features by analyzing the image histogram firstly. The obtained parameters are then used to approximate edges of the mandible by line segments. These edges are presented to PGH using geometric relationships between them. The shape correspondence is determined by comparing the PGHs of model and scene

Figure 2: Manual landmarks of the right mandible

data. A PHT is then used to identify hypothetical location of model landmarks on scene image. Finally, the hypothetical landmarks are performed by template matching. We now describe in details all these steps.
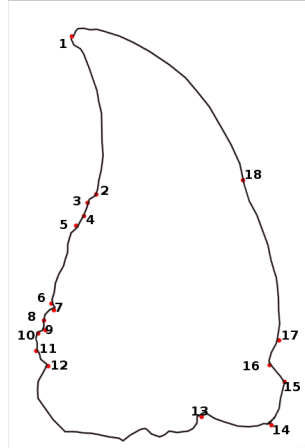
Segmentation step

Usual way to obtain automatically threshold value for segmentation is to take a look to the image's histogram (figure 5). In our case, per image we have only one object, the mandible, into a pretty uniform background, consequently the histogram exhibits only two picks. In this case, the retained threshold value is the average

Figure 3: Image Histogram

value (blue point in fig.3) between two mean values (red and green points in fig.3) of these two pick regions. The first region, begins from the beginning to the median of histogram and the second region is the rest.
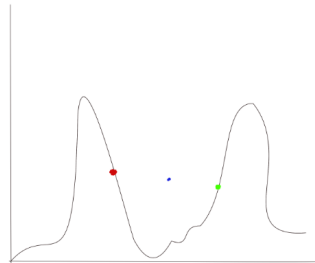
The Canny algorithm [2] is one of the relevant algorithms to detect segmentation edges. The result is a list of points for each retrieved edge. To compute the PGH another kind of geometric form, lines, is needed. Extraction of approximated lines from the list of points can be achieved by using the recursive algorithm [5] as below:

- Create a line connected by two edge endpoints
- For each point in the edge :
  - Calculate perpendicular distance to the line
  - Keep the point at max distance, i.e. max point
  - Divide edge at max point into two parts:
  - Repeat with the two new parts of the edge.

The algorithm stops when the edge cannot be broken more. Concretely, we stop the algorithm when the maximum perpendicular distance of max point is less than 3 pixels, i.e. enough small to create an approximated line.

Comparison between model and scene

To determine the correspondence between the model and the scene image, we compute the PGH[3] using the approximated lines of each image. The steps to construct the PGH as follows:

- Create a PGH matrix,
- Choose a reference line,
- For each other lines in the shape,
  - Calculating the perpendicular distance from two endpoints to the reference line,
  - Computing the angle between the considered line and the reference line,
  - Recording the perpendicular distance and angle into the matrix.
- Repeat step 2 (choose reference line) to all the lines in the shape considered as reference lines,

The algorithm stop when all lines of shape have been considered as reference line.

To be able to compare model and scene, a similarity metric is needed. The Bhattacharya[4] similarity metric is used to compare the distribution (PGH) for the model and the scene data. It computes the degree of match between them as a dot product correlation of the PGHs (equation 1).

$$d_{Bhatt}(H_i H_j) = \sum_{\theta}^{\pi} \sum_{d}^{d_{max}} \sqrt{H_i(\theta,d)H_j(\theta,d)} \quad (1)$$

Where $H_i(\theta,d)$ is an entry at row θ (i.e. angle) and column d (i.e. perpendicular distance) in the PGH of the image i.

Selection of matching points

The Probabilistic Hough Transform (PHT) is then used to determined the presence and location of the model in the scene image, as well as to determine the hypothesis of the model landmarks in the scene image[1]. Applying PHT includes two steps: first, we find the pair of scene lines that similar with a pair of model lines (named training process); second, we estimate the model landmarks in the scene image.

Training process includes the duration to construct the reference table for model image and process to find the similar pair of lines between model and scene image. The steps as follows:

- Create the reference table,
  - · Choose an arbitrary point in the model,
  - · Create a table to record the information,
  - · For each pair of model lines, calculate the perpendicular distance and angle from each line to the point and save into the table.

- Create an accumulator (a two dimension matrix (angle and perpendicular distance)),

- For each pair of scene lines, find the pair of model lines within correspondence in position, orientation and scale. Select the respective value in reference table,

- Increase the value in accumulator at respective position and keep the cell that have the maximum value.

The pair of scene lines having the best value is chosen. The estimated landmarks in the scene obtained by calculating the relatedness between the model's reference point and the model's landmarks are recorded. Besides, we also record the difference angle between model image and the scene image. Fig. 4 shows an example of result, the red points are estimated landmarks on the scene mandible (right one) from a model mandible (left one) landmarks.
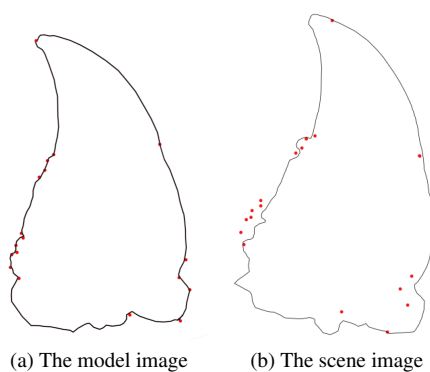

(a) The model image   (b) The scene image

Figure 4: The estimated landmarks by PHT

Template matching

The template matching is process to verify the landmarks estimation provided in the PHG stage. Cross-correlation method is hired for this work. By sliding the template on image by each pixel, cross-correlation will detect the best similarity between model and scene image. The progress of template matching as follows:

- Rotate the scene image (the angle has indicated by PHT),
- Create a bounding box around a model manual landmark (in model image),
- Create a bounding box around a estimated landmark (in scene image),
- Apply cross-correlation between the two bounding boxes.

