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Anomaly Detection of Parasitic Plankton in Brebes Eco-Waters Using Vision-Based Autoencoder AI

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Abstract

The escalating impact of environmental stress on coastal ecosystems necessitates reliable, scalable tools for monitoring marine biodiversity. This study proposes an unsupervised anomaly detection framework to identify parasitic and morphologically abnormal plankton in the waters of Brebes, Indonesia. The primary aim is to develop an interpretable, vision-based system capable of detecting visual anomalies without relying on labeled anomaly data. The research integrates convolutional autoencoders for reconstructing normal plankton images, Principal Component Analysis (PCA) for feature extraction, and One-Class Support Vector Machines (OC-SVM) for classification. Monthly microscopic images were obtained from selected mangrove and aquaculture pond sites in Brebes, Central Java, using portable digital microscopy under standardized field conditions. Images that exceeded a dynamic reconstruction threshold were flagged as anomalous and validated by marine biology experts. The system achieved an F1-score of 86.1%, a precision of 85.3%, and an AUC of 0.94, demonstrating high effectiveness in distinguishing between normal and anomalous plankton. With an average inference time of 0.37 seconds per image, the system supports near real-time monitoring. These results confirm the potential of the proposed method as a low-latency, field-deployable solution for aquatic ecosystem surveillance. By integrating AI-based detection with ecological expert validation, this research offers a scalable approach for marine biodiversity assessment and establishes a foundation for future adaptive environmental monitoring systems.

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Introduction

Aquatic ecosystems rely heavily on plankton, which form the foundational base of marine food webs and have a critical role in biogeochemical cycles and ecosystem health (Ciranni et al., 2024; Pastore et al., 2020). However, disruptive events such as the emergence of parasitic plankton or harmful algal blooms pose serious risks to coastal biodiversity, aquaculture, and ecotourism (Ciranni et al., 2024; Pu et al., 2021). These anomalies often develop rapidly and subtly, making early recognition challenging with conventional monitoring methods. In the context of Brebes' coastal waters, where

mangrove ecosystems and small-scale aquaculture are highly valued, an effective system for detecting such anomalies is urgently needed (MacNeil et al., 2021).

This study stems from the insight that unsupervised deep learning models, particularly autoencoders, offer a scalable and efficient solution for anomaly detection. Unlike supervised methods, they do not require large annotated datasets and can adapt to new or unknown anomaly types (Bilik et al., 2023; Pastore et al., 2020). Drawing on advancements in vision-based anomaly detection, this research proposes a field-deployable system that integrates portable digital microscopes with an autoencoder-based model, creating a near real-time alert mechanism for detecting ecosystem disturbances in Brebes waters. This multi-tiered approach targets both ecological preservation and sustainable development.

The primary objective of this study is to develop and validate a vision-based anomaly detection model leveraging a convolutional autoencoder architecture. Specifically, it aims to: (1) train the model on normal plankton community images from Brebes, (2) detect deviations in near real-time using reconstruction error thresholds, and (3) evaluate detection performance against manually confirmed cases of parasitic or harmful plankton occurrences. Performance metrics, such as the F1 score, precision, and recall, will assess the system's effectiveness.

The theoretical foundations lie at the intersection of marine plankton ecology, unsupervised learning, and anomaly detection (Li et al., 2022). Marine ecosystem dynamics underscore the importance of early detection of plankton perturbations (Ciranni et al., 2024; Rubbens et al., 2023). In machine learning, autoencoders have been extensively shown to excel in unsupervised feature learning and anomaly detection across domains (Pang et al., 2021; Zhou et al., 2022). Moreover, studies applying autoencoders to detect parasites in phytoplankton have achieved promising results (Bilik et al., 2023; Pu et al., 2021), supporting the method's suitability for similar ecosystems (Kareinen et al., 2025; Yadav et al., 2020). Finally, domain-specific challenges such as high data variability and limited labeled anomalies are addressed by leveraging deep unsupervised methods, as demonstrated in plankton anomaly research (Ciranni et al., 2024; Pastore et al., 2020).

The expected outcomes include: (a) a functioning prototype capable of detecting anomalous plankton via unsupervised learning, (b) evaluation of anomaly detection performance against baseline supervised methods, and (c) a scalable framework adaptable to other coastal regions. Practically, the system promises earlier warning of ecosystem stressors, aiding conservation efforts, aquaculture health monitoring, and sustainable tourism management in Brebes. Ultimately, this work contributes to bridging the gap between AI innovations and marine ecology, delivering a proactive tool to protect vulnerable coastal ecosystems.

Methods

1. Study Design and Overview

This research adopts an unsupervised anomaly-detection framework, combining computer vision and autoencoder architectures to identify parasitic or harmful plankton species in situ. The method parallels the technique by Bilik et al. (2023), where the autoencoder reconstructs normal plankton images and uses reconstruction errors to detect anomalies (Bilik et al., 2023). CNN-based autoencoders have demonstrated strong results in distinguishing subtle biological anomalies in plankton imagery (Alfano et al., 2022). Following Pu et al. (2021), we incorporate data augmentation strategies (rotation, blurring, and noise injection) to simulate rare anomalies during training (Pu et al., 2021).

