

# AI-Driven Solutions for Algal Bloom Monitoring and Management

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## Introduction

- Harmful algal blooms (HABs) threaten water quality, aquatic ecosystems, and public health by producing toxins, taste and odour (T&O) compounds, and depleting oxygen in water.
- Light microscopy remains the gold standard for identifying algal bloom species, but it is time-consuming, resource-intensive, and prone to human subjectivity.
- Artificial intelligence (AI), particularly deep learning models, has significant potential to automate microscopy and overcome its limitations.

## Objectives

- Develop AI-driven methods to automate microscopy for HAB monitoring.
- Evaluate two approaches:
  - Approach 1: Proof-of-Concept (Without annotated dataset)
  - Approach 2: YOLOv12 (With annotated dataset)

## Methodology

### Approach 1: Proof-of-Concept (Without Annotated Dataset)

- Segmentation of cells using Segment Anything Model (SAM).
- Clustering of cell shapes into seven defined benchmarks.



Machine learning driven image segmentation and shape clustering of algal microscopic images obtained from various water types

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Fig 1. Published work on Approach 1.

### Approach 2: Advanced YOLOv12 (With Annotated Dataset)

#### Dataset

- 1011 microscopy images collected and annotated.
- 3288 instances identified across 64 algal and cyanobacteria taxa.

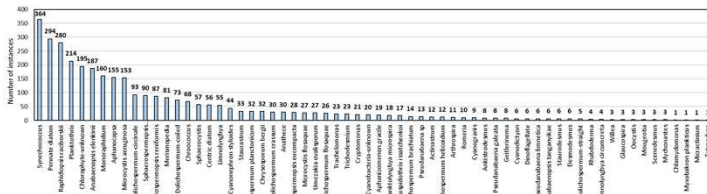


Fig 2. Per-class instance distributions for the microscopy image dataset.

#### Deep Learning Model for HAB Identification

- YOLOv12 (introduced 2025) used as the deep learning object detection model.
- Data-centric workflow applied to optimize dataset design choices (Fig. 3).

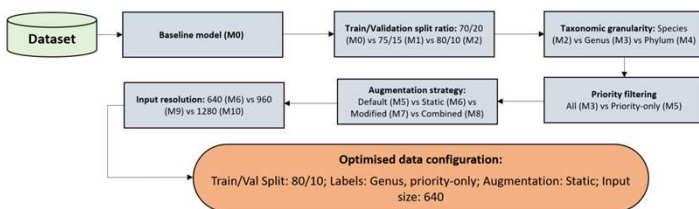


Fig 3. Data-centric workflow

## Results and Discussion

### Approach 1: Proof-of-Concept (Without Annotated Dataset)

- SAM segmentation performed well, especially for single cells and filaments.
- Identifications were limited to defined shape-based clusters; taxa could not be identified.

### Approach 2: Advanced YOLOv12 (With Annotated Dataset)

- Optimized YOLOv12 from the data-centric workflow outperformed the baseline, with ~23% higher performance.

Table 1. Performance of YOLOv12 models across data-centric workflow

	Model	mAP@0.5	mAP@0.5:0.95	Precision	Recall
Baseline	M0	0.5913	0.3857	0.6864	0.4835
	M1	0.6128	0.4231	0.7338	0.5215
	M2	0.636	0.4277	0.772	0.5801
	M3	0.6453	0.4195	0.7502	0.5985
	M4	0.6807	0.3645	0.706	0.6178
	M5	0.6697	0.4508	0.718	0.5705
Best	M6	<b>0.7255</b>	<b>0.4835</b>	<b>0.829</b>	<b>0.6131</b>
	M7	0.6823	0.4609	0.7408	0.5797
	M8	0.7157	0.4832	<b>0.8446</b>	0.5842
	M9	0.7009	0.4792	0.7706	<b>0.6674</b>
	M10	0.6421	0.4236	0.6227	0.6056

- Per-class analysis showed YOLOv12 performed very well on 1<sup>st</sup> Priority taxa that were well represented in the dataset.
- Performance remained lower for rare taxa with limited training samples.

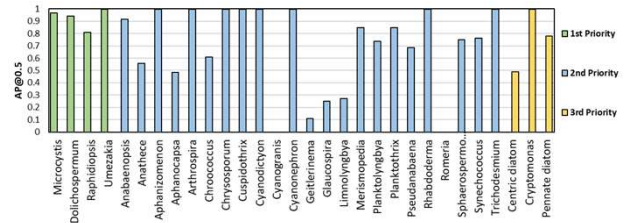


Fig 4. Per-class performance of best-performing model from the data-centric workflow

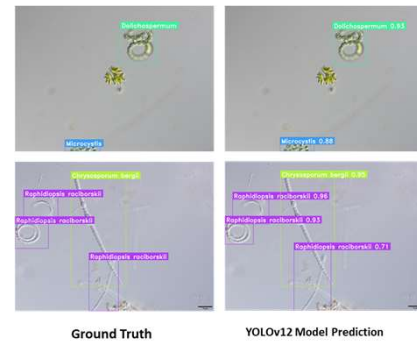


Fig 5. Representative examples comparing ground truth with predictions of YOLOv12

## Conclusion

- AI has strong potential to automate microscopy for HAB monitoring.
- Approach 1 (two-step proof-of-concept): effective for segmentation, but taxa could not be identified.
- Approach 2 (YOLOv12): showed strong performance, particularly for well-represented taxa in the dataset.

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