The template matching finishes when all estimated landmarks are refined. Fig 5 shows a complete result on one scene mandible with the segmentation (red lines), manual landmarks (yellow points) and estimated landmarks (green points).
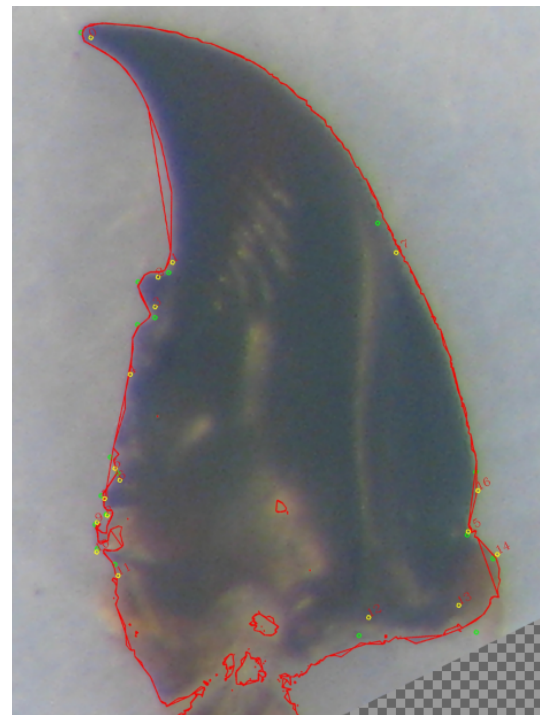

Figure 5: Automated landmarks in scene image after refining

3   EXPERIMENTS AND RESULTS

All the algorithms have been implemented in a framework MaeLab in C++ language[1]. The set of beetles images have been analyzed, right mandibles have been first studied. After verification of the image correctness, it remains 288 usable images. From the 3 images removed, 2 do not contain mandible and in the last one, the mandible is broken in 2 parts. All valid images have been segmented and the 18 landmarks have been set for each. Biologists have chosen to use in a first attempt the centroid size to measure the mandible. This size is obtained by determination of the centroid of the mandible and by sum of all square distances between each landmark and the centroid (see [6] for details).

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[1] MaeLab is a free software, it can be directly obtained by request to the authors.
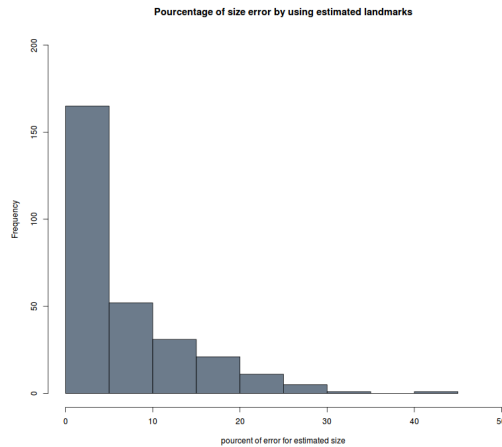
Figure 6: Percentage of error in computing centroid size from estimated landmarks

In that way, we have compared the size computed from manual landmarks and this one from estimated landmarks. The percentage of errors has been evaluated as below:

$$PercentOfErr = \frac{100 \star |(OriginalSize - EstimatedSize)|}{OriginalSize}$$

We can observe in fig. 6 that for more than 150 images, the error is less than 5%. Only 2 mandibles could be considered as wrongly measured with the estimated landmarks and exhibit more than 30% of errors. Finally 90% of images have less than 10% of error in their size computing and for which we can consider estimated landmarks as good enough to replace manual landmarks.

Perspectives and future works

Of course, centroid size is not the only feature we want to consider. It is also possible to compare image per image the exact position of manual and estimated landmarks, for example if we want to work with semi-landmarks by adding of curve measure between 2 landmarks.

In our case, the landmark couples 1 and 2 or 1 and 17 (figure 2) are good candidates to play this role. Figure **??** shows for one mandible the results which have been obtained for each landmark. What one can note is that for some of them, an offset appears. For example

4 CONCLUSION

Morphometric analysis is a powerful tool in biology in order to characterize species. Unfortunately, setting landmarks to run such analysis is time consuming and difficult to replicate through different experiments. In this project we have begun to design set of procedures to segment 288 beetle mandibles and to identify automatically landmarks which have been described by biologists. Each mandible is segmented by computing a approximated lines set. Using the Probabilistic Hough Transform method, these lines are used to align all mandibles scenes with one mandible model. The first results shows that in order to compute the mandible centroid size, the estimated landmarks are accurately enough. A framework

in C++ language has been developed to facilitate the using to biologists. From now, a next stage of this studying is to add features as measure of curves, in that way the landmark positions have to be set more precisely. To solve this problem, algorithms based on design of shape skeleton will be tried.

5 REFERENCES

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