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APHIS: A new software for photo-matching in ecological studies

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ABSTRACT

Unique body characteristics are increasingly used for individual recognition to avoid the effort and the potential negative effects of capture–mark–recapture technique. As a consequence there is a growing demand for computer procedures to assist users in photo-recognition of an individual. We present a new software for photo-matching developed to minimize the pre-processing time and maximize the speed of the matching procedure. In APHIS photos can be processed in batches of hundreds and users can select between two alternative matching procedures, one interactive, built as an extension of existing and freely available software, and one automatic. We assessed its performance in terms of individual recognition and time efficiency and illustrate its use with real capture-photo–recapture studies on a reptile and an amphibian species, the Balearic Lizard *Podiarcis lilfordi* and the Northern spectacled salamander *Salamandrina perspicillata*, with contrasting skin patterns.

1. Introduction

Detailed data on individual life-history are used in ecological and evolutionary studies for the estimate of demographic parameters such as population size, survival and fertility of wildlife populations (e.g. Fernández-Chacón et al., 2011; Lebreton and North, 1993; Tavecchia et al., 2001, 2005; Williams et al., 2001). A common solution for the individual recognition of the animals is to apply a mark to the animal body in the form of a tag or a ring with a unique alphanumeric code. However, rings, tags, flipper bands or other marks can alter individual fates and behavior (Gauthier-Clerc et al., 2004; McCarthy and Parris, 2004). In addition to ethical issues (e.g. May, 2004), these negative effects lead to bias the estimates of the parameters of interest. As a consequence there is an increasing interest in using non-invasive methods for individual recognition, such as unique natural marks or body characteristics. These methods have been applied with success in a wide range of taxa, in mammals (Karanth and Nichols, 1998; Langtimm et al., 2004; Martínez-Jauregui et al., 2012), amphibians (Gamble et al., 2008), reptiles (Sacchi et al., 2010), fishes (Speed et al., 2007; Van Tienhoven et al., 2007) or cephalopods (Huffard et al., 2008). However, with few exceptions (i.e. Perera et al., 2001), the photo-identification is restricted to those species featuring distinct colors, spots or marks. Photo-identification procedures consist of comparing a sample picture of an unknown individual with a library of candidate images of previously photographed individuals. This search is, in many cases, conducted by experienced observers who compare patterns and scars between photographs with the naked eye and might be extremely time-consuming when library contains hundreds of images (e.g. Martínez-Jauregui et al., 2012; Verborgh et al., 2009). Naked-eye comparisons are typically assisted by a preliminary grouping of the images using a multi-character score, for example by grouping images with a given chromatic pattern (e.g. absence or presence of specific marks, Carafa and Biondi, 2004). Unaided procedures may also become prone to errors when image libraries expand. There is now a growing demand in developing automatic or computer-aided procedures for photo-matching (Gamble et al., 2008). A computer-aided photo-identification system identifies the most probable sample–candidate matches, reducing the number of images to be inspected. Most photo-identification software solutions concatenate three processing steps. The first is a preprocessing step where a region of interest is selected and the image rotated, scaled or spatially corrected if required by comparison algorithms; the second is usually an automated comparison between the sample and the library of images, which arranges candidates by matching probability or likelihood values; a final step is a visual comparison of sample–candidate pairs for a limited number of plausible matches.

We present a new software solution, APHIS (Automated PHoto-Identification Suite), specially designed to deal with sample sets of over a hundred photographs per field campaign and image libraries containing more than a thousand samples. APHIS proposes two approaches for photo-matching, the Spot Pattern Matching (SPM) and

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the Image Template Matching (ITM). The former has been built on the already existing I^{3}S algorithm (Van Tienhoven et al., 2007) while the latter is a novel approach based on pixel matching that minimizes the user's preprocessing effort. ITM is a fast-running alternative to study species with apparent or easily recognizable spots or colored parts of the skin. The workflow and graphic interface of APHIS have been designed to reduce the time invested by the researcher in analytical tasks and to enhance user experience. We describe below the general features of the APHIS interface and illustrate the SPM and ITM procedures using real data from two capture-photo–recapture studies on the Balearic Lizard, *Podarcis lilfordi*, and on the Northern spectacled salamander, *Salamandrina perspicillata* (Fig. 1).

2. Material and methods

2.1. Automated PHoto-Identification Suite (APHIS)

APHIS (Automated PHoto-Identification Suite, freely available at http://www.imedea.uib-csic.es/bc/ecopob/) v. 1.0 combines C++ and Java modules. The idea behind APHIS was to provide users with a flexible environment for photo handling and matching. The Graphic User Interface (GUI) has been programmed using the Nokia Qt framework (http://qt.nokia.com/). The image preprocessing and analysis of the ITM approach implements functions from the openCV v. 2.2 libraries (Bradski, 2000). The two available approaches, SPM and ITM, differ in how they treat and match the sample pictures. They perform differently depending on photo and species characteristics (see below). APHIS also implements a metadata based filtering system for its SPM approach, a feature present in other photo-identification software solutions, i.e. Manta 2.1 and Contour 3.0 versions from the I^{3}S series (http://www.reijns.com/i3s/). This function allows the user to predefine species-specific descriptive features and their possible alternative values for characterizing each sample. For example, a commonly useful feature would be the sex of the individual. A filtered search will only be conducted among sample–candidate pairs having equivalent character values and will substantially reduce the photo-matching time.

Finally, an important feature in APHIS is the automatic creation of log files that register the score lists obtained at each comparison. It also produces a registry of the matches validated by the user, which will lead to an easy analysis of capture–recapture data.

