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Detection of Abnormal Fish Trajectories Using a Clustering Based Hierarchical Classifier

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Abstract

We address the analysis of fish trajectories in unconstrained underwater videos to help marine biologist to detect new/rare fish behaviours and to detect environmental changes which can be observed from the abnormal behaviour of fish. The fish trajectories are separated into normal and abnormal classes which indicate the common behaviour of fish and the behaviours that are rare/ unusual respectively. The proposed solution is based on a novel type of hierarchical classifier which builds the tree using clustered and labelled data based on similarity of data while using different feature sets at different levels of hierarchy. The paper presents a new method for fish trajectory analysis which has better performance compared to state-of-the-art techniques while the results are significant considering the challenges of underwater environments, low video quality, erratic movement of fish and highly imbalanced trajectory data that we used. Moreover, the proposed method is also powerful enough to classify highly imbalanced real-world datasets.

1 Introduction

Automatic analysis of animal and insect behaviour using computer vision techniques is a growing research area with many interesting studies such as mouse activity recognition [1], and behaviour identification of fruit flies [2] etc. The traditional way of analyzing the behaviour of animals is by visual inspection of human observers which is very time consuming and also limits the size of data that can be processed.

In this study, we present a novel framework for abnormal behaviour detection and especially focus on fish trajectories. Fish behaviour analysis is a fundamental research area in marine biology as it is helpful to detect environmental changes by detecting abnormal fish patterns and to detect new behaviours of fish. Detecting abnormal trajectories is useful when the system does not have any prior knowledge about the data which especially happens in the real-world data due to the uncontrolled naturalness. Recently, computer vision based fish trajectory analysis systems have been presented such as for water quality monitoring and toxicity detection [3, 4, 5], fish stress factor identification [6], fish school monitoring [7], abnormal trajectory detection in aquaculture sea cages [8]. The common aspect of these works is analyzing the fish trajectories in an aquarium [3], a tank [7] or a cage [8] which makes the analyses simpler, decreases the number of behaviour varieties and also removes the effects of habitat on the behaviour of fish. Compared to our work,

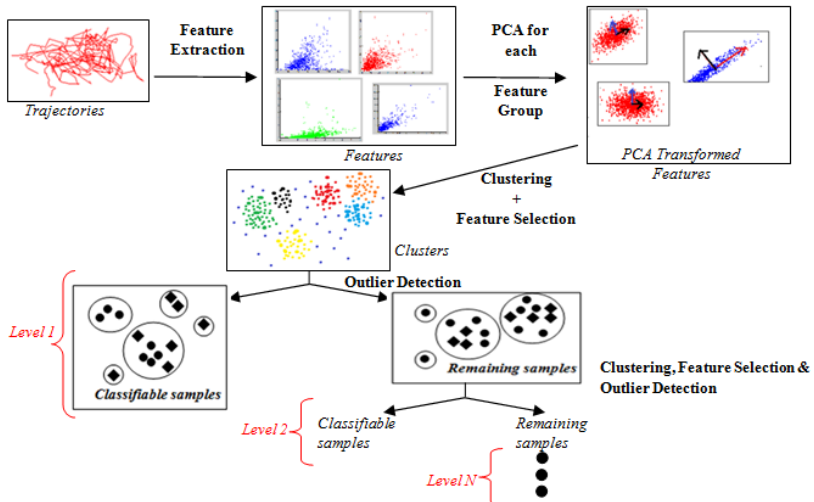


Figure 1: Overview of proposed method (See Section 2.1 for explanations).

those are limited in terms of number of trajectories. On the other hand, unconstrained underwater studies also exist such as [9, 10, 11, 12]. Those studies do not exactly consider abnormal fish trajectory detection but do contribute to fish trajectory analysis. A more detailed literature study on fish behaviour analysis can be found in [12].

