

**SharkID: A FRAMEWORK FOR AUTOMATED INDIVIDUAL SHARK
IDENTIFICATION**

A THESIS

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ABSTRACT

Recent progress in animal biometrics has revolutionized wildlife research. Cutting-edge techniques allow researchers to track individuals through noninvasive methods of recognition that are not only more reliable, but also applicable to large, hard-to-find, and otherwise difficult to observe animals. In this thesis, we propose a framework for automated individual shark identification based on semantic segmentation, boundary descriptors and bipartite perfect matching applied to shark dorsal fins. In order to identify a shark, we first apply semantic segmentation to extract the dorsal fin of the input source, then transform the fin's contour to a normalized coordinate system so that we can analyze images of sharks regardless of orientation and scale. Finally, we propose a metric scheme that performs a minimum weight perfect matching in a bipartite graph. The experimental results show that our metric is able to identify and track individuals from visual data.

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TABLE OF CONTENTS

ABSTRACT	ii
ACKNOWLEDGEMENTS	iii
LIST OF TABLES	v
LIST OF FIGURES	vi
1. INTRODUCTION	1
2. RELATED WORK	4
3. FRAMEWORK	6
4. IMAGE PREPROCESSING	8
5. BOUNDARY DESCRIPTOR	11
6. BOUNDARY DESCRIPTOR DISTANCE	15
7. MAIN RESULTS	18
8. CONCLUSION	21
APPENDICES	22
A. EXPERIMENT 1	23
B. EXPERIMENT 2	28
REFERENCES	30

LIST OF TABLES

1. Segmentation Model Summary	9
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LIST OF FIGURES

1. Overview of the framework.	3
2. Structure of the framework presented in this thesis.	7
3. Diagram of the deep learning model.	8
4. An example of a shark dorsal fin at each stage of the color-clustering algorithm. . .	10
5. Illustration of how the ridge partition of the dorsal fin is found.	13
6. Key points.	14
7. Akeru vs Zibbo	24
8. Akeru vs Wayne	25
9. Akeru vs Sydney	25
10. Sydney vs Zibbo	26
11. Wayne vs Zibbo	26
12. Wayne vs Sydney	27
13. <i>sharkvsOthers</i>	29

CHAPTER 1

INTRODUCTION

The ability to recognize individuals is a requirement for several aspects of ecological research and essential for environmental conservation [1]. Research in automatic animal identification started at the end of 1960s and first results were presented in 1976 [2]. Biometrics is a science usually applied to humans, but it has also shown promise for identifying, classifying, tracking, monitoring diseases in animal population [3]. Initially, studies were developed around cattle for their economic importance in agriculture and accessibility. More recent advances in technology have allowed researchers to apply these techniques to other species.

Currently, the most pervasive techniques for individual animal identification, including ear tags, leg rings, collars, number tattoos and hot branding, are invasive. Some of these procedures could potentially hurt the animals and are also unreliable, since tags and collars can fall off, resulting in financial and data loss. Advances in computer vision and research in unique animal characteristics has created potential for non-invasive solutions to animal identification [4], [5].

The first animal identification systems were reliant on large sets of unconstrained data, preferably taken in natural conditions in order to facilitate the identification, work done manually or semi-manually [6]-[10]. Fully automated systems capable of locating and identifying individuals in visual data have become the focus of more recent research. This approach eliminates the subjective human observer iteration and allows biologists to collect and process data on a large scale. Generally, these methods require a combination of a framework to detect the animal against a noisy background and a biometric system to identify the unique features and match them [4]. A recent example of a fully automated identification system is the deep learning framework for cattle recognition. Based on the uniqueness and immutable nature of cattle's muzzle beads and ridges, it was possible to develop a system that uses point image patterns to identify specific individuals [11].

Texture-based approaches are infeasible for aquatic animals though, since they are far less accessible than domesticated land animals.

A different approach emerged to satisfy the need of biometric identification that was not dependent on texture. Hughes and Burghardt [12] introduced the idea is based on an already existent technique of using the fin shape to track sharks manually and semi-automatically [13]. The proposed technique uses contour information from smooth or textureless objects, specifically white shark dorsal fins in an unconstrained environment. This was the first partially automated contour-based visual ID system in animal biometrics [12].

The primary objective of this thesis is to present a fully automated individual identification system for sharks, based on the unique pattern showed by their dorsal fin. This framework supports a novel biometric for shark identification using boundary descriptors and bipartite perfect matching.

Overview

The purpose of this thesis is to develop an automated framework for individual shark identification that supports the metric based on boundary descriptors and minimum perfect matching.

First, we discuss the related work in Chapter 2 with the previous work that inspired and guided our research.

We then present the problem and an overview of our framework in Chapter 3, where we describe the pipeline and the different sections of our process.

We extract the region of interest, dorsal fin, through semantic segmentation in Chapter 4. To do so, we use a *VGG-16* with pre-trained weights. Once the dorsal fin is extracted we use color-clustering to isolate the fin from the background noise and extract the its contour.

The next step is inspired by Affine Transformations [14]. We translate the contour to a normalized coordinate system in order to guarantee orientation and scale invariance, this and the

next steps are illustrated in Figure 1 of the metric overview.

