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An affine invariant curve matching method for photo-identification of marine mammals

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Abstract

Individual identification of marine mammals is of interest to marine biologists. This paper aims at the recognition of the edges associated with marine mammals whose pictures are taken under affine transformations. The introduced affine curve matching method uses the area of mismatch between a query and a database curve. This area is obtained by optimally aligning the curves based on the minimum affine distance involving their distinguishing points. The method is applied to databases of sea lions, gray whales, and dolphins, and its performance is compared with two other affine curve matching methods. The results show that the introduced curve matching approach outperforms the other approaches and thus further reduces the search time for identifying an individual. The developed method is of general purpose as it can be used for other affine curve matching applications.

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1. Introduction

This paper addresses the problem of individual identification of marine mammals, including dolphins, whales and sea lions. Recognition of individuals within a study population is of interest to marine mammalogists and is a key issue in many behavioral and ecological studies of marine mammals. Tagging of the animals (for example branding with heat or liquid nitrogen) has practical and legal obstacles associated with it and hence an alternative approach is useful. Among several existing identification approaches, photo-identification techniques provide a non-invasive approach. These techniques utilize the unique natural

markings or features, such as notches, scars, patches, blotches, etc., on the animals' bodies.

In this paper, we have introduced an affine invariant curve matching technique for photo-identification of marine mammals when utilizing an appropriate portion of their silhouettes. The motivation for using a curve-matching approach stems from the fact that the edges of dolphin dorsal fins, whale flukes, and sea lion flippers constitute relatively unique identifying information that remain mostly unchanged over time. In other words, these edges or curves can be regarded almost as fingerprints in humans. Typical images of the studied marine mammals and their corresponding edges or curves are shown in Fig. 1. We have previously developed several computer-assisted photo-identification techniques to identify dolphins and whales from the edges of their dorsal fins and flukes [1,2], respectively. Our research effort is directed at reducing the

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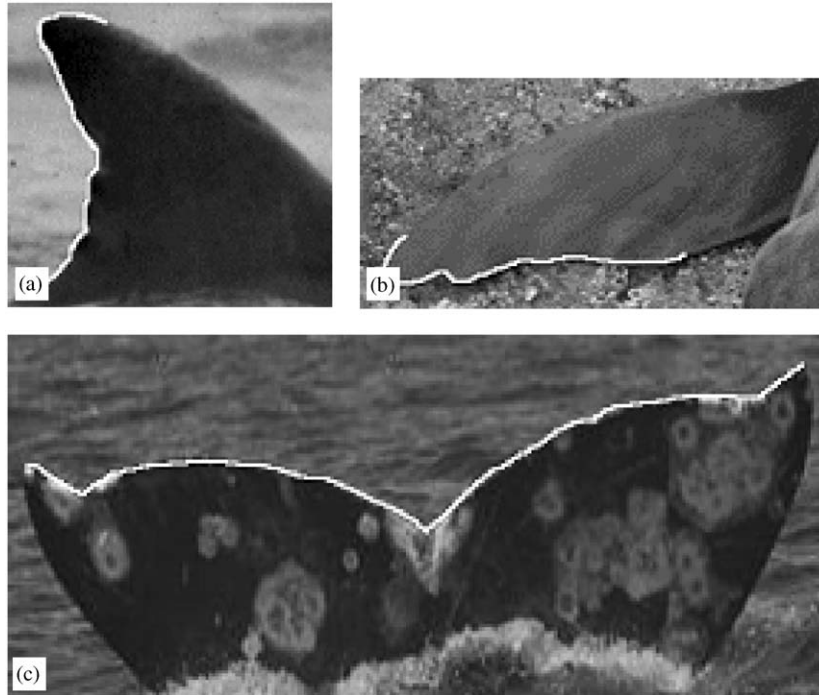


Fig. 1. (a) Sample image of a dolphin fin and its extracted edge (shown in white), (b) sample image of a sea lion flipper and its extracted edge (shown in white) and (c) sample image of a gray whale fluke and its extracted edge (shown in white).

time used for manual searching, in particular when going through large databases of photographs.

Section 2 provides an overview of the previous work on affine curve matching. Section 3 presents our affine curve matching method, named the area-of-mismatch method. The performance results on three different databases are shown in Section 4 followed by the conclusions in Section 5.