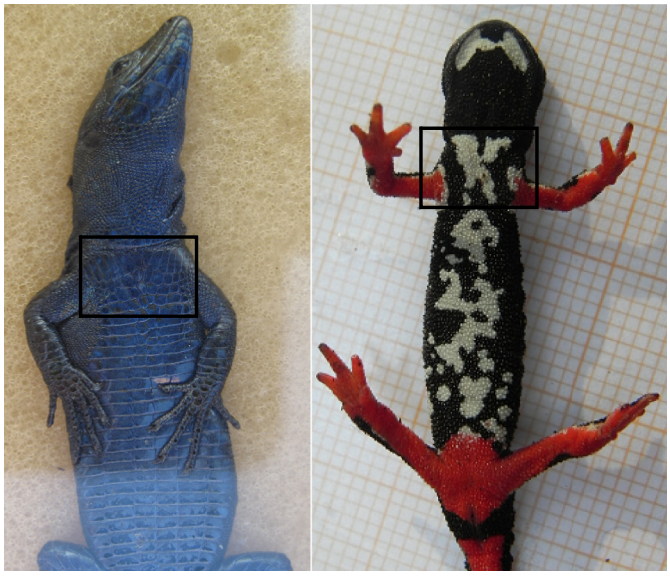

Fig. 1. The ventral side of a Balearic lizard (left) and of a Northern spectacled salamander (right). The black rectangles mark the region used for individual photo-recognition. (For interpretation of the references to color in this figure, the reader is referred to the web version of this article.)

2.2. The Spot Pattern Matching approach (SPM)

The Spot Pattern Matching approach is based on the algorithm implemented in the freely available software I^{3}S (Van Tienhoven et al., 2007). Each sample picture is pre-processed by the user before the photo-matching. During pre-processing the user delimits the region of interest with a given number of unequivocally identifiable reference points (typically three) and marks the set of spots within that will be compared during the matching of the defined area (Fig. 2; see Sacchi et al., 2010; Speed et al., 2007; Van Tienhoven et al., 2007 for practical examples). The coordinates of each spot in the space delimited by the reference points form a fingerprint-like statistic. At the matching step, the spatially-corrected cloud of spots from the sample is compared with the fingerprints stored in a repository. This correction is the result of an affine transformation of the sample pattern mapped onto that of candidate one. Matching scores are calculated as the sum of metric distances between spots from every pair created in a sample–candidate comparison divided by the square of the total number of spot pairs. Lowest scores point to likely matches, being the number of spot pairs used during calculation relevant to the resulting score value (Fig. 2), although it is not yet clear as to what extent (Speed et al., 2007). Sacchi et al. (2010) used a range of 20 to 40 spots per image and found a negative association between the matching score and the number of points, but this effect was not large enough to impair matching results. The matching algorithm used by SPM approach in APHIS was directly extracted from the I^{3}S Classic source code in accordance with its developers respecting its license agreement (GNU Public License v2). APHIS uses the exhaustive search version of the comparison algorithm described at Van Tienhoven et al. (2007). The exhaustive search uses every possible three spot pairs as reference points for different affine transformations, and not only those defined by the user (quick search). Score values are calculated for each transformation in comparison with the candidate and the lowest score is kept as final result. Exhaustive searches, although computer resource consuming, proved to be far more accurate than simple ('quick') searches (Van Tienhoven et al., 2007). Differently from the I^{3}S software, the pre-processing and the matching phases in APHIS occur separately. This permits to process sequentially a group of samples and then launch the matching calculations for the whole set. Once the automated matching is finished, the user is presented with a list of sample–candidate alternatives ordered from lower to higher matching scores (Fig. 3). If multiple pictures from the same candidate are available, APHIS only shows these with the lowest score. Finally, the user should inspect the possible candidates and accept the candidate as a recapture or discard the matching and register the sample as a new individual in the repository.

2.3. The Image Template Matching (ITM) approach

The Image Template Matching approach has been conceived to minimize the time invested by the user at the pre-processing step. It implements the *matchTemplate* function of the Open Computer Vision libraries (OpenCV, Bradski, 2000), a preprogrammed function that slides a template image patch over an input image looking for matches. This method provides three different algorithms and their normalized versions in order to calculate a matrix of likelihoods of match per comparison. APHIS implements the normalized version of the correlation coefficient algorithm, which is the most accurate of the three (Bradski, 2000). Normalization is recommended to minimize the effect of lightning differences among template and input while calculating matching scores (Bradski, 2000).

During the ITM pre-processing step the user selects only two reference points for each picture (Fig. 4). It is extremely important to use small, spot-like and easily recognizable parts or species-characteristic natural marks as reference points. The reliability of matching scores will depend on the reproducibility of this selection across pictures. APHIS automatically transforms to gray scale, rotates and resizes the

