A Registration Algorithm for the Identification of Individual Parrots Based on the Patterns of Filing Ridges on the Internal Surface of Their Upper Bill Tip

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Abstract

Ridges on the internal side of the upper bill tip (i.e., "filing ridges") of parrots and some cockatoos form patterns that are characteristic of genera and, therefore, can be used for the classification of parrots and cockatoos. These patterns are also individually variable and, thus, could be used to fingerprint individual parrots. The objectives of our project were to evaluate the degree of individual variability and to develop a method and algorithm for registering and comparing the patterns of ridges by using a rigid registration technique. Within the datasets, we have been successful in identifying each unidentified dataset using this method. For 22 of the 27 unidentified datasets, we found a degree of magnitude (i.e., the total error taken as the sum of distances between corresponding points) to be on the scale of 101 or greater between the match with the correct dataset and the match with all other datasets of the database via a squared residual error assessment. For the remaining datasets, instances occurred in which the difference was smaller for two birds, but the correct bird was identified, nonetheless, while accurately ruling out over 90% of the incorrect bird matches.

Keywords: Biometrics, Registration, Parrots, Conservation, Filing Ridges, Fingerprinting, Pattern Recognition, Non-invasive Tagging

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1. INTRODUCTION

Mapping and measuring biological structures has a well-documented history in biometrics and pattern recognition. It has been applied to areas such as fingerprint identification [1], retinal scans [2], facial recognition [3], growth and regeneration studies [4], and individual identification of members of animal populations [5]; [6]; [7]; [8]. The ability to identify individuals, species, or biological features accurately and efficiently has become an increasingly prominent issue in biology, medicine, and public safety. Another issue of increasing importance is the ability to follow identifiable structures in particular individuals through time (e.g., monitoring cell proliferation, tissue regeneration, or tumor growth; predicting changes of facial features of disappeared persons, etc.).

While human beings (and probably many mammals, birds, and even reptiles) recognize individuals of their own species through their Gestalt, or integrated complex of features, the recognition of individuals of a different species is more difficult for humans, although ethologists, who have studied particular populations of mammals and birds over many years, and farmers, who are in daily and intimate contact with domesticated animals, are capable of doing so. In general, however, when humans need to distinguish animals individually and cannot tag them with special markers, such as leg bands for birds, they rely on particular traits or features that can be measured or counted to identify, or fingerprint, individuals of non-human species [5]; [6]; [7]; [8]. The same approach to identify individuals is also used when the size of a human population exceeds the human brain capacity to memorize the identity of each individual. The type of features that can be used to fingerprint individuals depends on the morphology of the species and needs to be discovered afresh for each species, such as finger prints in humans, paw prints of fishers (*Marten pennanti*) [6], patterns of spots and stripes in whale sharks, birds and mammals [7], epidermal ridges on the muzzle of beef cattle [8], and retinal vascular pattern in lambs and sheep [9].

The need for fingerprinting methods to identify individual animals has been increasing with the intensifying illegal trade in wildlife [10]. Parrots have become one of the prime victims of the illegal wildlife trade for several reasons that make them highly prized [11]; [12]; [13]; [14]. If tame, they can make entertaining pets that can learn to understand and utter human speech. Their colorful plumage is exceedingly appealing. As specialized seed eaters, most parrots can be maintained in captivity on a simple diet of dry seeds at least for some time. Compared to most other birds, many parrots also breed relatively easily in captivity, thereby having encouraged a long tradition of aviculture in Europe, Japan, North America, and, more recently, the Middle East. At the same time, parrots have also become increasingly rare in their natural habitat because of habitat destruction that progresses too fast and radically for most parrots to adapt to the new conditions. All these attributes render many parrot species rare and, thus, very valuable and potentially the objects of poaching, theft, and contraband.

To facilitate the recovery of poached or stolen parrots and to distinguish them from captivity-bred parrots, a method of fingerprinting parrots is of fundamental importance. However, the tagging methods that are currently available are not completely satisfying. For example, DNA fingerprinting [15]; [16]; is expensive, and testing is not unproblematic as the data base for comparison is still small. Closed metal leg bands that are slipped over the feet of nestlings can occasionally lead to leg injuries and can be removed [17]; [18]; [19]. Implanted microchips are increasingly used to tag captive and wild populations, but are not recommended for small birds [20], and may induce infections and tumors at the implantation site [19]. They need to be registered and updated when parrots change hands, and they can be removed. Photographs for visual identification of parrots are problematic because the appearance of feathers through wear, molt, and metabolic or hormonal imbalances can change over time. Hence, a feature that is individually variable and cannot be removed or altered would facilitate the fingerprinting of parrots [19].

Our study explores the feasibility of using such a feature, namely the pattern of so-called filing ridges on the internal surface of the upper bill tip of parrots and most cockatoos. Filing ridges are

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rugosities on the inside of the upper bill tip of parrots and most cockatoos, which use them to sharpen the cutting edge of their mandible after a bout of seed shelling or wood gnawing [21]; [22]; [23]. They are part of the bill structures of parrots and cockatoos, which have originally evolved and been selected for the extraction of wood-boring insect larvae and the cracking of woody seed and nut shells [24]; [25]. Although the pattern formed by the filing ridges are not as clearly characteristic of genera as the ridges on the cornified palate [22]; [23], they were recently discovered to vary individually upon closer inspection [26], [27].

Filing ridges are formed by the cornified epidermis of the internal side of the rhamphotheca of the upper bill. They are underlain by ridges or rows of papillae that are formed by the underlying dermis in the same manner as the epidermal ridges of human fingerprints are preformed by the underlying dermis. Therefore, the filing ridges are not simply surface structures that could be removed by abrasion, but instead are manifestations of the intrinsic structure of the epidermis that is formed deep below the surface. For this reason, the patterns formed by the filing ridges are permanent and do not change during the life of an individual even when they are continuously worn down, except if wounds damage the dermis, just like the ridges of human fingerprints.

In the present study, we explored whether the pattern of filing ridges differ sufficiently among individuals to be used for fingerprinting purposes. In order to do so, we developed and evaluated a method and algorithm for fingerprinting parrots by using a rigid registration technique to register and compare the patterns of filing ridges on the internal side of the upper bill tip of 27 individuals of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the ultimate goal of developing a method to tag individual parrots and, thereby, curb the poaching, contraband, and theft of increasingly rare and valuable parrot and cockatoo species.

2. MATERIALS AND METHODS

2.1. Materials
Casts of the filing ridges on the internal surface of the upper bill tip were collected from 27 individuals of the Hispaniolan Amazon Parrot (*Amazona ventralis*). These individual parrots have been part of a captive population that has been under the supervision of Dr. Thomas N. Tully and has been housed in the Life Sciences Animal Care Facility at Louisiana State University, Baton Rouge, which has full AAALAC (Association for Assessment and Accreditation of Laboratory Animal Care) accreditation.