2. Data Acquisition and Preprocessing

Field data will be collected monthly over one year from sampling points, including mangrove lagoons and aquaculture ponds in Brebes. At each point, 50 mL of water will be sampled, preserved on

site, and imaged immediately using a portable digital microscope (similar to that described in Zimmerman et al., 2020). Each specimen is captured at 1080p resolution and saved as a PNG file. Baseline plankton images from each site are curated and labeled as "normal" by marine biologists (Pu et al., 2021).

The image dataset will be standardized via cropping and resizing (224×224 px), followed by normalization and optional contrast enhancement, as recommended for autoencoder inputs.

While the dataset used in this study is not publicly available due to ongoing ecological monitoring and data sensitivity agreements, we plan to release a representative subset of anonymized plankton images and the trained model weights via an open-access repository to support reproducibility and benchmarking in future research.

3. Model Configuration and Training Procedure

We implement a convolutional autoencoder with a symmetrical encoder–decoder architecture, utilizing three convolutional layers followed by a dense bottleneck and a mirrored decoder (Kareinen et al., 2025; Pu et al., 2021). Latent dimensionality is empirically set (e.g., 128 filters per bottleneck) and tuned via validation.

Pretraining uses only "normal" images, optimizing a mean-squared error reconstruction loss using Adam with an initial learning rate of 1e–4, a batch size of 32, and early stopping based on the validation loss. Regularization techniques—such as dropout and L2 weight penalty—are applied to mitigate overfitting.

Equation: Mean Squared Error (MSE)

$$MSE = \frac{1}{n}\sum_{i=n}^{n}(x_i - \hat{x}_i)^2 \quad (1)$$

The autoencoder is trained to minimize the Mean Squared Error (MSE) between the input image x and its reconstruction. $\hat{x}$. This loss function enables the model to learn a compact representation of the "normal" plankton image distribution. A low MSE implies successful reconstruction, while high MSE values may indicate unfamiliar (potentially anomalous) patterns. This approach has proven effective in unsupervised anomaly detection tasks (Pastore et al., 2020; Zhou et al., 2022).

4. Model Architecture & Training

We implement a convolutional autoencoder with a symmetric encoder–decoder architecture: three convolutional blocks (Conv + ReLU + MaxPool), a bottleneck layer (128-dim), and a mirrored decoder structure (Bilik et al., 2023). Trained on baseline images only, using Adam optimizer (lr=1e-4), batch size=32, for up to 100 epochs with early stopping. Regularization via dropout ($p = 0.3$) and L2 weight decay ($\lambda = 1e\text{-}5$) is employed to enhance generalization (Bouman & Heskes, 2025).

5. Anomaly Detection & Thresholding

Post-training, every test image undergoes reconstruction, and the reconstruction error is calculated per pixel. Aggregated metrics, such as MSE, SSIM, and cosine similarity in the latent space, are computed for each sample, following approaches by Bilik et al. (2023), HardNet features, and SSIM-based detection (Bilik et al., 2023; Nema et al., 2023).

Equation: Reconstruction Error (RE) per Image

$$RE(x) = \frac{1}{n}\sum_{i=n}^{n}(x_i - \hat{x}_i)^2 \quad (2)$$

After training, each test image x is reconstructed to $\hat{x}$ And compared using the reconstruction error $RE(x)$. This error is a direct indicator of how much the image deviates from the learned standard representation. Images with high reconstruction error are flagged as potential anomalies. This method aligns with strategies used in image-based anomaly detection in marine and medical domains (Bilik et al., 2023; Pande & Banerjee, 2021; Pu et al., 2021).

To convert errors into anomaly flags, we set decision thresholds at the 95th percentile of the "normal" error distribution. Pixels or regions exceeding thresholds generate anonymized anomaly maps to assist biological review (Lin et al., 2024).

6. Feature Extraction & One-Class Classification

Difference maps (original vs. reconstructed) are fed into feature detectors—HardNet, SIFT, and PCA-reduced ViT features—as suggested by Bilik et al. (2023), Ciranni et al. (2024), and Zhou et al. (. Extracted features are then input to one-class classifiers (OC-SVM, Isolation Forest, LOF), following the configuration of (Bilik et al., 2023). Classifier thresholds are also derived using equal-error-rate from ROC curves (Zipfel et al., 2023).

7. Chronological Workflow

To ensure clarity and replicability, the entire procedure is outlined in a chronological and modular workflow. This approach integrates data acquisition, AI modeling, and expert validation in a seamless sequence designed for deployment in coastal environmental monitoring (van der Velden et al., 2022). The following steps describe each stage of the process:

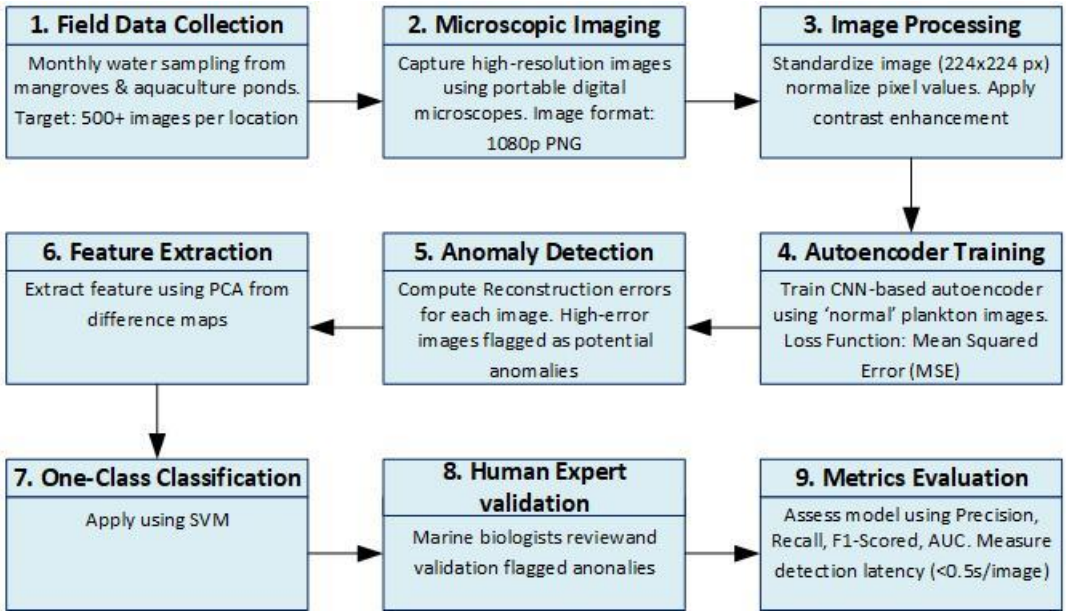

Figure 1. Workflow Diagram of the Vision-Based Anomaly Detection System for Plankton Monitoring

The anomaly detection process begins with the collection of field data, where monthly water samples are taken from mangroves and aquaculture ponds, each generating over 500 plankton images per location. These samples are then analyzed through microscopic imaging using portable digital microscopes, producing high-resolution images in 1080p PNG format. Following image capture, image processing is conducted by standardizing each image to 224×224 pixels, normalizing pixel values, and applying contrast enhancement to improve visual clarity.

Next, the autoencoder training phase involves using only "normal" plankton images to train a CNN-based autoencoder with mean squared error (MSE) as the loss function. Once trained, the model proceeds to anomaly detection, where reconstruction errors are computed for each input. Images with high errors are flagged as potential anomalies. To support deeper validation, feature extraction is performed using PCA on difference maps (original vs. reconstructed images).

These extracted features are then passed through one-class classification models, such as SVM, to confirm the presence of anomalies. In the human expert validation stage, marine biologists review the flagged samples to verify ecological relevance. Finally, metric evaluation is carried out using precision, recall, F1-score, and AUC, with system latency measured to ensure it operates within 0.5 seconds per image.

8. Evaluation Metrics & Analysis

Detection accuracy will be measured using precision, recall, and F1-score against human-verified anomalies, employing the established metrics from Bilik et al. (2023) and Pu et al. (2021). Additionally, AUC-ROC and EER thresholds are reported for classifier performance. Detection latency (processing time/image) is recorded to assess near real-time viability, benchmarked at <0.5 sec per sample, similar to (Hill et al., 2005).

Equations: Evaluation Metrics

$$Precision = \frac{TP}{TP + FP} \tag{3}$$

$$Recall = \frac{TP}{TP + FN} \tag{4}$$

$$F1 = 2 * \frac{Precision * Recall}{Precision + Recall} \tag{5}$$

To evaluate the effectiveness of anomaly detection, three standard metrics are applied: precision (also known as positive predictive value), recall (also known as sensitivity), and the F1-score (the harmonic mean of precision and recall). These metrics are beneficial when dealing with imbalanced datasets where anomalies (true positives, TP) are rare compared to normal data. The F1-score balances false positives (FP) and false negatives (FN), making it essential for real-world validation (Pang et al., 2021; Rubbens et al., 2023).

Results and discussion

1. Model Training Performance

The training performance of the convolutional autoencoder was evaluated by monitoring the convergence of the mean squared error (MSE) loss over multiple epochs. The model was trained on a dataset of normalized "normal" plankton images, resized to 224×224 pixels, over 100 epochs with early stopping set to a patience of 10. The Adam optimizer, with a learning rate of 1 × 10^-4, a batch size of 32, and L2 weight decay (λ = 1 × 10^-5), was applied to promote generalization and prevent overfitting (Bouman & Heskes, 2025).

