ANERIS

Operational Sensing Life Technologies for Marine Ecosystems

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Deliverable D3.6 – AIES-MAC Code and Documentation

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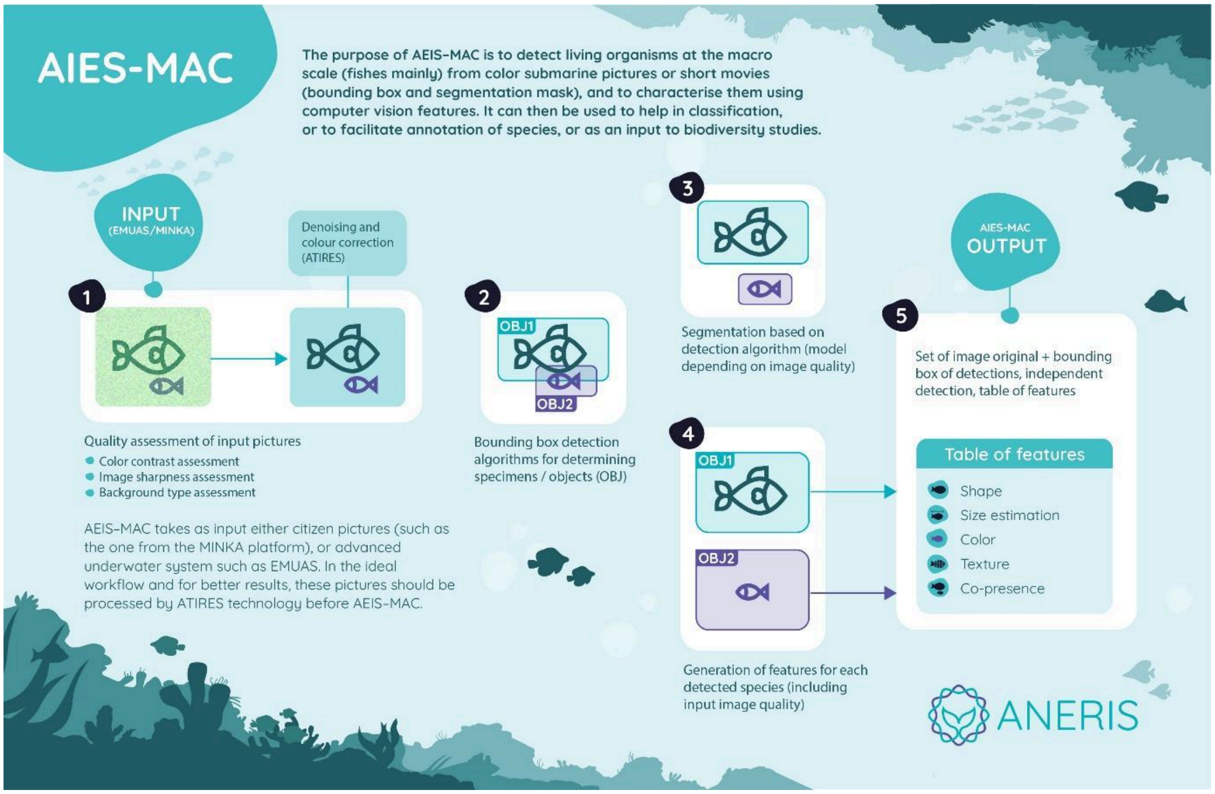
Table of Contents

Preface

In order to support the development of Operational Marine Biology (OMB) products, several technologies are developed within the ANERIS project. In particular, several digital image-based observations are now being collected in the context of the project, either based on participatory observations, gathered under the MINKA platform, either using underwater bio optics from a particular site, such as the technology EMUAS. These approaches of observations allow generating an important amount of digital images, for which the task is to recognise the species, which are present at these sites. The amount of data prevents a pure human based recognition, as this would be highly time-consuming and prone to human bias.

For this reason, one of the technologies developed in ANERIS is a system aiming to detect and characterize macro-organisms in the images collected, in particular underwater images, named AIES-MAC for Automatic Information Extraction System for MACroorganisms (Figure 1).

This deliverable introduces and documents the first version of the AIES-MAC open source code, which proposes to complete an automatic detection of the species on a digital image by their characterisation based on characteristics extracted from their automatic segmentation. It also gives the direction of the next developments before the end of the project.



The purpose of AEIS-MAC is to detect living organisms at the macro scale (fishes mainly) from color submarine pictures or short movies (bounding box and segmentation mask), and to characterise them using computer vision features. It can then be used to help in classification, or to facilitate annotation of species, or as an input to biodiversity studies.

AEIS-MAC takes as input either citizen pictures (such as the one from the MINKA platform), or advanced underwater system such as EMUAS. In the ideal workflow and for better results, these pictures should be processed by ATIRES technology before AEIS-MAC.

Figure 1: *Infographics introducing the AIES-MAC technology produced for co-design activities by PENSOFT and Science For Change.*

Summary

The technology focuses on detecting and identifying macroorganisms from single images acquired from citizen smartphones, underwater cameras or from EMUAS, after processing by ATIRES (Automatic underwaTer Image REstoration System). These single images can come from single shot captures or videos.

Given one image as input, AIES-MAC aims to recognize regions of interest (ROIs) containing one macroorganism. The purpose is to segment (not only detect) the macroorganisms and extract size, shape, texture, or other parameters that can feed the characterisation and the taxonomic classification. It focuses on explainable indices to add to the databases of measurements, which can be interpreted by humans, in opposition to black box classification by deep learning.

Identifying automatically the different organisms in underwater images is a challenging task, since many of the benthic images are considerably complex because of a rich background in the images, and pelagic images can suffer from blurriness and lack of resolution and do not focus on all the species present in the image.

