

Towards Automatic Model-Based Identification of Individual Sharp-Tailed Snakes from Natural Body Markings

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Abstract. This paper describes our work towards the development of a new computer vision-based method for the automatic photo-identification of spotted snakes. With respect to related work, our approach minimizes significantly the user intervention, which becomes a critical requirement when querying large databases. Our approach is model-based; its main advantage over existing semi-automatic model-free methods consists in the descriptive power of the model, and thus in the potential of the model to adapt to new images and to track the individual's evolution by quantifying changes in its appearance.

I. INTRODUCTION

OVER the past century, humans have caused unprecedented change to global ecosystems, causing the decline of many animal populations. A primary concern of ecologists and conservation biologists is to monitor population trends of these species, so that appropriate management strategies can be implemented to prevent decline and extinction. Traditionally, these population studies have used various methods to mark animals so that individuals could be recognized when recaptured over time. Common marking methods for small vertebrates include toe-clipping (excising a unique combination of toes) or attaching tags to various parts of the body.

Murray and Fuller [1] have shown that many such marking methods can have adverse effects on growth, movements, and even survival of marked animals. Attention has now focused on using natural body markings for individual identification. Such markings can be used for identifying individual animals for a variety of species [2-5].

Natural body markings that can be observed from photographs typically consist of colour patterns or spots. For example, the black marks under the chin of the endangered Sharptailed Snake (*Contia tenuis*) have been used to recognize individuals in population studies on southern Vancouver Island (Canada). Some individuals, recognized from their spot patterns, have been repeatedly captured for as many as 12 years.

The identification of visual patterns by comparing images of each newly observed animal to a set of images in the archives is both time- and resource-consuming, since it

requires extensive training and experience. Moreover, the task does not scale well and becomes impractical as the number of animals in the studied population increases beyond a certain limit. This creates the need for automating the process by using computer vision-based approaches.

Computer-aided approaches for identifying spotted animals via pattern matching were proposed by Arzoumanian et al [4], and by Tienhoven et al [5]. Both approaches rely heavily on user intervention. In [4], pre-processing via rotation, contrast enhancement, noise reduction and image cropping is applied manually on every image in the database. In [5], the user specifies first three pairs of corresponding spots on the two animals to be compared. These pairs are used for computing an affine transformation between the query and reference images. Next, the user specifies the location of a number of spots on the query image, and the algorithm attempts to match these spots on the reference image.

This paper describes our work towards the development of a new computer vision-based method for the automatic identification of spotted snakes from their pictures. In our approach, the user intervention is minimized and will be eliminated in the near future via new standards for the image acquisition protocol. Our approach describes the black spots underneath the chin of the snake via a geometrical model, which is subsequently used for classification purposes.

The remainder of the paper is structured as follows. Section 2 outlines our approach, while section 3 presents experimental results. Section 4 draws conclusions and outlines future work.

II. PROPOSED APPROACH

Input data for the proposed technique consists of a set of photographs of the ventral side of heads of sharp-tailed snakes. The first step extracts features relevant for individual identification and represents each individual as a feature vector in the feature space. This feature vector corresponds to a geometric model in the image space, which captures characteristics of the spot distribution. The classification step generates individual-representative

models via k-means and uses a minimum-distance classifier. All steps of the proposed approach are detailed below.

A. Database characteristics

This study uses a database of snake photographs acquired during field work. The acquisition process is largely unconstrained (variable type of camera, lighting, background etc.) and hence results in a significant variability in the general appearance of the photographs. We discuss here two effects of non-uniform lighting that significantly interfere with the process of feature extraction. Non-uniform lighting results in a variable shadowing pattern across images corresponding to the same individual. Specular effects are also generated by non-uniform lighting and by the ‘glossy’ nature of the snake’s skin. Both effects interfere with the segmentation of the natural markings (i.e. the dark spots). An example is shown in Figure 1.



Figure 1. Two images of the same snake taken in different spatio-temporal conditions. Shadowing (left) and specular highlights (right) interfere with the segmentation of the spots.