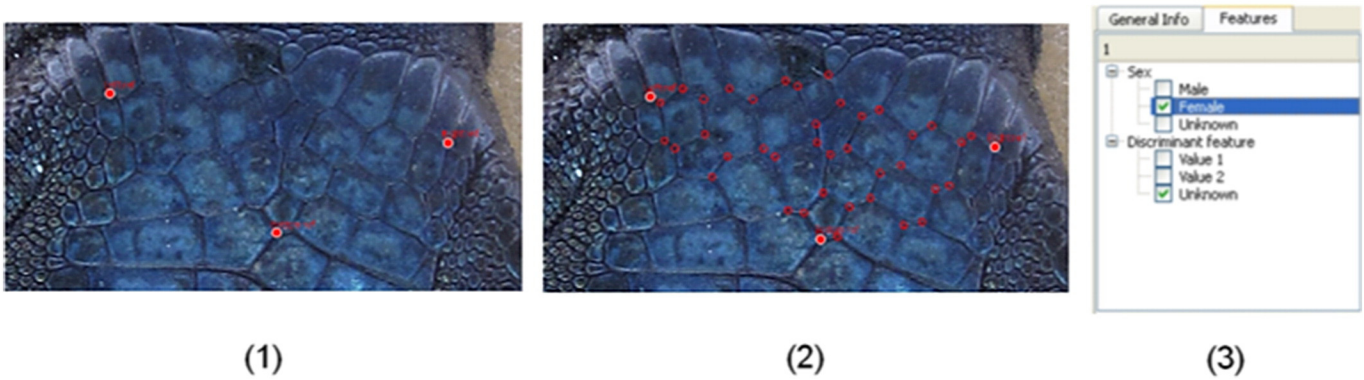

Fig. 2. Preprocessing for the SPM approach is divided into two steps: (1) manual selection of three reference points and (2) manual selection of between 30 and 50 intersections. Optionally, a third step (3) can be applied if the user decides to use individual discriminant characters to reduce processing times and to improve the quality of the resulting candidate list by constraining the analysis within individuals that show a given character.

images aligning the reference points along a horizontal axis. Next, a pattern, which is the region containing the natural marks used for identification, is cropped from the sample images (Fig. 4). The result is a rectangular area delimited by the pixel distance between reference points as base and a height 105% of this distance. The rectangle bottom is placed with a number of pixels below the reference points equal to 10% of the horizontal distance between them. A scale factor is applied to the resulting images such that all patterns finish aligned by their reference points and with a fixed resolution of 460 × 436 pixels. Finally, six templates of 91 × 103 pixels are homogeneously cut out from the pattern, distributed in two non-overlapping rows and three non-overlapping columns (Fig. 4). Using six non-overlapping templates the effect of local image defects has less impact on the final score, enabling real matches to be well positioned in the score list ahead of random

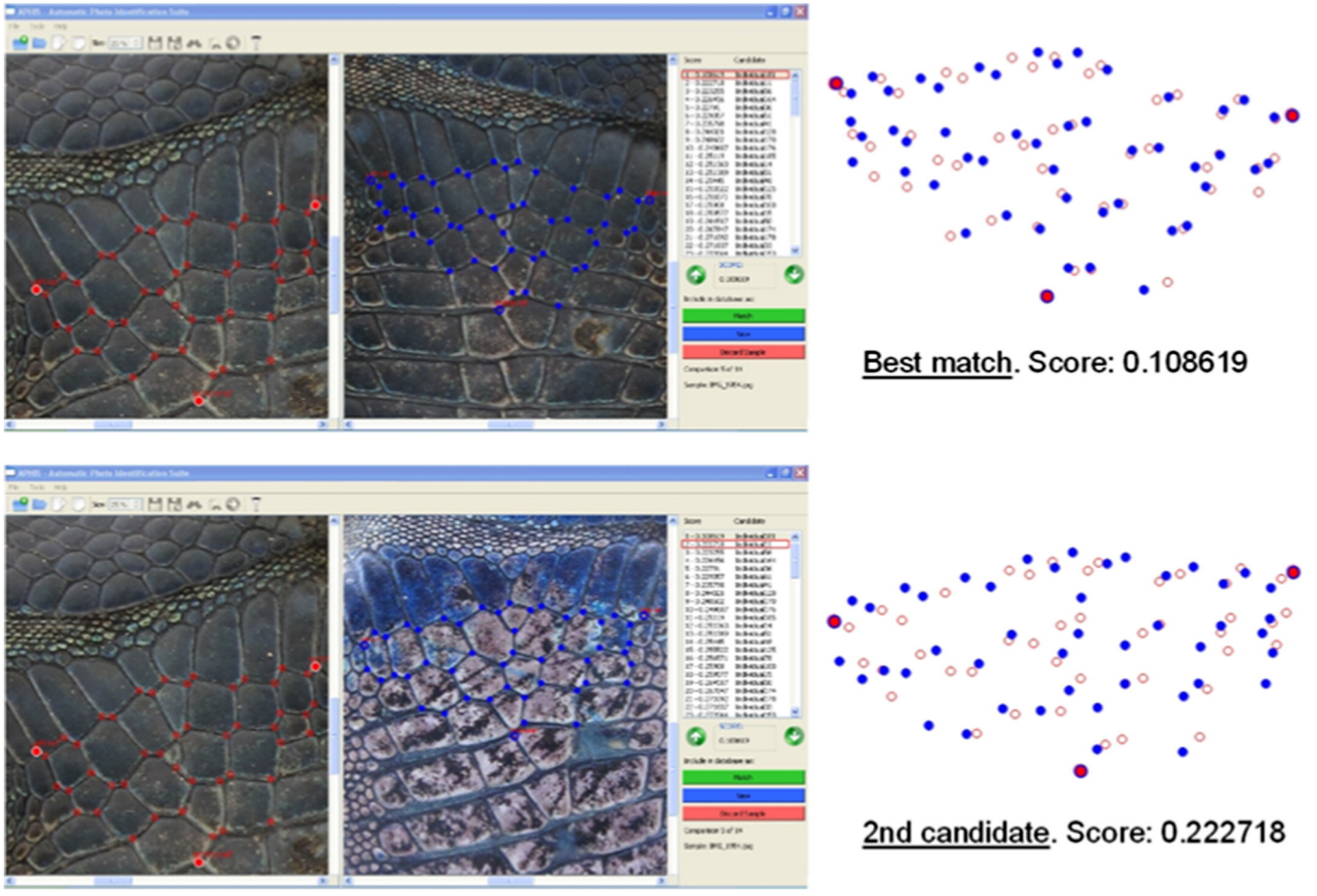

Fig. 3. The affine transformation of the fingerprint happens during the matching step and is comparison-dependent as far as it is applied for each sample–candidate pair under analysis. This figure shows the superposition of sample–candidate fingerprints for the first (best match) and second candidates of a SPM comparison from our study. It also includes two screen-shots of the APHIS display during the visual inspection of both comparisons. The sample is situated to the left of the screen, the candidate in the middle part and the controls used for decision-making to the right. The area reserved to display images has been maximized to show a general view of the animal that can be of help during the identification.