2. Previous work on curve matching

The literature contains a large number of methods on curve matching. The great majority of these methods address curve matching under similarity transformations. Some of such methods include *shape-signature* [3], *hidden Markov model* [4], *shape context* [5], and *curvature scale space* [6] methods. These and many other methods are not designed to cope with changes made to curves when they undergo affine transformations, in particular out-of-plane rotations. Thus, they cannot suitably address our problem at hand since the images are captured at different angles and different degrees of out-of-plane rotations.

As far as affine curve matching is concerned, Mokhtarian et al. [7] used affine curvature to make their *curvature scale space* method invariant to affine transformations. We have implemented this method and compared its performance to that of our method. In Ref. [8], an affine invariant curve nor-

malization was introduced based on a combination of curve attributes such as moments and Fourier descriptors. While being suitable for the recognition of closed curves, its applicability is limited when considering open-ended curves. In Ref. [9], a B-spline curve representation was used, from which control point parameters were estimated. While being invariant to affine transformations, in general, a B-spline curve is not uniquely identifiable by a single set of control points, creating difficulties in the matching process. In Ref. [10], Flusser et al. used affine moment invariants for character recognition. Affine moment invariants can also be used for affine curve matching by treating a curve as a set of points. We have also implemented this approach here and compared its performance to that of our method.

The next section describes our affine curve matching method, called area-of-mismatch curve matching. The basic idea behind this method is to bring a query and a database curve to the same “page” by applying an optimum affine transformation to the database curve, and then by employing the area enclosed between the two curves as a measure of dissimilarity between them.

3. Area-of-mismatch affine curve matching

The curve matching process starts by carrying out edge-detection. The extraction of the edge or curve from the

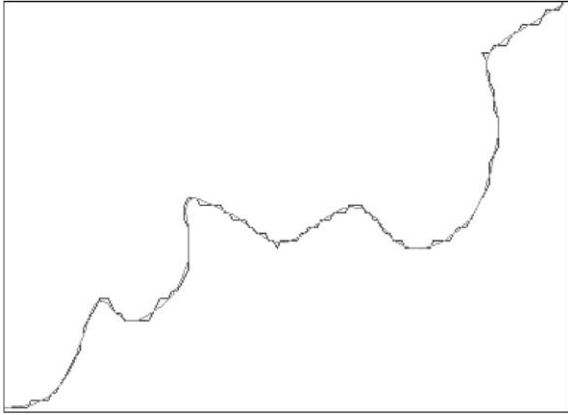


Fig. 2. B-spline representation of an extracted flipper edge.

animal's body is accomplished by a semi-automatic, live-wire [11] edge detection scheme. We have seen that this user-guided edge detection scheme is quite robust for the low quality of images with which we are dealing, noting that the images are taken under various outdoor lighting and water background conditions. Next, an extracted curve is modeled by a cubic B-spline curve, which forms a smooth description of the otherwise noisy digital curve. Fig. 2 shows the original curve data and its cubic B-spline representation. Properties such as smoothness, continuity, and shape invariance under affine transformation make B-splines suitable for curve representation; an affine transformed curve is still a B-spline curve whose control points are related to the original control points through the transformation. For a detailed description of B-spline curve representation, the reader is referred to Ref. [12].

Given a query and a database curve, the first step of the matching process consists of using an appropriate affine transformation to force the curves to overlap as closely as possible. The second step consists of computing the mismatch area between the curves after applying the transformation obtained in the first step. The third and final step comprises selecting the best matching database curves by ranking the area-of-mismatches. Fig. 3 illustrates the area-of-mismatches for two different database curves.

The optimum transformation which best aligns a given pair of curves is obtained by formulating an estimation problem via a few distinguishing points on the curves. These points correspond to the maxima and minima of the curvature vs. arc-length function at an appropriate smoothing scale. The estimation leads to finding the optimum affine transformation aligning a database curve with a query curve. The database curves are re-sampled so that they possess the same number of points as the query curve. Only a few points in correspondence are used to estimate the optimum affine transformation. After this alignment, the area enclosed between the query curve and each database curve is calculated,

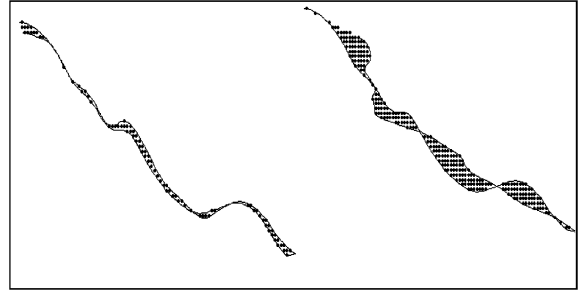


Fig. 3. Area-of-mismatch (dotted regions) for two affine normalized overlapping curves from the same individual (left) and a different individual (right).

providing a measure of dissimilarity between them. The area calculation can be carried out by any geometry technique that allows one to find whether a point lies inside or outside a closed polygon [13].

