# **APPENDIX II**

# PHOTO-IDENTIFICATION SOFTWARE FOR BOWHEAD WHALE IMAGES

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#### ABSTRACT

A computer program has been developed for identification of individual bowhead whales in aerial photographs. The program enables the user to create a collection of images and to compare an image to the collection. The collection is ranked by the program based on similarity to the query image, facilitating identification of the individual in the image. The program has been tested by the developer (GRH) with only a small number of images, but it appears to function accurately. Eleven successive versions of the program were provided to LGL Limited, who tested the program with a larger collection of images and provided reports on bugs in the system and feature requests to the developer. These bugs were fixed and features were added to make the program perform better, but further improvements to the program are likely to improve matching performance. Future potential improvements will be identified when larger numbers of images are processed through the program.

KEY WORDS: BOWHEAD WHALE, PHOTO-ID, MARK-RECAPTURE, ARCTIC, COMPUTER-MATCHING

#### INTRODUCTION

The photographic database of the Bering-Chukchi-Beaufort Seas (BCBS) population of bowhead whales (*Balaena mysticetus*) contains almost 18,000 images collected from the late 1970s to 2007. About half of the images that have been classified for image quality are of adequate quality to determine if the whales are marked and could be recognized if they were photographed in the future. All of the images in the database, but particularly the better quality images, have provided useful information on life-history parameters including calving intervals (Miller *et al.*, 1992; Rugh *et al.*, 1992a), growth rates (Koski *et al.*, 1992, 1993), population structure (Davis *et al.*, 1983; Koski *et al.*, 1993, 2006, 2007; Angliss *et al.*, 1995), population size (Rugh, 1990; da Silva *et al.*, 2000; Schweder, 2003; Schweder and Sadykova, 2007; Koski *et al.*, 2008) and survival rates (Whitcher *et al.*, 1996; Zeh *et al.*, 2002). On-going studies continue to use these data to further describe various parameters of bowhead whale life history and population dynamics (Rugh *et al.*, 2007).

The size of the bowhead photographic database has increased to the point where collection of new photographs results in a relatively high probability of re-sighting a previously photographed marked whale. This is because the proportion of the population that has been photographed has increased, and consequently, the likelihood of photographing a whale that has been photographed during previous studies has increased dramatically. Thus new photographs at this time provide much more information on individual whales and the population than the same number of photographs did during the early years of bowhead whale photography studies (Schweder and Sadykova, MS). However, as the number of marked whales in the collection has increased, the time to match each new photograph to earlier marked whales has also increased. To assist with the matching of the rapidly-growing number of photographs in the BCBS photographic collection, we have developed a computer-assisted matching program. This paper describes the development and current capabilities of the program and discusses future testing and development that will improve the efficiency of the program.

#### METHODS

#### Programming

All programming was done using the Matlab (The Mathworks, Inc., Natick, MA) development system. The program was written using Matlab's scripting language and graphical user interface (GUI) developer. The resulting files can be provided to any potential user who has a current Matlab installation. They can also be compiled by the programmer to produce MS Windows executable files, which run on any Windows XP or Vista machine. Executables for Mac and linux systems could also be created if needed. A Matlab runtime file, which the programmer is permitted by Matlab to distribute to end-users, must also be installed along with the executable file. For this project, the Matlab runtime and the executable files were sent to LGL Limited (LGL) and the National Marine Mammal Laboratory (NMML), and personnel there successfully installed and ran the program.

#### **Entering images into the program**

Bowhead whale images are opened in the matching program and can be TIF or JPG files; other common file formats could be accommodated. When an image is opened, the program automatically creates specific subfolders into which the program will insert metadata (information about the images). The metadata from all subsequent images in the same folder will be added to these subfolders.

Once an image is open, the user selects "Geometric Transform" from a menu. The image appears in a new window next to a provided "standard" image, which is simply a whale image of excellent quality. The user clicks on two points in the new image, such as the tip of the rostrum and the end of the fluke, and on the corresponding two points in the standard image. The program scales, rotates, and translates the new image so that it will be superimposable on the standard image, and therefore on all other images normalized to the same standard image. The normalization parameters are saved and are applied to that image each time it is read by the program.