Pictures in the initial database that exhibited severe shadowing and specular effects (more than 50% of the total head area affected) were eliminated. Since these effects are present to variable extents in the retained samples and affect local contrast ratios, the segmentation of the ventral side of the head was performed manually. It is worth mentioning that this segmentation process is the only one requiring user intervention in the proposed approach. Assuming that acquisition protocols will evolve towards obtaining higher-quality images, manual segmentation can be considered as a ‘place-holder’ into a fully automatic individual identification procedure.

B. Feature selection and extraction

The description of individuals for identification purposes is based on the generation of a feature vector to be further used for modeling and classification purposes.

The set of selected features describes the geometrical distribution of the five largest spots located on the ventral side of the snake’s head. This geometrical distribution is one of the main visual cues that field experts currently use for the identification of individual snakes.

The following information is measured for each of the five largest spots:

- Area: $a_s = \frac{A_s}{A_H}$ where a_s is the ratio between A_s (the

area of the spot, in pixels), and A_H (the area of the head, in pixels);

- Relative location with respect to the center of mass of the head C_H , described by:

- o Distance: $d_s = \frac{\|\vec{D}_s\|}{\|\vec{D}_M\|}$ where \vec{D}_M is the distance vector from the center of mass C_S of the spot and C_H ; and \vec{D}_M is the distance vector from C_H to the tip of the nose.
- o Orientation: $\alpha_s = \angle(\vec{D}_s, \vec{D}_M)$ where α is the angle between the distance vectors \vec{D}_s and \vec{D}_M .

Fig. 2a illustrates the feature measurement process on a synthetic snake head, while Fig. 2b shows an example of segmented spots and their relative positioning with respect to the center of mass of the head.

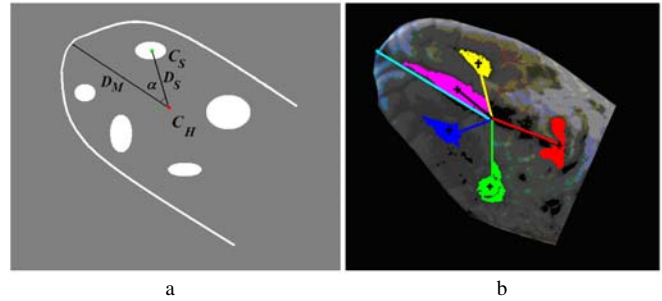


Figure 2. a) feature measurement process; b) geometric distribution of the five largest spots (presegmented) on a real snake head image.

The features describing each spot are used for modelling and classification purposes, as explained in section E.

One may note that the selected features are invariant to scaling, rotation, and translation of the snake’s head and therefore they can be used for the further classification of input images where the head is photographed from different angles and distance from the camera.

The feature extraction process is detailed in the flowchart shown in Fig. 3. The head contour is extracted from the input image via manual segmentation. Next, the head region is binarized using Otsu’s automatic thresholding technique. The five largest connected components are identified from the binary image as corresponding to the five spots of interest respectively. The feature vector captures information about the geometrical distribution of these five spots, as described above.