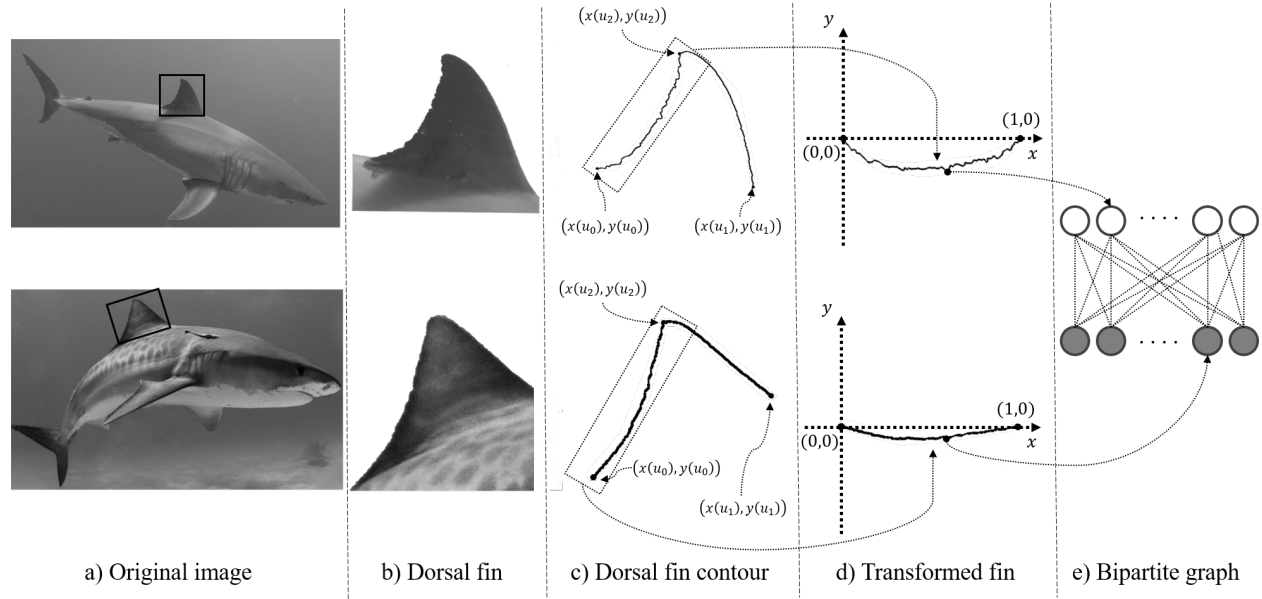


FIGURE 1. Overview of the framework.

Minimum weight perfect matching in a bipartite graph is a well-known technique for designing metrics [15], [16]. We designed a metric that can be computed in three steps. First, given two sets of dorsal fin contour key points, we create a bipartite graph such that every key point in the first set shares an edge with every key point in the second set. This is a fully-connected bipartite graph. Then, we weight each edge by computing the *Euclidean Distance* between each of the key points (in the normalized coordinate frame). Lastly, we perform a minimum weight perfect matching algorithm [17]. The sum of the edge's weights of the perfect matching is our metric. The comparison process is detailed in Chapter 6.

The results in Chapter 7 show that the metric is valid and is able to distinguish individual sharks.

The purpose of this thesis is to develop an automated framework for individual shark identification that supports the metric based on boundary descriptors and minimum perfect matching.

CHAPTER 2

RELATED WORK

Animal biometrics are defined by the measurable data related to appearance aspects [18], movement characteristics and vocalizations of animals that can be used as biometric entities [19]. In order to be a suitable biometric entity, such traits must be measurable by a recording device, adequately permanent, characteristic of the animal class of interest and universally displayed throughout the relevant population, such as the stripes on zebras [20] and tigers [21] or the spots on cheetahs [7]. However, not every physical characteristic fits the definition, for example, the injury marks in white sharks are salient and unique, but they heal quickly and such temporal variability can limit their use as biometric entity for long-term studies [4], [22].

Recently, deep learning has become a very popular approach when it comes to extracting features [11]. In “Deep Learning Framework for Recognition of Cattle Using Muzzle Point Image Pattern” [11] the goal was to develop a successful non-invasive biometric framework to manage cattle. The work involved preparing a database of muzzle point images, extracting the salient texture features and representation of muzzle point image using a convolutional neural network and deep belief neural network, and the use of a denoising auto-encoder technique to encode the extracted features. Our work uses deep learning to apply semantic segmentation to shark images to first eliminate the pictures that do not contain sharks, and then to isolate the shark’s dorsal fin [23].

A closely related work to ours is presented in “Automated Visual Fin Identification of Individual Great White Sharks” [12]. Hughes and Burghardt’s work discusses an automated visual identification of individual great white sharks from dorsal fin imagery. The approach considers the dorsal fin a textureless object, flexible and partially occluded. In order to identify an individual shark, they used a stroke model for fin detection, followed by a scale-space selective fingerprint to encode the fin individually. Also, they measured the species-specific distribution of

visual uniqueness along the fin contour, and finally use a non-linear model for individual animal recognition.

Their framework is a composition of all the previous steps and is classified as *fine-grained* since it takes into consideration the specific shape and ridges of individual dorsal fin, *multi-instanced* since the images can be multi-labeled semantically according to the shark present, *flexible* since fins can bend, and *fairly textureless* for its lack of texture [12].

Our research differs in that our framework can be applied to any individual shark independently of the species, although our work is not applicable to partially occluded fins.

CHAPTER 3

FRAMEWORK

The task of tagging a shark is not just costly, but highly unreliable. Tag expeditions are expensive and they are not always successful. Even when the sharks are successfully tagged, there is a risk of the device detaching from the animal.

One contribution of this thesis is a novel metric that can be used identify individual sharks non-invasively. Then, we develop an entirely automated framework that uses this metric to identify individual sharks without human interaction.

The framework presented in this manuscript is reliable, non-invasive, and monetarily inexpensive compared to current methods.

The framework can be divided into three phases:

- *Pre-processing*: A two-part segmentation process where we use a VGG-16 network to first find a shark in the frame, and then its dorsal fin. Then, we color-clustering to remove the background of the images.
- *Identification*: We extract the contour of the fin and use it to compute its boundary-descriptor. Using the metric described in Chapter 6, we compare the distance between fins of different sharks to identify the fin.
- *Analysis*: Finally, we analyze the results of the framework on a collection of fins from different sharks.