Some images were not sufficiently normalized by this procedure because the whale was flexed or twisted in the image. Therefore, an "Un-twist" option was added to the image capture procedure. The user selects "Un-twist" from the menu and then clicks on a point on the rostrum, a series of at least four points along the anatomic midline and one at the base of the fluke. The program

performs a nonlinear distortion of the image that causes the designated points to fall on the line between the rostrum and the fluke, with interpolation of all pixels between the selected points.

The user then selects the markings on the whale that are to be used for identification. First, a mouse click selects each mark. If the mark is a small dot, no further action is needed. If it is a large mark or has a distinctive shape, the user may outline the mark, and data about its size and shape are stored for use in matching. A capability has been added to review an image and its stored marks, and to add new selections, move, edit or delete previously selected marks without re-doing the entire mark selection process for that image. This feature allows updating of mark information for a whale from second and subsequent photos of the same whale. This ensures that the mapped image is an accurate representation of a whale and permits us to incorporate information from multiple images of a whale into a single image for matching.

Because some regions of a whale are not clearly visible on some photographs, the user may designate all or part of each image as a region of interest (ROI) for matching. If such a region is designated, the program will disregard marks in another image that are outside of the ROI during comparison of the two images. A ROI includes portions of the image which are not obscured by foam, glare, etc. The default includes the entire image if ROI is not selected.

The scaling and orientation, un-twisting, ROI, and locations and descriptions of the distinguishing marks are automatically stored in the subfolders, and are recalled by the program as needed.

When this pre-processing of an image is complete, the user selects "Add to Excel File." This adds the file name of the new image to a list maintained in a MS Excel file; this file stores the names of all files in the catalogue and the identity of the whale in the image. When the image is first added to the file, the program adds the identifier "0000" as its ID, later to be changed by the user when the image is identified either as a new individual or a match to a previous image. The files listed in the Excel document are the ones to which each new image is matched.

## Matching Images

The user selects any image that has previously been entered into the matching program. If the normalization and spot marking procedures have not been completed for the image, a notice reminds the user to complete them.

The size, orientation and shape of scars are sometimes distinctive and incorporation of these attributes into the matching process should increase the reliability of matching two photographs of the same whale. The user is therefore given an option to more heavily weight mark attributes that have been previously entered for the image, when the higher weighting is likely to improve the ability of the program to identify a match. For example, this option would be used if a whale had a distinctively-shaped mark so that all whales with a similar-shaped mark at the same location would be ranked higher on the list of potential matches than they might be without selection of this option. The parameters that are measured for each mark are: location, area (number of pixels), eccentricity (a number between 0, indicating round and 1, indicating a straight line), orientation (angle in degrees from horizontal of the major axis), length (the major axis of an ellipse that approximates the mark) and perimeter. When marks are matched, the difference between them is the Euclidean distance in the seven-dimensional space of these parameters (x position, y position, area, eccentricity, eccentricity×orientation [i.e., if it is round its orientation is not relevant], length and perimeter). Each of the parameters is weighted by a

default value. The default is 1 for all parameters except eccentricity which is 10 (because its native value is limited to 0 to 1) and 0.01 for area. The user can set the value to zero to have a parameter not count at all or any higher number to have the value weighted more heavily. The program saves the new weights in a file called "wtfile.mat."

Any two images may be compared by reading one as "Image 1" and the other as "Image 2." A "Compare two images" button measures and displays the difference between the two images. During testing of the program, this single matching process was useful for examining how the match was affected by the way spots were marked.

In the usual operation of the program, the user does not open an "Image 2", but instead, clicks a "Compare to List" button. In this case, all of the images listed in the Excel file are matched to Image 1. The program measures the dissimilarity between the query image and each listed image, and it sorts the entire list by the dissimilarity parameter, with the images that are most similar to the query image at the top of the list. It then displays a window with the sorted list and the dissimilarity value. The program also displays, as an array of small images, the six images that are most similar to Image 1, showing the file names and ID's (Fig. 1). Each small image has a button that allows its image to be displayed in a separate large window, with its selected marks shown. If the user sees a match among those six images, he enters the ID of the query image in a provided text box. If a match is not seen, the user may view the next six. The user can scroll through the catalogue of images in either direction, displaying them six at a time, until a match is found, or the user is convinced that there is no match. Either a pre-existing or a new ID may be entered, and it is recorded in the Excel file instead of the default "0000".

