

# SIFT descriptor to set landmarks in biological images

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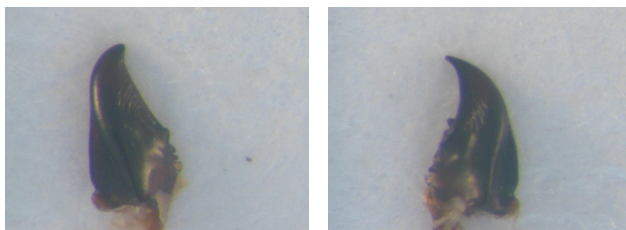
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**Résumé** – Les auteurs publiant au GRETSI et utilisant le traitement de texte  $\text{\LaTeX 2}_{\epsilon}$  trouveront ci-dessous quelques indications destinées à leur faciliter la tâche. Le fichier `gretsien.tex` qui contient le présent document respecte les contraintes fixées ; recopiez le, par exemple sous le nom `monarticle.tex`, et placez votre texte aux endroits appropriés.

**Abstract** – Image analysis is a large field of computer vision and it has applied in practice with many application in the different majors such as medicine, machine vision, biology, ... In the past of biology techniques, microscopic techniques were applied to study the structure details, but the current research requires more accuracy in the area, perimeter, localization of the object in the image by using the suitable features. In this content of this paper, we will focus on the problem of setting the landmarks on biological images which are used in many biological studies. The landmarks are indicated by applying a combination of SIFT and PCA. The efficiency of the method is evaluated on two set of images: left and right mandibles of beetle. The complete work is implemented in MAELab and freely available as a library.

## 1 Introduction

Morphometry analysis is an important field of image analysis in biology. It is used to characterize the shape variations of the organism. From obtained information, the biologists can evaluate the evolution of the organism or detect the difference between the organisms. Depending on the requirements of the application, the output of analysis process can be the shape, color, pattern,... or the landmarks (or dominant points). The landmarks are the points along an image outline that store a lot of important information about the shape of the image. They are used in many biological studies and included into the classification tasks.



(a) Left mandible

(b) Right mandible

FIGURE 1 – The pictures of beetle mandibles took by biologists.

In recently, we have a lot of techniques to indicate the dominant points such as SIFT, SUFT, ... [?] but the applying them into morphometry analysis is limit in scope. In this paper, we focus on the method to automatically determine the landmarks in 2D biological images (see Fig. 1), specify beetle images. This method is shown as a difference ways to apply the SIFT descriptor for keypoint detection along with the segmentaion and registration techniques.

## 2 Method

For each beetle, the morphometric landmarks have been manually identified on mandibles images by the biologists : 16 and 18 landmarks for each left and right mandible, respectively. The consideration problem is how to detect automatically the landmarks on the mandible image to replace the manual ones. In the whole of the process, a source and a target image are used. The landmarks will be estimated on the target image by using the manual landmarks of the source image. Note, the source image is chosen randomly from the set of images.

In this section, firstly, we have a summary about the general utilization of SIFT. Then, we will discuss detail about our method with a difference way of SIFT to estimate the landmarks.

## 2.1 SIFT method

SIFT method proposed by Lowe[] to extract distinctive invariant feature from images that can use to match between different views of source and target images such as rotation, scale, noise, 3D viewpoint. SIFT method includes four stages : (1) scale-space extrema detection, (2) keypoint localization, (3) orientation assignment, and (4) keypoint descriptor.

In the first stage, a difference of Gaussian (DoG) (Eq. 1) function is applied to identify the interest points on all scale and orientation of image. The keypoints are taken as the maximal and minimal of the result of DoG function at mutiple scale.

$$D(x, y, \sigma) = (G(x, y, k_i \sigma) - G(x, y, k_j \sigma)) * I(x, y) \quad (1)$$

Where :

- $D(x, y, \sigma)$  is the DoG image
- $I(x, y)$  is the original image
- $G(x, y, k\sigma)$  is the Gaussian blur at scale  $k\sigma$ .

The scale-space extrema detection produces too many keypoint candidates, some of them are unstable. In the second stage of SIFT, the key point candidates are localized and refined by suppress the key points which have the low contrast or are poorly localized along an edge.