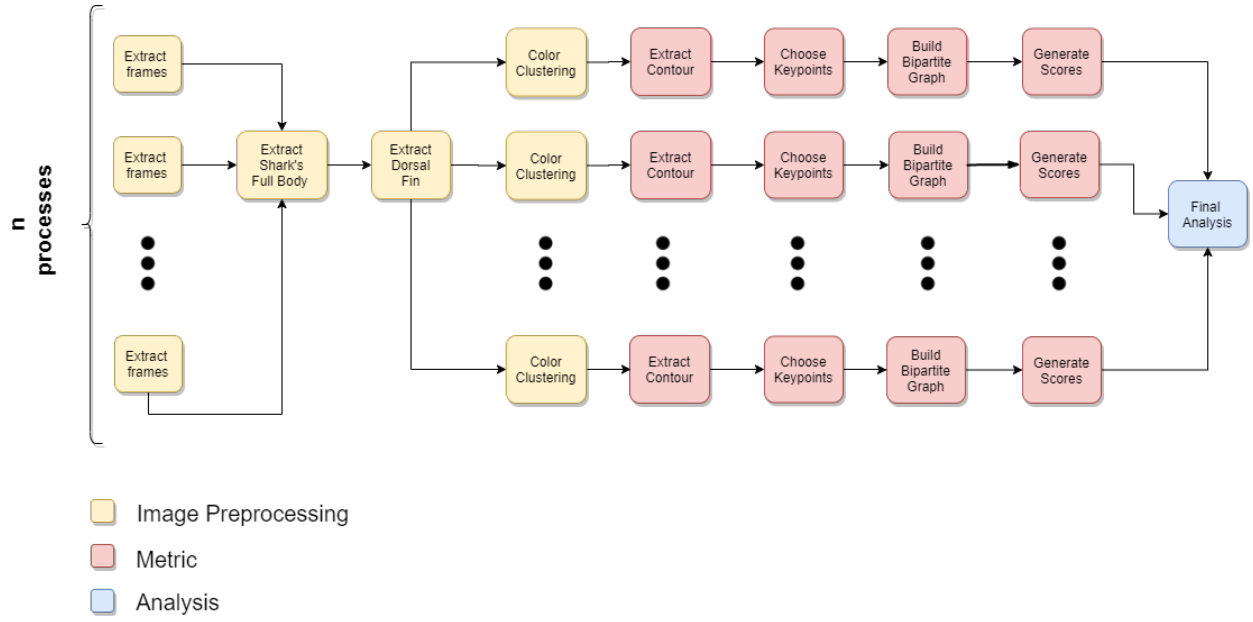


FIGURE 2. Structure of the framework presented in this thesis. Note that most of the tasks can be executed in more than one process, which accelerates the computing time and framework execution in general.

CHAPTER 4

IMAGE PREPROCESSING

The first step in our framework is to extract the region of interest to apply our metric. The framework accepts both video and image input (.MP4, .PNG, or .JPEG). If the input is a video, individual frames are extracted and fed into the rest of the framework. After the images are gathered, the framework filters out images that do not contain a shark using semantic segmentation to extract the shark from the image. If no shark is detected, the image is discarded, otherwise, it is fed into the rest of the framework. Next, we use semantic segmentation a second time to extract a bounding box around the dorsal fin of the shark. This whole process is illustrated by the yellow portion of the framework in Figure 2.

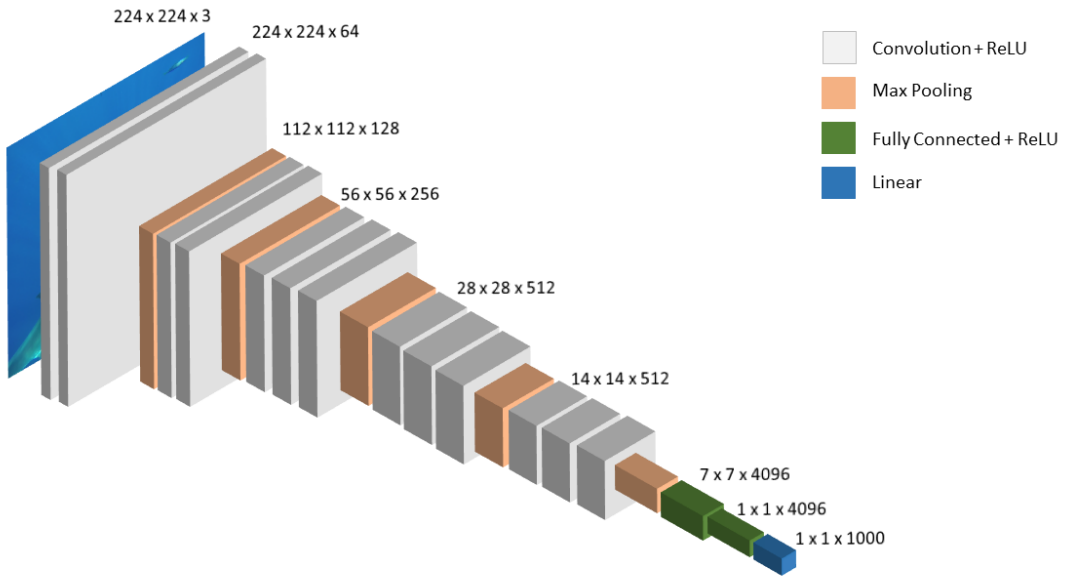


FIGURE 3. Diagram of the deep learning model.

The Deep Learning algorithm used in this portion of our work is a VGG-16 neural network that shapes the image input to a fixed $(224, 224, 3)$ size [23]. The image is passed through a series of convolutional layers with (3×3) kernel size and fully connected layers. Figure 3 shows

TABLE 1. Segmentation Model Summary

Layer (type)	Output Shape	Parameters Number
Input_1 (Input Layer)	(None, 224, 224, 3)	0
block1_Conv1 (Conv2D)	(None, 224, 224, 64)	1792
block1_Conv2 (Conv2D)	(None, 224, 224, 64)	36928
block1_Poll (MaxPooling2D)	(None, 112, 112, 64)	0
block2_Conv1 (Conv2D)	(None, 112, 112, 128)	73856
block2_Conv2 (Conv2D)	(None, 112, 112, 128)	147584
block2_Poll (MaxPooling2D)	(None, 56, 56, 128)	0
block3_Conv1 (Conv2D)	(None, 56, 56, 256)	295168
block3_Conv2 (Conv2D)	(None, 56, 56, 256)	590080
block3_Conv3 (Conv2D)	(None, 56, 56, 256)	590080
block3_pool (MaxPolling2D)	(None, 28, 28, 256)	0
block4_Conv1 (Conv2D)	(None, 28, 28, 512)	1180160
block4_Conv2 (Conv2D)	(None, 28, 28, 512)	2359808
block4_Conv3 (Conv2D)	(None, 28, 28, 512)	2359808
block4_pool (MaxPolling2D)	(None, 14, 14, 512)	0
block5_Conv1 (Conv2D)	(None, 14, 14, 512)	2359808
block5_Conv2 (Conv2D)	(None, 14, 14, 512)	2359808
block5_Conv3 (Conv2D)	(None, 14, 14, 512)	2359808
block5_pool (MaxPolling2D)	(None, 7, 7, 512)	0
fc1 (Conv2D)	(None, 7, 7, 4096)	102764544
fc2 (Conv2D)	(None, 7, 7, 4096)	16781312
predictions_1000	(None, 7, 7, 1000)	4097000

the architecture of the model used and Table 1 presents a layer-by-layer summary.