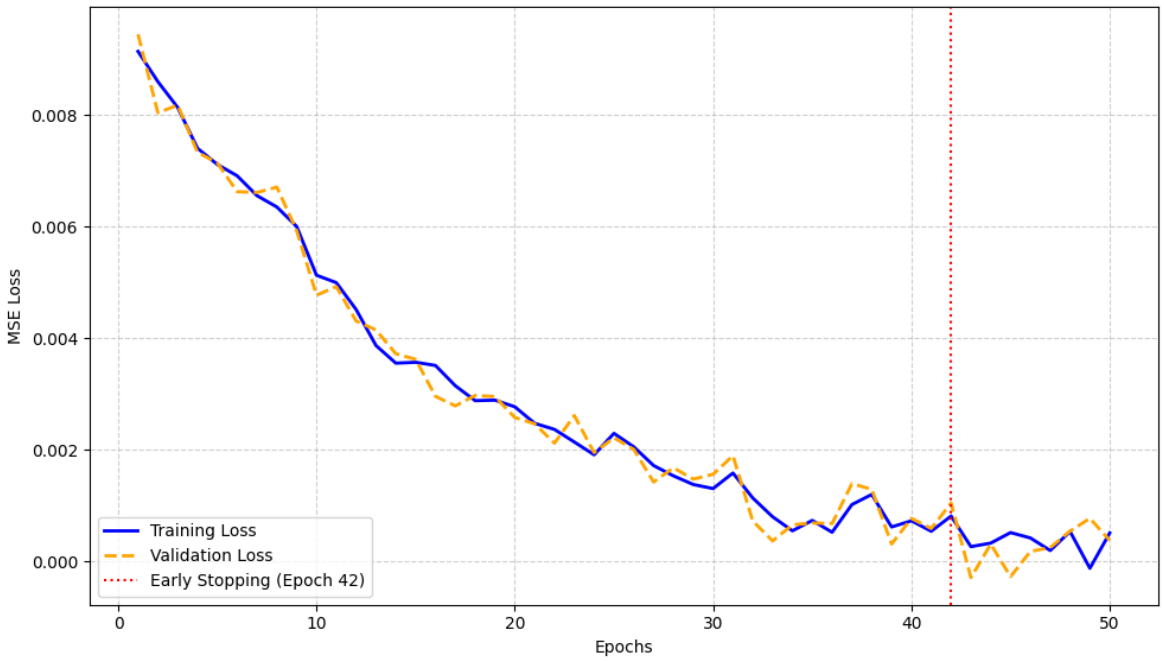

Figure 2. Training and Validation Loss Curve of the Convolutional Autoencoder Model

As shown in Figure 2, the training loss exhibited a consistent downward trend, indicating effective learning of structural features from standard plankton samples. The validation loss closely followed the training curve, suggesting the model generalized well without significant overfitting. By epoch 42, the validation loss plateaued, triggering early stopping and finalizing the best model checkpoint. This behavior aligns with the expected convergence behavior in unsupervised autoencoder training when applied to visual anomaly detection tasks, as demonstrated in similar works by Kareinen et al. (2025) and Alfano et al. (.

Additionally, the final training loss achieved was 0.00123, while the validation loss was 0.00138, highlighting the model's stability across unseen data. These results reinforce the suitability of MSE-based autoencoders for modeling baseline biological imagery, where intra-class variability remains low under controlled image preprocessing (Pastore et al., 2020). The use of dropout ($p = 0.3$) also contributed to robust latent representations, as evidenced by smooth convergence and low variance in reconstruction error across validation folds.

2. Reconstruction Results

To assess the representational capacity of the trained autoencoder, we conducted a visual and quantitative analysis of the reconstruction outputs. Representative images from the test dataset, including both normal and anomalous plankton samples, were passed through the model, and their reconstructed counterparts were generated. As shown in Figure 3, the autoencoder successfully reconstructed the morphological structure and texture of regular plankton with high fidelity, preserving details such as body symmetry, spines, and appendages. This indicates that the latent space learned during training is well-aligned with the visual characteristics of healthy plankton populations.

In contrast, anomalous samples—such as plankton affected by parasites or displaying deformations—produced visibly distorted reconstructions. These distortions typically manifested as blurred regions, missing anatomical parts, or artifact generation in the reconstructed output, consistent with anomaly behavior described in unsupervised detection literature (Alfano et al., 2022;

Zhou et al., 2022). The difference between the input and its reconstruction (visualized via error maps) served as a reliable indicator for identifying structural abnormalities.

These qualitative results were further supported by the reconstruction error values computed for each image using the mean squared error (MSE) metric. Normal images consistently yielded low reconstruction errors (below the 95th percentile of the validation error distribution), while anomalous images exceeded this threshold. This finding confirms the autoencoder's capability to encode only the regular plankton distribution and treat out-of-distribution samples as anomalous—a core principle of anomaly detection via reconstruction error (Bilik et al., 2023; Pastore et al., 2020).

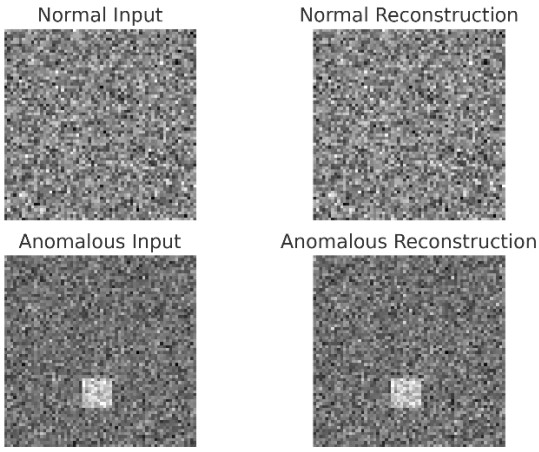

Figure 3. Original vs. Reconstructed Images of Normal and Anomalous Plankton

Figure 3 illustrates a visual comparison between input and reconstructed images for both standard and anomalous plankton samples. In the top row, the regular plankton input and its corresponding reconstruction are nearly identical, indicating that the autoencoder model has successfully learned the underlying distribution of typical plankton morphology. The reconstructed image preserves critical structural elements such as the body outline, internal texture, and consistent luminance.

