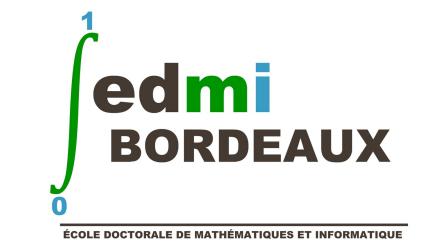


## SIFT descriptor to set landmarks on biological images

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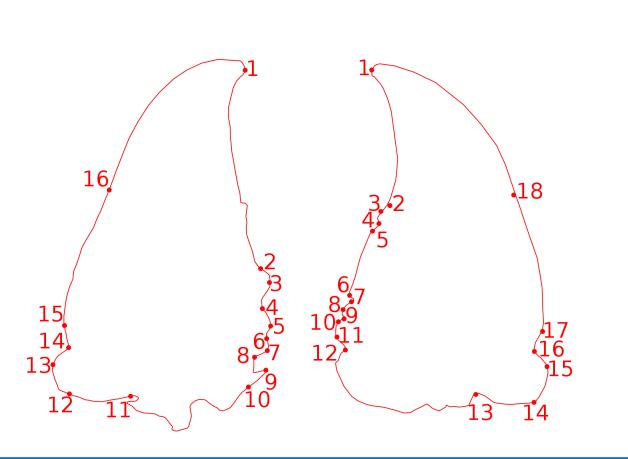


#### Context

Morphometry analysis is a way to distinguish the characteristics of organisms, i.e shape, size, form,.... It is used to appreciate the covariances between the ecological factors and the organisms. Landmark-based morphometry is known as one of the approaches to analyze the characteristics of organisms. Finding enough landmarks can give to biologists a comprehensive description of the organism. This work focuses on the automatic identification of landmarks on 2D biological images.

#### Landmarks

- ▶ Morphometric landmarks are points of interest in the biological object. They usually stay along the outline of the image.
- ▶ Landmarks characterize specificities through the shape most often linked to biological information,
- ► They are usually **defined manually** by biologists,
- ▶ Images at the right side show manual landmarks in **beetle mandibles** belonging to our sample: 16 and 18 manual landmarks have been defined for each left mandible and right mandible, respectively.



How to locate the landmarks automatically?

#### Mandibles and manual landmarks

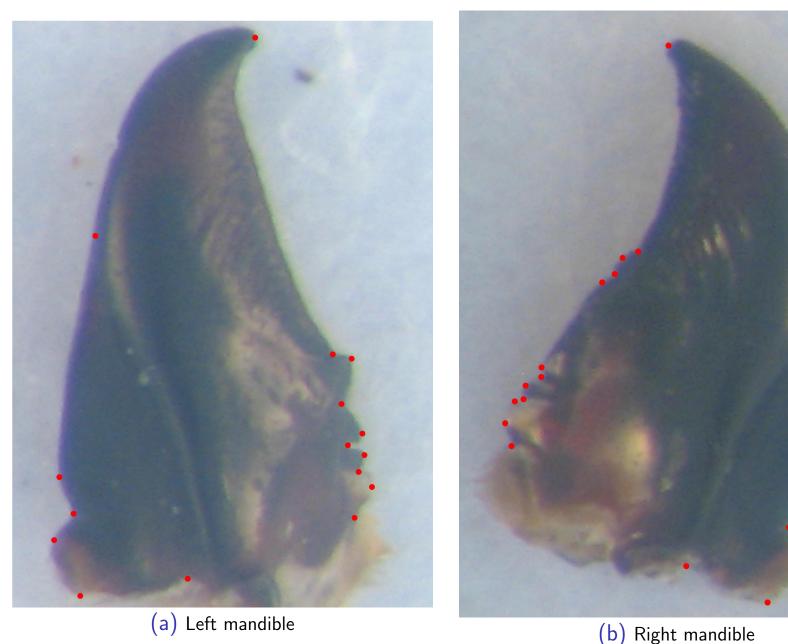


Figure: Example of beetle mandibles from the studied data set with manual landmarks.

