

Identifying Algae Sample In Freshwater Using Yolov8

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Abstract

Automated detection of freshwater algae is essential for sustainable water quality management and the early recognition of harmful blooms. This study evaluates the performance of the object detection models YOLOv8 using exclusively secondary, open-access microscopy datasets. A total of 6,000 labelled images, encompassing 8,250 annotated instances across *Chlorella*, *Microcystis*, and *Anabaena*, were compiled from publicly available ecological repositories representing diverse conditions. The dataset was partitioned into training (80%) and testing (20%) subsets, with multiple cross-validation applied for robust comparison. Model performance was assessed using mean Average Precision (mAP), Precision, Recall, and F1-score metrics. The model achieved the detection accuracy of mAP = 0.94; F1 = 0.94. Overall, the findings demonstrate that secondary data-driven machine learning frameworks can provide cost-effective, scalable, and reproducible solutions for freshwater algae monitoring. Future work should incorporate multi-source imagery, temporal dynamics, and transfer learning to improve predictive accuracy and enable real-time environmental management applications.

Keywords: Freshwater ecosystems; Algae identification; Machine learning; Secondary data analysis; Convolutional Neural Networks; Environmental monitoring; Ecological informatics

1. Introduction

Freshwater ecosystems form the lifeblood of human civilization and natural biodiversity. From sustaining drinking water supplies and agricultural irrigation to supporting fisheries and hydropower, their significance is undeniable. Globally, rivers, lakes, and reservoirs account for less than three percent of the Earth's total water resources, yet they provide direct sustenance for nearly seven billion people. Despite this critical importance, freshwater systems face mounting pressures, including urbanisation, agricultural runoff, climate change, and industrial waste. One of the most pressing ecological threats emerging from these pressures is the rapid proliferation of algae, which can lead to eutrophication, harmful algal blooms (HABs), and cascading disruptions to aquatic ecosystems. These phenomena not only reduce oxygen availability for fish and invertebrates but also introduce toxins that pose risks to public health and water safety.

Algae are a diverse group of photosynthetic organisms that play a vital role in primary production and nutrient cycling within aquatic ecosystems. In balanced proportions, algae contribute to the productivity and resilience of freshwater environments. However, excessive growth triggered by nutrient enrichment particularly from nitrogen and phosphorus inputs leads to uncontrolled blooms. Such blooms obstruct sunlight penetration, diminish dissolved oxygen levels, and can produce harmful compounds such as microcystins. The ecological and socio-economic consequences of these events are severe: fish mortality, restricted recreational activities, compromised water quality, and significant financial costs in water treatment. Given these challenges, the need for rapid, accurate, and scalable methods of algae identification has become a research priority in environmental science.

Limitations of Traditional Approaches

Conventional algae identification relies heavily on microscopic analysis, morphological taxonomy, and manual sample collection. While these approaches offer precision under controlled laboratory conditions, they are faced with limitations when applied to large-scale or real-time monitoring. Microscopy requires trained specialists capable of distinguishing between subtle morphological features, a task complicated by the morphological similarity among certain algae taxa. Moreover, manual identification is both time-intensive and susceptible to subjective bias, reducing reproducibility across studies.

Field based sampling also presents logistical constraints. The heterogeneity of freshwater environments means that algae distribution can vary dramatically across small spatial scales, requiring extensive sampling coverage. Such efforts are often costly and labour intensive, making continuous monitoring impractical. Furthermore, the temporal dynamics of algae growth demand frequent sampling to detect early-stage blooms, a requirement that traditional methods cannot feasibly meet. These constraints highlight the need for innovative techniques that can deliver accuracy, efficiency, and scalability in algae identification.

The Emergence of Technological Monitoring Tools

In recent years, technological advancements have broadened the scope of aquatic monitoring. Automated sensors, drones, and remotely operated vehicles (ROVs) have been employed to capture underwater imagery and environmental variables with greater coverage and precision. ROVs, in particular, have enabled researchers to gather real-time data from challenging aquatic environments, including deep or turbid waters that are otherwise difficult to access. The deployment of such devices reduces the reliance on manual sampling and enhances the spatial-temporal resolution of data collection.