The match or absence of a match is confirmed by a trained observer with assistance of the program. The goal of the program is to reduce the number of images that must be reviewed. If the program worked perfectly, its first suggestion would always be a match, if one existed. This ideal goal cannot always be achieved because some matching errors are inevitable, some images are unclear and some whales either lack distinctive markings or have markings resembling those on other individuals. Nevertheless, if a correct match occurs at or near the top of the list, much labour will be saved.

## **Comparison to earlier programs**

The overall design of the program is based on previous photo-ID programs that were developed for other species such as dolphins, sea otters, and gray whales (Hillman *et al.*, 2003; Markowitz *et al.*, 2003). The bowhead program code is entirely new, with many features that are specific to the bowhead whale application.

The processes of file access, Excel file access, image display and mouse-use take advantage of Matlab functions. The scale-rotation-translation normalization process uses Matlab's linear conformal transformation. However, the un-twisting function is a new algorithm. When the control points have been selected, the image is rotated such that the first and last points fall on the same horizontal row. A spline is then drawn through the intermediate points, with a spline point computed at each pixel column. Each column is then revolved along its vertical length so that the spline points all fall on the horizontal between the snout and the tail. The entire image is then rotated back to its original orientation. This process is fairly slow (at least several seconds), so it should not be used unless there is enough curvature or twisting to disrupt the location of identifying marks.

## Matching function

The matching function works as follows, with the process repeated as the query image is matched in turn to each image in the collection:

• The program recalls the locations and shape properties of the two images (A and B) being matched.

• If A or B has a designated valid region, the marks in the other image are tested to determine whether they fall within this region. Any marks that are outside the other image's valid region are temporarily discarded.

• The Euclidian distance is determined between each point in A and B in a 7-dimensional space comprised of the X distance, Y distance, mark area, mark eccentricity (a scale from 0 to 1 indicating shape from a circle to a line), angular orientation of the mark, length of the major axis of the mark, and perimeter of the mark. The closest points are determined. If the images have unequal numbers of marks, the smaller number is used (e.g. if A has 3 and B has 5 marks, the closest 3 pairs of points are found)

• Using a linear translation function and Matlab's optimization algorithm, the relative position of the two images is adjusted to minimize the distances between the corresponding closest-fit points.

The difference values between the query and all other images are accumulated and sorted, establishing the order in which images are presented for inspection.

A second matching algorithm was also implemented after discussion with an engineering colleague, Dr. Hemant Tagare at Yale. Rather than the successive-approximations optimization of the point locations, it uses an analytical minimization of the summed distance, with a specified number of iterations. The advantage of this method is that it can weight the distances in such a way that the matching value is weighted more heavily by points that fit more closely than those that are distant matches. The result of this weighting is to reduce the influence of outlying marks that might be due to errors or artifacts. The user of the program can select either of the two matching algorithms; experience will tell whether one is actually more effective than the other.

## DISCUSSION

A computer-assisted matching program has been developed and has been tested with a relatively small number of photographs. The program runs without errors when used correctly and identifies images quite accurately within the test dataset, but it has rough edges; for example, there is no internal help file and user error trapping is not complete. The latest version of the program was provided to LGL and NMML on 23 April 2008.

More study is needed of the weights that control the relative influence of distance, area, etc. of marks on the similarity of a matched pair of images; it is still uncertain what values to assign to these weights in order to provide the most accurate matching. Most importantly, there must be testing of the program with a large collection of images that have already been matched to determine how far down the list of potential matches actual matches may occur.

Additional program bugs will inevitably be found as more extensive testing is carried out, and these must be corrected. Some improvements are needed, such as a more flexible system of organizing the data files to facilitate the matching process. Additional features that may improve the reliability of the matching process have been requested by the testers at LGL and NMML.

Throughout the development process there has been frequent and effective communication between the programmer and the testing groups, and the result is a working draft of a program that may be extremely helpful for matching bowhead whale images.

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Fig. 1. - OPENING: When opening an unprocessed image in the Compare program, two prompts provide a warning that the image needs to be transformed and the spots to be marked.



Fig. 2 - GEOMETRIC TRANSFORM: To scale the whale brought up as Image 1, click 'Input Processing' in the menu and 'Geometric Transform.' Two images appear, Image 1 (Fig. 2) and the Reference Image (Fig. 3). To scale Image 1, click snout (left click) then tail (right click). On the Reference Image, click same spot on snout (left click) and tail (right click) that was clicked on image 1.



Fig. 3 - GEOMETRIC TRANSFORM: This is the reference image that image 1 is scaled to. On this reference image, click same spot on snout (left click) and tail (right click) that was clicked on image 1.