The approach taken in AIES-MAC is composed of many steps. First input images are automatically analysed to produce some quality metrics, which will serve as indicators of the quality and content of the images in order to automatically adapt the workflow to the images and their complexity. Then an adapted pretrained model for the creation of bounding boxes around each macroorganisms (detection) together with a prediction of its species (classification) is applied. The detected bounding boxes are then fed to a foundation model of segmentation to obtain the contour of the macroorganism within the bounding box. A list of human interpretable characteristics such as texture, colour, shape and size are then automatically extracted and associated to the detection. These characteristics can then serve to refine or correct a classification but also as indexes to search in the database of observations for instance.

The code takes for now the form of Jupiter notebooks in python and its current version associated to this deliverable is publicly released as Release associated to D3.6 · perrine paul-gilloteaux / ANERIS_AIES-MAC · GitLab. The minimum resources to run are under investigation: for now it was run on a cluster with a NVIDIA A100 graphical card and 16Gb RAM. The final form will depend on the prioritized OMB products.

The next steps will be mainly to apply and adapt if needed this code to the different OMB products defined in the consortium, in particular for participatory science and bio optics applications. For the latter, the video format will also allow defining and extracting information on the observed species dynamical behaviour by image-based tracking methods. Real cases will allow the validation and possible improvements of the technology, in particular to assess the need for a 3D estimation of the pose and for the segmentation of subparts of the organism (such as tail, head, eyes…). Another development to come is the calibration of the images

(giving a physical size and ideally 3D position of each pixel in the image). ATIRES is not yet embedded, but the aim is to use it both for the color restoration and quality improvement of the input images, but also to use the generated depth map estimation to help a 3D calibration.

List of Abbreviations

ATIRES – Automatic underwaTer Image REstoration System

DL – Deep Learning

DMP – Data Management Plan

DOI – Digital Object Identifier

EMUAS – Expandable Multi-imaging Underwater Acquisition System

OMB – Operational Marine Biology

ROI – Region Of Interest

ROIs – Regions Of Interest

SAM – Segment Anything Model

UCIQE – Underwater color image quality evaluation

UICM – Underwater Image Colorfulness Measure

UIConM – Underwater Image Contrast Measure

UISM – Underwater Image Sharpness Measure

UIQM – Underwater Image Quality Measure

YOLO – You Look Only Once

1. Documentation of the workflow

The approach taken in AIES-MAC is composed of several main steps, relying on computer vision tasks explained in Figure 2. First, input images are automatically analysed to produce some quality metrics, which will serve as indicators of the quality and content of the images in order to automatically adapt the workflow to the images and their complexity. Then an adapted pretrained model for the creation of bounding boxes around each macroorganism (**detection**) together with a prediction of its species (**classification**) is applied. The detected bounding boxes are then fed to a foundation model of **segmentation** to obtain the contour of the macroorganism within the bounding box. The segmentation is an **instance segmentation**, since there is a possibility for a bounding box to contain several macroorganisms if one is above the other one. A list of human interpretable characteristics such as texture, colour, shape and size are then automatically extracted and associated to the detection. These characteristics can then serve to refine or correct a classification but also as indexes to search in the database of observations for instance. Figure 3 summarizes the main steps of this strategy.

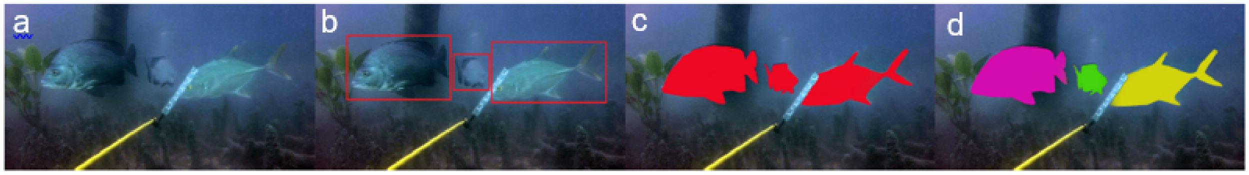


Figure 2: *Adapted from [1] : a) image-level classification (list of taxonomic species presented in the images without position); b) object detection (list of bounding box with detected objects: object classification can be added to give a taxonomic name to each detected object), c) semantic segmentation (mask of object of interest , separated from background), d) instance segmentation (every object has its own mask and identity).*

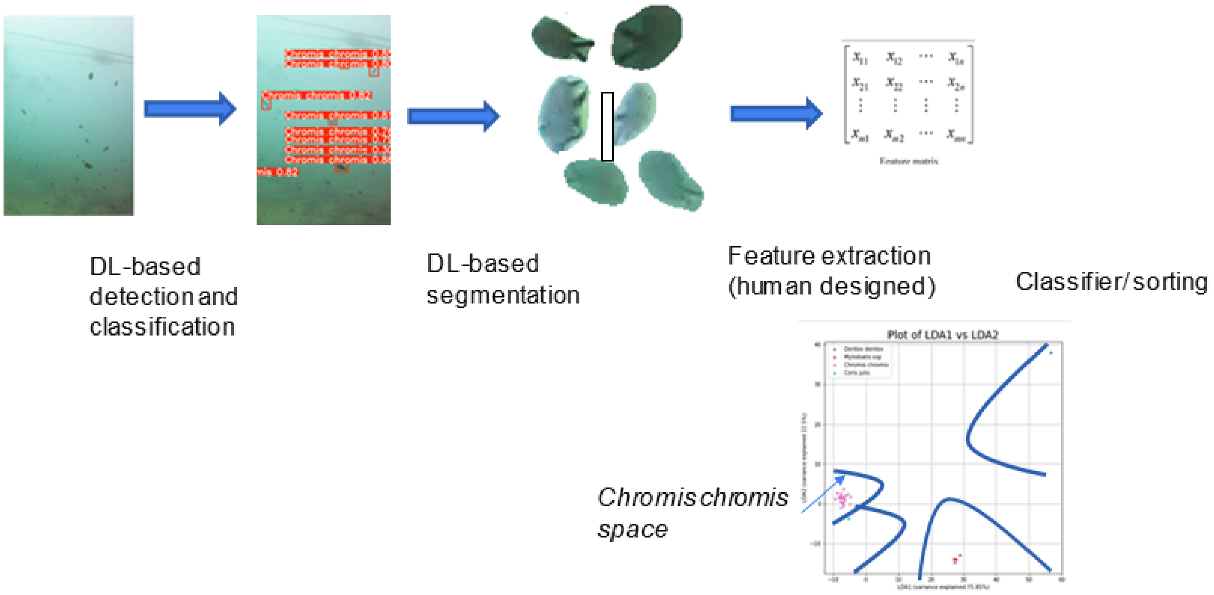


Figure 3: *Summary of the main steps of AIES-MAC: from an input image, candidate-bounding boxes are automatically extracted, together with a preproposal of classification of the species (DL-based detection and classification). Each bounding box is then used to compute a mask of the species (DL-based segmentation). Features are then extracted from this mask and the*

original image based on the mathematical expression of human interpretable characteristics (size, shape, texture..) which can then be used in a classifier or for sorting.