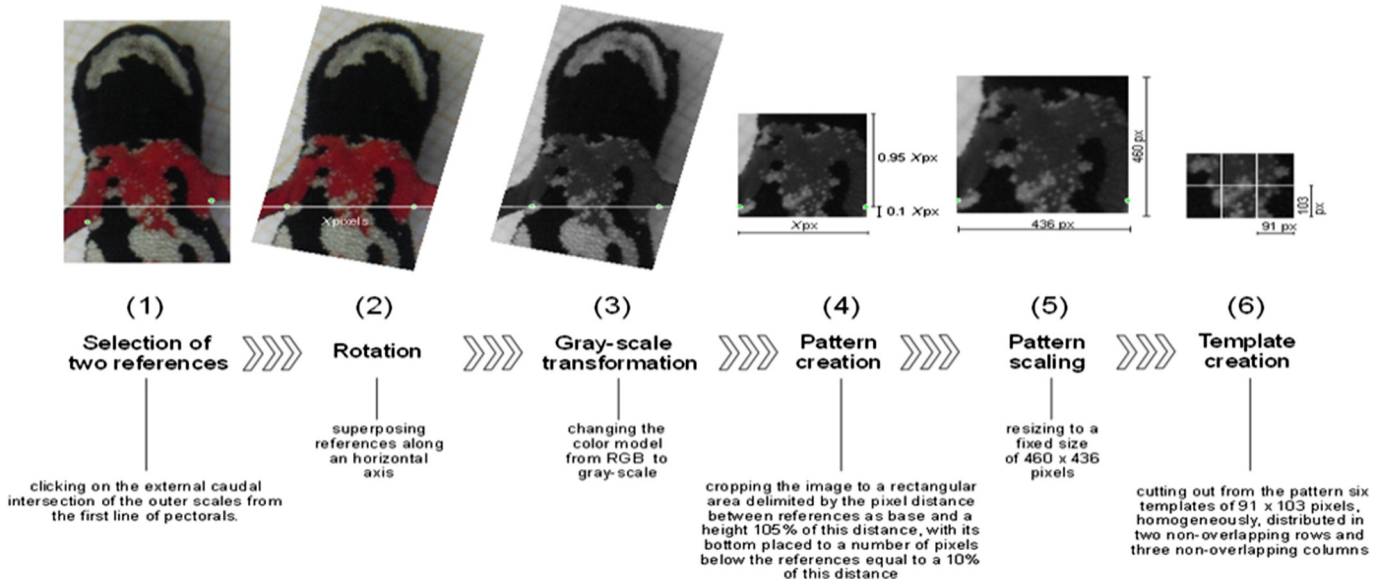

Fig. 4. Preprocessing for the ITM approach is divided into six steps: (1) manual selection of two references, (2) references are aligned with the horizontal axis, (3) the RGB image is transformed to gray-scale, (4) a region of interest is selected, (5) the image is resized to a fixed resolution, the resulting image is the pattern and (6) six non-overlapping contiguous templates are extracted automatically from the lower half of the pattern. Steps (2) to (6) are automatically performed by the software and do not need supervision.

ones. It has to be noted that values used to delimit patterns and templates are not arbitrary; they were expressly set to delimit and subdivide the region of the animal that includes the natural marks. In the case of the common wall lizard, *Podarcis muralis*, for example, this region is the pectoral area which includes a scales pattern characteristic for each individual (Fig. 1; Sacchi et al., 2010). Note that the rectangular area is fixed in the current version of APHIS (460 × 436 pixels) to fulfill the needs of the current studies; however it can be set to any arbitrary value. At present this can be done only by changing the source code (line 12–16 of the source code 'ITM.cpp') but further development of APHIS will make it possible to set the area directly using the GUI. The six resulting templates extracted from a single sample are individually compared with the candidate pattern and the scores resulting from the comparisons are added up to produce the final sample–candidate matching score. APHIS produces an ITM score list per comparison where candidates are ordered, from highest to lowest, by their matching likelihood (the final score). Individual template scores range from −1 to 1, this being the score obtained when the template is a portion of the own input image. Therefore a value of 6 would be a perfect sample–candidate match.

2.4. The capture-photo–recapture studies

We used real data from a capture-photo–recapture study on the Balearic lizard and on the Northern spectacled salamander to assess software matching performance in terms of individual recognition and time efficiency. Both studies aimed to estimate survival and population size using longitudinal data collected during multiple capture-photo–recapture sessions (e.g. Ruiz de Infante Antón et al., 2013; Tenan et al., 2013; Williams et al., 2001). The ventral region of both species is highly variable and preliminary studies have shown that the ventral patterns can be sued for individual recognition (Carafa and Biondi, 2004; Perera et al., 2001). In the Balearic lizard (dark morph) the ventral region is characterized by a uniform dark-blue or dark-gray color (Fig. 1) and individuals differ in the position and dimension of their ventral scales. The ventral region of the spectacled salamander has white, black and red areas of variable shapes and dimensions (Fig. 1) with marked differences across individuals in the color patterns.