When we compare fish trajectory datasets from underwater videos with the other abnormal behaviour detection datasets (for instance traffic surveillance, human abnormal trajectory detection and nursing home surveillance), there are certain differences. First, fish in the open sea can freely move in 3 dimensions hence there are no defined rules or roads such as exist in a traffic surveillance scenario. Fish are not goal-oriented which produces highly complex trajectories in contrast to people or vehicles. Fish usually make erratic movements due to currents in the water which increases the complexity of trajectories and also makes encoding the behaviour more difficult than is in human or animal behaviour recognition [9]. In this study, we present an approach to detect abnormal fish trajectories using a hierarchical classifier. Normal fish trajectories are defined as the trajectories which contain frequently observed behaviours while abnormal trajectories are defined as outliers or rare trajectories. Clustered and labelled data are used together and the hierarchy is automatically built using similarity of data instead of using a taxonomy between features or classes as is common in the literature. Different than the studies which use the same feature space for classification, we use different feature sets at different levels of the hierarchy which allows more specific features to be used once the data focuses onto specific subclasses. The proposed method is compared with the state of art methods of abnormal trajectory detection (fish and also in general) and performs better classification compared to them.

The main contributions of this paper are: **i)** presenting a novel approach for abnormal behaviour detection which builds a feature or class taxonomy independent hierarchy, **ii)** demonstrating improved performance on abnormal trajectory analysis of fish in unconstrained underwater videos. Besides, we show that using different feature spaces in the classification at different levels can improve the performance (see performance of K-NN, flat classifier and the proposed method in Section 3). The results showed that the proposed method successfully classifies imbalanced datasets especially when classes contain sub-classes even though they are considered as the same class.

2 Proposed Method

The tracker in [13] is used to obtain the fish trajectories and a trajectory is defined by the centre of fish bounding boxes. For fish i tracked through n frames the trajectory can be represented as:

$$T_i = \{(x_1, y_1), (x_2, y_2), \dots, (x_{n-1}, y_{n-1}), (x_n, y_n)\} \quad (1)$$

The basics of the proposed hierarchical method (Figure 1) are i) feature extraction (section 2.3, includes the pre-processing of fish trajectories and Principal Component Analysis (PCA) of extracted features), ii) clustering (section 2.4), iii) outlier detection (section 2.5) and iv) feature selection (section 2.6). Clustering of data based on selected features without initially using the known labels is the key to partitioning the data into separable subsets. To automatically generate the hierarchy during training (section 2.1), clustered and labelled trajectories are used together. Different from the traditional way which uses the same feature set for every level of hierarchy or for a flat classifier, we use different feature sets at different levels of the hierarchy, which allows selecting more specific features.

2.1 Hierarchy Construction

At each level of the hierarchy (training phase), data is first clustered using a subset of features by adding a single feature at each iteration of feature selection. Then, outlier detection is applied to each cluster and outliers are found. Following this, the class accuracies are determined using the ground truth labels which represent the normal and abnormal fish trajectories. This procedure is repeated by adding features to the subset of features and feature selection stops when the average of class accuracies on the training set (for the specific hierarchy level) decreases. After the best feature set is found (which is specific to that hierarchy level), the clusters which do not have any false positives (FPs) and false negatives (FNs) are fixed (called classifiable samples) for that level. The hierarchy building recurs with the remaining samples. The tree is extended until there is no cluster which is perfectly classifiable. The leaf nodes of the hierarchy can be either a) perfectly classified clusters (pure clusters; which contains only abnormal (True negative: TNs) or only normal trajectories (True positives: TPs) or mixed clusters which are separable by outlier detection, section 2.5) which can be observed mostly in the leaf nodes while not belonging to the last level of hierarchy, b) mixed non-separable clusters. These occur only in the leaf nodes belonging to last level of hierarchy.

2.2 Trajectory Classification using the Hierarchy

In the testing phase, to classify new trajectories, the constructed hierarchy (all clusters including the not classifiable ones for each level), selected feature sets in each level, and outlier detection parameters are used. At each level, the closest cluster to the new fish trajectory is found using the Euclidean distance between its feature vector (using the features selected for the current hierarchy level) and all cluster centres in that level. At this step there are six possibilities based on the type of the closest cluster. For a specific level, **i)** the closest cluster is classified pure abnormal cluster which makes the new trajectory a candidate abnormal fish trajectory, **ii)** the closest cluster is classified pure normal cluster where the new trajectory is further from the outlier detection threshold found during training which makes the new fish trajectory a candidate abnormal fish trajectory, **iii)** the closest cluster is a classified pure normal cluster where the distance between the new fish

trajectory and the cluster centre is smaller than the outlier detection threshold which makes the new trajectory a candidate normal fish trajectory, **iv**) the new trajectory becomes a candidate abnormal fish trajectory if the closest cluster is classified as a mixed cluster (having normal and abnormal trajectories) which was segmented by outlier detection during training and the new trajectory is further from the outlier detection threshold, **v**) the new trajectory becomes a candidate normal fish trajectory if case **iv** occurs but the distance between the new trajectory and cluster centre is smaller than the threshold, and last **vi**) the closest cluster is a “not classifiable” cluster during training which does not have any effect to the decision of the new trajectory’s class. Once the class decisions (candidate normal or candidate abnormal fish trajectory) computed at each level, a new trajectory is classified as normal if the decision from any level is normal. Otherwise, it is classified as abnormal trajectory.