The following sections explain each step of the workflow, together with the link to the corresponding jupyter notebook. Respecting ANERIS DMP, all the notebooks are part of the release associated to this deliverable Release associated to D3.6 · perrine paul-gilloteaux / ANERIS_AIES-MAC · GitLab. The associated DOI to the source code of this release is https://doi.org/10.5281/zenodo.14329537. The minimum resources to run are under investigation: for now it was run on a cluster with a NVIDIA A100 graphical card and 16Gb RAM.

1.1 Select and load image

This step is for development purposes only and allows selecting the image to be processed in the following steps from a list of files in one given directory. A list of available image database for testing is available as Annex 1

The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/SelectAndLoadImage.ipynb?ref_type=heads

1.2 Quality assessment and denoising

This step computes some quality metrics from the image, and optionally performs some denoising.

The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/Quality_Assessment_Denoising.ipynb?ref_type=heads

The following metrics are computed using the definition and implementation described in [2] and [3].

- **UICM** Underwater Image Colorfulness Measure (chroma)
- **UISM** Underwater Image Sharpness Measure
- **UIConM** Underwater Image Contrast Measure

- **UIQM** Underwater Image Quality Measure, linear combination of sharpness, chroma and contrast.
- **UCIQE** Underwater color image quality evaluation, linear combination of chroma, saturation and contrast.

1.3 Detection and default proposed classifications

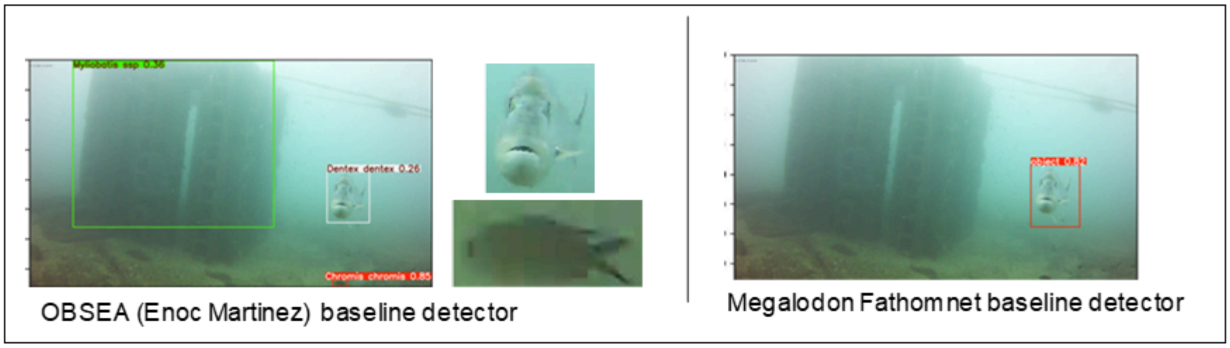
This step performs detection and classification using pre-trained models. An important notion to have about these detection and classification models is that they are trained using a defined list of species, and which a particular type of images, and will fail with new species or completely different images. A few pretrained models are available, in particular YOLOv8 OBSEA, which was trained on the OBSEA (Barcelona, Spain) images and should be used with EMUAS images. A "How to train you own model" section will be added to the AIES-MAC GitLab. YOLO developers are also providing some guidelines and notebook [4] to do so if a partner of the project has his/her own dataset, in order to adapt it to a particular OMB product.

The list of currently implemented models is given in [Annex 2](#)

The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/Detection.ipynb?ref_type=heads

This step provides as output a list of bounding boxes (the minimally sized box containing the object of interest) of detections and some species names as proposed by the model. Note that we keep for now all detections in order to assess the capacity of our feature extraction to remove false detections such as the background element detected as a fish in Figure 4.



OBSEA (Enoc Martinez) baseline detector

Megalodon Fathomnet baseline detector

Figure 4 : *Example of YOLOv8 based automatic detection with two different model weights : left from YOLOv8 trained by OBSEA as proposed in the European project Imagine and right from the Megalodon detector from Fathomnet. Links to the models are provided in Annex 2.*

1.4 Segmentation

Segmentation is performed for each detected bounding box using the foundational model Segment Anything [5].

Segment Anything Model SAM is a promptable foundation model for instance segmentation (Figure 5), the point prompt can be replaced by a grid of point generation. In AIES-MAC, the bounding boxes generated at the previous detection step are used as input prompts.

