

Automatic morphology: Application on biological images

LE Van Linh	BEURTON-AIMAR Marie	KRAHENBUHL Adrien	PARISEY Nicolas
LaBRI-CNRS 5800 ITDLU, Dalat Univ-V linhlv@dlu.edu.vn/ van-linh.le@labri.fr	LaBRI-CNRS 5800 Bordeaux University 33400 Talence-F beurton@labri.fr	LaBRI-CNRS 5800 Bordeaux University 33400 Talence-F adrien.krahenbuhl@labri.fr	IGEPP INRA 1349 35653 Le Rheu-F nparisey@rennes.inra.fr

ABSTRACT

Phenotype of species are characterized by several informations like, age, sex, morphological measures and environment parameters. Biologists are familiar to manually getting morphological measures. In the case of analysis at the macro level (tissues, small parts of animal ...) that can be done directly by measuring the element geometry: length, width, diameter, angles Another way is to take pictures of these elements and to run image processing algorithms. From a collection of beetle pictures, we have initiated this work to test the feasibility of automatically positionning landmarks on biological images. The set of images contains 293 beetles and for all an image of the left and right mandibles. For each mandible, a set of 16 and 18 landmarks (resp. left and right) have been set manually. In a previous work[2] based on Palanaswami article [4] we have shown that if we consider the centroid measure of the mandible as the parameter to obtain, the probabilistic Hough Transform can provide very interesting results. But in the case of the main goal is to fix landmarks to get property about specific area (defined by biologists) the result is not as precised as we have expected. In this next turn, we have kept the same method to segment and to register scene images with model but we have change the way to set the model landmarks on the scene. This new procedure uses a SIFT algorithm as the last operation of our process. We will compare all the obtained results in order to define the new workflow to label the mandible images.

Keywords

Automatic morphology, landmarks identification, image registration.

1 INTRODUCTION

In biology, morphology analysis is widely used to keep the changing information of the organism or detecting the difference information between the organisms. From the result of morphology analysis, we can conclude the evolution of an organism family, or we may classify the organisms. Especially in agriculture, morphology is one of best ways to learn about the variations of the insect on crops. The morphology methods may be divided into the groups by the features which are used by the methods such as shape, structure, color, pattern or size of the object. In the aim to study the potential links between these variations and agricultural ecosystems, a set of 291 beetles has been collected with all the information about the sex, place where they are found and agricultural practices in each field were recorded. For each beetle, the morphometric

landmarks has been defined on each part (each insect includes five parts: head, pronotum, body, left and right mandible) of the insect by the biologists. In this context, we try to indicate the landmarks on two parts of beetle (left and right mandible (see figure 1)). Morphometric landmarks are points that can be defined in all specimens and located precisely. Landmarks are widely used in many biological studies and they are currently included into the classification procedures.



(a) Left mandible (b) Right mandible

Figure 1: The mandibles of beetle

Permission to make digital or hard copies of all or part of this work for personal or classroom use is granted without fee provided that copies are not made or distributed for profit or commercial advantage and that copies bear this notice and the full citation on the first page. To copy otherwise, or republish, to post on servers or to redistribute to lists, requires prior specific permission and/or a fee.

In this paper, we focus on a method that can automatic identification of landmarks on 2D images of beetle, specify the mandibles of beetle. Through whole the article, we use two images to automatic extraction the landmarks: model image and scene image. The method

mainly includes three stages: firstly, we extract the features of the object in the image; secondly, principal component analysis iteration is used to register two images, the translation and rotation between two images are also determined; finally, a refinement of the estimated landmarks is done by SIFT method.

In section 2, the steps of our methods will be discussed. All experiments and evaluation are described in section 3. Finally, we have some conclusion in section 4.

2 METHOD

Given a model image with its manual landmarks and a scene image, we estimate the location of the scene's landmarks based on the model and its manual landmarks. The landmarks of the model are the points in the image that have been set by biologists corresponding to the morphological points of interest (18 landmarks for each right mandible and 16 landmarks for each left mandible). An overview of the proposed method is shown in figure 2.

