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SHORT COMMUNICATION

Semi-automated software for dorsal fin photographic identification of marine species: application to *Carcharodon carcharias*

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Abstract When dealing with large marine species, individual photographic identification plays a very important part in capture–mark–recapture studies. The success of this method is determined by the consistent correct identification of individuals, but as the number of images in the database increases, the task becomes increasingly time-consuming, affecting the accuracy of the matches. Although a few software packages are available, universally applied methods remain problematic in long-term studies, suggesting the need for species-specific software. This study presents new image recognition software tested on white sharks' dorsal fins and is based on a dynamic time warping algorithm. The software is specifically designed to improve the matching success of individuals, to standardise the data collection and to increase the overall accuracy when managing a large capture–mark–recapture database.

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The software is available upon request from Dr Pieter Holtzhausen (holtzhau@gmail.com).

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Introduction

During the past 15 years, photographic identification techniques have been used extensively to study the population ecology and life history of several species. Photographic identification proved particularly useful to study species under threat, mostly in the marine environment (Würsig and Jefferson 1990; Langtimm et al. 2004; Chapple et al. 2011; Marshall and Pierce 2012) and are often used to estimate the population size of species through capture–mark–recapture (CMR). It has specific advantages over standard tagging techniques in terms of non-invasiveness and reduced cost (Carbone et al. 2001; Jackson et al. 2006; Kelly et al. 2008; Schofield et al. 2008). For sharks, dolphins and whales, CMR studies often rely on the unique notched pattern of the individual's dorsal fin or the tail fluke, since an identification photograph can be taken from either side of the individual (Hammond 1990; Gowans and Whitehead 2001; Stevick et al. 2004; Calambokidis and Barlow 2004; Larsen and Hammond 2004; Marshall and Pierce 2012). Having a mark that is symmetrical on both sides of the animal allows for all individuals to have the same capture probability from a single photograph, which is an essential assumption when applying CMR models for estimating population abundance (Carbone et al. 2001; Jackson et al. 2006; Kelly et al. 2008; Schofield et al. 2008; Chapple et al. 2011; Marshall and Pierce 2012; Andreotti et al. 2014, 2016a).

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While different ad hoc (i.e. case-specific) image recognition software packages have been developed successfully to assist researchers in the matching process for marine mammals (e.g. DARWIN, Stanley 1995 and FINSCAN, Hillman et al. 2003), success in the photographic recognition of large elasmobranchs varies (Van Tienhoven et al. 2007; Chapple et al. 2011; Dureuil et al. 2015; Andreotti et al. 2016a). Specifically, the use of software originally developed for use with marine mammals (e.g. DARWIN, FINSCAN) has most likely resulted in unacceptably high levels of errors in matching elasmobranchs images (Chapple et al. 2011; Andreotti et al. 2016a). Alternatively, a pattern-matching program called I³S (Interactive Individual Identification System) was developed in Java 1.4.2 and C++ to identify individuals of *Carcharias taurus*, relying on their unique pigmentation marks (Van Tienhoven et al. 2007). I³S proved to be a valuable aid for the identification of *C. taurus* (Van Tienhoven et al. 2007) and *Rhincodon typus* (Speed et al. 2007), but it had the limitation of relying on marker features that differ on the two sides of the fin. For I³S, only photographs taken from the left side of the animals were used to prevent the addition of false-negatives in the database (e.g. the same animals, photographed on the left side, cannot be matched if the subsequent photo will be taken of its right side; Van Tienhoven et al. 2007). A further development of I³S was tested for adapting it to *Carcharodon carcharias* (I3S Contour), and focused on the contour from the posterior edge of the nostril to the first gill slit, along the irregular border between the ventral white and dorsal grey colouration (Dureuil et al. 2015). The reliability of I3S Contour to match the photographs proved to be highly dependent on the quality of the underwater photographs; thus, the amount of usable data were affected by the water visibility (Dureuil et al. 2015). Also, similarly to the original I³S, one image for each side of the animal is needed; this will alter the probability of capture of each individual (it depends on from which side the animals swim towards the camera).