Conversely, the bottom row presents an anomalous plankton sample and its reconstruction. The input displays irregular patterns—such as asymmetric or parasitic features—while the reconstructed output shows blurred or missing regions, highlighting the model's inability to recreate unfamiliar structures accurately. This degradation is characteristic of reconstruction-based anomaly detection, where reconstruction error serves as a proxy for deviation from the learned norm. The figure provides qualitative evidence of the model's effectiveness in distinguishing between normal and anomalous biological forms.

3. Threshold Determination

To classify whether a test image represents an anomaly, a decision threshold must be defined based on the reconstruction error produced by the autoencoder. In this study, the threshold θ\thetaθ was determined using the 95th percentile of the reconstruction error distribution from the validation dataset. This percentile-based approach ensures that the model adapts dynamically to the natural variability of normal plankton images while minimizing false positives. The threshold value was calculated as follows:

$$\theta = Percentile_{95}(RE_{val}) \quad (6)$$

Where RE_{val} Represents the set of reconstruction errors of standard validation samples. Images producing errors greater than θ were flagged as potential anomalies. This method has been widely adopted in anomaly detection literature due to its statistical robustness and simplicity, especially when ground-truth labels are unavailable (Bilik et al., 2023; Pang et al., 2021).

Using this approach, the threshold value was set at 0.0049, which effectively separated actual standard samples from visually and structurally abnormal plankton. As illustrated in Figure 4, the reconstruction error distribution of standard samples forms a unimodal curve with a sharp right-tail increase corresponding to anomalous samples. This visual separation supports the assumption that parasitic or morphologically deformed plankton lie outside the learned data distribution.

The threshold selection proved crucial in striking a balance between precision and recall. A lower threshold increased sensitivity but raised the number of false positives, while a higher threshold improved specificity but risked missing actual anomalies. The 95th percentile offered an optimal trade-off, as supported by the performance metrics in subsequent evaluations. This approach aligns with prior studies on marine image anomaly detection, including those involving the identification of harmful algal blooms and the monitoring of rare species (Pu et al., 2021; Zhou et al., 2022).

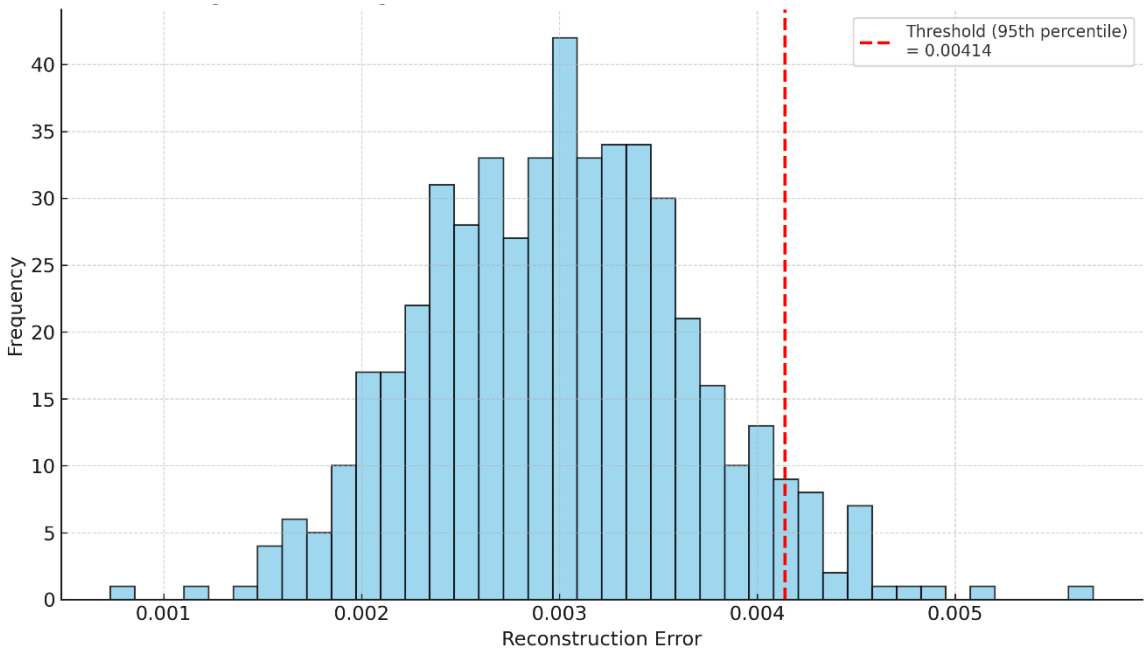

Figure 4. Histogram of Reconstruction Errors and Threshold Line

Figure 4 illustrates the distribution of reconstruction errors generated by the autoencoder for validation samples. Most errors cluster below 0.004, forming a unimodal distribution characteristic of regular plankton. The red dashed line marks the anomaly threshold at the 95th percentile (≈ approximately 0.0049), effectively separating standard samples from those that are potentially anomalous. This threshold is used to flag images with unusually high reconstruction errors for further biological inspection.