2.3 Feature Extraction

The challenges of fish detection and tracking in the underwater environment sometimes cause gaps in the fish trajectory. To handle this, before extracting features, all trajectories are linearly interpolated as a pre-processing step. To classify trajectories as normal or abnormal 10 groups of features are extracted.

2.3.1 Curvature Scale Space (CSS) Based Features

The CSS was first presented in [14] as a trajectory representation to classify and represent activities. It is calculated using the curvature at every point (x_i, y_i) on the curve formula given in Eq. 2 which is rotation and translation invariant and helpful to distinguish trajectories by their shapes in terms of convexity and concavity.

$$K_i = \frac{x_i'y_i'' - y_i'x_i''}{(x_i'^2 + y_i'^2)^{3/2}} \quad (2)$$

To find the CSS, a Gaussian smoothing kernel is applied. At each level of scale space the standard deviation (σ) of the kernel is increased and by finding the correspondence between the zero crossings of curvature for all levels, the CSS is constructed. As σ increases, the trajectory shrinks, becomes smoother and the number of zero crossing points on it decreases. Finally, the trajectory becomes a convex curve with no zero crossing [15]. The location of zero crossings of the trajectory is determined and the result is represented as a binary image called the CSS image (a more detailed description can be found in [14]).

In this study, we adapted the CSS based features to represent fish trajectories. We extract different statistical properties based on [14] using the CSS image and the absolute curvature at each scale level. Some of the extracted features are the length of curves in CSS image, the number of zeros crossings for each σ in CSS image, the total number of curves in CSS image and statistical features (such as mean, variance etc.) of absolute curvature are used and in total 580 features are obtained.

2.3.2 Moment Descriptors Based Features

For recognition of object and patterns, moment invariants are commonly used. Similarly, fish trajectories shape can be distinguished by using moment descriptors. We utilize affine moment invariants proposed in [16] in addition to moment, central moment and translation and scale invariant moments. In total 55 features are extracted using those moment descriptors.

2.3.3 Velocity and Acceleration Based Features

Even though a fish trajectory is spatially similar to normal trajectories its speed and/or speed change may represent an anomaly. Therefore using velocity and acceleration based features can be useful to detect possible abnormal trajectories. Statistical properties: mean, standard deviation, minimum, maximum, number of zero crossings, number of local minima and maxima etc. of velocity and acceleration are extracted in 3 dimensions considering the fact that fish can swim in 3 dimensions in an open sea. However, since we describe the trajectories of fish in 2 dimensions in Eq. 1, the width (w) and height (h) of fish bounding box in each detection are combined ($z=1/\sqrt{wh}$) to estimate the displacements of objects in third dimension. In total 42 features (7 properties x {velocity, acceleration} x 3 dimensions) are obtained.

2.3.4 Turn Based Features

Trajectory turnings give an idea about the shape of the fish trajectory. Calculating the trajectory slope is given in [17] (Eq. 3). From θ_i we extract the same 7 statistical properties as in Section 2.3.3.

$$\theta_i = \frac{y_{i+1} - y_i}{x_{i+1} - x_i} \quad (3)$$

2.3.5 Centred Distance Function (CDF)

CDF is the distance of each point in a trajectory from the centre of the trajectory [14]. In total 18 features including mean, maximum, minimum, standard deviation, number of mean crossings, number of local minima and maxima, skewness and kurtosis of 3D and 2D CDFs are extracted to represent the fish trajectories.