Based on the trailing edge pattern of their dorsal fins, *C. carcharias* was one of the first elasmobranch species for which a photographic identification approach was implemented (Anderson and Goldman 1996; Klimley and Anderson 1996; Domeier and Nasby-Lucas 2007; Anderson et al. 2011; Chapple et al. 2011; Towner et al. 2013; Andreotti et al. 2016a). However, despite significant improvements relating to the visual protocol, the organisation of the photographs in a categorisation system, and the subsequent manual matching techniques, becomes increasingly time-consuming as the database increases in size (Andreotti et al. 2014, 2016a). Furthermore, to manually generate an accurate binomial matrix of the history of captures, as used in CMR analyses, is problematic when dealing with a large number of individuals [i.e. in the categorisation system proposed in Andreotti et al. (2016b), each image collected during the study period must be renamed according to the date of capture and stored in a structured folder system].

Errors in the accurate assignment of individuals lead to false-negatives and can result in an over-estimate of the population size in CMR analyses (Burgess et al. 2014; Andreotti et al. 2016a). Thus, recent attempts to utilise marine mammal image recognition software on *C. carcharias* (Towner et al. 2013) or the development of image recognition software for non-permanent marking traits (Robbins and Fox 2012; Dureuil et al. 2015) have become causes for concern, since they might result in disproportionately high error rates in the matching process (Chapple et al. 2011; Andreotti et al. 2016a).

The aim of this study was to develop ad hoc software ('ad hoc' in the sense that it is specifically geared towards the recognition of *C. carcharias*) to aid white shark researchers in the photographic matching process as well as the subsequent data analyses. Differently to the other software, this ad hoc software aims to: (1) focus on a natural mark symmetrical on both sides of the animal, for meeting the equal capture probability criteria required in CMR studies, and (2) to be applicable independently from the environmental variables (e.g. water visibility). The ultimate goal is to provide a platform that can be used internationally and in the long term for monitoring *C. carcharias*, with the potential of also being applied to other marine species, such as humpback whales *Megaptera novaeangliae* (Borowski, 1781).

Materials and methods

From April 2009 to December 2011, photographic data were collected during the daily white sharks cage-diving ecotourism activities of Shark Diving Unlimited (Laroche et al. 2007). Data were collected during a period of 314 days in the proximity of the Dyer Island Nature Reserve (Kleinbaai, Gansbaai, South Africa), following the protocols and guidelines of Andreotti et al. (2014). The photographs were visually matched and used to build a dataset comprising 4398 photographic identifications from 426 individual *C. carcharias*. One or two of the best quality photographs of each identified *C. carcharias* were then copied to a separate folder (the 'database'), which, in total, comprised 744 images (Andreotti et al. 2014). To test the accuracy of the software, 50 new photographs of sharks known to be in the database were matched against the 744 images. The prime identification trait used in the software is the distinct notch pattern of the trailing edge of the dorsal fin, since they are bilaterally symmetrical (i.e. the do not differ between the left and right sides) and are not subjected to significant changes over time, as for the body pigment patterns (Anderson et al. 2011; Robbins and Fox 2012; Andreotti et al. 2014; Dureuil et al. 2015). The recognition software consists of two

(a)

(b)

(c)

(d)

