

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 current topics in agronomical research. Phenotypes is the observable physical characteristics of an organism like its age, sex and more, often extracted with the help of image analysis of its morphology. Nowadays, 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 data. 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*"[6]. They proposed a method based on calculus of a probabilistic Hough transform coupled to a template matching algorithm. They applied their method to the *Drosophila* 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 if we use centroid size to characterize mandibles, the size computed from automatic landmarks is close to the one computed from 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 such as sex, place where they were found and agricultural practices in each field were recorded. To perform quantitative analysis of beetle's shape, a set of landmarks has been defined. Morphometric landmarks are points that can be defined in all specimens and located precisely [8]. Landmarks are widely used in many biological

studies and analysis of geometric characteristics are currently included into classification procedures.



(a) Right mandible (b) Left mandible

Figure 1: The mandibles of beetle

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In this paper, we focus on a method which addresses automatic identification of landmarks in digital images. Palaniswamy et al. [6] 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 (see 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 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 background extraction is to take a look to the image's histogram (figure 3). 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 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.

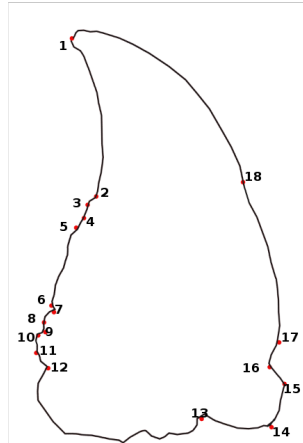


Figure 2: Manual landmarks of the right mandible

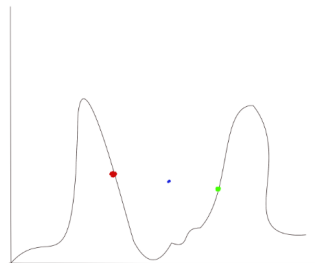


Figure 3: Image Histogram

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 [7], which is a new improved version with the Lowe's method[5] as below:

- Create a line connected by two edge endpoints
- For each point in the edge :
 - Calculate the perpendicular distance from it to the line,
 - Keep the point which have max distance, i.e. max point
- Divide edge at max point into two parts: the first part includes the points from the beginning endpoint to the max point and the last one is the points from the max point to the endpoint.
- Repeat step 1 with 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. small enough to create an approximated line.

Comparison between model and scene

In the previous stage, we converted edges from list of points to list of lines. It is useful to represent the image in a compact and invariant way. To determine the correspondence between the model and the scene image, we compute the similarity metric between two images. This value is indicated by comparing the PGH[3] of the images.

The PGH is constructed from the geometric relationships of the lines (i.e relative angle and perpendicular distance). The relative angle is defined by angle between two lines; and the perpendicular distance uses the distance from two endpoints of the first line to the second line. For a line in an image, we record the geometric relationships between it and other lines in this image when we consider it as reference line. It means that the PGH of an image is combined from all PGHs of all lines in the image.

The PGH is represented as a two dimension matrix with axis for relative angle and perpendicular distance. Each axis is divided into a number of rows (or columns) which are determined by the expected accuracy of process. The steps to construct the PGH for an image are as follows:

- Create a 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) until all lines in the image are considered as reference lines.

To be able to compare model and scene, a similarity metric is needed. The Bhattacharya similarity metric [6] 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).

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

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 determine 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 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 reference table is created when we consider relative position between each pair of lines in model image and an arbitrary point (i.e reference point). It contains the relative information (angle and distance) from each line of pair to the reference point. The used angle is the angle between horizontal axis (begin from reference point) and perpendicular line from the reference point to the line. The used distance is the perpendicular distance from the reference point to the line. The steps to construct the reference table as follows:

- Create the table to record relative information (3 columns¹),
- Choose the reference point in model,
- For each pair of model lines, calculate the distance and angle from each line to the point and save into the table.