The casts were made by placing individual parrots under general anesthesia, which was induced using 5% isoflurane (Hospira, Inc., Lake Forest, IL, USA) with a 1.5% flow of oxygen through a face mask. Once under anesthesia, the parrots were fitted with an endotracheal tube and maintained under a surgical level of anesthesia with 2.5% isoflurane and 1L flow of oxygen. The mouth cavity was cleared of any debris. The two-phases of the casting putty (3M™ ESPE™ Express™ STD Putty) were mixed, and the putty was gently pressed against the internal surface of the upper beak when the putty had achieved the proper consistency and until it started to set. The casts were checked for quality after they were removed from the beak, and additional casts were made until a satisfactory cast was achieved. Upon completion of the procedure, the isoflurane anesthetic agent was discontinued, and the individual parrots were maintained on a 1L flow of oxygen until they recovered approximately 1-2 minutes later, after which they were returned to their cage.
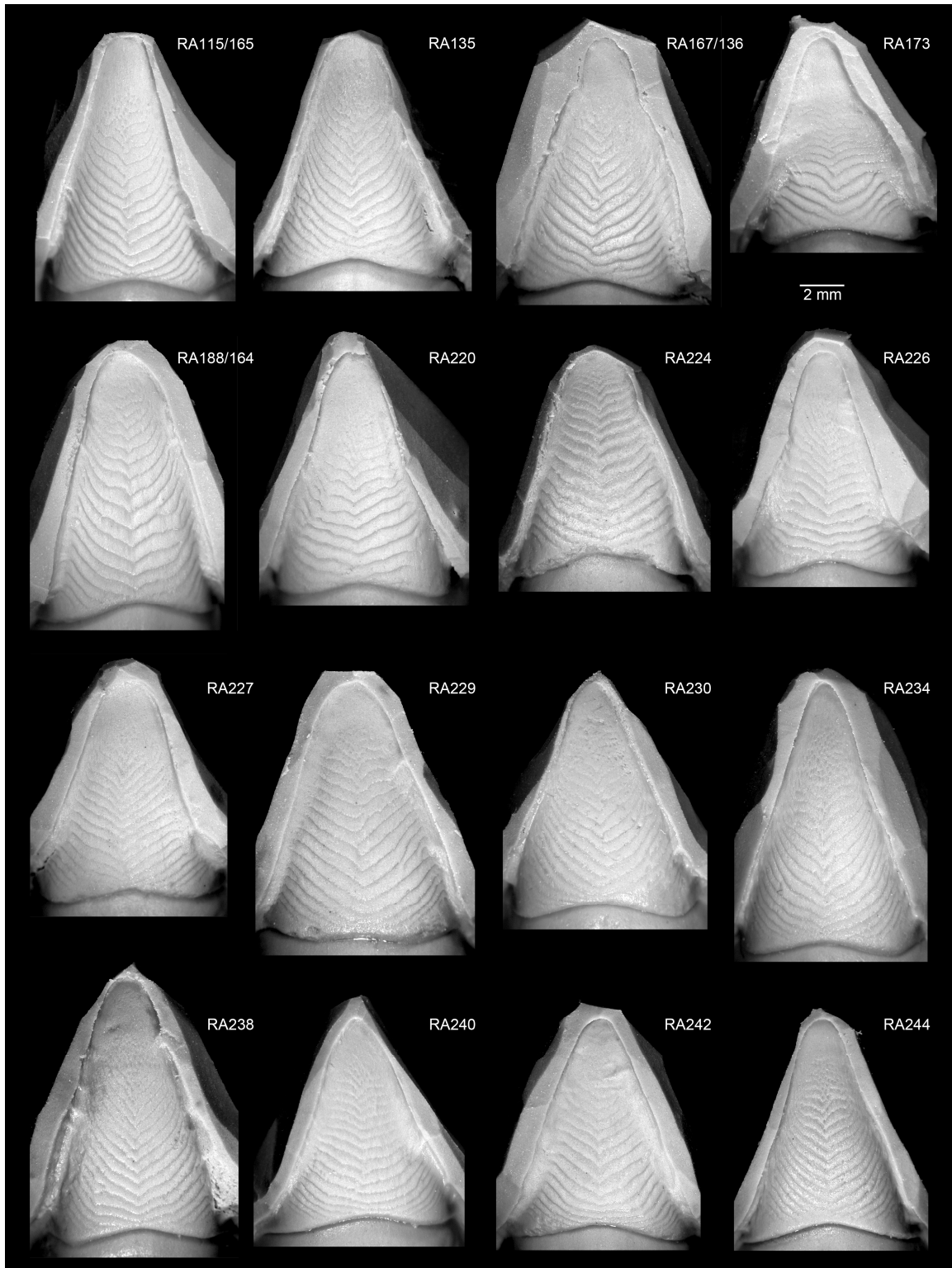
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FIGURE 1A : Digital images of casts of the filing ridge patterns of the internal surface of the upper bill tip of 16 individuals of the Hispaniolan Amazon Parrot (*Amazona ventralis)* used in our study to show the high degree of individual variability in the ridge pattern. The images are scaled to the same magnification (see scale bar), and the numbers represent catalog identification numbers.
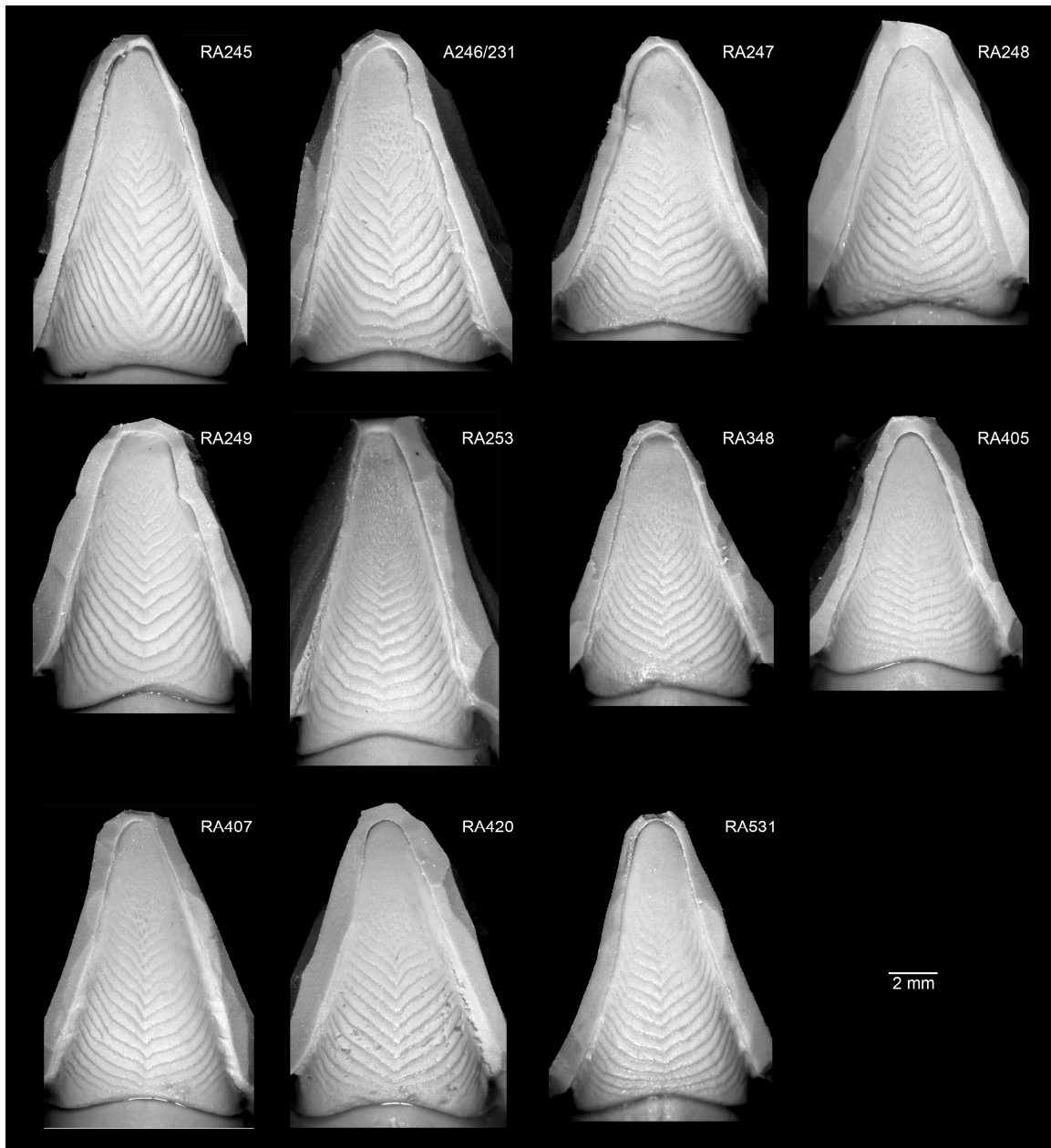
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FIGURE 1B. Digital images of casts of the filing ridge patterns on the internal surface of the upper bill tip of the remaining 11 individuals of the Hispaniolan Amazon Parrot (*Amazona ventralis)* used in our study to show the high degree of individual variability in the ridge pattern. The images are scaled to the same magnification (see scale bar), and the numbers represent catalog identification numbers.

The casts were photographed with a stereomicroscope (Leica MZ6) with a digital camera attachment (Spot Insight Firewire, Diagnostic Instruments, Inc., Sterling Heights, MI, USA), extended focus computer software (Image-Pro Plus 5.1 and In-Focus 1.60), and ring-light and gooseneck fiber-optics, which were equipped with polarizing filters and connected to a light box (Intralux 6000, Volpi USA, Auburn, NY, USA). Care was taken to place the casts under the stereomicroscope in such a manner that the surface bearing the imprints of the filing ridges would be oriented horizontally to ensure a sharp focus over the entire, slightly curved surface. This orientation could be reproduced fairly consistently for all 27 casts.