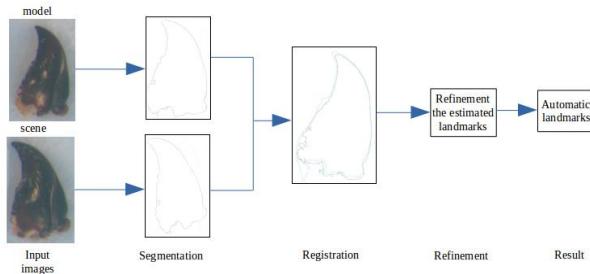


Figure 2: Overview of the proposed method

In this section, we will describe three steps in our method: segmentation, registration and refinement the estimated landmarks. During the method, we assume that the input images are regarded as the same size and same part; it means that do not have the confusion between the parts of the beetle and not yet to mention about the scale between the images.

2.1 Image segmentation

In the methods of image processing, feature extraction is always an important stage. It has a strong decide to the result of the method. During feature extraction, depending on the nature of the method, some techniques are applied before (pre-processing) or after (post-process) the main process extracting the features. In our approach, the original Canny algorithm[1] is idea for detect the curves on the image. The ratio between lower threshold and upper threshold which are used in Canny algorithm is 1:3 (lower threshold approximated to 1 times *threshold value* and upper threshold set to 3 times threshold value). This ratio is evaluated by the experiments. The *threshold value* has been determined by

analyzing the image histogram (see [2] for detail). During applying the Canny algorithm to detect the curves of object, the gradient direction of each pixel which belongs to the curves is kept for the next steps of the method.

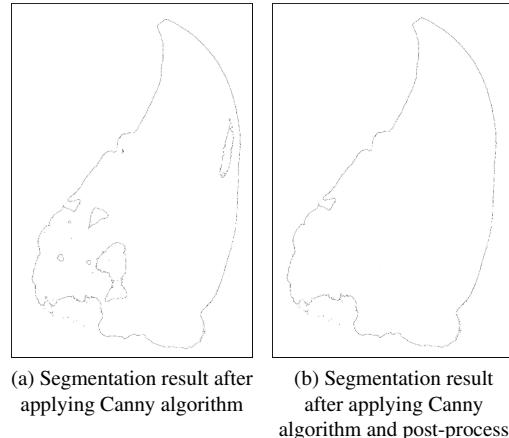


Figure 3: The segmentation results of the image

In this study, the aim of segmentation stage is determined the outer border of the object which can be used to reconstruct the shape of the object as well as provide the best data for next step. The curves from Canny algorithm will be post-processed to remove the unnecessary curves i.e hole inside the border (see figure 3).

2.2 Image registration

Our study is working on the 2D image, and the transformation between two images are inevitable. At this step, we will try to align the segmentations of two images before estimating the landmarks. Besides, the translation and rotation between the images are determined by Principal Component Analysis Iteration (PCAI). PCAI is the method that is improved from PCA method[5]. The work flows of PCAI are illustrated in figure 4