¹ The first column contains pair of lines, two last columns contain the relation position of each line (in pair of lines) with reference point

After obtaining the reference table of the model image, we consider the presence of the model in the scene image by finding the similar pair of lines between them. Then a probabilistic statistical is applied to finish this work. With the “vote” for each similar pair between model and scene, we will obtain the pair of lines which have the largest “vote” value, and there lies the pair of scene line similar with model’s pair. The steps to find the similar pair of lines between model and scene image are as follows:

- 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 (relative information) 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 presence of the reference point (of model) in the scene[1] image is indicate by the respective information from the reference table. 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.

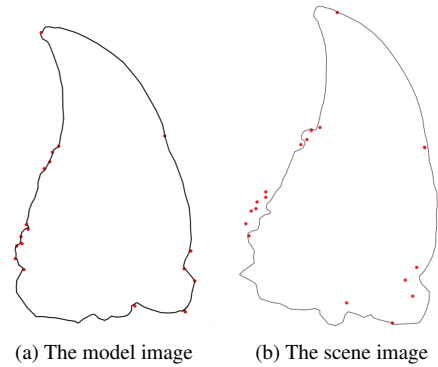


Figure 4: The estimated landmarks by PHT

Template matching

The template matching is a process to verify the landmarks estimation provided in the PHG stage. Cross-correlation method[4] 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. To save time during work, we should rotate the scene image to match with the model image (using difference angle extracted from PGH stage) and we just consider in a square around the landmarks (instead

of over the whole image) when applying the cross-correlation. The process of template matching is 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) (the size of this box should larger than the size of box in model 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).

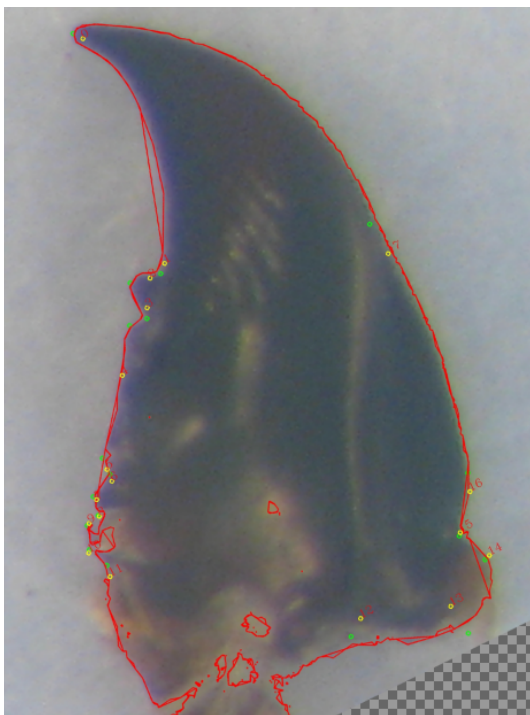


Figure 5: Automated landmarks in scene image after refining

3 EXPERIMENTS AND RESULTS

All the algorithms have been implemented in a framework called MaeLab (coded in C++)². 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

² MaeLab is a free software, it can be directly obtained by request to the authors.

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 [8] for details).

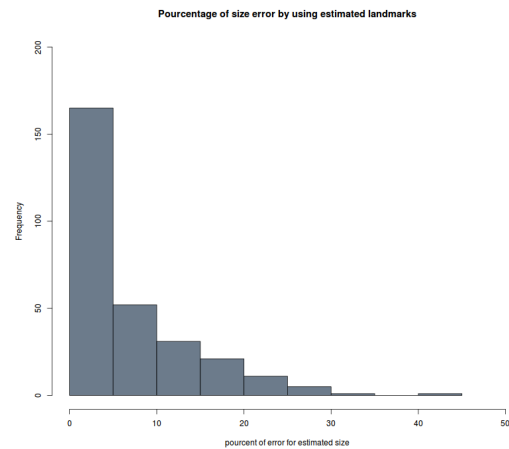


Figure 6: Percentage of error in computing centroid size from estimated landmarks

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 5 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.

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 accurate enough. A framework in C++ language has been developed to facilitate use by 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.

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