The color clustering algorithm is the last step of the *Image Preprocessing* portion of the framework. The underwater pictures contain similar blue hues and distinguishing the fin from the background is a challenging task. Our framework uses a K-Means algorithm [24] to remove the background. For every fin picture, the algorithm separates the colors in 3 clusters. Observe that each cluster is associated with a single color, composed of a red, green, and blue channel, or $r, g, b \in [0, 255]$. Let B be the blueness of an image:

$$B(r, g, b) = b - \frac{(g + r)}{2}$$

We threshold the image by assigning the cluster with the highest blueness, which we assume is background (water is blue), to 255 (white), and the other two to 0 (black) (Figure 4).

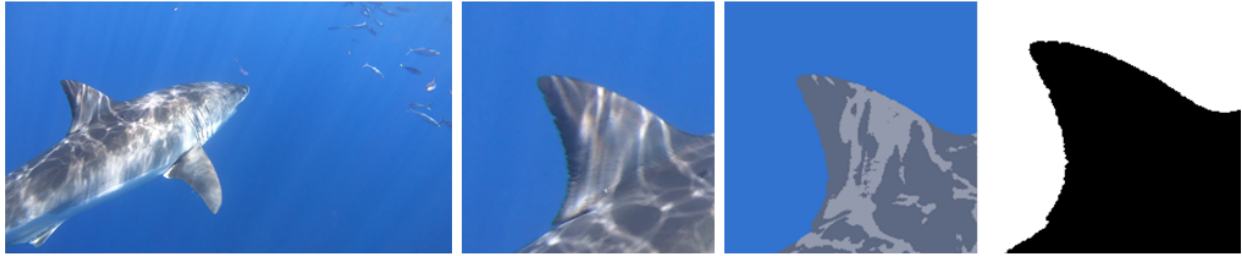


FIGURE 4. An example of a shark dorsal fin at each stage of the color-clustering algorithm.

CHAPTER 5

BOUNDARY DESCRIPTOR

In this chapter, we describe the boundary descriptor computed from the extracted contour of the dorsal fin for a shark. The steps from Chapter 5 and Chapter 6 are illustrated in the red portion of Figure 2.

Let $c(u)$ represent the contour of an object as following;

$$c(u) = (x(u), y(u)) \quad (5.1)$$

where u is the any parameter, and $x(u)$ and $y(u)$ denote coordinate functions of the contour, respectively. The contour is smoothed by (G)

$$C(u, \sigma) = G(u, \sigma) * c(u) = (G(u, \sigma) * x(u), G(u, \sigma) * y(u)) \quad (5.2)$$

where $G(u, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{u^2}{2\sigma^2}}$, σ is a standard deviation, and $*$ denotes the convolution operator [25].

The corner response function is defined

$$D(u, m, \sigma) = ((G(u, m\sigma) - G(u, \sigma)) * x(u))^2 + ((G(u, m\sigma) - G(u, \sigma)) * y(u))^2 \quad (5.3)$$

where $m\sigma = m \times \sigma$, “ \times ” denotes ordinary multiplication, i.e., $m > 1$ is a multiplier factor [25].

Viewed as a bandpass filter, by varying m and σ , the operator can be tuned to different frequency components of contour shape [12].

After contour is determined, the specific region of the fin to be analyzed is where the protuberances are. Let *partition* be a list of the 3 sets of points that describe each side of the fin.

To find which element of *partition* contains the protuberances to be analyzed, first the vertices of

the fin must be found.

Algorithm 1 shows how the three points correspond to the vertices of the fins are found. Note that, in Algorithm 1 *minEnclosingTriangle* is a function that returns the vertices of the minimum enclosed triangle that fits the contour.

ALGORITHM 1. Find Vertices of the Fin.

```

1: procedure FINDTIPS(contour)
2:   vertices  $\leftarrow$  minEnclosingTriangle(contour)                                 $\triangleright$  3-element list
3:   fin_tips  $\leftarrow$  null 3-element list
4:   for i in 0, 1, 2 do
5:     fin_tips[i]  $\leftarrow$   $\underset{point \in contour}{\operatorname{argmin}} (\sqrt{(v - point)^2})$ 
6:   end for
7:   return fin_tips
8: end procedure

```

The vertices of the fin are used to calculate the mid-point of each *partition*. The mid-point that is the furthest away from the *Minimum Enclosing Triangle* belongs to the *partition* element that represents the concave (ridges) part of the fin.

Figure 5 illustrates this process showing the *Minimum Enclosing Triangle*, the fin vertices and the mid-points.

With the right *partition* in hand, the next step is to find the featured points that are going to be used for the metric comparison step. Definition 1 describes how to find the locations that are more protuberant on the ridges partition.

Definition 1: (Salient Locations) Let S' be the set of salient locations defined by

$$S' = \left\{ u \mid \frac{\partial D(u, m, \sigma)}{\partial u} = 0 \right\} \quad (5.4)$$

In Definition 2 we organize the points found previously and describe the prominence function to collect the n most protuberant points.

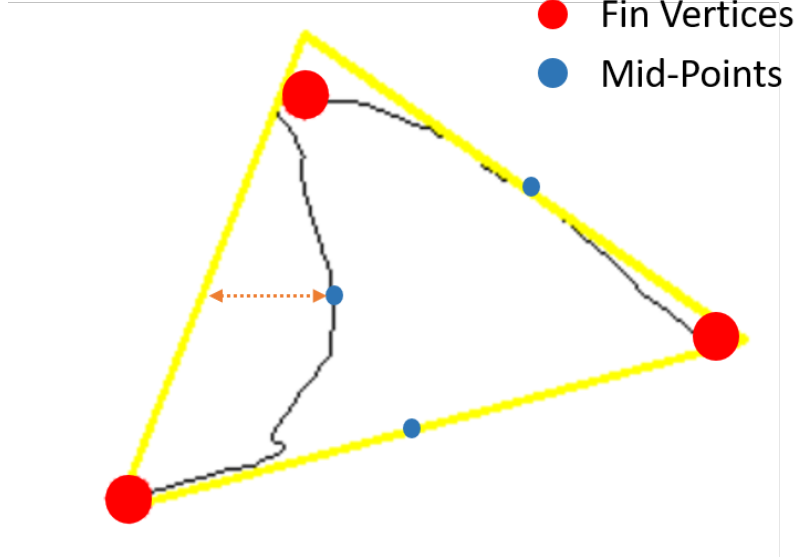


FIGURE 5. Illustration of how the ridge partition of the dorsal fin is found.