3.1. Selecting distinguished points

Curve representation of the edge data is followed by its curvature description. Curvature $k(s)$ of a curve $C = [x(s), y(s)]$, parameterized by s , is given by

$$k(s) = \frac{d\alpha}{ds} = \frac{x'y'' - y'x''}{(x'^2 + y'^2)^{3/2}}, \quad (1)$$

where α represents the angle between the tangent to the curve and the positive x -axis, x' represents the first derivative of x with respect to s and x'' represents the second derivative of x with respect to s .

Here the distinguishing points on the curve are chosen to be the points corresponding to the local maxima and minima of the curvature vs. arc-length function [14]. High curvature points have the useful property that they are relatively stable, which means that despite different affine distortions, these points on the curve can be consistently detected.

To cope with noise, the curvature function is normally smoothed. An appropriate smoothing scale can be chosen in a consistent way by using the scale-space approach [15]. The scale-space approach consists of filtering at a continuum of smoothing scales. Gaussian kernels are primarily used for smoothing due to their causality property: i.e., new zero crossings can appear but the existing ones do not disappear as the smoothing scale is reduced [16]. Due to the difficulties posed by numerical integrations, B-splines have also been used to provide various degrees of smoothing. Given data points (x_i, y_i) , this involves finding a curve f by minimizing the functional

$$\mathfrak{J} = \sum_i (y_i - f(x_i))^2 + \rho \int (f''(x))^2 dx, \quad (2)$$

where ρ denotes the smoothing scale. It can be shown that cubic spline is a solution of the above equation [17].

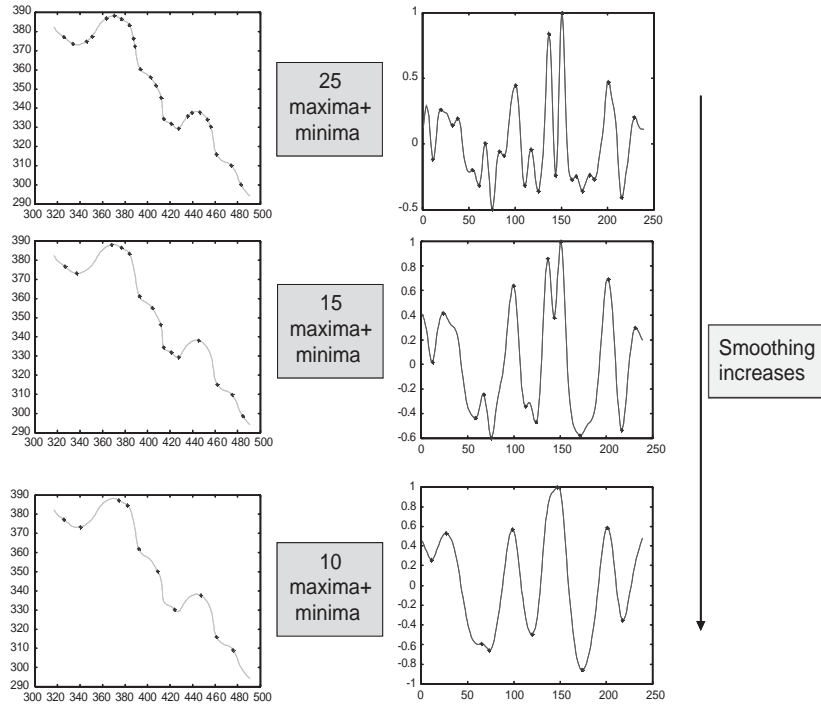


Fig. 4. Curvature vs. arc-length functions (right) at various smoothing scales, the maxima and minima of which correspond to distinguished points on the spatial domain curve (left).