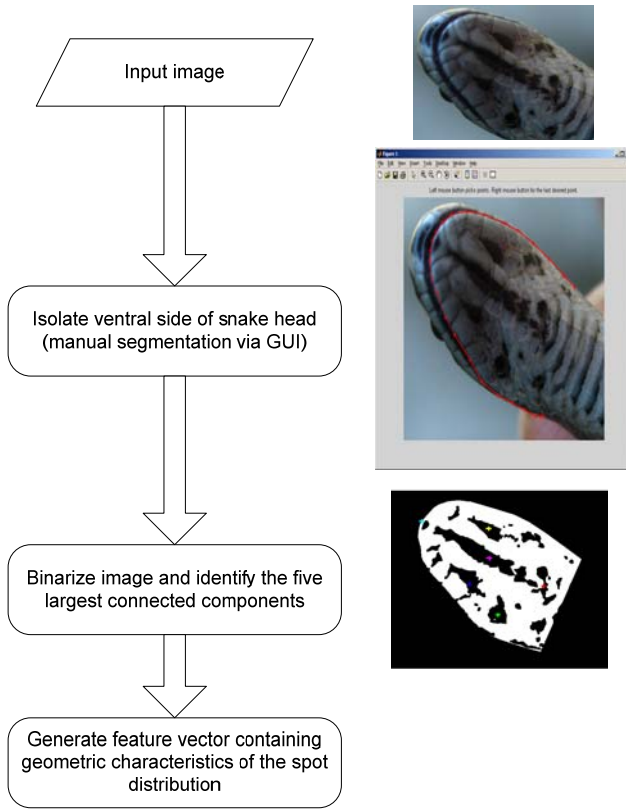


Figure 3. Flowchart of the feature extraction process

C. Modelling and Classification

For each snake in the database, our approach creates a geometric model that captures representative characteristics of the spot distribution across all images in the training set that represent the same individual. Our hypothesis is that, for a given individual, the feature vectors (a_s, d_s, α_s) that represent each spot in the individual-specific training database form clusters in the feature space. An illustration of our hypothesis is given in Fig. 4.

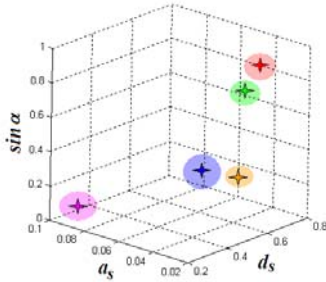


Figure 4. Our hypothesis: feature vectors corresponding to the same spot on the same snake form clusters in the feature space. Clusters corresponding to different spots are represented by different colours. The “centroids” of these clusters, detected via K-means, are chosen as representative points for their corresponding spots.

In the individual-specific model, we aim at representing each cluster/spot by one representative point in the feature space. The K-means algorithm represents a natural choice

for finding these representative points. The output of this algorithm is a feature vector that contains the coordinates of the ‘centroids’ of each cluster/spot. This feature vector represents the geometric model in the feature space, but it can also be used for a direct representation of the model in the image space (see Fig. 5).

The geometric model generated via K-means is used for classifying test images via a naïve Bayes classifier. For each spot on the tested candidate, each feature’s distance to the corresponding ‘centroid’ is normalized by its standard deviation, which is equivalent to a minimum-distance classifier using as distance $d(x_i, \mu_i) = \frac{\|x_i - \mu_i\|}{\sigma_i}$ where x_i is the feature of the spot, $x_i \in (a_{si}, d_{si}, \alpha_{si})$ and μ_i is the corresponding feature in the ‘centroid’ representing the spot. Fig. 5 illustrates the process of modelling and classification described above.

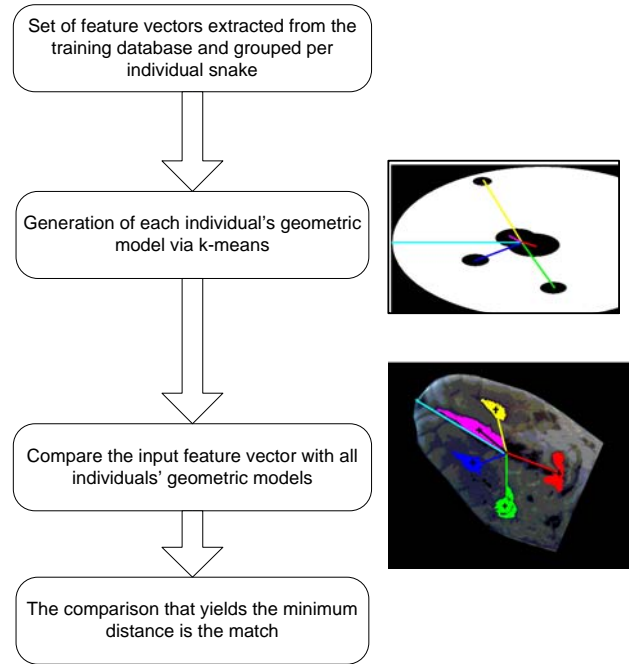


Figure 5. Flowchart of the modelling and classification process

III. EXPERIMENTAL RESULTS

There are five distinct individual snakes in our database. The modelling phase used a training database of four images per snake (twenty images in total). The query (testing) database consisted of ten images.