Definition 2: (Boundary Descriptor) Let S'' be an ordered list of u , $\forall u \in S'$. For $u_i \in S''$ where $i = 1, 2, \dots, |S''| - 1$, we use the prominence function as $p(u_i) = |D(u_i, m, \sigma) - D(u_{i+1}, m, \sigma)|$. For δ largest values of $p(u_i)$ where δ is a user-defined parameter, we collect the respective u_i 's in a multi-set S , called the boundary descriptor.

The parameter n is user-defined, and for the experiments in Chapter 7 we use $n = 50$, or 50 *key points*.

Definition 3: (Key points) The Key points of a contour is a subset of $c(u)$, which is denoted by K .

$$K = \{c(u) \mid u \in S\} \quad (5.5)$$

The *key points* are the features used to calculate the distance in between sharks, a process we detail in Chapter 6.

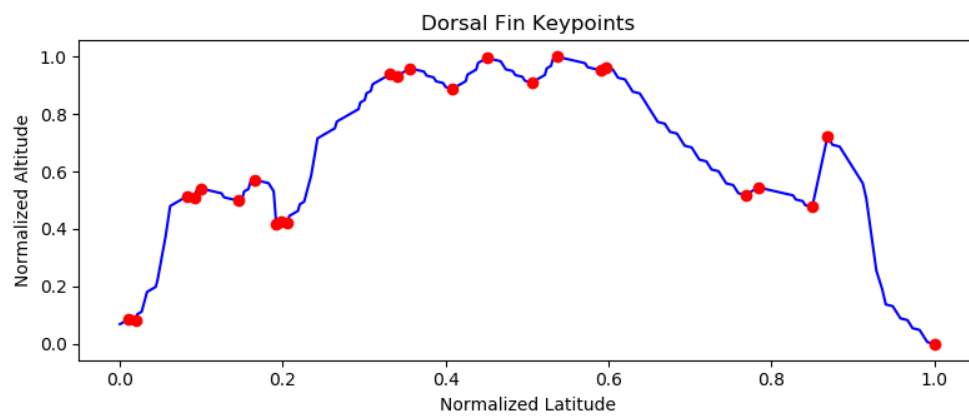


FIGURE 6. Key points.

CHAPTER 6

BOUNDARY DESCRIPTOR DISTANCE

In this chapter, we describe one of the main contributions of this thesis: a metric for comparing boundary descriptors of shark fins. We present all the definitions, lemmas and proofs to show our metric is valid. We start by clearly defining the fin vertices computed in Algorithm 1.

Definition 4: (Critical Points) We define $c(u_0) = (x(u_0), y(u_0))$ be the point at the back of the base of the fin, $c(u_1) = (x(u_1), y(u_1))$ be the front of the base of the fin, and $c(u_2) = (x(u_2), y(u_2))$ be the point at the tip of the fin as shown in Figure 1.

Comparing features of different individuals can be challenging when they have different sizes and shapes. In Definition 5 we propose a transformation function to make contours orientation and scale invariant from each other.

Definition 5: (Transformation Function) For a given contour $c(u)$ and its boundary descriptor S , the transformation function, $f: c(u) = (x(u), y(u)) \rightarrow C(u) = (X(u), Y(u))$ is defined by

$$\begin{pmatrix} X(u) \\ Y(u) \end{pmatrix} = \begin{pmatrix} \frac{1}{\alpha} & 0 \\ 0 & \frac{1}{\alpha} \end{pmatrix} \begin{pmatrix} \cos \beta & \sin \beta \\ -\sin \beta & \cos \beta \end{pmatrix} \begin{pmatrix} x'(u) \\ y'(u) \end{pmatrix} \quad (6.1)$$

where $x'(u) = x(u) - x(u_0)$, $y'(u) = y(u) - y(u_0)$, $\alpha = \sqrt{(x(u_2) - x(u_0))^2 + (y(u_2) - y(u_0))^2}$, and $\beta = \arctan\left(\frac{y(u_2) - y(u_0)}{x(u_2) - x(u_0)}\right)$.

Now given two boundary descriptors S_1 and S_2 , a fully-connected bipartite graph $B(S_1, S_2)$ is defined with $E = \{(u, v) | \forall u \in S_1 \text{ and } \forall v \in S_2\}$. For an edge (u, v) , the weight of the edge is defined by

$$W(u, v) = \sqrt{(X(u) - X(v))^2 + (Y(u) - Y(v))^2} \quad (6.2)$$

where $(X(u), Y(u)) = f((x(u), y(u)))$ and $(X(v), Y(v)) = f((x(v), y(v)))$, which is the Euclidean distance between $(X(u), Y(u))$ and $(X(v), Y(v))$.

Finally, we can compare the two fins and provide the proof that our method is in the metric space.

Definition 6: (Boundary Descriptor Distance) $\mathcal{BD}(S_1, S_2)$ is the *Boundary Descriptor Distance* between two boundary descriptors S_1 and S_2 is the weight of the minimum weight perfect matching in $B(S_1, S_2, E)$ with the weighting scheme W .

Lemma 1: The boundary descriptor distance is $\mathcal{O}(n^{2.5} \log n)$ time computable where $n = |S_1| = |S_2|$.

Proof: Let S_1, S_2 be boundary descriptors with n elements. Computing the weights of the edges in $B(S_1, S_2)$ requires $\mathcal{O}(n^2)$ time. The minimum-weight perfect matching problem can be solved by using the faster scaling algorithm that is asymptotically bound by $\mathcal{O}(n^{2.5} \log(n))$ [17], from which the desired runtime follows. \square

Lemma 2: The boundary descriptor distance is a metric, i.e., for boundary descriptors S_i, S_j , and S_k , the following four properties are satisfied.