Lizards were captured at the island of Moltona off the southern coast of Mallorca (Balearic archipelago, Spain) for three consecutive days in two sessions, June and October 2010 with pit fall traps positioned along and inside shrubs within an area of c. 0.21 ha (Ruiz de Infante Antón et al., 2013; Tenan et al., 2013). Captured individuals were held under a glass to ensure a clear picture of their ventral scales (Figs. 1, 2, 3 and 5). Photos were taken using a digital camera (Canon© G10) fixed to a stand and positioned inside a photo-cube to standardize light conditions. The picture was made after aligning lens marks with the collar of the individual to diminish differences in rotation, translation or lighting across the pictures. After manipulation, lizards were released. To assess the performance of the photo-identification method, all individuals were double-marked using a low-temperature medical cauterizing unit (Winne et al., 2006). Images of the Northern spectacled salamander have been collected in an area of c. 1 ha of the "Monte di Mezzo" Natural Reserve as a part of a large-scale ecological study (MANFOR CBD; LIFE09 ENV/IT/000078). Animals were captured by hand during their terrestrial activity in two sessions of two consecutive days twenty days apart (8–9 and 28–29 October 2013). Images were taken at low resolution (1280 × 960 pixel) using a digital camera (Nikon© Coolpix P100), at variable distance from the subject and without standardizing light conditions. Individuals were first identified by assigning a binary code to each image on the basis of four chromatic characters as suggested in Carafa and Biondi (2004). These results were used to assess the percentage of correctly identified matches by APHIS. Given the belly pattern of salamanders and the absence of clearly identifiable spot-like points, the ventral images were processed using ITM approach, only.

In each study the images taken the first day were used to create the initial repository. APHIS classified each subsequent photo as a recapture or as a new individual whether a match was found in the existing catalog or not, respectively. When a match is found the processed image is stored in the same directory of the matched sample, otherwise a new directory is created. Each processed image is considered as candidate for next comparisons, so that multiple images from the same individual taken in different capture-photo–recapture sessions are treated as independent samples. The reliability of both approaches implemented in APHIS was assessed by recording the number of correctly classified recaptures. For each misclassified picture we assessed the phase in which it occurred and inspected photo characteristics to identify possible physical character responsible for the misclassification. In addition to the real sets of image, to evaluate time efficiency of the SPM and ITM

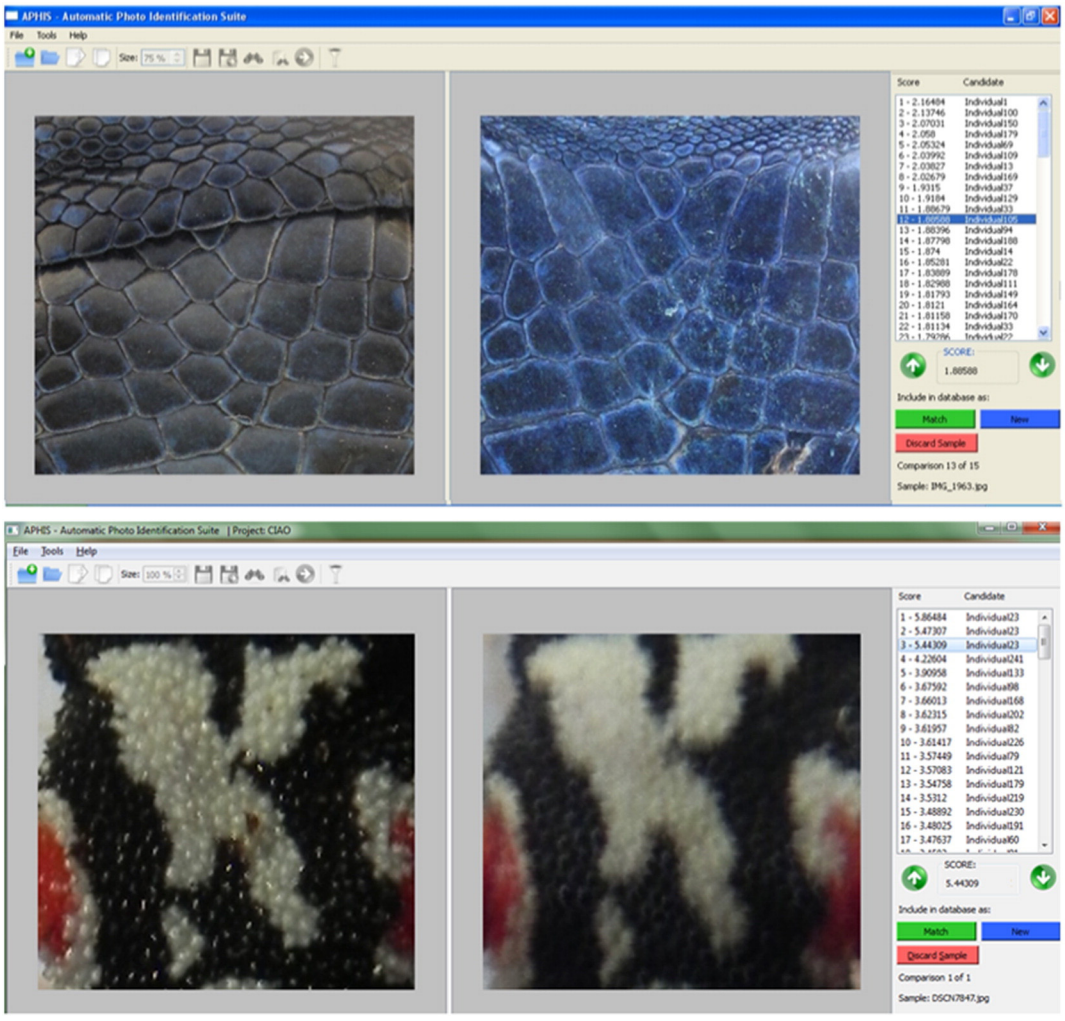

Fig. 5. Matching between a sample image (left) and each of the candidates (right), classified according to the match score (e.g. the likelihood of a correct match). When the pattern to match is uniform, ITM is sensitive to image luminosity, local bright spots or shadows and body torsion. The upper photo shows a correct match that was classified at position twelve in the list of candidates, probably due to the difference in brightness between the sample and the candidate images. However, when the pattern to match is highly contrasted ITM has proved to be less sensitive to image quality. The lower figure shows a match classified among the first three even when the library image (right) was blurred.