2.3.6 Vicinity Features

Features extracted from the trajectory vicinity were used in [18] for handwriting recognition. We adapted this idea to represent fish trajectories. Three kinds of properties: 1) aspect of vicinity, 2) vicinity curliness (the length of trajectory in the vicinity divided by maximum ($\Delta x(i)$, $\Delta y(i)$) while $\Delta x(i)$ and $\Delta y(i)$ represents the difference between x and y coordinates of vicinity points respectively) and 3) vicinity linearity (the average square distance of each point in the vicinity to the straight line from the last and first vicinity point) are extracted. Statistical measures obtained from those properties such as number of local minima, mean etc. are used as features. Different than [18], the vicinity features are calculated in two different ways as given in Eq. 4. In total 40 features are extracted from trajectory vicinity.

$$\text{Type1: } (\Delta y(i) - \Delta x(i)) / (\Delta y(i) + \Delta x(i)) \quad \text{Type2: } \Delta y(i) / \Delta x(i) \quad (4)$$

2.3.7 Loop Features

The trajectory of a fish can be complex and might contain many loops due to the erratic motion of fish and the undersea current. Therefore, representing the trajectory in terms of loops can be useful. As features the number of loops, maximum, minimum and median of number of points in a loop (in total 4 features) are extracted.

2.3.8 Fish Pass By Features

Fish trajectories can be affected by the geographical properties of the underwater environment and can be different in the open sea, under the coral and above the coral.

Considering those properties can be helpful to find normal and abnormal trajectories. In this study, we manually segmented each video scene once as the cameras are fixed as shown in Figure 2 and extract descriptors: the frequencies of being in different locations and frequency of crossings from one location to another using the segmented image and the trajectory of the fish. In total 12 features (4 features for each location) are obtained.

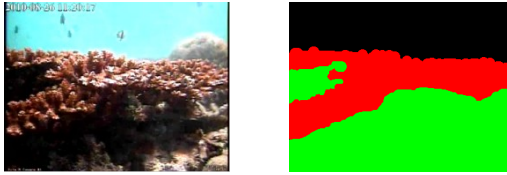


Figure 2: Segmented regions of underwater image; black for open sea, red for above the coral and green for under coral.

2.3.9 Features Based on Normalized Size of Bounding Box

Fish can frequently change their posture. Even for adjacent frames its posture can be different and this fact can be useful to distinguish the erratic motion of fish, aggressive motion of fish and/or sudden changes in its trajectory. To model this, we extract the width (w) and height (h) of the fish bounding box for each detection and define a function from the ratio of width of fish bounding box to its height (w/h). This function is z-normalized to eliminate the effect of small and big fish differences. The number of zero crossings, number of local minima and number of local maxima obtained from this function are the extracted features (in total 3 features) in this step.

2.3.10 Features Based on Displacement on the Location

Using the segmented locations given in section 2.3.8, we extract the statistical properties such as maximum, minimum and median etc. of average displacement in different locations. In total 15 features are obtained.

Altogether 776 features are obtained in the feature extraction step. These features are generally correlated with each other which might cause over-training in case of being selected by feature selection. To handle this, dimensionality reduction is used which also reduces the curse of dimensionality. Therefore, as a post processing step of feature extraction, PCA is applied to the data from each feature group individually. To obtain a useful set of components the smallest number of components that represent 90% of the sum of all eigenvectors is used. This left $\{115, 12, 12, 3, 8, 14, 2, 6, 2 \text{ and } 5\} = 179$ features for the 10 feature groups respectively.

2.4 Clustering

Affinity propagation (AP) is the clustering method [19] that we used in this study. It has been used by many studies for different applications including anomaly detection. Different from many other clustering methods AP identifies the cluster centres from actual data points (exemplars). The pair-wise similarity between each pair of feature vectors is the negative of the Euclidean distance between the vectors. Given the similarity matrix AP tries to find the exemplars that maximize the overall sum of similarities between all exemplars and their data points. It is based on two kinds of messages between data points. The first message (responsibility) is from a data point i to j that represents the accumulated evidence for how well it would be for the data point j to be the exemplar for data point i .

The second message (availability) represents how well it would be for data point i to choose data point j as its exemplar. More information can be found in [19].

AP has many advantages over traditional clustering methods (our experiments using k -means, mixture models and mean-shift clustering also show that AP performs better for our problem). The most important properties of AP given our assumption for outlier detection are its capability to produce smaller clusters and to be able to produce uneven sized clusters by minimum error rate. Additionally, its fast processing speed, being non-parametric, not requiring initialization, not depending on sample order (such as hierarchical clustering) and scalability property (which makes our method scalable as well) are other benefits of this method.