Although the casts of the filing ridges are less crisp than the actual filing ridges, they retain the shape and arrangement of the individual ridges and, thus, the pattern of the filing ridges (Figure 1a, b). Because of the individual differences of the length, proportion, and curvature of the beaks, it was not possible to ensure that all photographs were taken at exactly the same angle. The introduction of this slight error was deemed acceptable as it would test the robustness of the method.

2.2. Registration Method
To compare the filing ridge patterns of the various individuals, a registration-based technique was applied. Methods of registering morphological datasets with one another are well established and readily available in the literature [28], [29], [30]. We used a rigid method in our study, because differences in the size and shape of the upper bill tip and, thus, of the area covered by the filing ridges needed to be preserved and even emphasized to enable the differentiation of the individuals.

Primary registration techniques in general include point-based, surface-based and intensity-based methods. Surface-based methods were not used in our study because of the nature of the data, which are two-dimensional images of the filing ridges and not the filing ridges themselves. Surface based methods often also involve larger datasets, which require more computing power and longer match times. Another deterrent for using surface-based methods was the difficulty of removing from the images artifactual data that were the result of imperfect casts. Finally, a surface based method is not appropriate given the material and tissue properties of the actual filing ridges. The surface structure of the filing ridges of an individual could change temporarily through mechanical abrasion due to normal behaviors, such as eating hard-shelled nuts. Such modifications of the filing ridge pattern could produce inaccurate results in a surface comparison of filing ridge patterns of a particular bird taken at different points in time. However, intensity-based methods are generally more appropriate for the differentiation of high contrast features, such as tumors *versus* normal tissue, or of bone *versus* soft tissue in CT-scans. Therefore, point-based methods seemed to be best suited for our purposes, especially since the preservation of color information was not needed. Point-based methods use morphological landmarks or introduced fiducial markers to represent datasets. The locations of these markers are selected *a priori* and are used to determine the best alignment of two or more datasets. In our study, fiducial markers based on morphological landmarks are used to compare the filing ridge patterns of the individual parrots.

On images of the casts of the internal surface of the upper bill tip, the filing ridges of each individual were first discretized into a pared-down dataset by using the termination points of the filing ridges along the edges of the upper bill tip and the points along the midline, where the filing ridges usually form an angle, as fiducial markers to represent landmarks in the dataset. The pared-down dataset of a particular individual parrot can then be registered with the pared-down datasets of other individuals for comparison and classification. An added benefit of this approach is that the pared-down dataset is much smaller than the full dataset and, therefore, facilitates the manipulation and cataloguing of the datasets. The method presented here is an amalgamation of techniques and concepts based on morphology and image registration.

2.3. Data Extraction
The initial issue that needed to be addressed in our study was the extraction of the information contained in the patterns of filing ridges. Once extracted, the datasets could be used to compare the patterns of two individuals at a time. As the images of the casts of the filing ridges preserved the physical distances, arrangements and shapes of the filing ridges, they could be used for a physical match between the various datasets.

Several methods of extracting the filing ridge patterns were considered. While datasets representing the entire pattern might have been ideal, extracting the pattern is not an inherently simple task because the datasets are two-dimensional images of three-dimensional structures. To perform comparisons, the relationship between corresponding points on the structures must

be known, in advance. In extracting the data, the data must be sampled in some regular interval or in a manner that maintains an expected correspondence of markers in different datasets. Several edge detector-based techniques were used to attempt to delineate the filing ridges, but the images did not have enough contrast to extract the filing ridge pattern consistently and accurately. Therefore, markers were introduced to represent the shape and orientation of the filing ridges.

The criteria for these markers were developed so as to make the selection of the markers consistent and reproducible. In standardizing the marker selection process, an expected correlation was determined between corresponding points, while retaining the information that would allow the identification of unique filing ridge patterns. Initially, markers were placed along the longitudinal axis where the vertices, or troughs, of the filing ridges align themselves (Figure 2). These axial markers were placed starting caudally near the transverse step and cornified palate and progressing towards the tip of the upper bill. At least six axial markers are required to make a comparison using this algorithm. This number was chosen based on the integrity of the available data. Some filing ridge patterns were marred by trauma or artifacts, but each such instance was found closer to the tip of the upper bill than to the cornified palate. In using six points starting caudally, the filing ridge pattern was more likely to be complete, and each dataset could be used for comparison. By their very nature, the axial markers are in very close proximity to the axis of symmetry of the upper bill tip. If a set of markers to the right and to the left at equal distances from the central axis returned the same match value, incorrect identification of a filing ridge pattern could result, because two or more birds could have a filing ridge pattern with the same error value. However, bilaterally symmetrical filing ridge patterns appear to be the exception rather than the rule (Figure 1a, b).

Because of the fairly linear alignment of the axial markers, additional markers are needed to identify individuals and to avoid a false positive. A false positive would occur if two different birds returned the same error value. To aid in generating a unique identification, left and right terminal markers were added at the end points of the filing ridges along the edges of the internal surface of the upper bill tip (Figure 3). To add terminal markers, we identified first the caudalmost axial marker and followed the filing ridge to the left side to its end point where a terminal marker was placed. This procedure was repeated by sequentially following the axial markers towards the tip of the upper bill. If filing ridges bifurcated, the branch with the shortest distance to its end point was followed. This procedure of placing terminal markers was then repeated on the right side of the internal surface of the upper bill tip. Whereas it is generally irrelevant on which side the terminal markers are placed first, the computer code developed for our study required that the same sequence of placing terminal markers be maintained for all images of the filing ridges.

The combination of axial and terminal markers created a pared-down dataset representing the filing ridge pattern of a particular individual parrot. This pared-down dataset has the advantage of being smaller than the original image, while retaining essential information concerning the pattern of filing ridges because the markers are based on the actual shape of filing ridges. This pared-down dataset was used for the comparison of the filing ridge patterns of the various individuals by using a rigid, point-based registration method.

2.4. Data Registration
To make the comparisons, the axial and the left and right terminal markers were combined into a single nx2 matrix, A, where the columns of A contained the x- and y- coordinates of the markers. As order was non-trivial in this comparison, the axial markers were entered first in this matrix, followed by the left terminal markers and finally by the right terminal markers. Only the first six markers of each set of markers were used in this initial comparison. This number was chosen empirically based on the minimum number of filing ridges with well-defined end points in all 27 individuals in our study. The procedure of combining the markers into a single matrix was repeated for all datasets of the 27 parrots. This resulted in two databases, one with the original images of the filing ridge patterns of the 27 parrots and the other with the pared-down data sets.
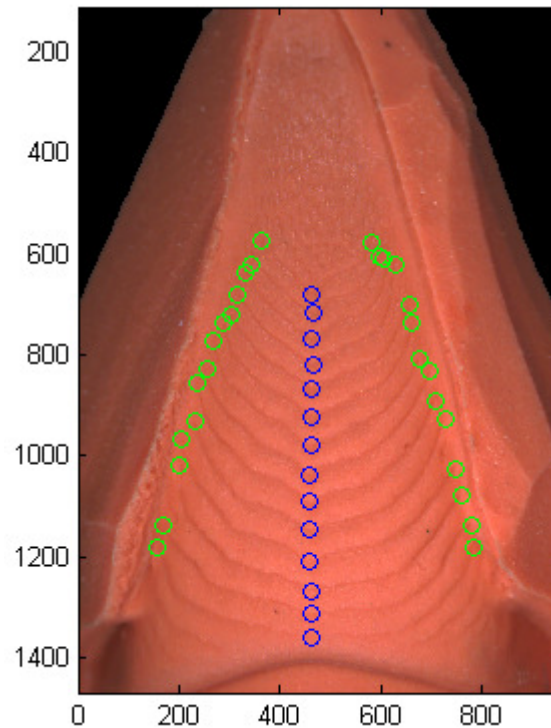
FIGURE 2. Fiducial markers based on the shape of the filing ridges on a cast of the internal surface of the upper bill tip of the individual RA253 of the Hispaniolan Amazon Parrot (*Amazona ventralis*). The blue circles represent axial markers, and the green circles represent terminal markers.

According to the algorithm of Fitzpatrick, *et. al.* [28]; [29]; a rigid registration can be performed to compare datasets. Given two datasets x and y, this algorithm consists of:

1) Calculating the centroids of the filing ridge pattern datasets, x' and y'.

2) Redefining the datasets in terms of distance from their centroids.