(e)
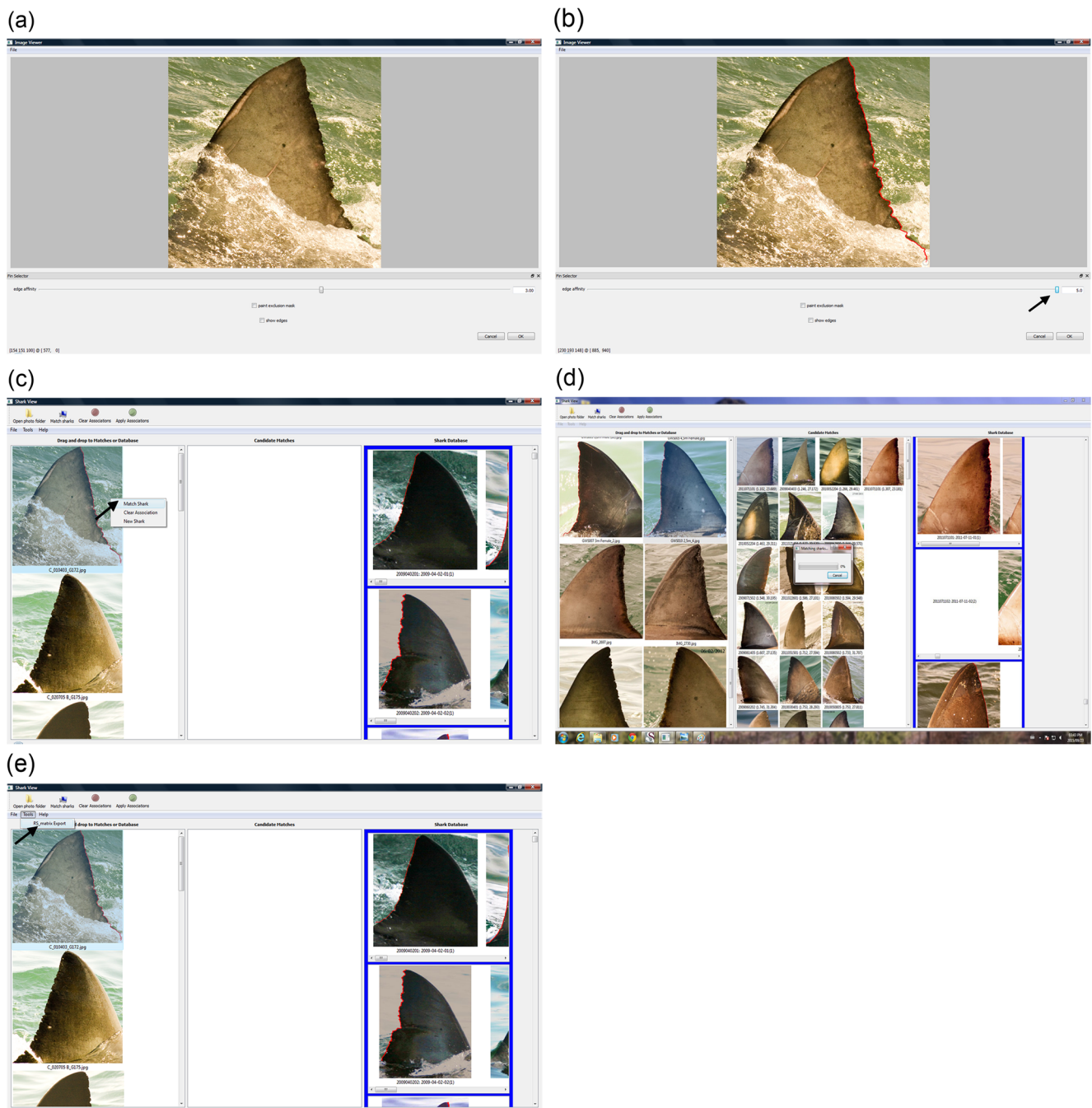
Fig. 1 Interface of the *Carcharodon carcharias* fin matching program. **a** Original photograph to be traced, with the bottom of the dorsal fin partially covered by water. **b** Once the researcher indicates the top and the bottom of the fin, the software automatically traces the notches pattern (*in red*). The affinity to the edge can be improved, as indicated by the *arrow*. **c** The researcher asks the software to match the traced photograph with existing images of potentially the same shark. **d** The interface of the

software is organised as follows (from left to right): images to match, candidate matches from the database in order of similarity and uses the complete database for comparing the matches; in this case, the software found the correct match in the first position of the selected image. **e** In the software, there is an embedded function to create the matrix of the history of recaptures, used ultimately for population estimates

sections: the first semi-automated section separates the foreground (fin) from the background (ocean and sky), allowing the extraction of the trailing edge of the dorsal fin; the second section matches the dorsal fin pattern with the patterns stored in the database. Note that both sections of the

algorithm are of fundamental importance, since no matching algorithm can provide reliable results with an inaccurately extracted pattern, and a poor matching algorithm won't give the expected outcome, even given a perfectly extracted pattern.