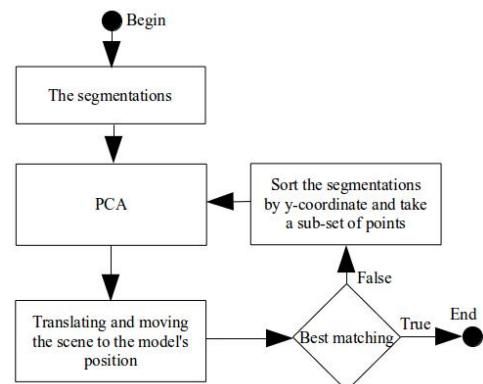


Figure 4: The flows in PCAI

PCAI received the result from segmentation step as

the input. Firstly, the centroid point and principal axis of each image are defined: the centroid point is the point which has the coordinate by getting the mean coordinate of all boundary points; the principal axis is a connected line from the centroid point to a point in the list of curve points. The second endpoint on curve points are determined as described: For each point in the curve, we assume that it is the second endpoint of the principal axis. Then, the mean of the perpendicular distance from the remaining points to the axis is calculated. This work is finished for all points on the curve, and the principal axis is the line that has the minimum mean perpendicular distance to other points. The translation is indicated by the difference coordinate between the centroid points. The rotation angle is the angle between the principal axes. As well as, the rotation direction is determined by checking on each direction. Then, the scene is moved to matching with the position of the model. However, in some case, the translation and rotation between two images are wrong indicated because the result of the segmentation may be not perfect. To make sure that we have obtained the best match between the images. We extract a sub-set of segmentation points to re-calculate the PCA. Before extracting, the points have been sorted by y-coordinate to suppress the unnecessary points. The iteration is continual until we get the best register of the segmentation.



Figure 5: A registration result between two images.

Figure 5 shows an example of PCAI. In this figure, the aquamarine curve and blue curve are presented for the segmentation of the model and the scene image, respectively.

At the end of PCAI, a hypothesis is made to judge the scale between the images. For each image, the bounding boxes are indicated by the coordinates of the points on the curve. The scale of x and y-direction are determined by the ratio between the corresponding

sides of the bounding boxes. Then, the scene curve is scaled to fit the model curve.

As the result of PCAI, we have fitted between the model and the scene. So, by using the landmarks of the model image, we can also estimate the location of the scene image. Hence, before estimating their location, the translation and rotation are applied on scene image to match the pose between the scene and the model.

2.3 Refinement the estimated landmarks

The registration step provides to us the best presence between the model and the scene. The automatic landmarks can be estimated for the scene by the manual landmarks of the model. However, the estimated landmarks can be located at the incorrect location. So, we need a method to verify each position of the estimated landmarks. For this reason, in the last step of the method, we apply a step in the SIFT[3] method to verify the location of automatic landmarks. Firstly, the regions around each manual and corresponding automatic landmark are created. Then, the orientation and gradient magnitude of each pixel in the region are calculated and presented into a descriptor. At the end, the comparing between the descriptors is done by using L_2 distance which is given by the equation (1).

$$L(x, y) = \sum_{x_i, y_i} \sqrt{(x_i - y_i)^2} \quad (1)$$

Where x_i, y_i are the corresponding location in the descriptors.

The figure 6 is the illustration of this process. For each manual landmark on the model and corresponding estimated landmark on the scene, the small patches I, T are created with the size s_1, s_2 , respectively ($s_1 < s_2$). Next, for each pixel in the patch T , a sub-patch T' is extracted with the same size of the patch I . Then, their descriptor and measure distance are determined(between I and T'). This process is finished when all the pixels on the patch T are considered.

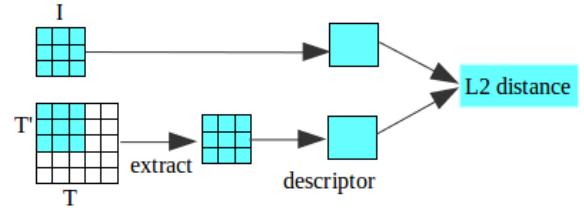


Figure 6: Illustrate the steps of descriptors comparing.

During the descriptor creation (I and T'), the orientation and gradient magnitude are calculated for each their pixel by the equation:

$$\begin{aligned} m(x, y) &= \sqrt{(L(x+1, y) - L(x-1, y))^2 + (L(x, y+1) - L(x, y-1))^2} \\ \theta(x, y) &= \tan^{-1}((L(x, y+1) - L(x, y-1)) / (L(x+1, y) - L(x-1, y))) \end{aligned} \quad (2)$$

Where:

- $m(x,y)$ is the gradient magnitude of the pixel at position (x,y)
- $\theta(x,y)$ is the orientation of the pixel at position (x,y)
- $L(x,y)$ is the value at position (x,y) in the image

Then, the descriptor is created for the patch. This is a histogram with eight direction for orientation, with the length of each bin is sum of the gradient magnitude of the pixels that corresponding with the orientation. The descriptor is formed from a vector containing the value of all the bins in the histogram. Finally, the vector feature is modified to reduce the effects of illumination change by normalization.