2.5 Outlier detection

In this study, we adapted the outlier detection method from [20] and present two types of abnormal (outlier) trajectories: those located in small clusters and those that exist in dense clusters but deviate from other trajectories in its cluster. To detect small clusters we defined a threshold which is based on the cardinality of all clusters. Hence, a cluster which has less data samples than $threshold=A\%$ (such as 10%) of the median cardinality of clusters or a cluster that has only one data point is defined as a small cluster and all trajectories belonging to that cluster are abnormal. Otherwise it becomes a dense cluster, whose outliers are detected by using the Euclidean distance between the trajectories in that cluster and exemplar. In this case, a trajectory whose distance is greater than the threshold ($\tau=\mu+w\sigma$), (which is based on the mean (μ), weight (w) and standard deviation (σ) of all distances between the trajectories in that cluster) from the cluster's exemplar, is defined as abnormal.

2.6 Feature Selection

At each level of the hierarchy, sequential forward feature selection is applied in combination with clustering and outlier detection. This provides finding the proper features for that level using the remaining data from the higher level of hierarchy and also to decrease the chance of over-fitting during training. Moreover, by using this, irrelevant, redundant features and features that might even misguide clustering are eliminated. We use the average of class accuracies instead of using overall accuracy since highly imbalanced data (where the number of normal trajectories is much larger than the number of abnormal trajectories) drives overall accuracy to misclassify the minority class.

In detail, for a specific level of hierarchy, given the current set of features, an additional feature is added one by one, afterwards clustering and outlier detection are performed with the extended feature set. The classification accuracies are found using the ground-truth labels. After all possible additional features are tried; the extended feature set with the best classification performance is kept. The feature addition stops when the average of class accuracies on the training set decreases compared to the previous iteration.

3 Results

The proposed method was applied to 3102 trajectories (3043 normal, 59 abnormal, which is the largest fish trajectory data set in the underwater environment to the best of our knowledge) from 93 different videos (320x240 resolution, 5 frames per second) which belong to *Dascyllus reticulatus* in the Taiwanese coral reef in the morning. The normal and

abnormal (rare) behaviours are determined by visual inspection. The most usual and frequent behaviours in the dataset are freely swimming fish in open sea and hovering fish on the coral (Figure 3a-b) which represent normal behaviours. On the other hand, abnormal trajectories are: i) fish suddenly (in one frame) diving under the coral, ii) fish suddenly (in one frame) changing direction (predator avoidance, Figure 3c), iii) fish biting at coral (also interaction with plankton, Figure 3d), iv) diving quickly between the coral branches when frightened or to hide from predators, and v) aggressive fish which is moving fast. A trajectory that has normal and abnormal segments is assumed as abnormal.

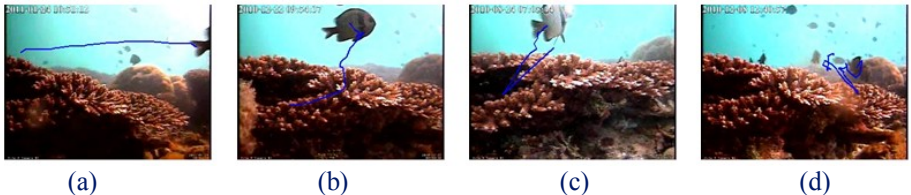


Figure 3: (a-b) Examples of normal fish trajectories, (c-d) Examples of abnormal (rare) fish trajectories.

The proposed method was compared with the state of art methods of fish trajectory analysis and other popular trajectory analysis researches. 9-fold cross validation was performed. Training and test sets were constituted randomly and the normal and abnormal trajectories are distributed equally in each set. The proposed method is compared with classifiers: k-nearest neighbour (k-NN) and Support Vector Machines (SVM). k-NN was chosen to show the differences between using different feature spaces in the classification of different samples and using a single set of features and also to have an idea about the distribution of data in feature space. SVM is a very popular technique for trajectory analysis which has already used in many studies such as [21, 22, 23]. Different k values including $k=1$ for k-NN, different kernel parameters for the radial basis function of SVM were tested to obtain the best performance for each method. The proposed method is also compared with method [12] (the most similar study that can be compared) which tries to filter out normal fish trajectories while not filtering any abnormal trajectories especially when normal trajectories are many more than abnormal trajectories. We also applied the flat classifier using the same methods for clustering, outlier detection and feature selection. The new trajectories are classified applying clustering and outlier detection with the selected features, and parameters learned during training. While performing those methods sequential forward feature selection was performed for k-NN, SVM and flat classifier as done in the proposed method. Lastly, spectral clustering and Gaussian mixture model based method [24] (which is very popular method for trajectory analysis) were applied to fish trajectories. In this context, as done in [24], Normalized Cuts spectral clustering was applied to abnormal and normal trajectories individually and each cluster of behaviour was modelled as a mixture of Gaussians in the spectral embedding space. A new track is classified by projecting it into the spectral embedding space for normal and abnormal classes and based on the likelihood the new track is classified as a normal or abnormal trajectory.