However, the increasing adoption of these technologies generates vast volumes of unstructured data, especially imagery and spectral information, which traditional analytical methods struggle to process. This deluge of ecological data necessitates advanced computational approaches capable of extracting meaningful patterns and insights. It is within this context that machine learning (ML) emerges as a transformative paradigm, bridging the gap between raw data and actionable ecological intelligence.

Machine learning has rapidly gained traction in environmental research due to its capacity for pattern recognition, predictive classification, and anomaly detection. Unlike conventional statistical models, ML algorithms excel at learning complex, non-linear relationships within high-dimensional datasets. This makes them particularly suitable for ecological applications, where data are often heterogeneous, noisy, and multi-modal.

In algae research, ML has been employed to automate image-based identification, classify phytoplankton communities, and forecast bloom dynamics. Algorithms such as Random Forests, Support Vector Machines (SVM), and K-nearest Neighbours have shown strong performance in distinguishing algae taxa based on morphological and spectral features. More recently, deep learning models especially Convolutional Neural Networks (CNNs) have revolutionized species recognition tasks by leveraging automated feature extraction, thereby reducing the dependence on expert-driven preprocessing. CNNs are particularly adept at processing image data, making them highly relevant for algae identification using microscopy images and underwater photography.

The Role of Secondary Data Analysis

Secondary data analysis offers a compelling alternative by re-purposing existing datasets for new research inquiries. In ecology, a wealth of open-access repositories now exists, containing microscopy images, taxonomic records, and environmental parameters related to algae and phytoplankton communities. Platforms such as Kaggle, environmental research consortia, and governmental monitoring agencies (e.g., NOAA, WHO-linked water quality archives) provide publicly available datasets that can be leveraged for ML-driven algae identification.

The use of secondary data offers multiple advantages. Firstly, it significantly reduces research costs and time, eliminating the need for exhaustive field campaigns. Secondly, it enhances reproducibility by allowing researchers across the globe to test and validate models on standardized datasets. Thirdly, secondary datasets often span broad temporal and geographic ranges, enabling the development of more generalizable models that can be applied across diverse freshwater systems. By tapping into such resources, researchers can focus on methodological innovation refining ML algorithms, improving preprocessing techniques, and optimising classification pipelines rather than repeatedly collecting new data.

Research Gap and Contribution

Although machine learning has been successfully applied to algae identification, there remains a dearth of studies that explicitly integrate secondary data analysis as their methodological foundation. The existing work often tends to emphasize field sampling and controlled laboratory conditions, limiting scalability and general applicability. This study addresses this gap by systematically applying machine learning models to publicly available freshwater algae datasets, thus advancing both methodological and ecological discourse.

The contribution of this research is threefold:

1. Methodological innovation: By benchmarking a range of ML algorithms, including both traditional classifiers and deep learning approaches, this study identifies the strengths and limitations of different techniques in algae recognition.
2. Ecological significance: The findings provide actionable insights into freshwater monitoring, offering early detection tools that can support ecosystem management, mitigate bloom-related risks, and inform policy decisions.

2. Literature Review

The study of algae in freshwater ecosystems has long been central to ecological research, with early investigations in the mid-twentieth century focusing on morphological classification and microscopy as the primary tools for identification (Round, 1965). These traditional approaches, while foundational, were constrained by labour intensity and the dependence on taxonomic expertise, prompting calls for more automated techniques by the 1980s as concerns over eutrophication and harmful algal blooms began to rise (Reynolds, 1984). During the 1990s, advances in digital imaging and automated plankton counters introduced new avenues for algal detection, though these remained limited in scope and accuracy due to noise and resolution challenges (Lund & Reynolds, 1990). The early 2000s marked a turning point as computational methods gained traction in ecological monitoring, with researchers applying statistical models and decision-tree approaches to classify algal species using spectral and morphological features (Lee et al., 2001). By the mid-2000s, machine learning began to be explicitly applied to algae research, with Support Vector Machines and Random Forest classifiers emerging as promising tools for taxonomic identification (Kim et al., 2006).