Fig. 2 Results of the trial performed using 50 randomly selected images against the database of 744 images, using the *C. carcharias* fin matching program software
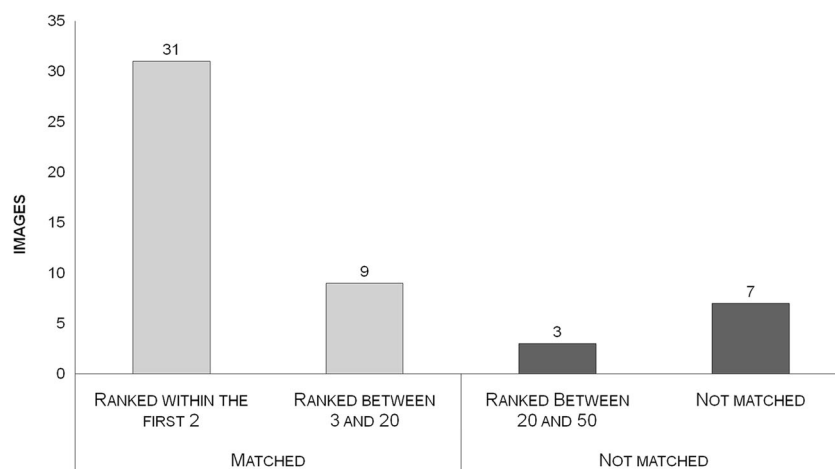
The algorithm uses a dynamic time warping approach (Bellman and Kalaba 1959; Sakoe and Chiba 1978; Myers et al. 1980; Tappert et al. 1990; Efrat et al. 2007; Senin 2008) to match a fin with the best ranking candidates in the database. The result is a list of individual fins of greatest similarity. We detect each fin path by following the trailing edge of the dorsal fin using a shortest path algorithm on the Sobel edges, from the top to the bottom of the photo. Due to the flexible nature of the dorsal fin and water that tends to cover the base of the fin (Fig. 1a), the researcher is required to manually indicate the tip and the bottom of the dorsal fin before the software will extract the trailing dorsal fin pattern. The latter was done to resolve possible ambiguities and to ensure an accurate identification of the fin start and end (Fig. 1b).

We orientate the fin path by aligning it to the principal component axis of the spatial coordinates. The dynamic time warping algorithm then does a comparison of various normalised (e.g. scaled) path versions, with a representative path of each *C. carcharias* fin in the database. Firstly, we scale the path according to the image size in order to capture the real-life magnitude of the fin features better. Then, we scale according to the maximum peak amplitude of the fin path in order to better express the unique detailed features of each fin. The software will then be asked to match the new photograph (Fig. 1c) with the most suitable one available in the database. The best matches from the database are then ranked in order of probability and displayed in the middle of the screen, as illustrated in Fig. 1d. We consider the fin that returns the lowest cost as a good candidate: a perfect match is when the first, most probable image, is the correct one (Fig. 1d).

The performance of our software was tested by matching 50 randomly selected images of different *C. carcharias* against the database consisting of 744 images [of 426 individual *C. carcharias* positively identified through manual and, in some instances, also genetic matching; Andreotti et al. (2016a, b)]. Similar to the test conducted with DARWIN in Andreotti et al. (2016a), a match is deemed to be positive if the correct