Then, the orientation and gradient magnitude of key points are calculated by applying the following equations (Eq. 2) :

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

Where :

- $v_x = I(x + 1, y) - I(x - 1, y)$
- $v_y = I(x, y + 1) - I(x, y - 1)$
- $I(x, y)$  is the gray value at position  $(x, y)$  in the image,
- $m(x, y)$  is the gradient magnitude of the pixel at position  $(x, y)$ ,
- $\theta(x, y)$  is the orientation of the pixel at position  $(x, y)$ .

At the end, the descriptor is computed for each key point based on the orientation and gradient magnitude to ensure the invariance to image location, scale, and rotation. First, an orientation histogram with 8 bins is created on  $4 \times 4$  pixel neighborhoods. This histogram is computed from the magnitude and orientation values of each pixel in the  $4 \times 4$  region. The descriptor around a keypoint is a histogram of a  $16 \times 16$  region around it which is combined from the 4 histograms of the  $4 \times 4$  subregions. Then, all the values of the histogram are presented as a vector. To reduce the effects of illumination changes, the vector is normalized and applied a threshold of 0.2 and the vector is again normalized.

show an

By applying the original SIFT into our problem, we have succeeded indicating the keypoints in the image (see Fig. 2). But we do not have the result when we try to extract correspondence keypoints between the source and target image. The problem is carried from the choosing the best points from the large set of the candidates. This problem is solved in our method by limit the spatial before applied the SIFT along with changing the size of the grid to calculate the SIFT descriptor.

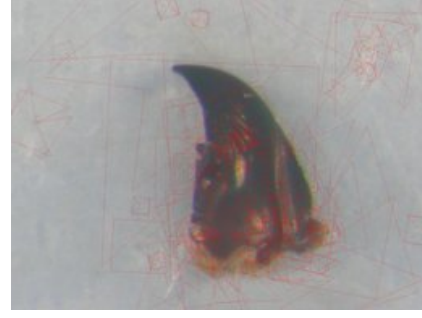


FIGURE 2 – SIFT keypoints in an right mandible

## 2.2 A difference way of SIFT descriptor

### 2.2.1 Image segmentation

The first step in the method is segmentation. It is hired to detect the contours belonging to the shape of the mandible. In our case, the Canny algorithm [?] was chosen to finish this step. To use the Canny algorithm, two thresholds value must be provided (lower threshold ( $T_{lower}$ ) and the upper threshold ( $T_{upper}$ )). As mentioned in [?], indicating the threshold values is a difficult problem. If the threshold values are unsuitable, the contours could be far with ground truth (fewer contours or more noise). Most often working on Canny, the threshold values are chosen by manual or experiment with a ratio of  $T_{lower} = (1/2) \times T_{upper}$ . In order to consider a larger range of values, we prefer set  $T_{lower} = (1/2) \times T_{upper}$  and the threshold value is determined by analyzing the histogram of image [?]. During Canny computing, the direction of the gradient of each pixel belonging to the contours is kept and will be used later. To finish the segmentation step, a simple algorithm is applied to remove the edge inside the main contours. As shown in Fig. 3, the mandible contours is determined by the Canny algorithm.

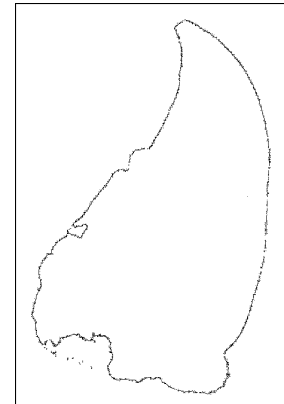


FIGURE 3 – The mandible contours after finishing the contours detection

### 2.2.2 Image registration

The input images have been learned with the same scale. But under the camera, the orientation between from a beetle to another one is the difference. In the next step, we consider the registration between a source and a target image.