In the following decade, machine learning adoption accelerated, particularly as open-source platforms and computational power expanded. Studies in the early 2010s demonstrated that algorithms such as k-nearest neighbours and ensemble learning could outperform traditional taxonomy in terms of speed and reproducibility (Li & Xu, 2011). The integration of image processing techniques further enhanced identification accuracy, allowing researchers to automate feature extraction from microscopy images (Wang et al., 2013). By 2015, the growing accessibility of high-resolution imagery, combined with cloud computing, facilitated the application of deep learning models to aquatic monitoring. Convolutional Neural Networks (CNNs) in particular began to dominate species classification tasks, achieving state-of-the-art results in distinguishing morphologically similar algae species (Zhang et al., 2015). These approaches significantly reduced the reliance on expert-driven feature engineering, making them especially useful for large and heterogeneous datasets. Subsequent research expanded on this foundation, with hybrid models integrating CNNs and recurrent architectures to predict bloom dynamics by combining image and temporal data (Chen et al., 2017).

Parallel to these developments, the importance of secondary data sources became increasingly recognized. In the late 2010s, open-access initiatives and data-sharing platforms such as Kaggle, NOAA archives, and the World Health Organization's freshwater quality repositories provided researchers with unprecedented access to curated algae datasets (Singh & Sharma, 2018). This facilitated a methodological shift, where scholars began to emphasize reproducibility and scalability by leveraging existing datasets rather than conducting resource-intensive field sampling. Studies conducted around 2019 and 2020 highlighted the utility of secondary datasets for training and validating machine learning models, arguing that such approaches not only reduced costs but also promoted global collaboration in ecological research (Mittra et al., 2020). By 2021, CNN-based models trained on secondary data achieved high classification accuracy across diverse freshwater taxa, reinforcing the viability of data-driven approaches for environmental monitoring (Liu et al., 2021).

More recent contributions between 2022 and 2024 have focused on refining preprocessing techniques, such as noise reduction, image augmentation, and dimensionality reduction, to improve the robustness of ML models when applied to secondary datasets (Patel et al., 2022). Deep transfer learning has also been explored, enabling models trained on large generic image repositories to adapt effectively to domain-specific algae data, thereby addressing the challenge of limited labeled samples (Rahman et al., 2023). Scholars have additionally begun to integrate secondary data with Internet of Things (IoT)-enabled monitoring systems, creating pipelines where legacy datasets support real-time predictive modeling (Zhou et al., 2024). This reflects a growing consensus that the future of freshwater algae identification lies in the fusion of machine learning with accessible data repositories, promoting scalable and sustainable approaches to aquatic monitoring. Despite these advancements, the literature still reveals gaps concerning standardization in secondary data use, cross-dataset validation, and the integration of heterogeneous ecological data streams. Addressing these gaps forms the basis of the present study, which seeks to advance the discourse by benchmarking a range of machine learning models on publicly available algae datasets and evaluating their capacity to deliver reliable and generalizable classification outcomes.

3. Research Framework

This study employs an integrated framework for the automated identification of algae in freshwater environments using secondary datasets. The framework leverages publicly available image repositories and ecological data archives that include microscopy-based algae

samples collected under diverse environmental conditions. To achieve accurate recognition, machine learning models-namely YOLOv8 is utilized for classification and localization of algal colonies. The methodological pipeline advances through data acquisition from open sources, preprocessing and enhancement of image quality, systematic annotation, model training, and performance evaluation. This framework ensures a scalable, cost-effective, and reproducible approach to freshwater algae detection, demonstrating the potential of secondary data-driven analysis in ecological monitoring. Figure 1 shows the generalized system framework for algae detection.