3.2. Selection of appropriate smoothing scale

An appropriate smoothing scale can be decided based on a prescribed number of maxima and/or minima of the curvature function. Maxima and minima of the curvature function, when mapped back to the spatial domain, correspond to distinguishing points on the curve that reflect bumps and notches. At least three points in correspondence are needed to estimate the affine transformation between two given sets of points. In the case of gray whales, it is fairly easy to locate three well-distinguished points on the fluke edge in a consistent manner, namely the two tips and the middle notch-like point. In this case, the affine transformation can be calculated almost exactly. On the other hand, the flipper edges of sea lions and the dorsal fin edges of dolphins do not have such well-distinguished points. In such cases, more than three such points should be located. For sea lions, the appropriate smoothing scale is considered to be that scale where the total number of maxima and minima of the curvature function is 10. This choice is made based on the fact that the protrusions on the flipper edge correspond to the underlying bones, which are 5 in number. This number was also found to be a good choice in dolphins.

Fig. 4 illustrates the process of curvature function smoothing at various scales while Fig. 5 shows how the distinguishing points on an extracted edge correspond to the protrusion

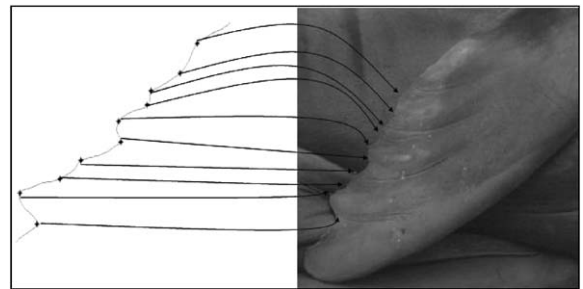


Fig. 5. Distinguishing points on the extracted edge and corresponding points on the flipper boundary.

points on the actual animal boundary (sea lion flipper in this example).

3.3. Comparison of point-sets

Given two point-sets, the estimation of the best affine transformation can be viewed as an optimization problem. Let $Q_{2 \times M}$ and $D_{2 \times M}$ be two point-sets, each consisting of the (x, y) coordinates of M points in correspondence, where the two matrices Q and D represent the query and database point-sets, respectively. To compare two matrices,

a matrix norm must be defined. Here, we have considered the *Frobenius* norm of the difference matrix, which is the same as the Euclidean distance between points in two point-sets. The Frobenius norm $\|P\|_F$ of a $m \times n$ matrix P is defined as

$$\|P\|_F^2 = \sum_{i=1}^m \sum_{j=1}^n p_{i,j}^2 = \text{trace}(P P^T), \quad (3)$$

where $p_{i,j}$ is the (i, j) th element of matrix P . Thus, $\|Q - D\|_F^2$ provides a difference measure between the two matrices Q and D . However, before computing the norm of the difference matrix, it is essential to normalize them with respect to affine transformations, or to bring them to the same “page”.

3.4. Affine transformation

Affine transformation is an important subgroup of the general class of projective transformations. It includes translation, rotation, scaling, out-of-plane rotation, and skewing. For the two-dimensional case, it can be represented mathematically by

$$\begin{pmatrix} u \\ v \end{pmatrix} = A_{2 \times 2} \begin{pmatrix} x \\ y \end{pmatrix} + b_{2 \times 1}, \quad (4)$$

where $(u \ v)^T$ represents the transformed coordinates of an original point $(x \ y)^T$, matrix A represents rotation, scaling, and skewing, while vector b represents translation. It is necessary to consider invariance to affine transformations because the images are captured not only from different distances but also with different degrees of out-of-plane rotations.

3.5. Optimal affine transformation

Before they can be compared, Q and D matrices need to be normalized with respect to affine transformations. Without loss of generality, it can be assumed that the point-sets are mean-centered, so that their first moments are zero. Therefore, the only component of the affine transformation that needs to be estimated is the linear transformation matrix A . We have considered the following optimality condition to choose the “best” matrix A relating Q and D ,

$$\min_{A'} \|A' D - Q\|_F^2. \quad (5)$$

The matrix A_{opt} which satisfies the above optimality criteria can be derived to be

$$A_{opt} = Q D^+ = Q D^T (D D^T)^{-1}, \quad (6)$$

where D^+ represents the pseudo-inverse of D . Hence, the affine distance d_{aff} between D and Q is given by