3) Computing the weighted fiducial covariance matrix.

4) Determining the singular value decomposition of the covariance matrix.

5) Using the left and right matrices of eigenvectors to determine optimal alignment.

6) Determining the translation that best aligns the datasets in a minimum error sense, based upon the centroids.

$$\varepsilon = \| P_k - T(P_u) \|_2^2$$

The error assessment is typical of methods for registering datasets used in identification algorithms [31], [32], [33]. In the error equation, P_k is the known filing ridge pattern dataset, and $T(P_u)$ is the optimally aligned, unidentified filing ridge pattern dataset. The minimum error sense takes the form of an L_2 – norm squared, consisting of the difference between the locations of the landmarks from dataset 1, and the rotated and translated landmarks in dataset 2. Whereas a

weighted centroid could have been used, we deemed all points to have been equally viable, thus, no weighting value was included. The rotation and translation matrices that were generated form the T transformation and provide the optimal alignment of two datasets in a rigidly transformed sense. The sum distance between optimally aligned, corresponding points in the two datasets is the basis for the comparisons of individual filing ridge patterns.
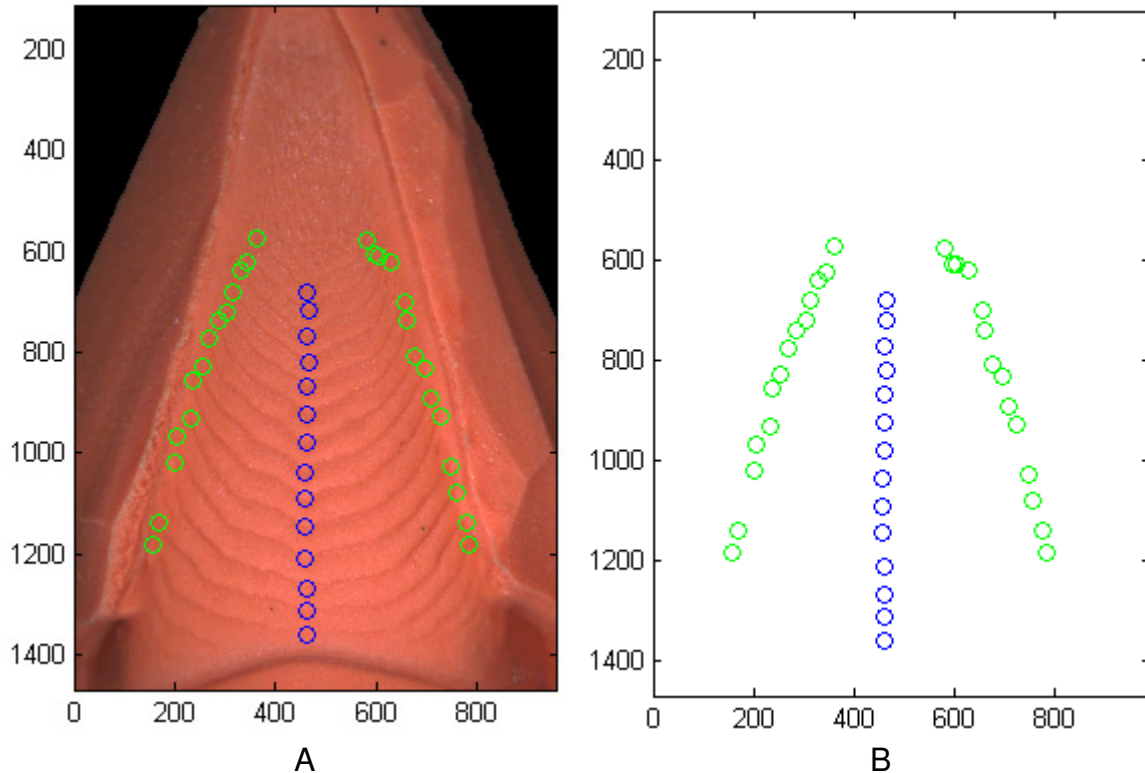

FIGURE 3. The filing ridge pattern on a cast of the internal surface of the upper bill tip of the individual RA253 of the Hispaniolan Amazon Parrot (*Amazona ventralis*). A: Fiducial markers mapped on the original image of the cast. B: Fiducial markers creating a pared-down dataset. The blue circles represent axial markers, and the green circles represent terminal markers.

A rigid registration is often performed with the intention of determining the optimal alignment of two images with a known correspondence. However, this registration procedure can also be used to find the optimal alignments of several images with a given image. The image that returns the smallest error value can then be argued to be the image that is most similar to the given image. If the images under consideration are known to be unique, then this process can be used to help identify specific images.

Several unidentified datasets were analyzed to test whether the applied rigid registration procedure was able to identify specific filing ridge patterns. Using the previously outlined process, several test datasets, U_n, were discretized appropriately into pared-down datasets and then compared one by one with the datasets in the pared-down database, S, in an effort to identify them. Using the same criteria that were used to create the pared-down datasets, S_n, the unidentified test datasets, U_n, were loaded into the computer program. Landmarks along the axis, and the left and right termination points were introduced following the same procedure that was used in creating the pared-down datasets. Once the landmarks representing an unknown test dataset were selected, an automated comparison of the unidentified dataset with all the datasets in the pared-down database was performed. The goal of this comparison was to identify
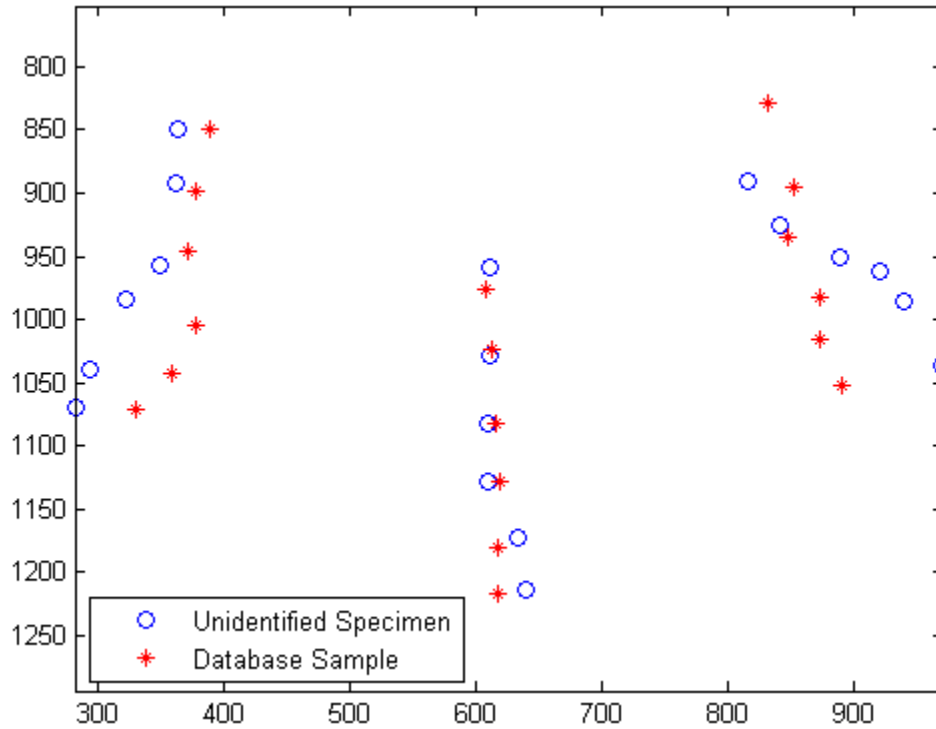
the dataset, K, which most closely matched the unidentified test dataset, U_n. The optimal match was defined as the match that returned the lowest error value, ε.

3. RESULTS

The alignment that was returned after an unidentified dataset was compared to the datasets of the pared-down database is provided in Figure 4a-h. For many datasets, the match was very poor in a quantitative sense, which means that they returned a relatively large value for ε. This is a direct result of the sum of the distances between data points being larger for these matches than for others. The aforementioned issue of non-uniqueness in a set of approximately linear axial data points can be seen in Figure 4b. Here, although the markers on the axis line up very well for this individual, the right and left terminal markers fail to generate an appropriate match and help to rule out this filing ridge pattern as a match. It is the individual RA240, seen in Figure 4f, which returns the most favorable match with the unidentified test dataset, both from inspection and in a quantitative sense.