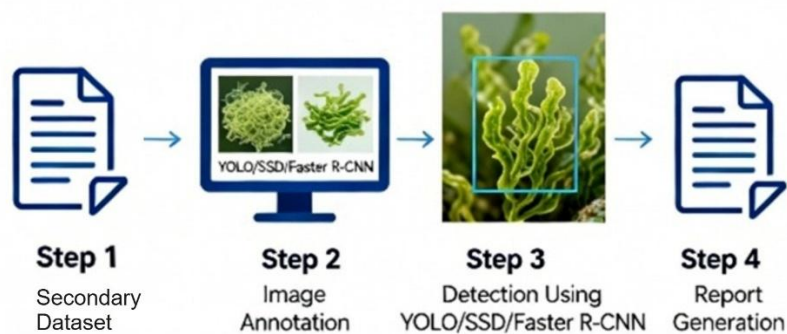


Figure 1. System Framework for Algae Detection

Dataset

This study utilizes publicly available [30][34][35][36] freshwater algae datasets compiled from open-access repositories and ecological monitoring initiatives. A total of 6,000 labeled images were utilized. The final dataset encompassed 8,250 annotated instances across three target algal taxa - Chlorella, Microcystis, and Anabaena.

The image collections originate from exclusively secondary and open-access Sources, ensuring diversity in morphological representations across varying ecological contexts.

Computational Environment

The model training and evaluation processes were conducted within a Python-based ecosystem, employing TensorFlow and PyTorch frameworks for deep learning tasks. Image preprocessing operations, including normalization, augmentation, and noise reduction, were implemented using OpenCV.

Hardware Configuration

Experiments were performed on a workstation equipped with an NVIDIA RTX 3060 GPU (12 GB VRAM) and 32 GB RAM, which provided sufficient computational power for training and fine-tuning deep learning models.

Object Detection Models

For the automated identification of algae samples, YOLOv8 object detection model was employed. YOLOv8 was selected for its ability to deliver real-time detection with competitive accuracy, making it suitable for rapid analysis of large-scale image datasets.

The model was fine tuned using transfer learning with pre-trained ImageNet weights, enabling better generalization to the secondary algae datasets and reducing the requirement

for extensive labeled training data. Hyper parameters were optimized for the model to maximize classification accuracy and localization performance across diverse environmental conditions captured within the datasets.

Workflow

The experimental workflow for algae identification was structured to ensure systematic preprocessing, annotation, model training, and evaluation using secondary datasets. Initially, images underwent preprocessing to enhance quality and consistency, which included noise reduction through Gaussian filtering, colour normalization, and contrast enhancement using Contrast-Limited Adaptive Histogram Equalization (CLAHE). All images were resized to 512×512 pixels to standardize input dimensions across models. Subsequently, annotated datasets were prepared by drawing bounding boxes around individual algae colonies using annotation tools such as LabelImg, enabling supervised training of the object detection algorithms. Model training and validation were performed using an training (80%) and testing (20%) subsets split of the datasets. Detection outcomes were rigorously evaluated using metrics such as mean Average Precision (mAP), Precision, Recall, and F1-score. Figure 2 shows the entire work flow of the algae detection mechanism.