$$d_{aff}^2 = \text{trace}((A_{opt} D - Q)(A_{opt} D - Q)^T). \quad (7)$$

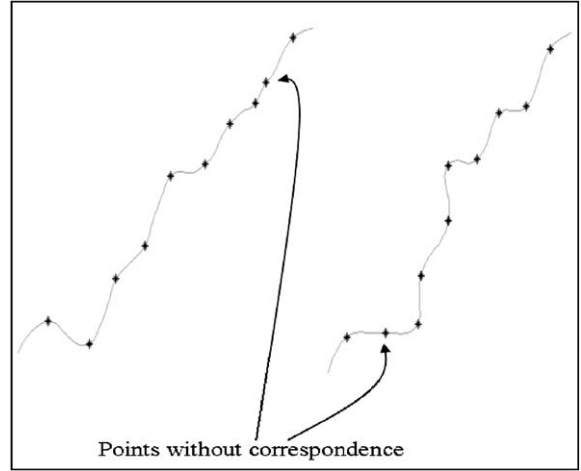


Fig. 6. Two curves extracted from different flipper images of the same animal, having points without correspondence.

3.6. Correspondence between point-sets

Two edges or curves of the same individual, obtained from two different images, may contain some points without any correspondence. Fig. 6 illustrates such a situation. Such a problem is caused either by the finite resolution of the images or by noise during the edge detection and/or the curvature computation steps. In our case, it is reasonable to assume that there are no more than two such points between a pair of curves. As a result, during the matching phase, we attempt to obtain the best possible correspondence between point-sets (the one that gives the least affine distance) by considering point-sets of cardinality ten, nine, and eight. This means that we consider 56 possible combinations of points for each curve. Establishing correspondence between point sets is not of concern in the case of gray whales, as we have exactly three well-distinguished points on the fluke edge with known correspondences.

4. Results and discussion

Three different databases of marine mammals have been examined in this study. The sea lion database consists of 92 images of 37 individuals. It has 2, 3, or 4 different images per individual sea lion. The gray whale database consists of 95 images of 37 individuals with 2 or 3 different images per individual. The dolphin database consists of 624 images of 164 individuals with the number of images per individual ranging from 2 to 15.

While matching a query image against the database, the query image itself was not taken as a candidate match. Fig. 7 shows the matching performance plots for the sea lion database using our area-of-mismatch (AOM) method, together with the affine moment invariants (AMI), and affine

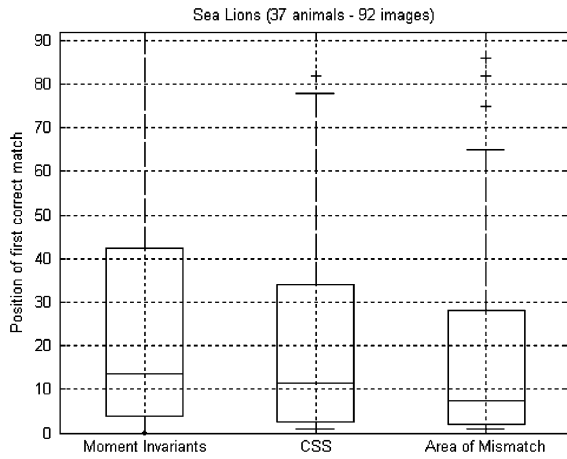


Fig. 7. Boxplots exhibiting identification performances for three affine curve matching techniques applied to a sea lion database.

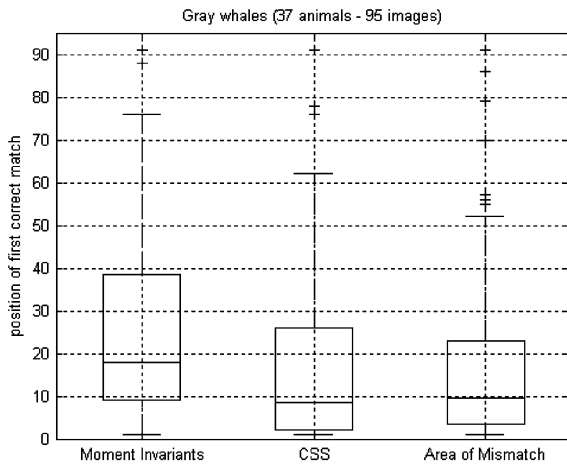


Fig. 8. Boxplots exhibiting identification performances for three affine curve matching techniques applied to a gray whale database.

curvature scale space (CSS) methods. Boxplots have been used to show the position of the first correct match for various percentages of the test images. A boxplot has horizontal lines at the lower quartile, median, and upper quartile values. Such boxplots are commonly used to exhibit performance of identification systems.