#### ► Input:

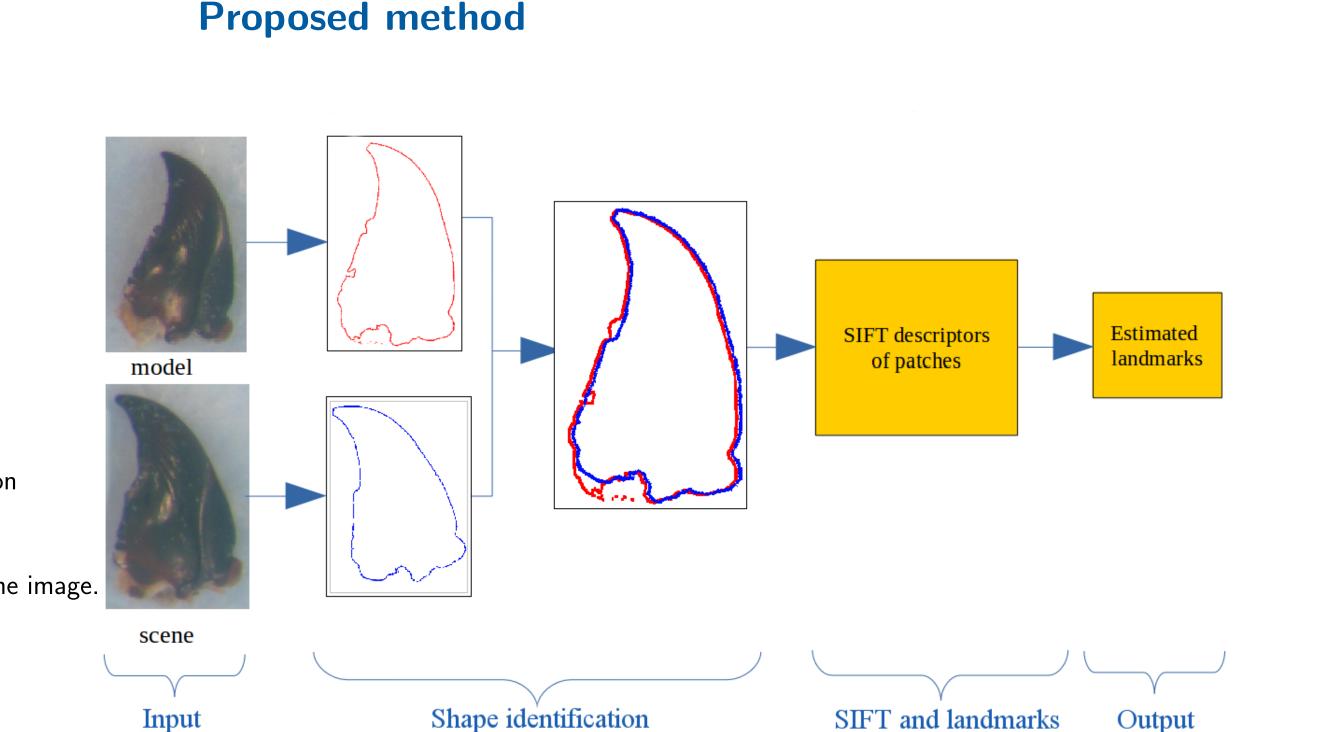
- ► A model image
- ► The manual landmarks of model image
- ► A scene image

#### ► Output:

► Landmarks of scene image

#### ► Steps:

- ► Shape identification: segmentation and registration
- ▶ SIFT and landmarks: Extract the patches, calculate the SIFT descriptors and
- estimate the coordinates of landmarks on the scene image.



#### Segmentation

- . Converting the image to binary one by applying a threshold determined by histogram analysis [1],
- 2. Contours points are extracted by Canny algorithm [2]. The thresholds ratio in Canny:  $T_{lower} = (1/3) \times T^{upper}$ , in which  $T^{lower}$  equals to the threshold value in step 1.

#### Registration

Model and scene images are segmented to extract the contours points. The contours points are registered by applying Principal Component Analysis [3] Iteration (PCAI).

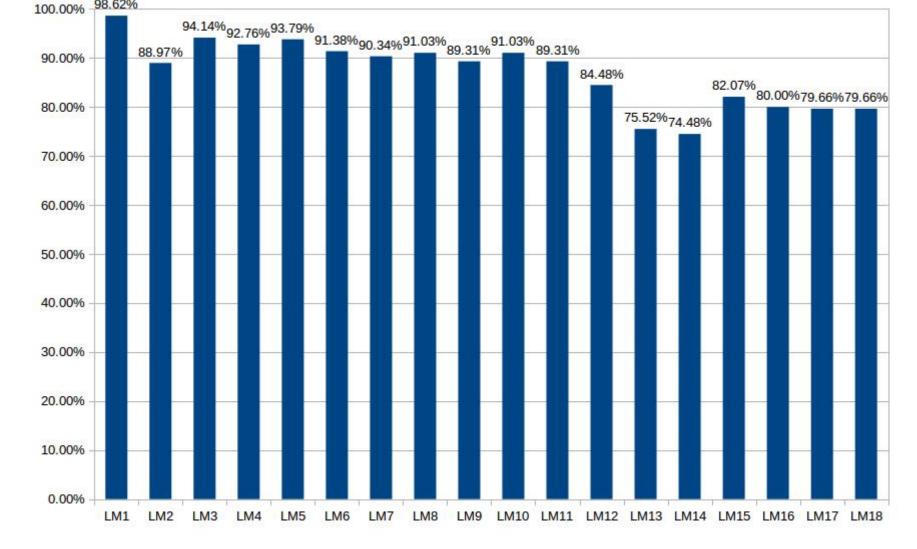
- 1. Compute the centroid point and principal axis of each list of contour points,
- 2. Compute the **translation** and **rotation** values between two lists of contour points,
- 3. Register the two lists of contour points,
- 4. Sort the contour points of scene image followed y-direction,
- 5. Select a subset of contour points of scene image and repeat step 1,
- 6. PCAI stop automatically when the **angle difference** between two lists of contour points is less than 1.5 **degree**.