Table 1 shows the best result of each method in terms of the average of true positive rate (TPR; the normal trajectory classification accuracy), the average of true negative rate (TNR; the abnormal trajectory classification accuracy) and the average geometric mean of TPR and TNR which is a common metric to evaluate performance of imbalanced datasets. For each evaluation metric the standard deviation is also given after \pm sign. For the proposed method the best performance was observed when the A is 10 and the w is 0.1 as

outlier detection parameters. The depth of the hierarchy was at most 3 while mostly 2 for the 9-folds. The results show that the proposed method has highest abnormal trajectory detection rate while also the best method in overall. Additionally, t-tests were applied to the geometric mean of TPR and TNR between each method and the proposed method. It is obtained that the proposed method is significantly better than all methods (except SVM) with p-value under 0.01. It also performs better than SVM however that p-value is close to 0.05.

	k-NN	SVM	Rule based method [12]	Flat Classifier	Spectral clustering based method [24]	Proposed Method
TPR	0.99±0.004	0.93±0.03	0.77±0.04	0.76±0.02	0.85±0.11	0.88±0.02
TNR	0.37±0.28	0.81±0.16	0.80±0.2	0.81±0.17	0.57±0.2	0.94±0.1
Geo.Mean TPNR	0.55±0.27	0.86±0.09	0.78±0.09	0.78±0.09	0.66±0.04	0.91±0.05

Table 1. Comparison with the state of art methods

To show that the proposed hierarchical classifier is not limited to fish trajectory analysis and is a general framework for classification of imbalanced datasets, we applied it to 3 popular imbalanced sets (even though our primary aim in this paper is detecting abnormal fish trajectories): the Scene dataset (2230 samples from majority, 177 from minority class) [25] for semantic scene classification, the Pima dataset (500 from majority, 268 from minority) [26] and the Ionosphere dataset (225 from majority, 126 from minority) [27]. For these datasets, we choose the smallest class as the minority class (TNs; abnormal) and collapsed the rest of the classes into one to obtain normal class (TPs). 5 fold cross validation is applied in all cases. Table 2 compares the proposed method with k-NN and SVM using those datasets. The proposed method performs the best in terms of both the TNR and the geometric mean of TPR and TNR. In all cases, our TNR rate is significantly better ($p < 0.01$), which is desirable as we are looking for the minority class (abnormal class).

		k-NN	SVM	Proposed Method
Scene [25]	TPR	0.93±0.01	0.68±0.08	0.67±0.10
	TNR	0.17±0.05	0.60±0.09	0.64±0.03
	Geo.Mean TPNR	0.40±0.09	0.64±0.05	0.74±0.04
Pima [26]	TPR	0.73±0.04	0.64±0.06	0.65±0.02
	TNR	0.46±0.05	0.68±0.08	0.75±0.07
	Geo.Mean TPNR	0.58±0.04	0.66±0.05	0.71±0.03
Ionosphere [27]	TPR	0.94±0.02	0.95±0.01	0.95±0.06
	TNR	0.71±0.06	0.75±0.16	0.92±0.07
	Geo.Mean TPNR	0.82±0.04	0.84±0.09	0.93±0.05

Table 2. The performance of the proposed method in other popular datasets

4 Conclusions

We presented a hierarchical classifier to detect abnormal fish trajectories in underwater videos which is useful to help marine biologists to automatically detect new fish behaviours. To represent fish trajectories novel descriptors were developed. The comparison between different methods and the proposed algorithm showed that the proposed method is significantly better at detecting abnormal fish trajectories while also

presenting better classification in overall. It is also efficient at classifying new tracks as it is only based on distance calculations between the new sample and the cluster centres of each level of the hierarchy.

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