1. $\mathcal{BD}(S_i, S_j) \geq 0$ (non-negativity)
2. $\mathcal{BD}(S_i, S_j) = 0 \iff S_i = S_j$ (identity)
3. $\mathcal{BD}(S_i, S_j) = \mathcal{BD}(S_j, S_i)$ (symmetry)
4. $\mathcal{BD}(S_i, S_k) \leq \mathcal{BD}(S_i, S_j) + \mathcal{BD}(S_j, S_k)$ (subadditivity)

Proof: Observe that non-negativity, identity, and symmetry properties follow directly from definition of the \mathcal{BD} distance (i.e., Definition 6). To show the remaining subadditivity property suppose that M_{ij} and M_{jk} are the minimum weight perfect matchings in $B(S_i, S_j)$ and $B(S_j, S_k)$

respectively. Now, define a new matching in $B(S_i, S_k)$ by $M_{ik} := \{(u, w) \mid (u, v) \in M_{ij} \wedge (v, w) \in M_{jk}\}$, where $u \in S_i$, $v \in S_j$, and $w \in S_k$. For u , v , and w , $W(u, w) \leq W(u, v) + W(v, w)$ since the weighting function W is based on the Euclidean distance which is a metric. We have

$$\begin{aligned} \mathcal{BD}(S_i, S_k) &\leq \sum_{(u, w) \in M_{ik}} W(u, w) \leq \sum_{(u, v) \in M_{ij}, (v, w) \in M_{jk}} (W(u, v) + W(v, w)) \\ &= \sum_{(u, v) \in M_{ij}} W(u, v) + \sum_{(v, w) \in M_{jk}} W(v, w) = \mathcal{BD}(S_i, S_j) + \mathcal{BD}(S_j, S_k) \quad \square \end{aligned} \tag{6.3}$$

We use the metric on the framework to generate scores, which are the distances (result of minimum weight perfect matching) for each frame. Let *sharkA* and *sharkB* be the sharks compared in our framework. We have two types of scores: the scores obtained by comparing the frames of *sharkA* to itself and the scores obtained by comparing the frames of *sharkA* to *sharkB*. Those scores are going to be used to classify our shark at the analysis portion of the framework.

CHAPTER 7

MAIN RESULTS

In this chapter, we present the results of our framework on sample images of sharks obtained from California State University, Long Beach - Shark Lab, this step is correspondent to the blue portion of Figure 2.

The goal of our metric is to identify an individual shark by analyzing how distant it is from pictures of itself and how distant it is from pictures of other sharks. As we described before in Chapter 6 the distance is given by the sum of weights of a minimum perfect matching, we also refer to this distance as score in this paper.

Let *Sharks* be the set of sharks used in the experiment of this research defined by $Sharks = \{Akeru, Sydney, Wayne, Zibbo\}$. Our dataset is composed of two video files of each $shark \in Sharks$, which are the inputs to our framework. The details and results for those inputs are described in Experiment 1 and Experiment 2.

For the rest of this thesis, we use fin and frame interchangeably to refer to pictures of the dorsal fin.

Experiment 1

In this first experiment we compare pairs of sharks at a time. For each $shark \in Sharks$, we fed both videos into the framework. After the first round of the *Segmentation* step, described in Chapter 4, 50 frames per shark were selected by the framework. We performed the rest of the pre-processing on the 50 selected frames.

Let \mathcal{F}_{shark} be the set of all frames for $shark$, and $K(F)$ be the set of all key points for a frame $F \in \mathcal{F}_{shark}$.

After pre-processing, contour extraction, and boundary-descriptor computation, for each pair $shark_1, shark_2 \in Sharks$ where $shark_1 \neq shark_2$, we have 50 key points for each frame. We compare two sharks at a time, namely:

- Akeru vs Zibbo
- Akeru vs Wayne
- Akeru vs Sydney
- Sydney vs Zibbo
- Wayne vs Zibbo
- Wayne vs Sydney

Let *shark* be our subject and *other* be a different shark or *Others*. For each $F \in \mathcal{F}_{shark}$ we calculate two different distances (or scores):

- from F to F' for each $F' \in \mathcal{F}_{shark}$.
- from F to F' for each $F' \in \mathcal{F}_{other}$

The results are plotted in Appendix A.

Notice for each comparison, there is a clear distinction in between the two distributions showing the effectiveness of our metric.

Experiment 2

In this experiment we have results for all *sharks* \in *Sharks* vs *Others*, where *Others* represent a random choice of 50 images of the combination of the three sharks that are not the subject of that run. Appendix B) illustrates the combinations:

- Akeru vs Others
- Sydney vs Others
- Wayne vs Others

- Zibbo vs Others

Note that for *Zibbo vs Others* there is a complete overlap of the histograms. This result is due to the very low resolution of most of this shark's images. An idea to improve this results is presented in Chapter 8 as a future work.

CHAPTER 8

CONCLUSION

Animal biometrics are essential for several fields of research and ecological preservation. Most existing non-invasive identification methods are expensive and unreliable, especially for animals that are difficult to access. This thesis was written to introduce an automated framework for individual shark identification based on a novel metric.

Throughout this thesis we described all the steps involved for the automated identification process. Starting with the raw data files (videos or images), through semantic segmentation for the dorsal fin extraction, background removal, contour extraction, and boundary descriptor computation. We showed that our metric, the boundary descriptor distance, is in fact an effective individual identification method by reporting such distinguishing distributions.

Since our metric relies on high resolution images to get clear contours and quality key points for comparison, future work on this project will involve an image enhancing step to the pipeline. It is valid to mention that our dataset is growing as we receive more videos from the *Shark Lab*, however we also would like to introduce Big Data to this project. The idea is to use pictures gathered by surfers, divers, fisherman, and all kinds of resources, and use them to expand our dataset.