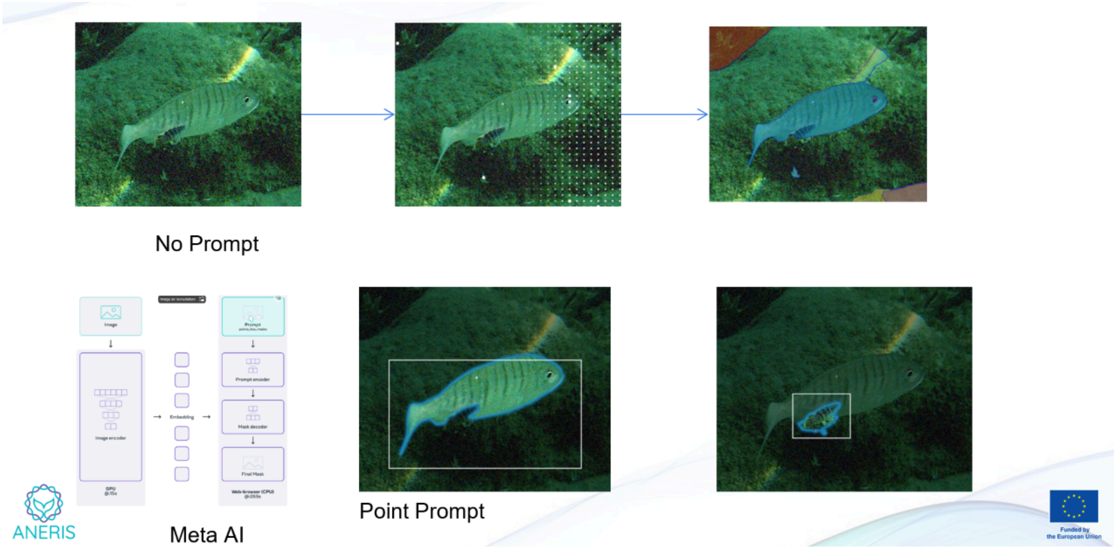


Figure 5 : *example of grid prompt (first row) and point prompts on the elements of interest (second row) given to SAM.*

The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/Segmentation.ipynb?ref_type=heads

The output of this step is a list of segmentation masks (Figure 6) which allows getting the contours and their content in the original image by simply multiplying the mask by the image, setting all pixels not in the segmentation mask to zero in the original image.

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Figure 6 : *example of segmentation mask multiplied by the original color image.*

1.5 Feature extraction

This step gathers information from previous notebooks and extracts features from masks. It appends all the results in an excel file with one line per detection.

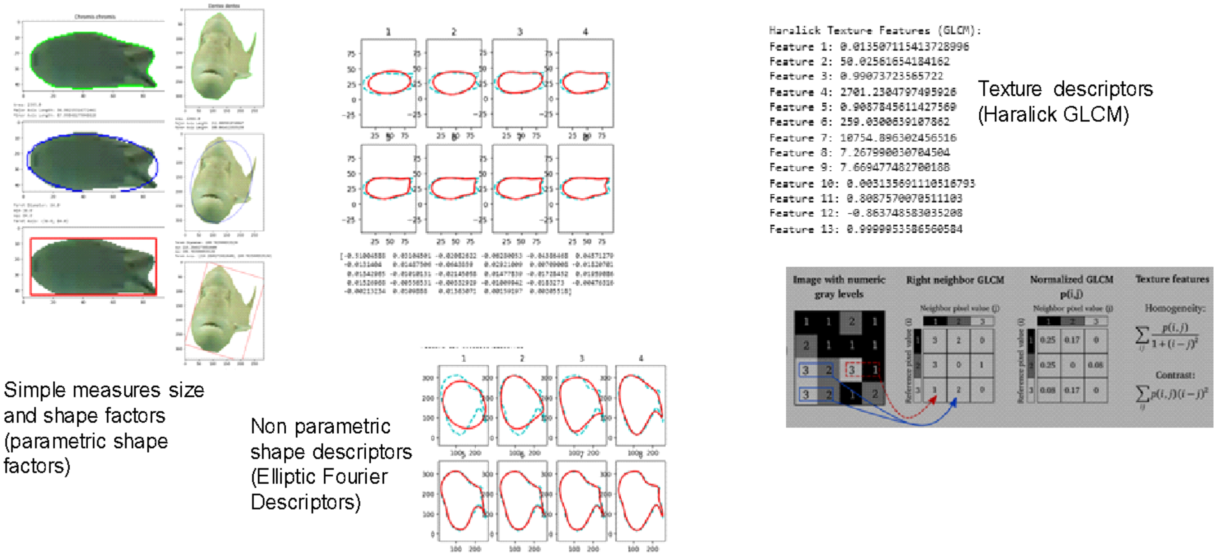
The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/Feature_extraction.ipynb?ref_type=heads

In the version of AIES-MAC at the date of this deliverable, the implemented features, as illustrated in Figure 7 are:

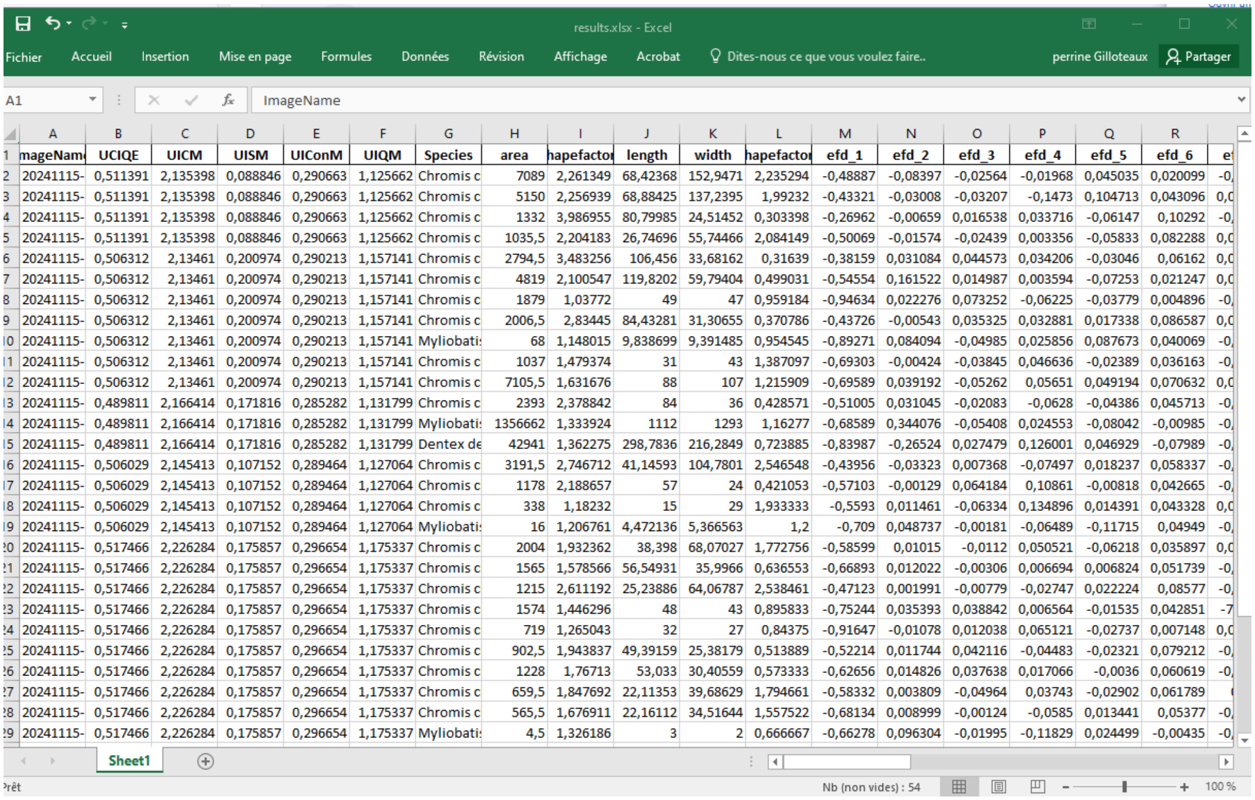
- Parametric shape descriptors (simple length based measurements such as the Feret's lengths that can be combined to obtain aspect ratio, roundness etc… , as exemplified in the notebook)
- Non parametric shape descriptors: AIES-MAC uses the Elliptic Fourier Descriptors as described in [6], normalized to be rotation- and scale-invariant.
- Texture descriptors, using the gray-level invariant Haralick texture features as described in [7].

The output is, for now, an excel file (Figure 8) that can be further analysed, for example using the Data Visualisation step provided.



```
Haralick Texture Features (GLCM):
Feature 1: 0.013507115413728996
Feature 2: 50.02561654184162
Feature 3: 0.9907372356572
Feature 4: 2701.2304797495926
Feature 5: 0.9087845611427569
Feature 6: 259.0300639107862
Feature 7: 10754.896302456516
Feature 8: 7.267990030784504
Feature 9: 7.669477482700188
Feature 10: 0.003135691110516793
Feature 11: 0.8087570070511103
Feature 12: -0.863748583035208
Feature 13: 0.9999953586560584
```

Figure 7 : *Illustration of features generated by the feature extraction step. The Haralick features schema explanation is extracted from* [7].



mageNam	UCIQE	UICM	UISM	UIConM	UIQM	Species	area	hapefactor	length	width	hapefactor	efd_1	efd_2	efd_3	efd_4	efd_5	efd_6	e
20241115-	0,511391	2,135398	0,088846	0,290663	1,125662	Chromis c	7089	2,261349	68,42368	152,9471	2,235294	-0,48887	-0,08397	-0,02564	-0,01968	0,045035	0,020099	-0,
20241115-	0,511391	2,135398	0,088846	0,290663	1,125662	Chromis c	5150	2,256939	68,88425	137,2395	1,99232	-0,43321	-0,03008	-0,03207	-0,1473	0,104713	0,043096	0,0
20241115-	0,511391	2,135398	0,088846	0,290663	1,125662	Chromis c	1332	3,986955	80,79985	24,51452	0,303398	-0,26962	-0,00659	0,016538	0,033716	-0,06147	0,10292	-0,
20241115-	0,511391	2,135398	0,088846	0,290663	1,125662	Chromis c	1035,5	2,204183	26,74696	55,74466	2,084149	-0,50069	-0,01574	-0,02439	0,003356	-0,05833	0,082288	0,0
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	2794,5	3,483256	106,456	33,68162	0,31639	-0,38159	0,031084	0,044573	0,034206	-0,03046	0,06162	0,0
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	4819	2,100547	119,8202	59,79404	0,499031	-0,54554	0,161522	0,014987	0,003594	-0,07253	0,021247	0,0
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	1879	1,03772	49	47	0,959184	-0,94634	0,022276	0,073252	-0,06225	-0,03779	0,004896	-0,
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	2006,5	2,83445	84,43281	31,30655	0,370786	-0,43726	-0,00543	0,035325	0,032881	0,017338	0,086587	0,0
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Myliobati	68	1,148015	9,838699	9,391485	0,954545	-0,89271	0,084094	-0,04985	0,025856	0,087673	0,040069	-0,
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	1037	1,479374	31	43	1,387097	-0,69303	-0,00424	-0,03845	0,046636	-0,02389	0,036163	-0,
20241115-	0,506312	2,13461	0,200974	0,290213	1,157141	Chromis c	7105,5	1,631676	88	107	1,215909	-0,69589	0,039192	-0,05262	0,05651	0,049194	0,070632	0,0
20241115-	0,489811	2,166414	0,171816	0,285282	1,131799	Chromis c	2393	2,378842	84	36	0,428571	-0,51005	0,031045	-0,02083	-0,0628	-0,04386	0,045713	-0,
20241115-	0,489811	2,166414	0,171816	0,285282	1,131799	Myliobati	1356662	1,333924	1112	1293	1,16277	-0,68589	0,344076	-0,05408	0,024553	-0,08042	-0,00985	-0,
20241115-	0,489811	2,166414	0,171816	0,285282	1,131799	Dentex de	42941	1,362275	298,7836	216,2849	0,723885	-0,83987	-0,26524	0,027479	0,126001	0,046929	-0,07989	-0,
20241115-	0,506029	2,145413	0,107152	0,289464	1,127064	Chromis c	3191,5	2,746712	41,14593	104,7801	2,546548	-0,43956	-0,03323	0,007368	-0,07497	0,018237	0,058337	-0,
20241115-	0,506029	2,145413	0,107152	0,289464	1,127064	Chromis c	1178	2,188657	57	24	0,421053	-0,57103	-0,00129	0,064184	0,10861	-0,00818	0,042665	-0,
20241115-	0,506029	2,145413	0,107152	0,289464	1,127064	Chromis c	338	1,18232	15	29	1,933333	-0,5593	0,011461	-0,06334	0,134896	0,014391	0,043328	0,0
20241115-	0,506029	2,145413	0,107152	0,289464	1,127064	Myliobati	16	1,206761	4,472136	5,366563	1,2	-0,709	0,048737	-0,00181	-0,06489	-0,11715	0,04949	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	2004	1,932362	38,398	68,07027	1,772756	-0,58599	0,01015	-0,0112	0,050521	-0,06218	0,035897	0,0
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	1565	1,578566	56,54931	35,9966	0,636553	-0,66893	0,012022	-0,00306	0,006694	0,006824	0,051739	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	1215	2,611192	25,23886	64,06787	2,538461	-0,47123	0,001991	-0,00779	-0,02747	0,022224	0,08577	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	1574	1,446296	48	43	0,895833	-0,75244	0,035393	0,038842	0,006564	-0,01535	0,042851	-7
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	719	1,265043	32	27	0,84375	-0,91647	-0,01078	0,012038	0,065121	-0,02737	0,007148	0,0
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	902,5	1,943837	49,39159	25,38179	0,513889	-0,52214	0,011744	0,042116	-0,04483	-0,02321	0,079212	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	1228	1,76713	53,033	30,40559	0,573333	-0,62656	0,014826	0,037638	0,017066	-0,0036	0,060619	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	659,5	1,847692	22,11353	39,68629	1,794661	-0,58332	0,003809	-0,04964	0,03743	-0,02902	0,061789	0
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Chromis c	565,5	1,676911	22,16112	34,51644	1,557522	-0,68134	0,008999	-0,00124	-0,0585	0,013441	0,05377	-0,
20241115-	0,517466	2,226284	0,175857	0,296654	1,175337	Myliobati	4,5	1,326186	3	2	0,666667	-0,66278	0,096304	-0,01995	-0,11829	0,024499	-0,00435	-0,