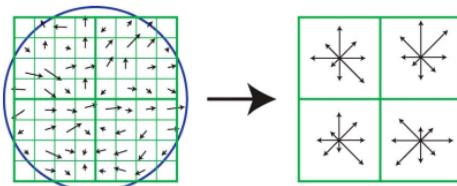


Figure 7: A landmarks descriptor is created by computing the orientation and gradient magnitude

In the example at figure 7, a patch with the size 16×16 is created around the landmark. For each pixel in the region, the orientation and gradient magnitude are calculated (the orientation and length of the arrows). Then, the patch is divided into 4 sub-blocks 4×4 . The descriptor of each sub-block is determined by using 8-orientation histogram and the length of each arrow corresponding to the sum of the gradient magnitudes near that direction within the region.

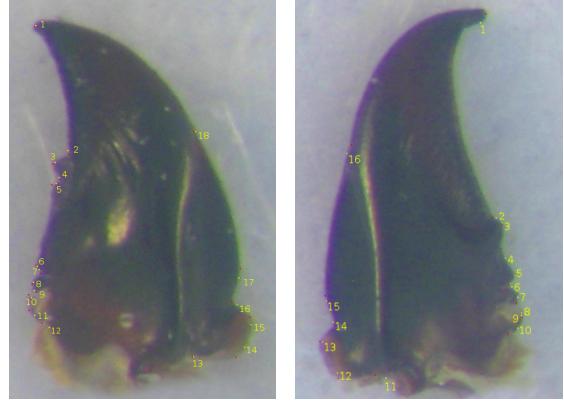
As we mentioned before, the last location of estimated landmarks is the pixel in template T that has the smallest measure distance value (by L_2 distance). Finally, the automatic landmarks are inverted to match with the real location in the scene image (by inverting the transformation and rotation).

Figure 8 shows a complete result on one scene mandible with the manual landmarks (red points) and estimated landmarks (yellow points).

3 EXPERIMENTS AND RESULT

All the steps in our method are implemented in MAE-Lab¹. Two sets of beetle have been analyzed, right and left mandible. After verifying the quality of the image, it remains 290 usable images for right mandible and

¹ MAELab is a free software in C++. It can be directly obtained by request the authors.



(a) Result on right mandible (b) Result on left mandible
Figure 8: The automatic landmarks on mandibles

286 images for left mandible. The removed images include the images that do not contain the mandible and the mandible is broken.

In all valid images, a set of 18 manual landmarks of right mandible (16 landmarks for left mandible) are indicated by biologists. Along with choosing the centroid size to measure the mandible. This size is obtained by sum of all square distance from each landmarks to the centroid point (see [6]).

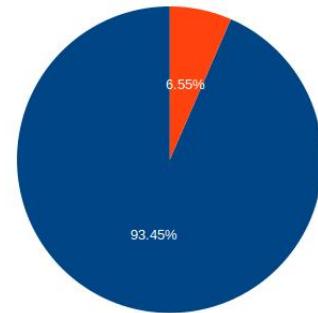


Figure 9: The percentage of correct proportions on right mandibles

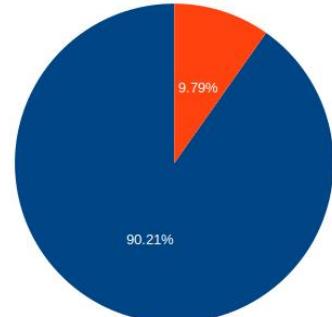


Figure 10: The percentage of correct proportions on left mandibles

Firstly, our evaluation is done on comparing the

centroid size of the estimated landmarks and manual landmarks. The experiment is done by choosing an arbitrary image in the dataset as the model. The automatic landmarks are estimated on remaining images with the method that we have described. Then, the centroid size of each image is calculated and evaluated. We can see in figure 9 and figure 10 for all images, the correct proportions of centroid size which based on the estimated landmarks are 93,45% for the right mandible and 90,21% for the left mandible. And the results in figure 9 and 10 were a vindication of the propriety of the method.