FIGURE 4A. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA226 from the pared-down database.
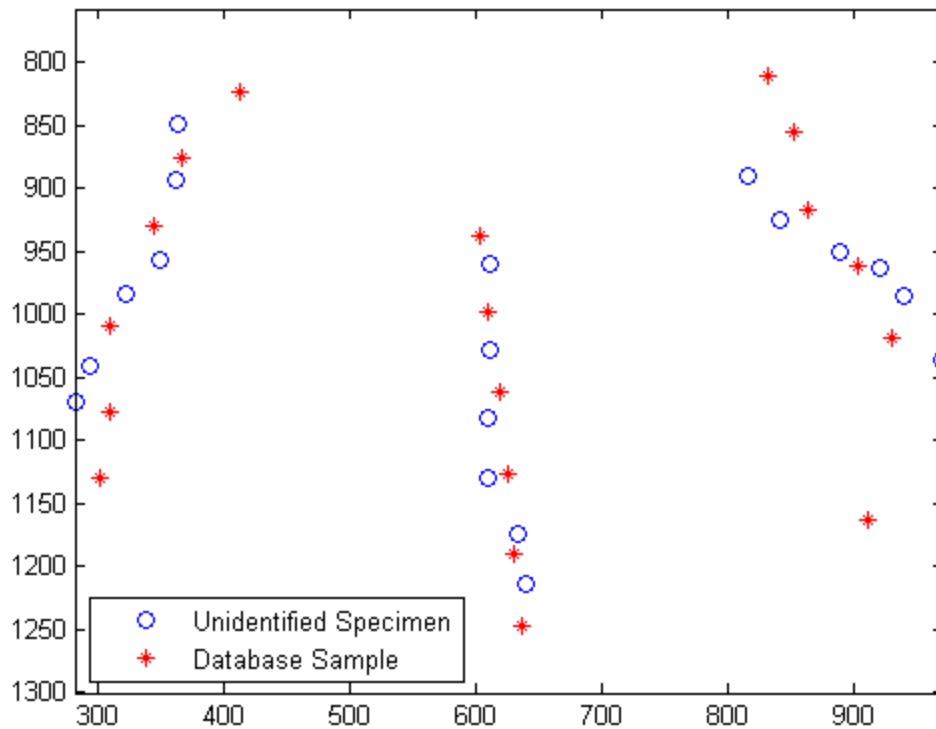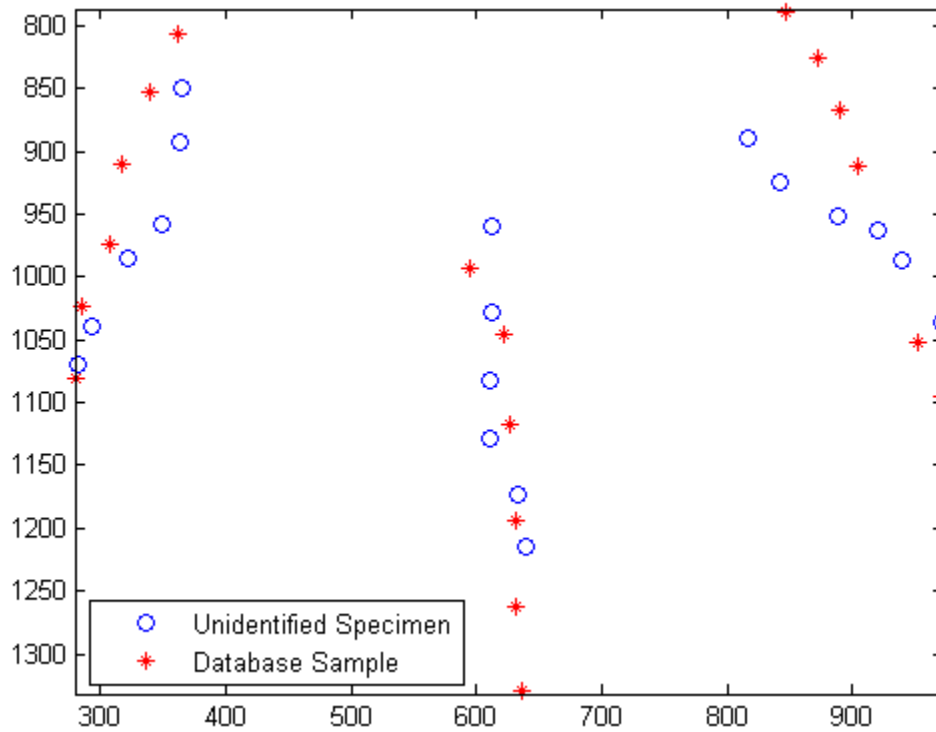
FIGURE 4B: Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA227 from the pared-down database.
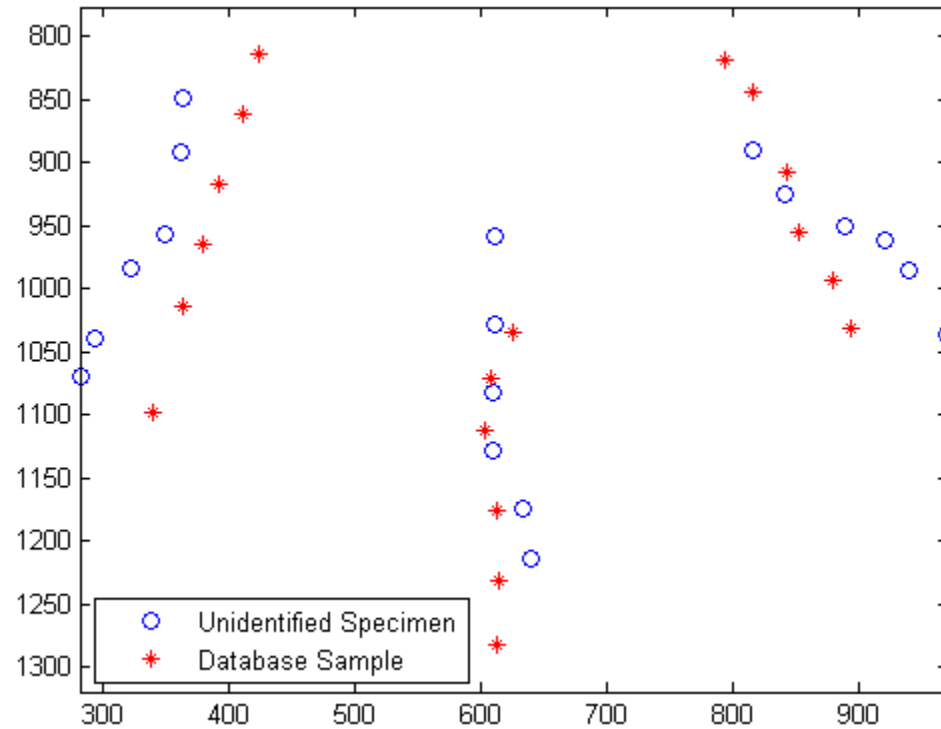
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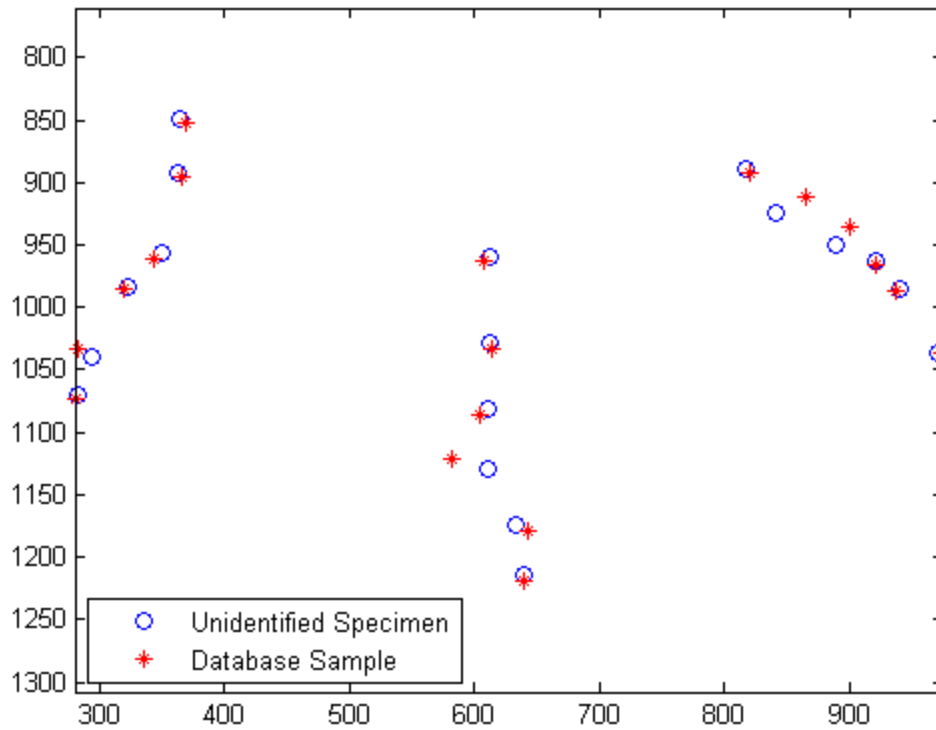
FIGURE 4C. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA220 from the pared-down database.