approaches we randomly choose 100 samples of Balearic lizard and analyzed them against a repository of a thousand candidates in a computer with an Intel Core Duo 2.40 GHz processor with 3 GB of RAM memory. In general, SPM approach required between 30 and 50 points per individual and, in both approaches the 20 first candidate pictures proposed by APHIS as potential matches were inspected before assignment. We have calculated the total time invested by the user in supervised tasks of this analysis, which include the pre-processing steps (i.e. the marking of scale intersections in SPM approach) and the visual comparison of likely matches after the processing phase occurred.

3. Results

The 287 images, of which 91 were recaptures, were analyzed using the SPM and the ITM procedures. The two approaches, ITM and SPM, delivered similar results, however, the overall number of photos classified as new captures by both approaches were different. The SPM approach correctly classified all newly photographed individuals (percentage of correctly classified pictures = 100%), while ITM found 85 of the 91 recaptures (93.4%). Excluding user's mistakes (e.g. reference points placed wrongly), ITM approach resulted in 95.6% of correctly classified recaptures. The three errors were due to image characteristics such as marked differences in luminosity, local shadows, or variations in pigmentation or lepidosis, i.e. the scale pattern deformation due to body torsion. Nineteen of 305 images of northern spectacled salamander were recaptures. In this case the ITM approach correctly classified them all (100%). The whole ITM analysis took 52 min against the 215 min of the non-automatized method originally used to determine the number of recaptures. The analysis of 100 recaptures on a repository of a thousand took a total of 329 min with ITM and 266 min with SPM (Table 1), done in separate intensive batch sessions. However, the time invested in supervised tasks for the ITM approach (104 min) was nearly a half of this invested at the SPM approach (197 min; Table 1). The unsupervised task took 225 min for ITM and 69 min for SPM.

Table 1
Time spent in photo-matching of lizard images using a batch search of 100 samples against a repository of 1000 individuals. Supervised tasks include pre-processing (reference points and pattern edition) and post-processing (visual inspection of likely matches); the calculation of scores for each sample–candidate pair is automatically conducted by the software, therefore it is an unsupervised task.

Approach	Time (min.)		
	Total	Supervised tasks	Unsupervised task
SPM	266	197	69
ITM	329	104	225

Hence the ITM approach had a longer processing time but the pre-processing phase was faster. On the other hand the longer pre-processing phase in SPM was paid off by a short processing period.

4. Discussion

Individual identification by photo recognition is becoming an increasing area of research. At present, there are several routines available for photo-matching, for example 'I^{3}S' (van Tienhoven et al., 2007),'MantaMatcher' (Town et al., 2013), 'StripeSpotter' (Lahiri et al., 2011), Sloop (Gamble et al., 2008) and 'Wild-ID' (Bolger et al., 2012). Some are highly customized and some are very flexible. Our purpose here was neither to compare them nor to create yet another procedure for a particular problem. Rather it was to provide users with a new integrative tool conceived to grow modularly offering common features and different algorithms (two at the moment) with user friendly options, metadata filtering, short pre-processing time and enough flexibility to be used on different ecological cases. A significant feature of APHIS that distinguished it from most of the existing software is that pictures can be processed in batches because the pre-processing and the photo-matching phases are independent. The software was designed to pack unsupervised and supervised tasks into separate working phases, allowing the sequential treatment of pictures in a batch. The photo-matching is an automated task that requires long computation times and does not need to be monitored. Such work-flow should limit the time invested by the user to the pre-processing and the post-processing phases only. This minimizes the time spent by the user in front of the computer. This is a simple but relevant improvement in front of solutions where automated photo-matching should be started and inspected independently for every picture. Another novel aspect is that APHIS creates log files that can be used to track the analyses and kept for successive examinations. A companion procedure ('ResultsDigest', freely available at http://www.imedea.uib-csic.es/bc/ecopob/) was built to extract results from the log files generated by APHIS. It generates a table by ordering images of each individual according to date. Users can obtain the photo-history of each individual for further analysis and any image can be inspected by simply selecting its name from the table. At present APHIS allows users to choose between two matching approaches, the Spot Pattern Matching (SPM) and the Image Template Matching (ITM). In the SPM approach, based on the algorithm of the existing I^{3}S software (Van Tienhoven et al., 2007), the comparison between sample and candidate pictures is made only across pairs of spots marked at both pictures. This reduces differences among patterns and focuses the analysis on common or easily identified body marks. The SPM approach tolerates some discrepancies in the image rotation angle between sample and candidate pictures (Speed et al., 2007). This is possible because of the affine spatial correction applied, which simulates a comparison between spot patterns in the same two-dimensional space. Although this method unrealistically assumes that the individual is two-dimensional, it can be considered a good approximation if the region of interest is selected at a flat and rigid part of the individual's body (Van Tienhoven et al., 2007). The major drawback of the SPM is that pre-processing time is long as far as the user has to manually select 20–50 spots on each photograph to create the image 'fingerprint'. However, this method correctly identified 100% of recaptures when applied to the lizard dataset. Another remark is that the metadata based filtering system provided for SPM can reduce the computing time but an erroneously assigned value can prevent the detection of a real match. In contrast, the ITM approach reduces the pre-processing effort to only the setting of two reference spots per picture that will be used for rotation as well as processing starting points (Fig. 3). However, it is important to set uniquely recognizable body parts or marks as reference points because the reliability of matching scores is extremely dependent of the reproducibility of this selection across samples. In this case, we decided to use the normalized versions of the template matching algorithm to minimize the effect of differences in brightness between templates in calculating the matching scores (Bradski, 2000). Additionally, the simultaneous use of six templates was incorporated to prevent possible distortions affecting only a specific portion of the image (Fig. 3). Despite these efforts to optimize the robustness of the method, the study of lizards shows that ITM keeps being especially sensitive to luminosity differences from sample to sample, local bright spots or shadows, the angle between the individual and the photographic axis or the body torsion. These drawbacks can affect the score values and mask real matches, although with very contrasted and defined chromatic patterns, as in the case of the spectacled salamander, the procedure succeeded in finding matches among images of very different quality (Fig. 5). The need to assume that the individual is two-dimensional also limits this method. However, if photo characteristics can be kept similar across samples or if the patterns are highly contrasted the ITM becomes a fast and versatile analytical approach to be used for comparing almost any visually identifiable natural mark. Another aspect of ITM is that the pre-processing is limited to the set-up of reference points. This simplifies the standardization of manual annotation and facilitates the use to non-experienced users. Also ecological studies where matching accuracy is not critical, i.e. age determination based in the observation of progressively changing patterns in skin, feather or fur pigmentation, could benefit from approaches minimizing user intervention. In conclusion, the SPM is a highly precise photo-identification method for species showing variable patterns of lepidosis (see also Sacchi et al., 2010) and resulted in no identification errors. The ITM approach is recommended when marks are clearly visible, i.e. highly contrasted with the background color, and/or light conditions similar across pictures while SPM is optimal when photo conditions cannot be standardized, i.e. animals are not always in the same position or the exposure changes across pictures. Strengths of both approaches are summarized in Table 2, providing basic guidelines to researchers deciding which approach could better suit their studies.