We have chosen to use PCA [] to determine the rotation and translation parameter values between two images. In this step, we use the lists of contour points as the input. Firstly, the centroid point and principal axis are detected for each image contours. Then, two images are registered by computing the translation and rotation parameter values. The translation is computed as the distance between the centroid points of the source and the target. The rotation angle is the angle between the principal axes of two images. However in some case, the result of the segmentation step could exist the noise, it could affect to the registration step. To improve the registration, we have built up the PCA by iterating until stabilization (PCAI). The Fig. ?? shows an example of the results obtained from PCAI. The red contours belong to the source, the black ones are the target contours after one iteration, and the blue contours are the finally resulting contours.



FIGURE 4 – The step in iteration of PCA between the source contours (red) and the target contours

### 2.2.3 Landmarks estimation

The last task in this method is estimating the landmarks of the target image from the manual one of the source image. As mentioned before, we will use the SIFT [] without the usually way.

## 3 Experiments and result

## 4 Conclusion and discussion

### 4.1 gretsi class

Your paper should not exceed 4 pages, including tables and figures. It should consist of 2 columns each measuring 88mm

wide, with a gap of 6mm between the columns. We advise you to use the gretsi.cls L<sup>A</sup>T<sub>E</sub>X 2<sub>ε</sub> class file to perform automatic page setting :

```
\documentclass{gretsi}
```

In your file preamble, you have to enter the following informations :

- paper title :  
`\title{Paper title}`
- Christian and first names of each author, with a number linking to its address :  
`\author{\coord{Pierre}{Dupont}{1},  
          \coord{John}{Smith}{2}}`
- authors' addresses :  
`\adresse{\affil{1}{Laboratory \\  
          street, town, country}  
          \affil{2}{University \\  
          street, town, country}`
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`\frenchabstract{R\'esum\'e fran ais}  
  \englishabstract{English written abstract}`
- then, your text, and the bibliography :  
`\begin{document}  
  \maketitle  
  Paper text  
  \begin{thebibliography}{99}  
    The references  
  \end{thebibliography}  
  \end{document}`

## 4.2 Section and subsection

This example file uses `\section` and `\subsection`. For lower level sectioning commands, you obtain :

### 4.2.1 Subsubsection

By means of `\subsubsection`.

**Subsubsubsection** By means of `\paragraph`.

## 5 Tables, figures and mathematics

The title of tables should appear at the top, as in table 1.

TABLE 1 – 2 to the power

$n$	1	2	3	4	5	6	7	8
$2^n$	2	4	8	16	32	64	128	256

1. French written abstract is optional, but highly recommended.

Captions should appear below graphical objects, as in figure 5.

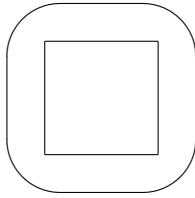


FIGURE 5 – a square in an oval

Including Postscript graphics files is easily performed by means of `graphics`, `graphicx` or `epsfig` packages. To insert `fig.eps` file, with automatic width adjustment, using `graphics` package, you have to enter :

```
\begin{figure} [htb]
\begin{center}
\resizebox{88mm}{!}{
\includegraphics{fig.eps}}
\end{center}
\legende{title}
\end{figure}
```

With `graphicx` package, you have to enter :

```
\begin{figure} [htb]
\begin{center}
\includegraphics[width=88mm]{fig.eps}
\end{center}
\legende{title}
\end{figure}
```

With `epsfig`, you have to enter :

```
\begin{figure} [htb]
\begin{center}
\epsfig{file=fig.eps,width=88mm}
\end{center}
\legende{title}
\end{figure}
```

Mathematical formulas appearance can be improved by means of `amsmath` package from  $\mathcal{A}\mathcal{M}\mathcal{S}\text{-}\mathcal{L}\mathcal{T}\mathcal{E}\mathcal{X}$ . They have to be numbered as formula 3 :

$$F(x) = \int_{-\infty}^x f(u) du \quad (3)$$

## Références

- [1] M. Goossens, F Mittelbach et A. Samarin. *The  $\mathcal{E}\mathcal{T}\mathcal{E}\mathcal{X}$  Companion*. Addison-Wesley, 1994.
- [2] L. Lamport.  *$\mathcal{E}\mathcal{T}\mathcal{E}\mathcal{X}$  User's Guide and Reference Manual*. Addison-Wesley, 1994.