Figure 8 : *example of excel file generated by the feature extraction step*

1.6 Data visualisation

This step aims to provide some preliminary data mining on the results generated by the previous steps.

The corresponding notebook is available at the following link:

https://gitlab.univ-nantes.fr/paul-gilloteaux-p/aneris_aies-mac/-/blob/master/PrototypingNotebooks/DataVisualization.ipynb?ref_type=heads

Two examples are provided. One is the exploration of features after reduction by linear composition, with unsupervised (Principal component Analysis, Figure 9) or supervised (Linear Discriminant Analysis, Figure 10) methods. This aims to demonstrate how the features could be used for the species classification. The principal component analysis could be used to detect any outlier in a classification based on interpretable features, or to refine a particular classification. It also shows which features are the most discriminant. The Linear Discriminant Analysis can tell how useful the selected features are to discriminate species and if they are sufficient. It could also be used to perform some machine learning based classification of species, when an unclassified object can be classified according to its distance to the classified species in this space. The second example exploits the generated image quality metrics to detect a problem of visibility in the images from one of the EMUAS sites on the 15th of November 2024 (Figure 11).

Note that these examples are very preliminary and use a very limited set of images, and are only used for documentation and demonstration purposes.

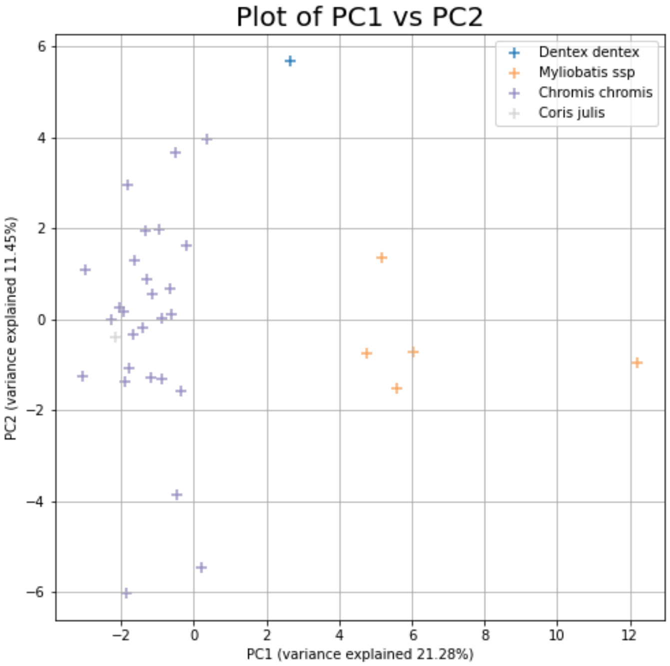


Figure 9 : *Example of use of the extracted features from macroorganisms extracted on 7 arbitrary selected images from the 15/11 EMUAS public database (listed in Annex 1) for unsupervised analysis. All extracted features are reduced to two axes using a Principal Component Analysis. For information, the texture descriptors and Elliptic Fourier Descriptors are the ones with more weights in the first and second principal axes. The proposed species as proposed by the detection and classification steps are added in legend but were not used to create the linear composition of the principal axes. The Coris julis for example is not discriminated from the Dentex dentex by this combination of features.*