APPENDICES

APPENDIX A
EXPERIMENT 1

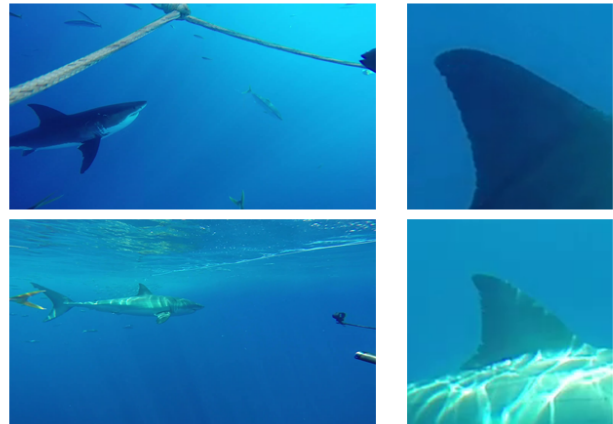
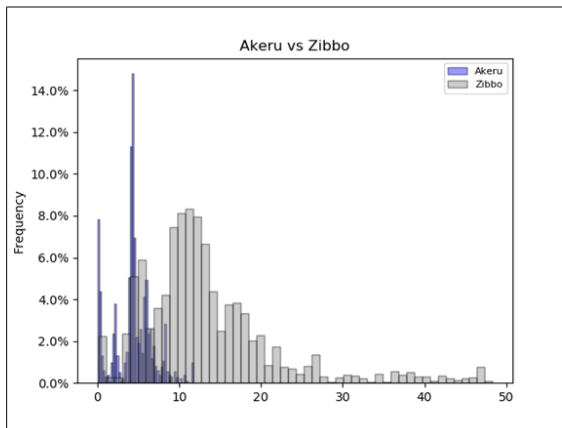


FIGURE 7. Pairwise comparison in between Akeru and Zibbo.

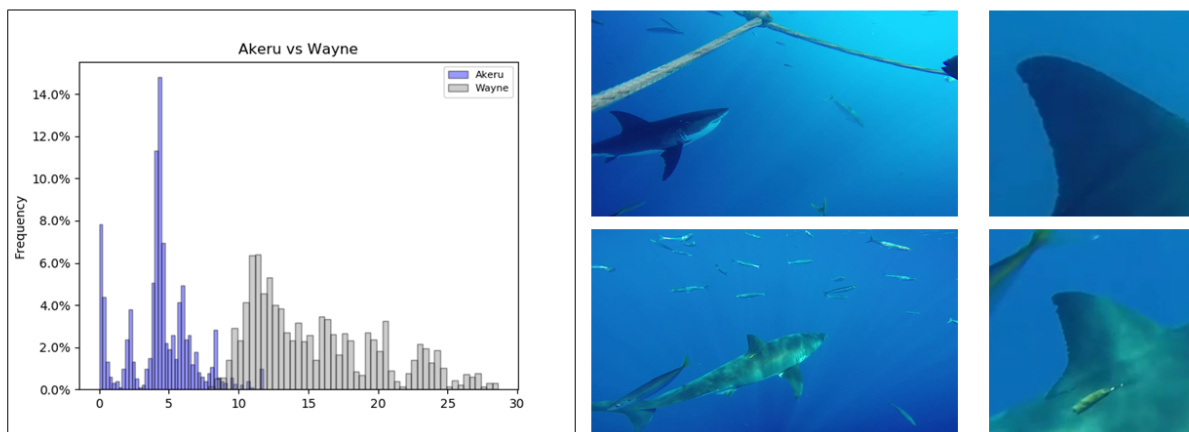


FIGURE 8. Pairwise comparison in between Akeru and Wayne.

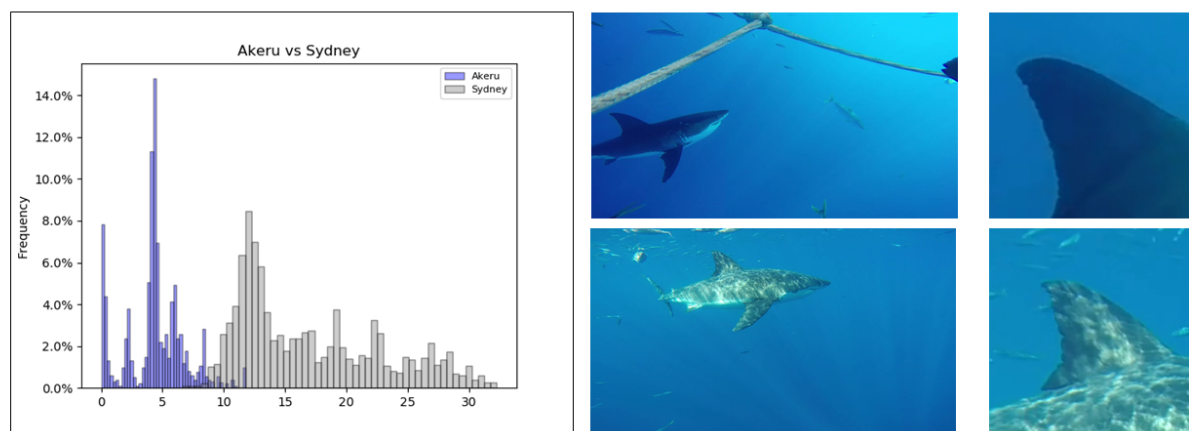


FIGURE 9. Pairwise comparison in between Akeru and Sydney.

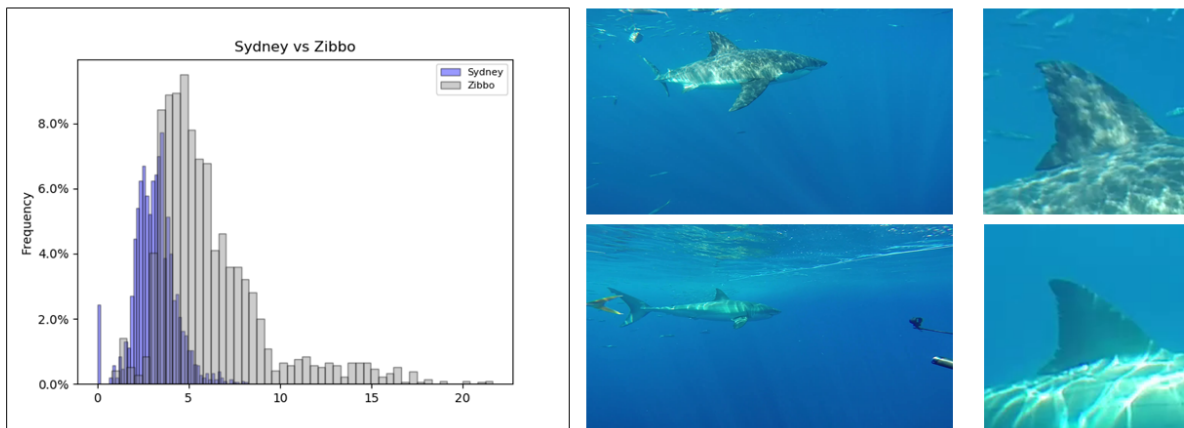


FIGURE 10. Pairwise comparison in between Sydney and Zibbo.