Fig. 3 Simulated adaptation of the image matching algorithm for *C. carcharias* to a matching algorithm for *Megaptera novaeangliae*
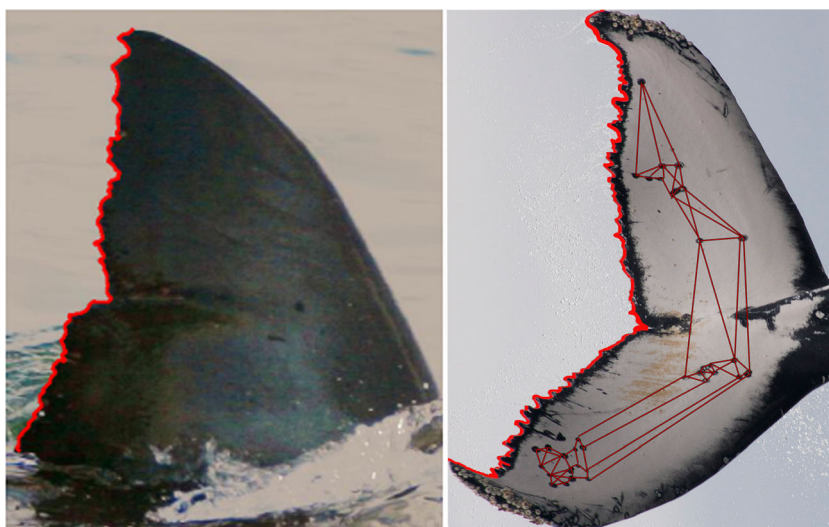
image is within the top 20 best matches as ranked by the algorithm. A paired *t*-test was applied to the results to quantify the accuracy of the performance (see also the ESM of Andreotti et al. 2016b).

Results and conclusions

The algorithm correctly matched 80% of the images (40 images out of 50), with 62% of the correct matches ranked within the first two positions (Fig. 2). Seven images couldn't be matched and a rank couldn't be assigned. A paired *t*-test (on the 43 ranked photos) was used to quantify how much the means of the software result (e.g. rank obtained) against the correct result (e.g. rank = 1) differ among each other, allowing for a hypothesised difference of 20, compared to the real mean difference between the two.

The average difference (95% confidence) between first rank and the software's match is 5.86. The paired *t*-test confirmed the hypothesis that the software can successfully match a *C. carcharias* dorsal fin image in the upper range of up to 20 ranked images (t-stat = −5.82, $P = 3.54 \times 10^{-7}$).

Once the matching process is completed and the result visually confirmed, a copy of the correctly matched image is automatically renamed after the name of the individual *C. carcharias* (following the protocol suggested in Andreotti et al. 2016a) and saved in the appropriate folder. Subsequently, an ad hoc algorithm included in the software (Fig. 1e) extracts the information of the day on which the photo was taken from the metadata of the images, to generate a binomial re-capture history matrix (1: captured; 0: non-captured) of all the sharks (Y-axis) captured in each sampling occasion (X-axis), for population estimates analyses (RS_matrix—see also Andreotti et al. 2016a).

To conclude, the newly developed algorithm presented in this study proved to be effective in matching *C. carcharias* dorsal fin photographs providing a reliable tool for long-term monitoring of the species. The performance of the *C. carcharias*-specific software shows an average difference between the first rank and the software's match of 5.86 (95% C.I.), which is a great improvement from the 66.34 (95% C.I.) score obtained with the software DARWIN (see the ESM of Andreotti et al. 2016a). Notably, the same database and photographs used in the present work were used to test the software DARWIN in the ESM of Andreotti et al. 2016a. Further, the combination of the matching process, automated storage and the matrix generator algorithms allows for the development of a large, user-friendly database that should prove to be an invaluable tool for the researcher. The concept expressed in this study has the potential of being applied to other marine species by simply modifying the matching algorithm to be species-specific. Additional algorithms could classify the pigment pattern to assist the matching of trailing edge patterns.

For example, *M. novaeangliae* can be identified from images of their flukes by replacing the identification module (Fig. 3).

Photographic identification also has the potential to be the common denominator to link different research fields. Once an individual is identified, its biological characteristics can be linked to its genotype (when available), size at the time of capture, history of re-captures, tagging data and any other information that researchers wish to investigate. Furthermore, the utilisation of the software will standardise the data collection among different research groups. In our instance, the standardisation of the datasets will allow for the creation of an international database for *C. carcharias*, and, with limited modifications, it can also be extended to other marine species. Finally, the long-term monitoring dataset that will be generated has the potential to give unprecedented insight into the population dynamics, growth rate and migration of the vulnerable species investigated, without harming its natural activities.

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