In the area-of-mismatch method (Fig. 7, sea lion performance plot), about 75% of the time the user needed to search through only the first 28 images to get a match to a query image, and about 50% of the time the user needed to search through only the first 7 images to get a match to a query image. Similarly, Figs. 8 and 9 show the performance plots for the gray whale and the dolphin databases, respectively. Tables 1–3 provide numerical comparisons for the three curve matching techniques. The high

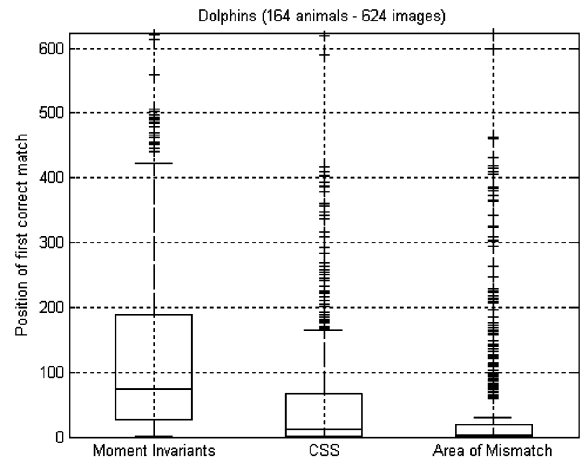


Fig. 9. Boxplots exhibiting identification performances for three affine curve matching techniques applied to a dolphin database.

Table 1

Position of first correct match for various percentiles of query images

Sea Lion database (37 animals—92 images)

Curve matching technique	Percentile of query images		
	25	50	75
Affine moment invariants	5	13	42
Curvature scale-space	3	11	34
Area of mismatch	2	7	28

Table 2

Position of first correct match for various percentiles of query images

Gray whale database (37 animals—95 images)

Curve matching technique	Percentile of query images		
	25	50	75
Affine moment invariants	10	18	39
Curvature scale-space	3	9	27
Area of mismatch	4	10	23

Table 3

Position of first correct match for various percentiles of query images

Dolphin database (164 animals—624 images)

Curve matching technique	Percentile of query images		
	25	50	75
Affine moment invariants	40	80	190
Curvature scale-space	1	10	70
Area of mismatch	1	3	30

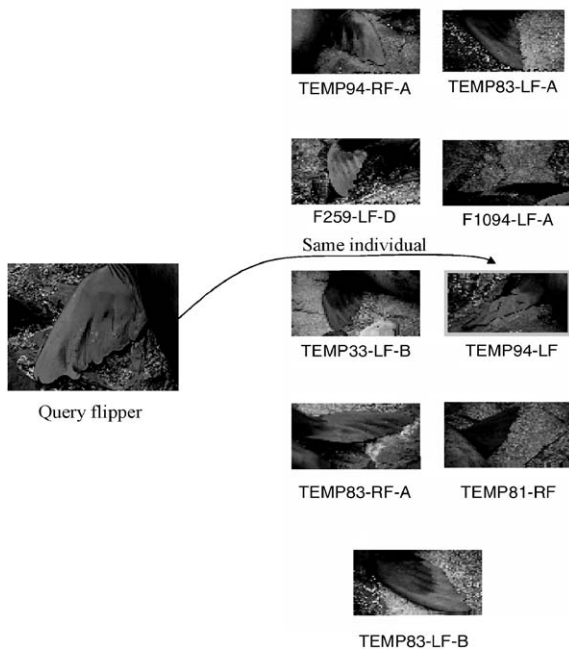


Fig. 10. Identified matches for a query flipper.

identification rate for the dolphin database, as compared to the other two databases, is due to the fact that a large number of different images for the same individual were available in the dolphin database.

The steps involved in the curve matching method were incorporated into a MATLAB-based graphical user interface program, called *CurveMatch*, to allow efficient and easy user-interaction. Fig. 10 shows an instance of the matching process using *CurveMatch*. The images in the database get ranked depending on their distances from the query image and then displayed 9 at a time for visual inspection by a marine biologist.

5. Conclusion

In this paper, a computer-assisted photo-identification technique has been developed for the identification of marine mammals based on their unique identifying edges. It is evident from the performance plots that in most cases, this approach considerably reduces the number of images to be searched and hence can be utilized by marine biologists in their identification studies. The curve matching technique discussed in this paper is of general purpose, as it can be used for other curve matching applications.

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