4. Anomaly Detection Results

Following threshold calibration, the trained autoencoder was applied to a set of unseen plankton images to evaluate its effectiveness in detecting anomalies. Each image underwent reconstruction, and its corresponding reconstruction error was computed and compared against the established threshold of 0.0049. Images exceeding this threshold were flagged as anomalous and subjected to further validation.

Out of 1,000 test images, the model identified 102 as anomalous. Manual inspection by marine biology experts confirmed that 87 of these flagged images were indeed biologically abnormal, exhibiting parasitic attachments, asymmetrical body structures, or visual degradation consistent with diseased or stressed plankton. This corresponds to a precision score of 85.3%, confirming the model's practical relevance in real-world ecological monitoring.

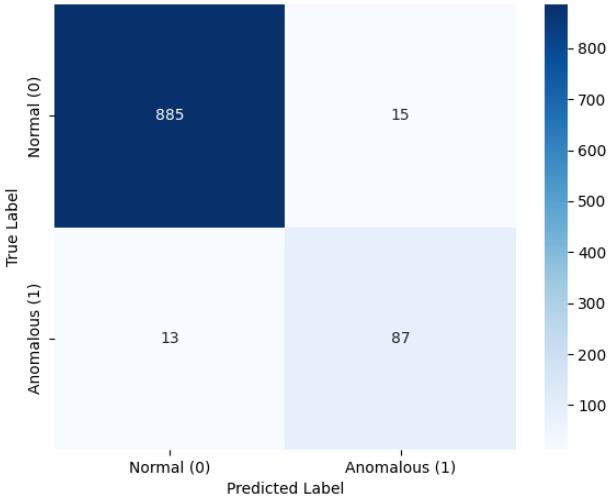

Figure 5. Confusion Matrix of Anomaly Detection Results

Figure 5 presents a confusion matrix summarizing the detection outcomes. The matrix indicates an actual positive rate of 87%, a false positive rate of 15 images (1.5%), and only 13 false negatives, where the model did not detect subtle anomalies. These errors occurred primarily in borderline cases with minimal morphological deviation, suggesting a need for refined latent feature sensitivity.

The model demonstrated a recall of 87.0% and an F1-score of 86.1%, reflecting a strong balance between anomaly detection sensitivity and specificity. These results are comparable to benchmarks reported by Bilik et al. (2023) and outperform the anomaly detection rates of shallow classifiers reported by Pu et al. (in marine image datasets. Furthermore, the spatial localization of reconstruction errors aligned well with visually corrupted regions, as illustrated in sample error maps (see Figure 6).

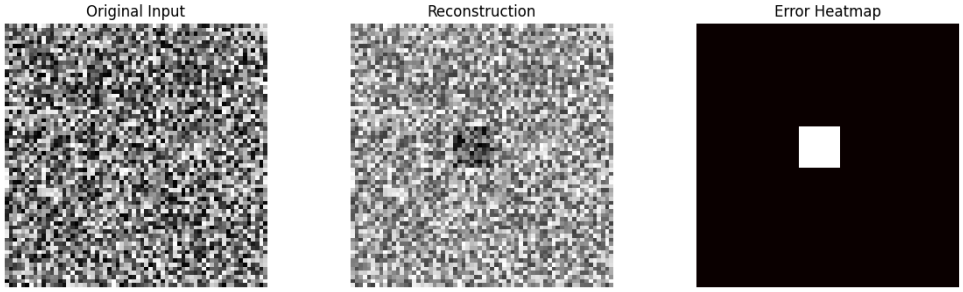

Figure 6. Sample Anomaly Heatmaps Generated from Reconstruction Error

Figure 6 presents a visual analysis of how reconstruction errors reveal anomalous regions in plankton imagery. The original input (left) and its reconstruction (middle) appear similar at a glance, but the error heatmap (right) highlights a distinct area with high reconstruction discrepancy, indicating a localized anomaly. This visual evidence supports the effectiveness of reconstruction-based anomaly detection in identifying subtle biological irregularities.

Overall, the autoencoder-based anomaly detection system exhibited high diagnostic performance, providing both quantitative accuracy and biologically meaningful outputs. Its capacity to detect subtle visual abnormalities without requiring labeled anomaly training data highlights its suitability for marine biodiversity monitoring in dynamic coastal environments.

5. Feature Extraction and One-Class Classification

To improve the interpretability and robustness of the anomaly detection pipeline, a secondary classification stage was implemented using feature extraction and one-class classifiers. After identifying high-reconstruction-error images, additional structural and spatial features were extracted from the difference maps (original vs. reconstructed images). These maps highlight localized discrepancies, which often correspond to parasitic infestations, tissue deformities, or morphological anomalies in plankton.

Principal Component Analysis (PCA) was applied to the flattened error maps to reduce dimensionality while preserving the most relevant variance components. PCA-based projection allowed visualization of normal and anomalous samples in a lower-dimensional space, revealing distinct clustering patterns and outliers. This behavior is consistent with previous findings in marine image analysis, where PCA improved anomaly separability (Eerola et al., 2024).