FIGURE 4D. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA229 from the pared-down database.
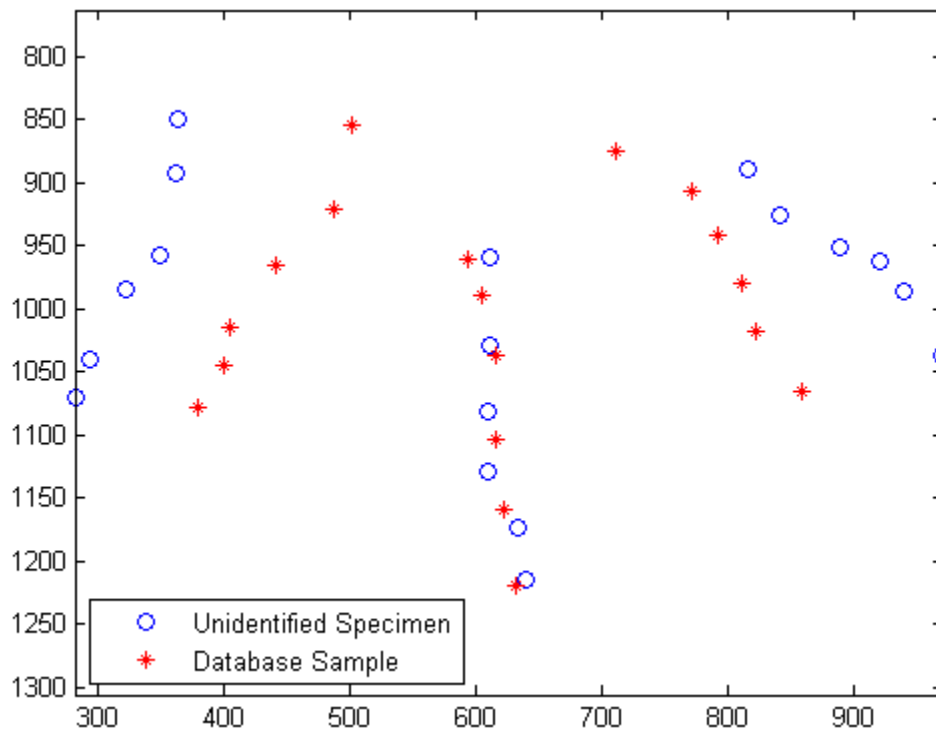
FIGURE 4E. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA348 from the pared-down database.

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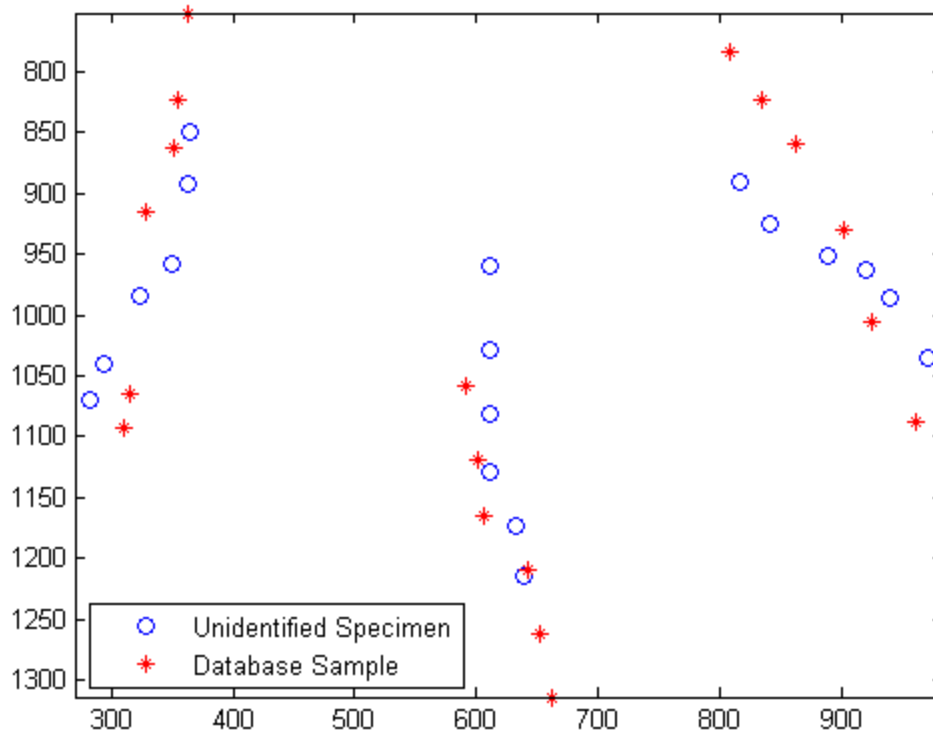

FIGURE 4F. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA240 from the pared-down database.

FIGURE 4G. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA173 from the pared-down database.

FIGURE 4H. Comparison of the test dataset of the filing ridge pattern on the internal surface of the upper bill tip of the unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with the dataset of the individual RA135 from the pared-down database.

The results of the comparisons of four unidentified test datasets with the datasets in the pared-down database are provided in Figure 5a-d. In each figure, the error value, ε, which is generated by comparing the unidentified dataset with each dataset of the database, is plotted relative to each specimen's catalog number. The error value represents the sum of the distances between corresponding points of two datasets after alignment. Optimally aligned datasets whose ε-value is lower represent a better match than datasets that have a higher ε-value despite being optimally aligned. In some cases, the total distance between corresponding points of two datasets is an order of magnitude lower than the error values given by the optimal alignment with any other dataset. Even in cases, in which the difference in error values is not as pronounced, the difference is significant enough to rule out the majority of the datasets as matches and to narrow the pool of possible matches. The distances between corresponding points in the compared pared-down databases in Figure 5a-d are machine units or pixels. Through a directly proportional (rigid) conversion, the machine units can be converted back to physical distances, which are more meaningful, given the datasets being used. For our datasets, 10^2 machine units are equal to 1 millimeter on average. Thus, errors on the order of 10^{-3} machine units convert to about 10^{-5} millimeters of physical distance. This suggests that the ε-measurements of datasets that differ by an order of magnitude or more are highly unlikely to be from the same dataset.

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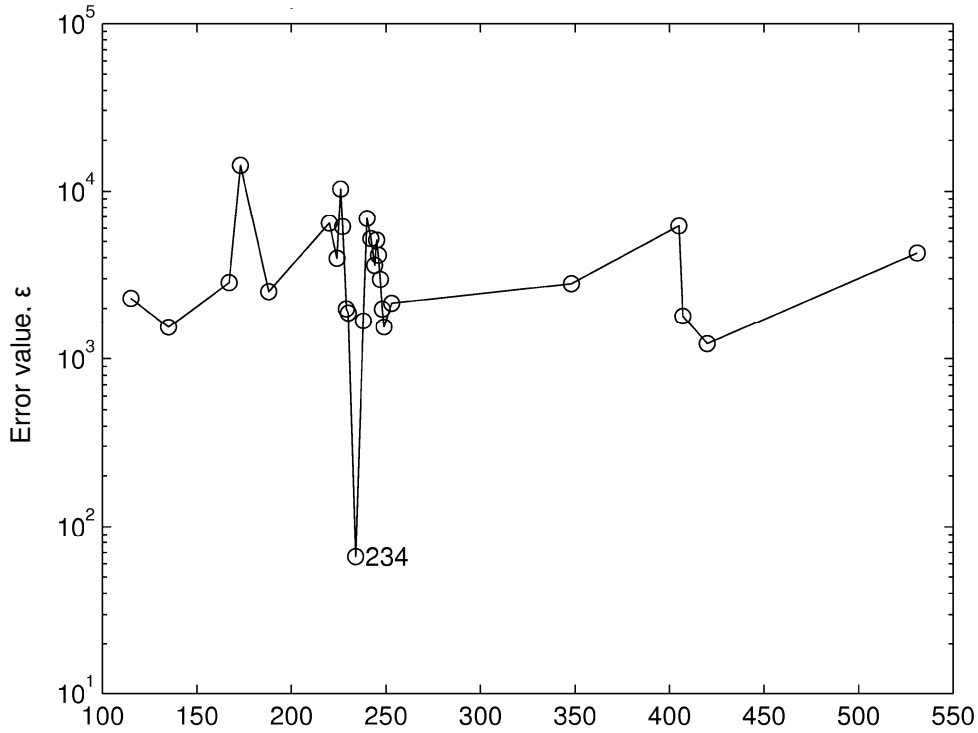