Finally, the two procedures available in APHIS are semi-manual and images need to be pre-processed by the user before the matching routine begins. Although the pre-processing phase is fast and not demanding (especially in ITM), there are photo-matching procedures, such as training algorithms for facial or shape recognition, for example, that do not need pre-processing (Journaux et al., 2008; Smach et al., 2007). However these procedures typically use multiple images from different angles or with different luminosity to train the algorithms. In many ecological studies, like ours, only one image is taken for each individual and shooting multiple pictures would increase animal handling time. In addition in a semi-manual procedure the process is interactive and users decide which features of the image have to be matched or discarded (Van Tienhoven et al., 2007). For this reason, most available procedures for animal photo-matching (see a list above) are semi-manual.

4.1. Further development

APHIS aims to provide a 'suite' to incorporate different photo-matching routines so that users would choose the most appropriate one. At present APHIS include two alternative approaches, the SPM

Table 2
Comparisons between the two photo-matching approaches currently available in APHIS. 'Tolerance' is the tolerance to brightness, image definition and body deformations; 'Versatility' is the possibility to customize the parameters used by the matching routine.

	Need of visible marks	Tolerance	Pre-processing effort	Matching efficiency	Versatility
SPM	Low	High	High	High	Moderate
ITM	Moderate to high	Low	Low	Moderate to high	High

and the ITM. A natural future advance would be to include other approaches as those recently developed on the Scale Invariant Feature Transform (SIFT, Lowe, 2004). The SIFT is a computer vision approach that has been proposed by several authors as suitable for photo-identification ecological studies (Buonantony, 2008; Yu et al., 2013). The approach has shown to perform a reliable matching between images of the same object, being robust in front of scale, rotation, affine, 3D viewpoint, noise and illumination differences (Lowe, 2004). Examples of software with a SIFT-based routine are Wild-ID (Bolger et al., 2012) and Manta Matcher (Town et al., 2013). APHIS offers a metadata filtering mechanism (Fig. 2), which is not present, as far as we know, on most of the available photo-matching software. Also the ITM includes an interesting characteristic that is to divide the pattern into six sub-patterns that are analyzed independently and contribute partially to the final score. A measure that minimizes the effect of local distortions. Finally, it will be interesting to include an initial procedure to assist users in choosing the best routine available for the case considered.