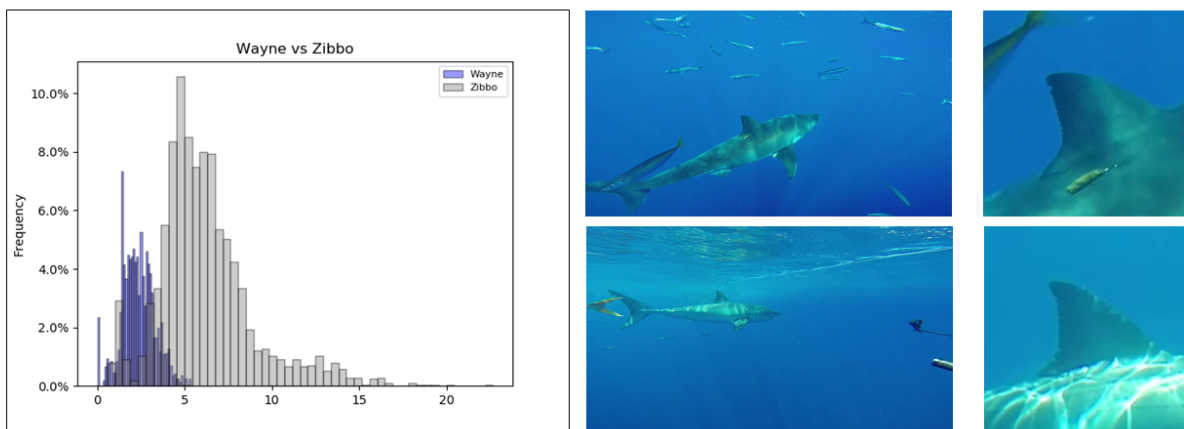


FIGURE 11. Pairwise comparison in between Wayne and Zibbo.

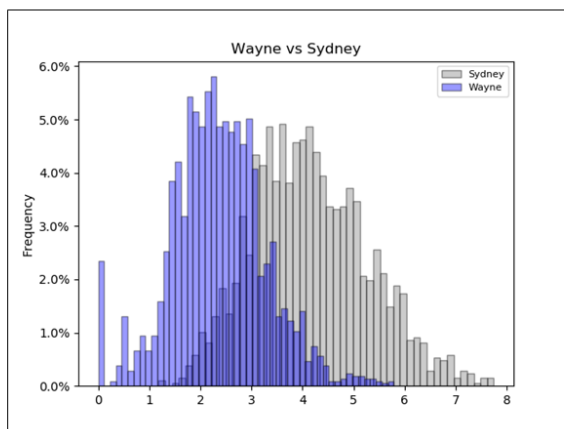


FIGURE 12. Pairwise comparison in between Wayne and Sydney.

APPENDIX B
EXPERIMENT 2

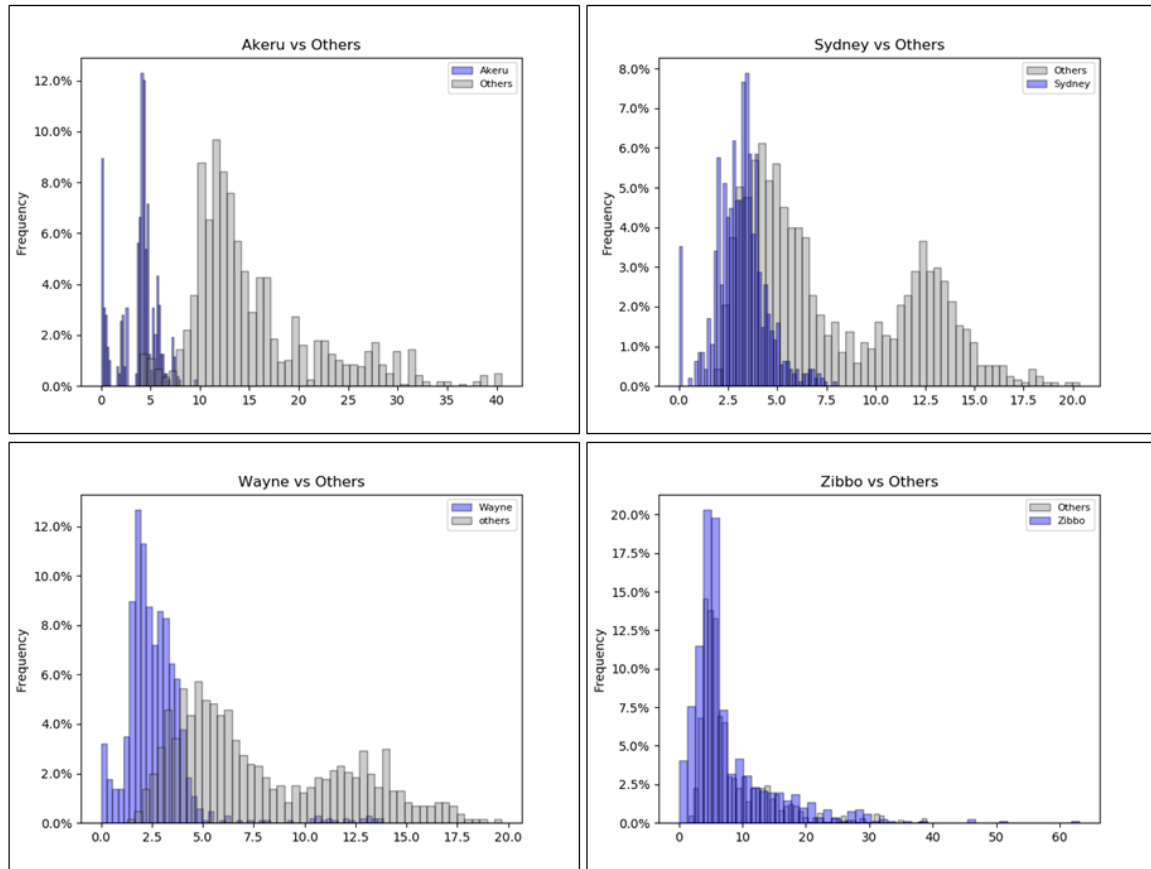


FIGURE 13. Pairwise comparison in between a shark and a random selection of the combination of the other sharks.

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