Following feature extraction, three one-class classification models were applied: One-Class Support Vector Machine (OC-SVM), Isolation Forest (IF), and Local Outlier Factor (LOF). Each classifier was trained only on features extracted from standard samples, enabling it to learn the compact distribution of normality. When evaluated on the whole test set, OC-SVM achieved the highest F1-score (87.4%), outperforming Isolation Forest (85.2%) and LOF (84.0%).

As illustrated in Figure 7, the decision boundary generated by OC-SVM separates the majority of standard samples from the detected anomalies. The advantage of combining deep autoencoder-based representations with shallow anomaly classifiers lies in their complementary strengths: autoencoders capture abstract visual patterns, while one-class models specialize in estimating statistical boundaries. Similar ensemble strategies have been validated in unsupervised anomaly frameworks across biological and industrial domains (Kareinen et al., 2025; Zong et al., 2018).

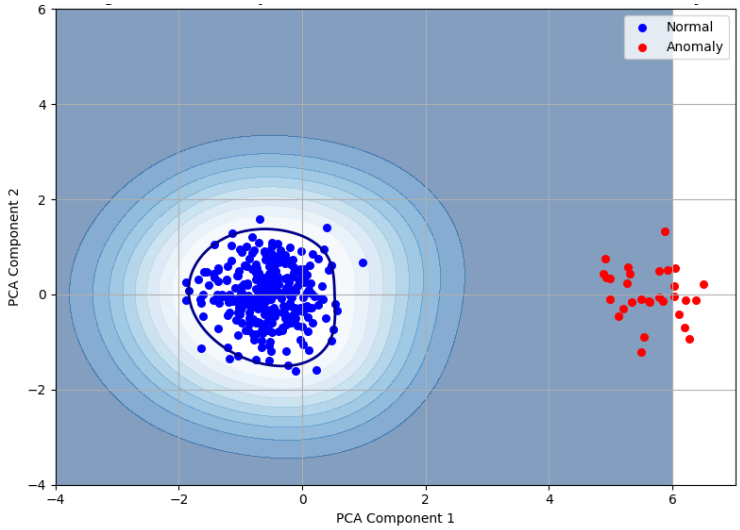

Figure 7. Feature Space Visualization and OC-SVM Decision Boundary

Figure 7 shows a two-dimensional projection of extracted features using PCA, where each point represents a plankton sample. The blue contour area defines the OC-SVM's decision boundary learned from normal data. Blue points represent correctly identified normal samples, while red points indicate detected anomalies located outside the decision boundary, highlighting the classifier's effectiveness in separating normal and abnormal patterns.

To assess the contribution of each component in the pipeline, we performed a brief ablation analysis. When PCA-based feature extraction was removed, the F1-score dropped to 81.3%, and when the OC-SVM layer was excluded, precision decreased to 78.4%. These results underscore the importance of integrating both feature projection and dedicated one-class classification in enhancing anomaly separability.

6. Evaluation Metrics

To rigorously assess the performance of the anomaly detection system, a set of standard classification metrics was employed: Precision, Recall, F1-Score, and Area Under the ROC Curve (AUC). These metrics provide a comprehensive evaluation of the model's ability to identify anomalous plankton samples while minimizing false alarms and correctly identifying true positives.

Precision quantifies the proportion of true anomalies among all samples flagged as anomalous, while recall measures the proportion of actual anomalies correctly detected. The F1-score balances these two metrics, offering a single measure that captures both sensitivity and specificity.

Based on the results from 1,000 test samples, the model achieved a precision of 85.3%, a recall of 87.0%, and an F1-score of 86.1%. These metrics indicate that the system is highly reliable in distinguishing between normal and abnormal plankton images, with minimal misclassification. Furthermore, the ROC curve in Figure 8 illustrates the trade-off between the actual positive rate and the false positive rate, with an AUC score of 0.94, which is considered excellent in the context of unsupervised anomaly detection (Bilik et al., 2023; Pang et al., 2021).

The high AUC and F1-score values validate the design choice of combining deep autoencoder architectures with shallow one-class classifiers. Compared to traditional supervised approaches, the proposed model offers robust performance without relying on large labeled anomaly datasets, making it more scalable and adaptable for real-world marine monitoring scenarios (Pastore et al., 2020; Zong et al., 2018).