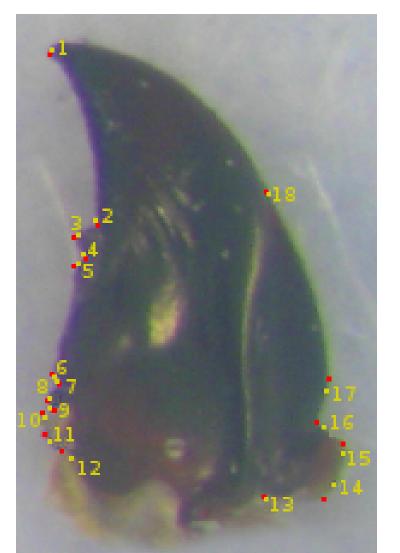
# **SIFT** and landmarks L2 distance $\mathbf{P}'$ extract descriptor P

- 1. A patch  $P_s$  is initialized at each manual landmark of model image (size of  $9 \times 9$ ),
- 2. Calculating the SIFT[4] descriptor for  $P_s$ ,
- 3. At the same position in the scene image, a patch  $P_t$  is created (size of  $36 \times 36$ ),
- 4. For each pixel in  $P_t$ , a patch  $P'_t$  is extracted with the same size than  $P_s$ ,
- 5. Calculating the SIFT descriptor for all  $P'_t$ ,
- 6. Computing the distance between the descriptor of  $P_s$  and each  $P'_t$ ,
- 7. At the end, the pixel that has the **minimum distance** with  $P_s$  is kept.

### Results on right mandibles

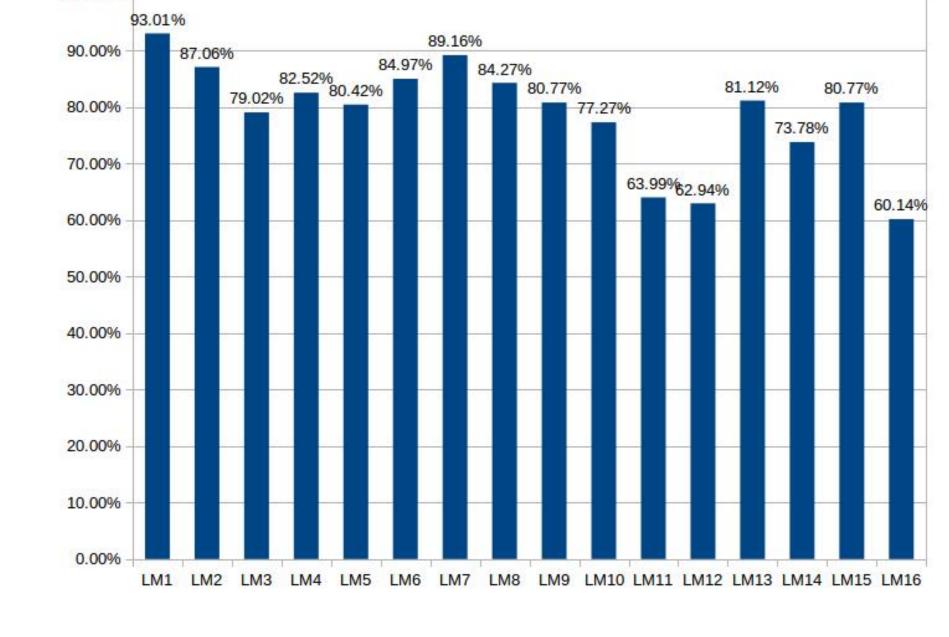
- ► Highest accuracy: 1<sup>st</sup> landmark with 98.62%
- ▶ Lowest accuracy:  $13^{th}$ ,  $14^{th}$  landmark with app. 75%

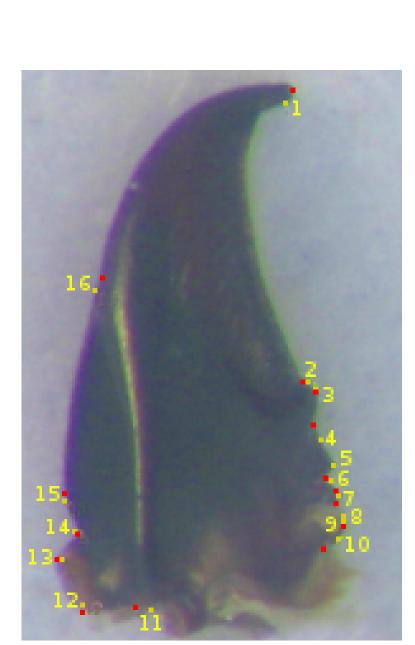




#### Results on left mandibles

- ► Highest accuracy: 1<sup>st</sup> landmark with 93.01%
- ▶ Lowest accuracy:  $11^{th}$ ,  $12^{th}$  and  $16^{th}$  landmark from 60% to app. 63%





#### Conclusion

- ▶ A solution based on SIFT descriptor for landmark estimation is presented,
- ▶ The results show that method **succeed in locating** all landmarks in request images,
- ▶ The accuracy of method is sufficient to be proposed to biologists as a replacement of manual positioning, and to characterize the shape.

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