FIGURE 5A. The originally unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) has been identified as specimen RA234 through computation of the Residual Error, ε, after comparison of the test dataset of the unidentified specimen with each dataset of the pared-down database.
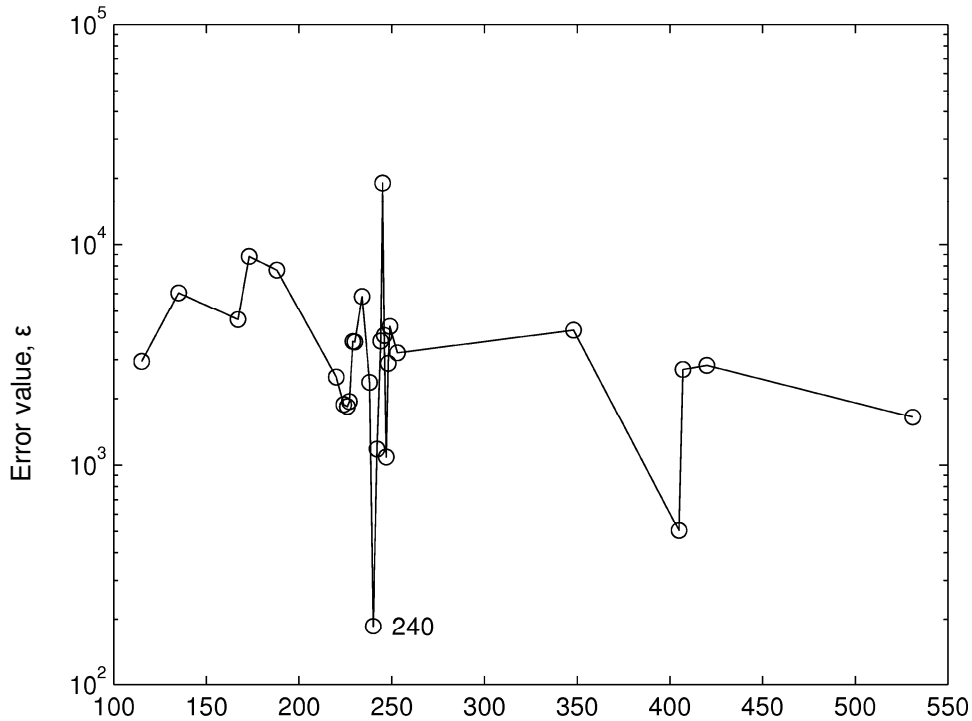

FIGURE 5B. The originally unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) has been identified as specimen RA227 through computation of the Residual Error, ε, after comparison of the test dataset of the unidentified specimen with each dataset of the pared-down database.

FIGURE 5C. The originally unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) has been identified as specimen RA240 through computation of the Residual Error, ε, after comparison of the test dataset of the unidentified specimen with each dataset of the pared-down database.
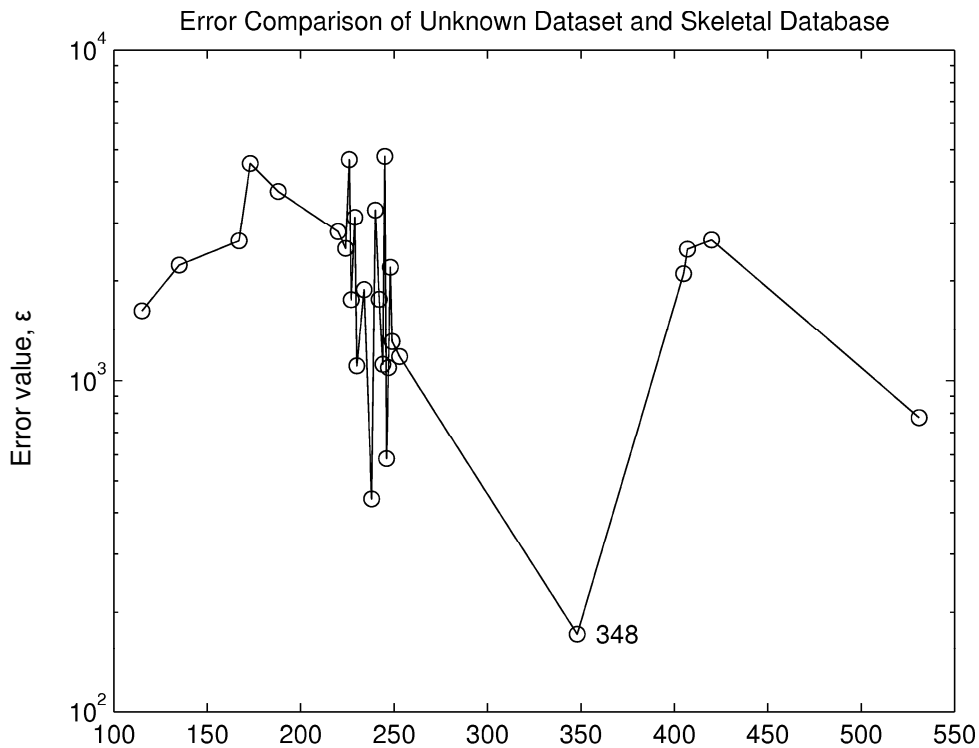

FIGURE 5D. The originally unidentified specimen of the Hispaniolan Amazon Parrot (*Amazona ventralis*) has been identified as specimen RA348 through computation of the Residual Error, ε, after comparison of the test dataset of the unidentified specimen with each dataset of the pared-down database.

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The identification process involves a degree of user interaction as the program requires a user to select the landmarks. Some of the errors in the results are due to differences in user perception when selecting the landmarks. While individual users varied slightly in their selection of the landmarks, the selection algorithm and landmarks were nevertheless able to generate accurate matches of unidentified test datasets with datasets of the pared-down database of known datasets.

Catalog Number	$FRE(U_1)$	$FRE(U_2)$	$FRE(U_3)$	$FRE(U_4)$
RA115	2.2964E+03	2.9521E+03	3.2171E+03	1.6259E+03
RA135	1.5413E+03	4.2585E+03	6.5689E+03	2.2336E+03
RA167	2.8513E+03	3.3646E+03	5.6702E+03	2.6441E+03
RA173	1.4199E+04	2.3867E+03	7.9959E+03	4.5421E+03
RA188	2.5181E+03	3.6033E+03	8.3479E+03	3.7351E+03
RA220	6.4138E+03	1.7986E+03	2.6990E+03	2.8201E+03
RA224	3.9707E+03	2.2424E+03	2.0512E+03	2.5108E+03
RA226	1.0296E+04	1.8456E+03	1.4097E+03	4.6635E+03
RA227	6.1160E+03	218.3418*	1.8910E+03	1.7579E+03
RA229	1.9917E+03	5.0464E+03	4.2970E+03	3.1174E+03
RA230	1.8787E+03	3.2462E+03	3.8623E+03	1.1094E+03
RA234	66.0830*	4.3637E+03	6.6045E+03	1.8846E+03
RA238	1.6801E+03	1.5212E+03	2.7634E+03	4.4064E+02
RA240	6.8514E+03	2.0818E+03	142.6456*	3.2792E+03
RA242	5.1965E+03	7.3428E+02	1.0897E+03	1.7625E+03
RA244	3.6043E+03	1.3947E+03	3.6402E+03	1.1198E+03
RA245	5.0777E+03	8.7219E+03	1.9827E+04	4.7670E+03
RA246	4.1366E+03	1.1030E+03	3.7910E+03	5.8328E+02
RA247	2.9813E+03	1.6010E+03	1.2869E+03	1.0951E+03
RA248	1.9828E+03	3.3066E+03	3.1574E+03	2.2016E+03
RA249	1.5486E+03	3.3005E+03	4.4730E+03	1.3119E+03
RA253	2.1469E+03	1.6756E+03	3.5746E+03	1.1825E+03
RA348	2.8076E+03	1.2978E+03	4.2021E+03	171.9901*
RA405	6.1778E+03	1.1494E+03	521.6445	2.1066E+03
RA407	1.8005E+03	4.5177E+03	3.1929E+03	2.4975E+03
RA420	1.2290E+03	4.9117E+03	3.4399E+03	2.6613E+03
RA531	4.2632E+03	1.1637E+03	1.8145E+03	7.7718E+02

TABLE 1: Comparison of error values for datasets of filing ridge patterns from unidentified specimens of the Hispaniolan Amazon Parrot (*Amazona ventralis*) with datasets from the pared-down database. *Denotes lowest value and correctly identified dataset.