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References

Bolger, D.T., Morrison, T.A., Vance, B., Lee, D., Farid, H., 2012. A computer-assisted system for photographic mark–recapture analysis. Methods Ecol. Evol. 3, 813–822.
Bradski, G., 2000. The OpenCV library. Dr. Dobbs J. 25 (11), 120–126.
Buonantony, D., 2008. An Analysis of Utilizing the Leatherback's Pineal Spot for Photo-identification. Duke University (Doctoral dissertation).
Carafa, M., Biondi, M., 2004. Application of a method for individual photographic identification during a study on *Salamandra salamandra gigliolii* in central Italy. Ital. J. Zool. 2, 181–184.
Fernández-Chacón, A., Bertolero, A., Amengual, A.D., Tavecchia, G., Homar, V., Oro, D., 2011. Spatial heterogeneity in the effects of climate change on the population dynamics of a Mediterranean tortoise. Glob. Chang. Biol. 17, 3075–3088.
Gamble, L., Ravela, S., McGarigal, K., 2008. Multi-scale features for identifying individuals in large biological databases: an application of pattern recognition technology to the marbled salamander *Ambystoma opacum*. J. Appl. Ecol. 45, 170–180.
Gauthier-Clerc, M., Gendner, J.P., Ribic, C.A., Fraser, W.R., Woehler, E.J., Descamps, S., Gilly, C., Le Bohec, C., Le Maho, Y., 2004. Long-term effects of flipper bands on penguins. Proc. R. Soc. B Biol. Sci. 271, S423–S426.
Huffard, C.L., Caldwell, R.L., DeLoach, N., Gentry, D.W., Humann, P., MacDonald, B., Moore, B., Ross, R., Uno, T., Wong, S., 2008. Individually unique body color patterns in octopus (*Wunderpus photogenicus*) allow for photoidentification. PLoS One 3 (11), e3732.
Journaux, L., Destain, M.-F., Miteran, J., Piron, A., Cointault, F., 2008. Texture classification with generalized Fourier descriptors in dimensionality reduction context: an overview exploration. In: Prevost, Lionel, Marinai, Simone, Schwenker, Friedhelm (Eds.), In Artificial Neural Networks in Pattern Recognition. Lecture Notes in Computer Science 5064. Springer, Berlin Heidelberg, pp. 280–291.
Karanth, K.U., Nichols, J.D., 1998. Estimation of tiger densities in India using photographic captures and recaptures. Ecology 79, 2852–2862.
Lahiri, M., Tantipathananandh, C., Warungu, R., Rubenstein, D.I., Berger-Wolf, T.Y., 2011. Biometric animal databases from field photographs: identification of individual zebra in the wild. Proceedings of the ACM International Conference on Multimedia Retrieval (ICMR 2011), Trento, Italy.
Langtimm, C.A., Beck, C.A., Edwards, H.H., Fick-Child, K.J., Ackerman, B.B., Barton, S.L., Hartley, W.C., 2004. Survival estimates for Florida mantees from the photo-identification of individuals. Mar. Mammal. Sci. 20 (3), 438–463.
Lebreton, J.D., North, P.M., 1993. In: Lebreton, J.D. (Ed.), Marked Individuals in the Study of Bird Population. Birkhäuser Verlag, pp. 373–386.
Lowe, D., 2004. Distinctive image features from scaleinvariant keypoints. Int. J. Comput. Vis. 60 (2), 91–110.
Martínez-Jauregui, M., Tavecchia, G., Cedenilla, M.A., Coulson, T., Fernàndez de Larrinoa, P., Muñoz, M., González, L.M., 2012. Population resilience of the Mediterranean monk seal *Monachus monachus* at Cabo Blanco peninsula. Mar. Ecol. Prog. Ser. 461, 273–281.
May, R., 2004. Ecology: ethics and amphibians. Nature 431, 403.
McCarthy, M.A., Parris, K.M., 2004. Clarifying the effect of toe clipping on frogs with Bayesian statistics. J. Appl. Ecol. 41, 780–786.
Perera, A., Pérez-Mellado, V., Cortázar, G., 2001. Searching for the fingerprint of lizards: an addition of a photographic identification technique. IV Symposium on the Lacertids of the Mediterranean Basin, Maó.
Ruiz de Infante Antón, J., Rotger, A., Igual, J.M., Tavecchia, G., 2013. Estimating lizard population density: an empirical comparison between line transect and capture–recapture methods. Wildl. Res. 40, 552–560.
Sacchi, R., Scali, S., Pellitteri-Rosa, D., Pupin, F., Gentilli, A., Tettamanti, S., Cavigioli, L., Racina, L., Maiocchi, V., Galeotti, P., Fasola, M., 2010. Photographic identification in reptiles: a matter of scales. Amphibia-Reptilia 31 (4), 489–502.
Smach, F., Lemaître, C., Gauthier, J.-P., Miteran, J., Atri, M., 2007. Generalized Fourier descriptors with applications to objects recognition in SVM context. J. Math. Imaging Vis. 30 (1), 43–71.
Speed, C.W., Meekan, M.G., Bradshaw, C.J.A., 2007. Spot the match—wildlife photo-identification using information theory. Front. Zool. 4 (2), 1–11.
Tavecchia, G., Radel, R., Boy, V., Johnson, A., Cézilly, F., 2001. Sex- and age-related variation in survival probability and the cost of the first reproduction in breeding Greater Flamingos. Ecology 82 (1), 165–174.
Tavecchia, G., Coulson, T., Morgan, B.J.T., Pemberton, J.M., Pilkington, J.C., Gulland, F.M.D., Clutton-Brock, T.H., 2005. Predictors of reproductive cost in female Soay sheep. J. Anim. Ecol. 74 (2), 201–213.
Tenan, S., Rotger, A., Igual, J.-M., Moya, O., Royle, A., Tavecchia, G., 2013. Population abundance, size structure and sex-ratio in a insular lizard. Ecol. Model. 267, 39–47.
Town, C., Marshall, A., Sethasathien, N., 2013. Manta Matcher: automated photographic identification of manta rays using keypoint features. Ecol. Evol. 3 (7), 1902–1914.
Van Tienhoven, A.M., Den Hartog, J.E., Reijns, R.A., Peddemors, V.M., 2007. A computer-aided program for pattern-matching of natural marks on the spotted raggedtooth shark *Carcharias taurus*. J. Appl. Ecol. 44, 273–280.
Verborgh, P., De Stephanis, R., Pérez, S., Jaget, Y., Barbraud, C., Guinet, C., 2009. Survival rate, abundance and residency of long-finned pilot whales in the Strait of Gibraltar. Mar. Mammal. Sci. 25 (3), 523–536.
Williams, B.K., Conroy, M.J., Nichols, J.D., 2001. Analysis and Management of Animal Populations. Elsevier Academic Press, San Diego.
Winne, C.T., Willson, J.D., Andrews, K.M., Reed, R.N., 2006. Efficacy of marking snakes with disposable medical cautery units. Herpetol. Rev. 37 (1), 52–54.
Yu, X., Wang, J., Kays, R., Jansen, P., Wang, T., Huang, T., 2013. Automated identification of animal species in camera trap images. EURASIP J. Image Video Process. 2013 (1), 52.