The model-based classification paradigm was compared to a model-free classifier, namely the k-nearest neighbors’ classifier ($k=5$). For every image to be classified, the model-free classifier receives as input a feature vector that is built as a concatenation of all the spot-specific features, in the decreasing order of the spot area.

We have used two metrics for evaluating the performance

of the two classifiers. The first one, referred to as ‘precise matching’ evaluates the percentage of correct matches across the testing database. The second metric, referred to as ‘close matching’ considers the classifiers’ output as a set of distances/neighbors ranked in decreasing order. Specifically, for the proposed model-based approach, a ‘close match’ is decided when the distance corresponding to the correct match falls within the three minimum distances calculated. For the k-nearest neighbors classifier, the ‘close match’ is decided if at least one neighbor belongs to the same class as the correct match.

The second metric is appropriate for evaluating the performance of the considered classifiers from a practical viewpoint. If a classifier performs well on ‘close matching’, then it restrains the search space to a very limited number of choices to be further evaluated by human experts.

Table 1 summarizes our classification results with respect to the two metrics presented above.

Table 1 Summary of classification results

Classification method	Precise matching	Close matching
Model-based (proposed approach)	50%	80%
5-Nearest neighbors	63.6%	81.8%

One may note that, in terms of precise matching, both classifiers have poor performance. Their performance rises significantly when considered in terms of ‘close matching’. While both classifiers yield comparable performances, the model-based approach has a significantly lower computational complexity, since it is based on a minimum-distance classifier. This characteristic will allow for a good scaling of this approach to large databases of individuals to be identified.

One explanation of the poor performance of the proposed approach in ‘precise matching’ can be found in the unexpected way that feature vectors characterizing the same spot in the training images of the same individual cluster together in the feature space. Specifically, one spot belonging to the same individual across the training database can be represented by more than one cluster in the feature space. This is evidenced by the classification results obtained when running the K-means algorithm for various numbers of clusters. Table 2 summarizes these results.

Table 2 Classification results for K-means algorithm (variable number of clusters)

Number of clusters	Precise matching	Close matching
5	10%	40%
6	50%	70%
7	50%	80%

The sensitivity of the model-based classification method with respect to the number of clusters indicates that more features need to be added in order to create individual-representative models that minimize intra-individual variability while maximizing inter-individual variability. This is one of the future work directions described in the next section.

IV. CONCLUSIONS

The work described in this paper represents a first attempt towards creating a model-based computer vision framework for individual identification from natural body markings. With respect to related work, our approach minimizes significantly the user intervention, which becomes a critical requirement when querying large databases. The main advantage of a model-based identification paradigm approach over model-free methods consists in the descriptive power of the model, and also in the potential of the model to adapt to new images and to track the individual’s evolution by quantifying changes in its appearance. This potential is to be investigated in future work.

This paper reports on a pilot project involving a limited number of images in the training and testing databases. One aspect that is highly likely to lead to immediate improvements in the performance of the proposed approach is the generation of reliable databases via standardization of the image acquisition protocol (i.e. minimization of variability of acquisition conditions, such as non-uniform lighting and shading, minimization of glare etc.).

The current state of our model relies only on simple geometrical information that is invariant to size, rotation, and scaling. Future work will focus on enriching the model by integrating morphological information about the shape of the spots on the snake’s head, as well as on improving the classification process via adaptive learning techniques. Moreover, the model-based identification paradigm will be generalized to other species of spotted animals.

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