4. DISCUSSION

There are currently various methods available for identifying individual members of a species. Some investigators have used methods based upon DNA, which have been shown to be one of the most valid methods of identifying individuals, though there is still a relatively small database compared to populations of individual species. Unfortunately, DNA identification can be very expensive in both the computational and monetary senses. The increased expenses occur at

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both at the acquisition and comparison phases. While fur spots [1]; [7], iris scans [2], and fingerprints [5] are effective methods of identifying individual members of a species in many instances, these methods cannot simply be applied to the identification of other species, if they differ in their characteristics. In humans, using the ridge pattern of fingerprints as an identification tool has been a well documented and established practice dating back over 200 years. Though the practice is not perfect, it is of sufficient accuracy to be admissible in the court systems of many countries, because the concept and theory behind its use is viewed as being sound. [34] Some critics have questioned the reliability of fingerprinting methods as a whole for identification based on the identification process's requirement for human interaction. Generally, the shortcomings of fingerprint identification in humans are related to the training of the technicians performing the match and the possibility of improper execution. [35] Just as with fingerprinting in humans, the method of comparison used to identify the parrots in our study is based on the assumption that filing ridge patterns on the internal side of the upper bill tip are individually unique. Our method provides a more quantitative approach and reduces (but does not eliminate) the dependence on human perception. Mathematically, a desired match value (zero) is known, reducing any human guess-work in calculations. Morphologically, the filing ridges are static and more rigid than the tissues that make up the human finger tips, thereby suggesting a higher confidence level in the results than in human fingerprinting. The greatest sources for possible errors in our method reside at the data acquisition phase, when the casts of the filing ridges are imaged, and at the discretization phase, when the landmarks are introduced to the images of the filing ridge patterns. Both phases can be refined to reduce or eliminate errors. Investigations are planned into human perception and interpretation of the landmark picking algorithm as well as into completely automating the landmark selection process.

Our identification procedure is based on a novel combination of established tools. In using established tools for image registration, it explored the possibility of using the patterns of filing ridges on the internal surface of the upper bill tip of parrots to identify individual members of one particular species, the Hispaniolan Amazon Parrot (*Amazona ventralis*). Each filing ridge pattern was represented by a pared-down dataset consisting of the coordinate pairs in two-dimensional space. The coordinate pairs were used to create a matrix of values that are representative of each filing ridge pattern. From a morphological perspective, the filing ridge patterns are hypothesized to be unique, like fingerprints in humans, suggesting that their representative matrices will be unique. Mathematically speaking, the difference in the norm values of two matrices is *0*, if they are not unique, and is non-zero, if they are unique. Due to possible errors in computation and data acquisition, values exactly equal to zero are generally not possible, making values closer to machine zero desirable. In our study, we have found that the match that minimizes the residual error between two datasets can be used to accurately identify unidentified filing ridge patters, though this value may not be identically zero. However, no particular value is required for the identification. Instead, the assessment is made relative to the matches of all other datasets in the pared-down database. In our experiments, we have found that there is often almost an order of magnitude difference between the correct match *versus* the matches with any other dataset of the database.

In a closed database, it is possible to locate the exact match for a given dataset by finding the minimum registration error between dataset pairs. In practice, the database would likely grow as more and more filing ridge patters are entered into the database. In an open database, it is possible to narrow the list of possible matches (the number of datasets in the database that are under consideration) by removing the datasets within the database with the largest registration error when compared with the unidentified dataset.

Our findings support our working hypothesis that the landmark selection and image registration processes are appropriate for determining an optimal match when correspondence is known *a priori*. By creating a database of pared-down datasets, we have created a repository of individually unique information that may be used to identify individual parrots. Our database allowed a simulation and assessment of an identification algorithm that compared a test filing ridge pattern with our database of known filing ridge patterns by using representative landmarks,

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aligning the images through a registration procedure, and then calculating the residual error between the compared datasets. The dataset with the lowest error value, in a minimum distance or least squares sense, was deemed to be most similar to the original dataset. The least squares problem (determining the residual error between two data sets) and minimizing the resulting function is well documented within introductory Linear Algebra texts. Using a single blind test, we were able to identify individual filing ridge patterns successfully based solely on a pared-down dataset of the filing ridge patterns.

Due to the required human participation in the selection process, there is an inherent error that is often included in the assessment of methods. The error is generally consistent, which allows the algorithm to identify individual datasets accurately nonetheless. The cumulative error in landmark selection due to human perception is on a scale that is much smaller than the error due to the variation between individual filing ridge patterns: The introduced human error was found to be on the scale of 10^{-2} to 10^{-3}, whereas the error between different filing ridge patterns was found to vary by a factor of 10^1 to 10^2. The results of this algorithm are a quantitative assessment of the total distance between markers. The perfect match then would return a match value of $\varepsilon=0$. The likelihood of returning a perfect zero match is small at present. However, if the goal is to eliminate patterns from a list or database, or to narrow a search for a particular pattern, the method of using landmarks on filing ridge terminals and performing a rigid registration to compare filing ridge patterns is appropriate. Further investigation is needed to determine the extent to which a match can be said to be unique, and to determine what, if any, threshold value, or order of accuracy, is needed to ensure a unique match. Currently, a match whose error value is a degree of magnitude (a power of ten) lower than matches with other datasets of the database provides the correct identification of the specimen. Through further refinement and the possibility of automating the landmark selection process, it may be possible to decrease the ε value at which a match is assumed.

In the future, communication between the biology, mathematics and visualization units of our research team must continue to make the landmark acquisition process more uniform and to refine the feature identification through an even more systematic selection of landmarks. The process of adding items to the pared-down database is currently in its initial stages of being automated to make the database creation more consistent and less time-consuming. This will lead to a more systematic identification of the patterns and will result in a more consistent database of pared-down datasets. A future development of this project will involve the ability to assess the volumetric data of the filing ridges on the curved internal surface of the upper bill tip from a 3D perspective. Future iterations of this process should minimize the human interactive component, thereby generating a faster, more consistent process for selecting landmarks and a larger, more physically meaningful disparity between the error values that are returned by the comparison.

The opportunity to test our hypothesis that the pattern of filing ridges is an individually unique pattern that can be used to fingerprint individual parrots of a species of *Amazona* turned out to be fortuitous, because a large number of *Amazona* species are endangered [12]. Hence, the result that the pattern of filing ridges is individually unique at least in our test population of *Amazona ventralis* raises the expectation that this may also be the case for a much larger population. Because the anatomy of the feeding apparatus and the ridge patterns of the cornified palate of *Amazona* and *Pionus* species are very similar (D.G. Homberger, unpublished observations), this expectation will have to be tested on a much larger population that encompasses as many species and individuals of *Amazona* and *Pionus* as possible.

The observation that the filing ridges of parrots are individually diverse within a general pattern that is diagnostic of genera and groups of genera may represent a nice example of developmental plasticity in which the final shape of a genetically controlled pattern is modified by multitudinous influences during the development of each individual.

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The probability that the pattern of filing ridges can be used reliably to tag individual parrots will be increased if the patterns of the more caudal palatal ridges are included so as to create a single, but much more complex pattern. The pattern of palatal ridges has been shown to be characteristic of genera or groups of genera [22]; [23] and has been discovered recently to vary individually within a basic pattern in *Amazona ventralis*. The more markers that can be considered for the identification of individuals, the less likely it will be that two individual parrots will have an identical pattern.

5. ACKNOWLEDGMENTS

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