Besides, using the centroid size to evaluate the method. We are also interested in the position of the estimated landmarks. In this experiment way, we calculate the distance between each manual landmark and corresponding automatic landmark. Through, we want to examine replacing the manual landmarks by corresponding automatic landmarks.

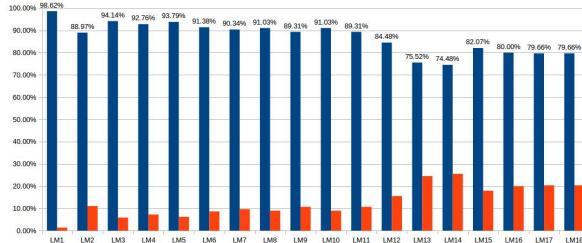


Figure 11: The correct proportions on each landmark of right mandibles

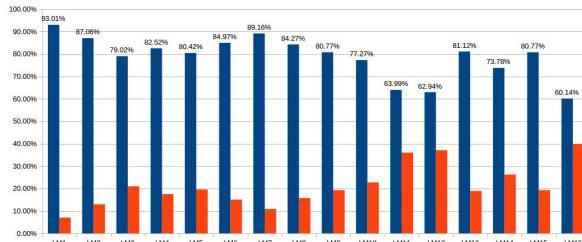


Figure 12: The correct proportions on each landmark of left mandibles

Figure 11 and 12 show the correct proportion on each landmark of mandible. The blue column is presented for the success rate. The orange column is expressed as the incorrect rate. With 18 landmarks of right mandible, the position of the first automatic landmarks is reasonably accurate with 98,62%, the lowest proportion is 74,48% for fourteenth landmark. The remaining landmarks are also indicated with a high proportion (with the accuracy proportion greater than 75%). For left mandible, the highest and lowest success rate are 93,01% for the first landmark and 60,14% for the sixteenth landmark. The statistic is

done on each automatic landmarks of all the images.

In both of experiments, the success rate on right mandible is always greater than left mandible. So, when we reconsider the datasets, the images in left mandible are having more type of size than on the right mandible (scale problem). This explains why the success rate on right mandible is always higher than left mandible.

From two experiment ways, we can see that the method is success in indicating all landmarks for each image; and the location of the landmarks is considered near with the manual landmarks in some aspect. In a different side, when comparing with our previous study (see in [2]). This method has more exactly about the position of automatic landmarks as well as the advantages for the implementation process. The memory to detecting the landmarks, along with the times to execute the process are decreased dramatically.

4 CONCLUSION

Morphometric analysis is a powerful tool in biology in classification the species. Automatic identification the characteristics biology of the organism is a difficult problem. In the content of this paper, we have begun to design a method to segment the beetle mandibles and to indicate automatically landmarks which have been determined by biologists. Each mandible is segmented by applying the Canny algorithm. Using PCAI to align the images and estimate the landmarks. Finally, a descriptor distance will be applied to refine the location of the estimated landmarks. The first version of this method has been implemented. From now, the next stage of our method is to add the features to have the position of landmarks more precisely, i.e diagnose on the scale of the image.

5 REFERENCES

- [1] John Canny. A computational approach to edge detection. *Pattern Analysis and Machine Intelligence, IEEE Transactions on*, (6):679–698, 1986.
- [2] L Lê Vănh, M Beurton-Aimar, JP Salmon, A Marie, and N Parisey. Estimating landmarks on 2d images of beetle mandibles. *WSCG*, 2016.
- [3] David G Lowe. Distinctive image features from scale-invariant keypoints. *International journal of computer vision*, 60(2):91–110, 2004.
- [4] Sasirekha Palaniswamy, Neil A Thacker, and Christian Peter Klingenberg. Automatic identification of landmarks in digital images. *IET Computer Vision*, 4(4):247–260, 2010.
- [5] Jonathon Shlens. A tutorial on principal component analysis. *arXiv preprint arXiv:1404.1100*, 2014.

- [6] M. Webster and H.D. Sheets. *Quantitative Methods in PaleoBiology*, chapter A Practical Introduction to Landmark-based Geometric Morphometrics, pages 163–188. J.Alroy and G. Hunt, 2010.