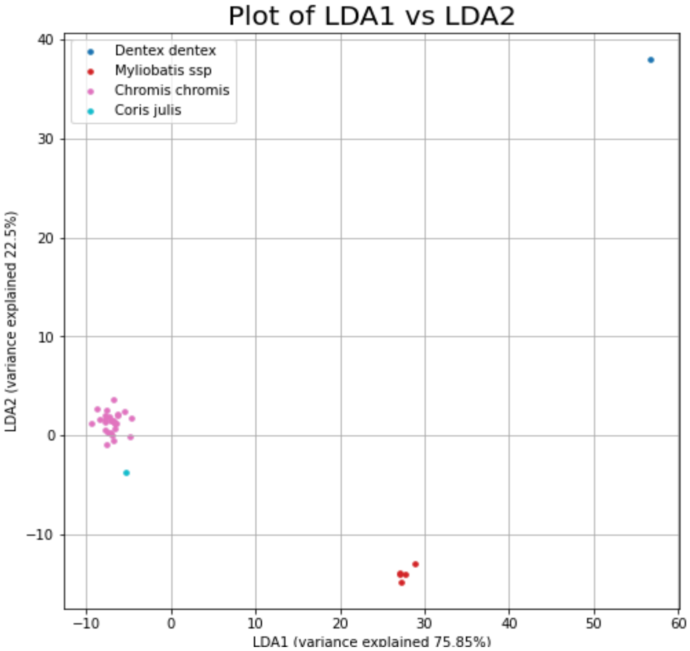


Figure 10: *Example of use of the extracted features from macroorganisms on 7 arbitrary selected images from the 15/11 EMUAS public database (listed in Annex 1) for supervised analysis. All extracted features are reduced to two axes using a Linear Discriminant Analysis, such that they maximize the distance between attributed species. The purpose of this analysis is to demonstrate that the features can discriminate between different species, and could be used in explainable machine learning for example.*

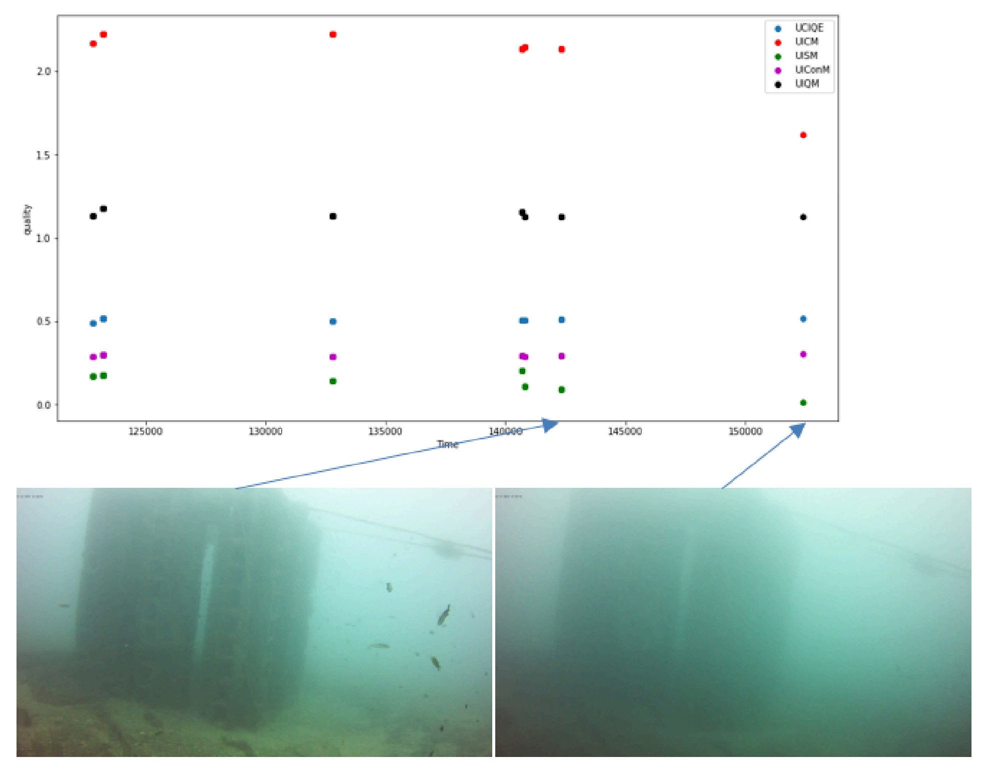


Figure 11 : *Example of quality monitoring over time on 7 arbitrary selected images from the 15/11 public dataset from EMUAS public database (listed in Annex 1), time is expressed as HHMMSS. A drop down in UICM metric (red dots) was detected, corresponding indeed as a blurrier image as expected.*

2. Road map for the next developments

ANERIS provides AIES-MAC (still 2 years of dev to come) which can be adapted to several questions. Figure 12 gives example results of segmentation for several images provided by partners. Note that the model used for detection and classification was not specifically trained for these species, and only the detection is used. We need to define together, within the project, the type of images to prioritize to refine the development (AGILE mode) (segmentation, feature extraction.., need for tracking or 3D pose estimation). Now that the workflow is defined, we can generate data for OMB products, validate it for these OMB products and add new features if needed, for example to discriminate species or to retrieve a list of images containing a species or candidate to be classified as a species. Also some features are available but not listed in an specific output file, such as a co-presence list and distance to other species within one image for example.

The features that will be implemented next are the calibration (for now all dimensions are expressed in pixel units and do not take into account the depth map) and denoising together with the technology ATIRES developed by the University of Haifa team.

We also aim to tune AIES MAC to be used on the BIOPOLIS participatory science observation on rocky intertidal ecosystems, that collect images out of water, during low tide, and we will work with BIOPOLIS team to train an adequate model based on the dataset that they have already prepared.