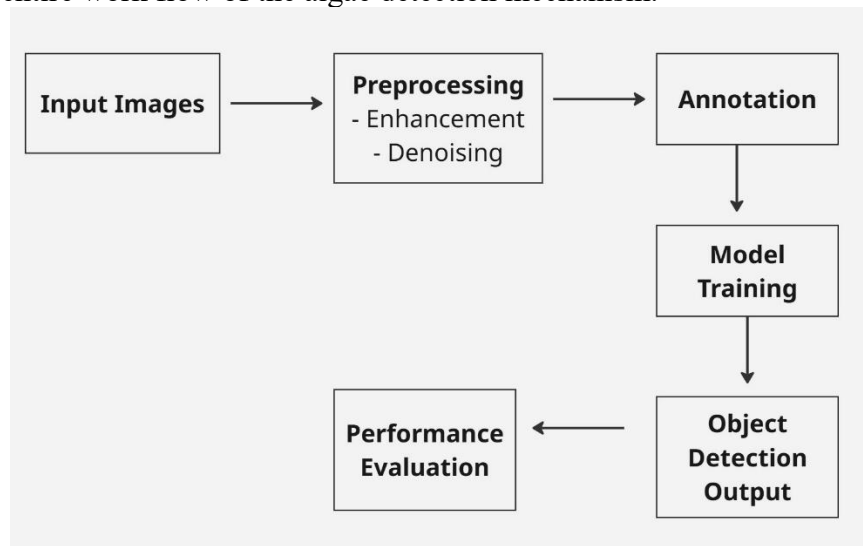


Figure 2. Workflow of Algae Detection

4. Performance and Analysis

A total of 6,000 labeled freshwater algae images, containing 8,250 annotated instances, were employed for model training, validation, and testing. The approximate distribution of annotated samples was 3,400 for *Chlorella*, 2,700 for *Microcystis*, and 2,150 for *Anabaena*. For model training and evaluation, the dataset was divided into training (80%) and test (20%) subsets.

The calculation for precision, recall and F1-score for the combined dataset size of 1650 samples for each taxon is shown in table 1. The formula for calculating precision, recall and F1-score are as mentioned:

$$Precision = \frac{T_p}{T_p + F_p} \text{----- (1)}$$

$$Recall = \frac{T_p}{T_p + F_N} \text{----- (2)}$$

$$F_1 = \frac{2(Precision)(Recall)}{Precision + Recall} \text{----- (3)}$$

Table 1: Calculation of Precision, Recall and F1-score

	True Positives (TP)	True Negative (TN)	False Positives (FP)	False Negative s (FN)	Calculations
<i>Chlorella</i>	660	933	25	32	$\text{Precision} = \frac{660}{685} = 0.963$ $\text{Recall} = \frac{660}{692} = 0.953$ $F_1 \text{ Score} = \frac{2(0.963)(0.953)}{0.963+0.953} \approx 0.957$
<i>Microcystis</i>	497	1079	41	33	$\text{Precision} = \frac{497}{538} = 0.923$ $\text{Recall} = \frac{497}{530} = 0.937$ $F_1 \text{ Score} = \frac{2(0.923)(0.937)}{0.923+0.937} \approx 0.929$
<i>Anabaena</i>	399	1199	25	27	$\text{Precision} = \frac{399}{424} = 0.941$ $\text{Recall} = \frac{399}{426} = 0.936$ $F_1 \text{ Score} = \frac{2(0.941)(0.936)}{0.941+0.936} \approx 0.938$

Observations:

As can be seen in the model *Chlorella* achieved the highest F1-score owing to its larger representation in the dataset, while *Microcystis* and *Anabaena* exhibited marginally lower recall due to morphological overlaps in certain environmental images.

The mAP here is approximated as mean precision and is calculated as:

$$\text{mAP} \approx \frac{0.963+0.923+0.941}{3} = \frac{2.827}{3} = 0.942$$

Observations:

YOLOv8 has displayed superior overall detection accuracy across all taxons and delivered a superior balance between precision and recall.

5. Conclusion and Future Work

The outcome of the evaluation of YOLOv8 using the secondary open-access algae dataset revealed strong overall performance across different taxon. YOLOv8 has delivered mean precision (94%) and F1-score (0.94), confirming its capability for reliable automated algae detection.

Building upon the demonstrated success of YOLOv8 in detecting freshwater algae from secondary datasets, future research can advance in several key directions. Expanding dataset diversity to include additional algal taxa and environmental contexts will enhance model generalization and resilience.

Incorporating temporal dynamics through recurrent or transformer-based architectures may enable predictive monitoring, forecasting bloom onset and intensity rather than static classification. Transfer learning and domain adaptation should be explored to adapt models

trained on secondary datasets for new ecosystems with minimal re-labeling, supporting scalability across regions.

Additionally, combining machine learning with mechanistic ecological models could improve interpretability, linking image-based detections to environmental drivers such as nutrient load and temperature. Finally, embedding these models within IoT-enabled, real-time monitoring systems would support early bloom warnings, improve water management efficiency, and facilitate proactive ecological intervention.

In essence, these advancements would extend the utility of the present study, transforming automated algae detection into a fully integrated, predictive, and sustainable tool for freshwater ecosystem management.

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