Fig. 4 - GEOMETRIC TRANSFORM: After last click on tail end of the Reference Image, the two image windows disappear, and the geometric transform shows in the main window and is prompted to be saved.



Fig. 5 - UNTWIST: To untwist whale in Image 1 choose 'Input Processing' then 'Untwist' and a image 1 will appear in a window. To untwist the whale, six or more asterisks must be clicked evenly spaced down the midline of the whale. The program takes about 15 seconds to untwist a whale image. Due to the time it takes to untwist the whale, the Untwist feature must only be utilized if spots on whale would be affected or not be able to be compared to a 'straight' whale.



Fig. 6 - SELECT SPOTS: At this stage, the whale image is untwisted. To indicate permanent marks and scars, there is a 'Select Spots' command in the 'Input Processing' menu option.



Fig. 7 - SELECT SPOTS: When selected, image 1 will pop up, and all scars need to be indicated by setting the asterisk with the mouse. When in doubt whether or not a mark is real, it should be indicated as a mark. After all the marks are indicated, the ones that are larger than an asterisk should be further processed (Fig. 8).



Fig. 8 - SELECT SPOTS: If a mark is larger than the asterisk or has a unique shape other than a circle, the mark can be zoomed in and the perimeter of the mark outlined. When you right click near the image, select 'Mark Attributes' to outline the perimeter of the mark (Fig. 9).



Fig. 9 - SELECT SPOTS: This is the mark from Fig. 8 being outlined to indicate its uniqueness.



Fig. 10 - IMAGE 1 WITH POINTS: When the Image 1 window has been closed, the main screen will be visible. At this stage, the image may be reviewed to add, move, remove, or outline more marks. Go to 'Viewers' in the Menu and select 'Image 1 w/ points.' Image 1 window will appear in a larger window (Fig. 11).



Fig. 11 - IMAGE 1WITH POINTS: This is Image 1, ready to be reviewed by zooming in and making changes. By right-clicking on Image 1, a menu will appear with the options to 'add point,' 'move point,' 'move point,' 'mark attributes' (outlining unique or large marks) and finally 'show attributes' (allow you to see characteristics of a mark, such as, perimeter, area, eccentricity, length, and orientation).



Fig. 12 - REGION OF INTEREST: If Image 1 is an incomplete picture of a whale where the whole body is not visible due to splash, ice, or placement, the 'Region of Interest' (ROI) may be indicated. This is only applied if you cannot tell if there are marks on the part of the whale that is obscured. This process is done after scaling, untwisting, and marks have been indicated (Fig. 13).



Fig. 13 - REGION OF INTEREST: This is Image 1 after it has been scaled ('Geometric Transform') and all marks have been indicated and outlined. It is not necessary to 'Untwist' this image since we are not using the part of the whale that is not clearly visible, therefore we will only mark the ROI which will be used in the matching part of the program.



Fig. 14 - REGION OF INTEREST: To mark the ROI, go to 'Input Processing' and then select 'Mark ROI.' Image 1 will appear in a larger window (Fig 15).



Fig. 15 - REGION OF INTEREST: Similar to how a unique mark is outlined, an outline will be drawn around the region of the whale that can clearly be seen and has already been marked.



Fig. 16 - REGION OF INTEREST: Once the ROI has been outlined, double clicking inside the area outlined will then appear so that the area marked can be reviewed. To go back to the main window, this Image 1 window can just be closed, and the ROI is automatically saved.



Fig. 17 - REGION OF INTEREST: This is the final view of Image 1 with the marks and the indicated ROI around the tail and fluke.



Fig. 18 - ADD TO EXCEL FILE: When the image is done being processed, go to 'File' and select "Add to Excel file." This copies the image name and pathway to an Excel spreadsheet used in running the matching part of the program.



Fig. 19 – COMPARE TO LIST: To run the program to produce a list of possible matches click the 'Compare to List' button on the lower right of the main screen (Fig. 1). The list is presented showing six images at a time in order of most likely matches to least likely matches.



Fig. 20 - COMPARE TO LIST: From the window with the list of six images (Fig. 19), an image can be enlarged and compared to Image 1. When you click 'Enlarge', you can see the points from Image 1 overlapped on the enlarged image from the list. From this point, a trained technician will sort through all the possible matches to confirm if there are true matches.