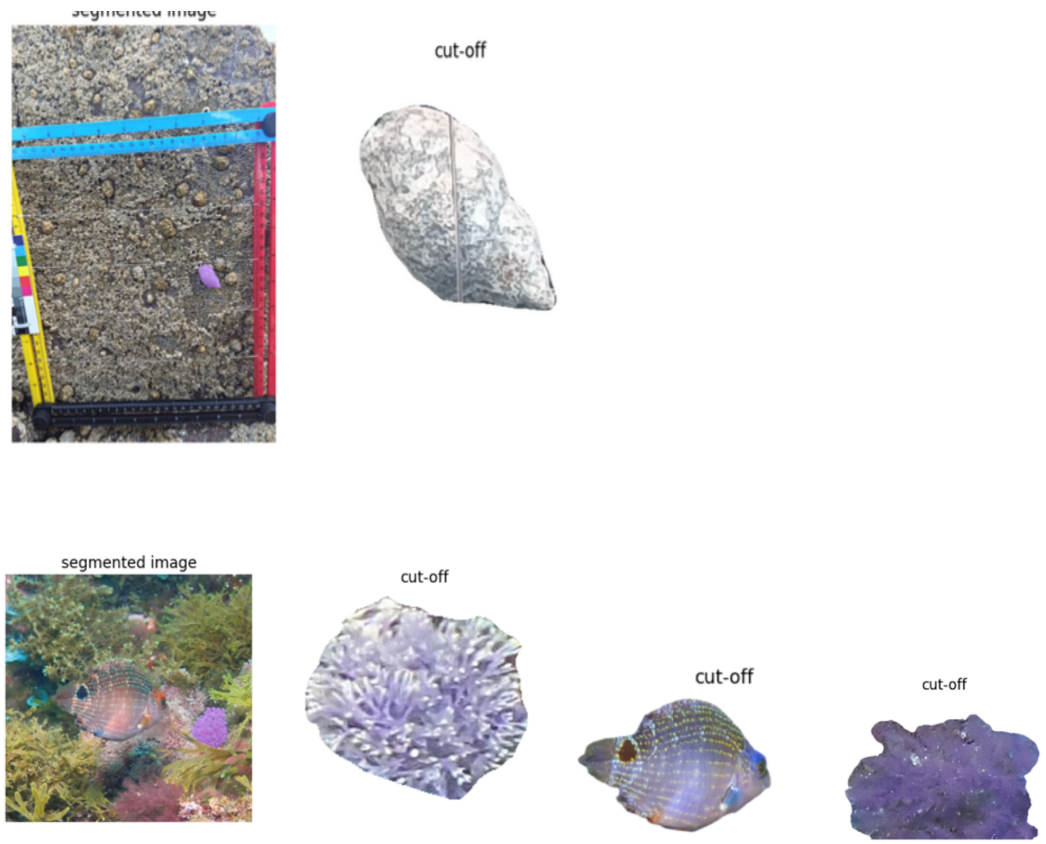


Figure 12: *Example of results obtained for out of water images and underwater images on crowdy background (below) from participatory sciences.*

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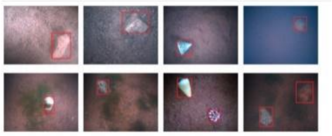
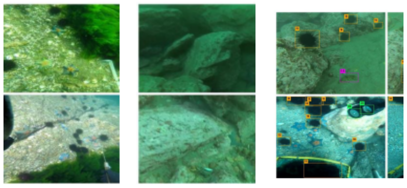
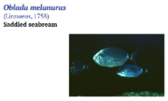
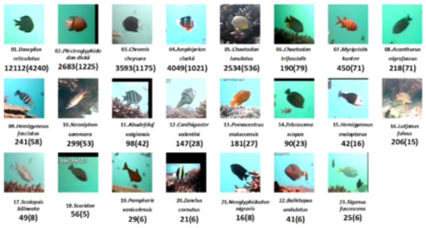
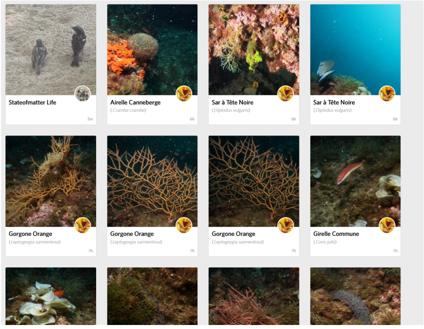
Annex

A.1 Non exhaustive list of Available public databases

Reference	Name and content	Aimed task	Example
https://doi.org/10.1016/j.asoc.2019.04.025	Marine Underwater Environment Database (**MUED**) 8600 images of 430 different salient object	Object recognition (detection)	

https://doi.org/10.1109/TIP.2019.2955241	890 images with related GT Underwater Image Enhancement Benchmark (**UIEB**)	Image enhancement	
https://doi.org/10.1109/TCSVT.2019.2963772	4000 images Real-time Underwater Image Enhancement (**RUIE**) Dataset	Image Quality , Underwater Color Cast , Object detection	
https://doi.org/10.1038/s41598-022-19939-2	**Fathom Net** (plus a model zoo of pretrained models)	Detection and Classification	
www.fishbase.org, version (10/2023).	**FishBase** (63800 pictures of 35400 species)	Classification	
https://universe.roboflow.com/g18l5754/fish4knowledge-dataset/dataset/3	**Fish4Knowledge** database	Fish classification	
https://minka-sdg.org/	**MINKA**	Classification	

A.2 List of implemented detection and classification models in AIES-MAC

Model Name and provider	Description of data it was trained on (location when available) and species covered	Architecture	trained model weight link
MBARI monterey bay benthic	https://zenodo.org/records/5539915 NE Pacific	Yolov5	https://zenodo.org/records/5539915/files/mbari-mb-benthic-33k.pt?download=1
MBARI Monterey Bay 315k YOLOv8	https://huggingface.co/FathomNet/MBARI-315k-yolov8	Yolov8	https://huggingface.co/FathomNet/MBARI-315k-yolov8/raw/main/mbari_315k_yolov8.pt
FathomNet Megalodon Detector	FathomNet/megalodon · Hugging Face	Yolov8	https://huggingface.co/FathomNet/megalodon/resolve/main/best.pt
OBSEA xlarge	https://dashboard.cloud.imagine-ai.eu/marketplace/modules/obsea-fish-detection	Yolov8	https://github.com/EnocMartinez/obsea-fish-detection/releases/download/model/12sp_1537img_xlarge_lr_0_000375_1920_best.pt
OBSEA nano	https://dashboard.cloud.imagine-ai.eu/marketplace/modules/obsea-fish-detection	Yolov8	https://github.com/EnocMartinez/obsea-fish-detection/releases/download/model/12sp_1537img_nano_lr_0_000375_1920_best.pt