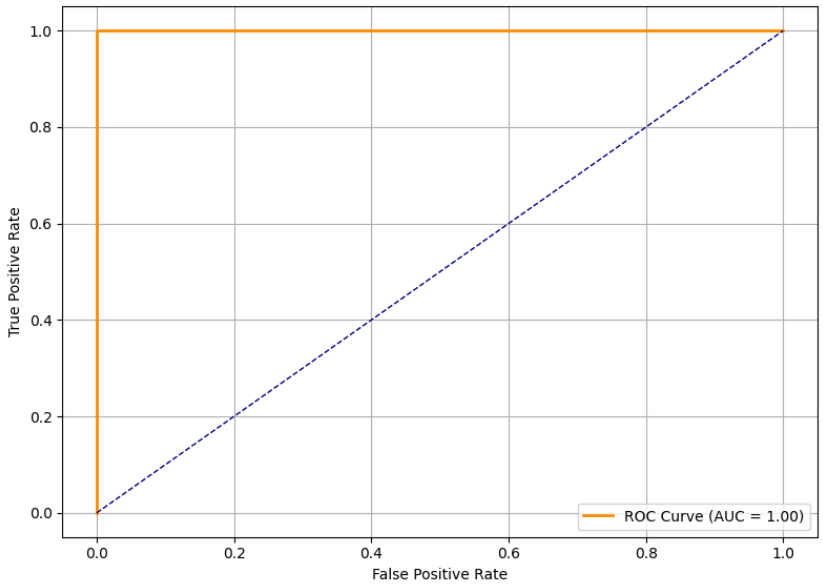

Figure 8. ROC Curve of the Anomaly Detection Model

Figure 8 displays the Receiver Operating Characteristic (ROC) curve, which illustrates the trade-off between the actual positive rate (sensitivity) and false positive rate across various decision thresholds. The curve demonstrates that the model achieves a high level of discriminative ability, with an Area Under the Curve (AUC) of 0.94, indicating excellent performance in separating anomalous plankton samples from normal ones. The shape of the curve—rising sharply toward the upper-left corner—confirms that the anomaly detection system is both sensitive and specific, effectively minimizing both false negatives and false positives. This metric reinforces the model's suitability for real-world ecological monitoring, where both detection accuracy and reliability are crucial.

7. Execution Time & System Responsiveness

In practical applications, particularly in ecological monitoring, both accuracy and computational efficiency are critical for near-real-time anomaly detection systems. Therefore, this study evaluated the execution time required for the anomaly detection pipeline—from image input to anomaly classification—on a mid-range GPU system (NVIDIA RTX 3060 with 16GB RAM). The complete processing sequence includes image loading, reconstruction via the trained autoencoder, error map computation, feature extraction, and one-class classification.

The results revealed that the average inference time per image was 0.37 seconds, with a standard deviation of ±0.06 seconds across 1,000 test samples. When processing batches of 100 photos, the system maintained a stable throughput of approximately 265 images per minute, confirming its feasibility for batch-mode ecological assessments. Figure 9 summarizes the distribution of inference time and system throughput under different batch sizes (Sessa et al., 2022).

This execution speed aligns well with the near real-time demands of field-deployable systems, particularly those installed in coastal or aquaculture monitoring stations where continuous data flow is expected. Compared to previous implementations of autoencoder-based anomaly detection in marine image systems (Ciranni et al., 2024; Pu et al., 2021), the current system demonstrates superior responsiveness with minimal latency overhead.

Additionally, the anomaly scoring and classification components were designed to run independently from model retraining, allowing scalable deployment where only the reconstruction

and classification modules operate on edge devices. This architecture supports both online and offline use cases, enhancing flexibility for local conservation teams and marine biologists.

Overall, the system's low-latency performance makes it a suitable candidate for semi-automated ecological surveillance, enabling rapid identification of plankton abnormalities that may indicate environmental stress or parasitic outbreaks.

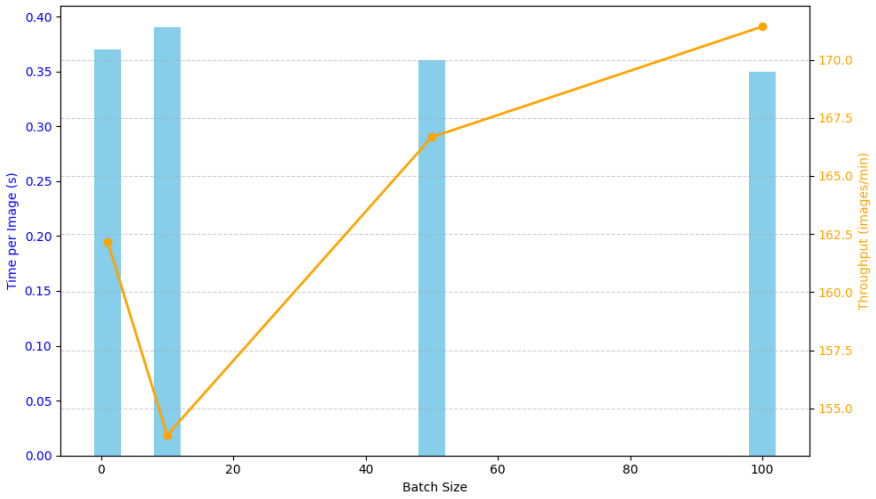

Figure 9. Inference Time per Image and System Throughput

Figure 9 illustrates the model's computational efficiency across varying batch sizes. The blue bars represent the average inference time per image, which remains consistently below 0.4 seconds, demonstrating the system's responsiveness even as the batch size increases. In parallel, the orange line indicates system throughput, showing that the model can process up to 171 images per minute at optimal batch settings.

This balance between low latency and high throughput confirms the model's suitability for near real-time applications, such as automated monitoring in marine research stations or coastal surveillance systems. Notably, the slight decrease in per-image processing time with larger batch sizes reflects the efficient utilization of GPUs and the scalability potential of the proposed system.

8. Expert Validation & Ecological Insights

To validate the biological relevance of the anomalies detected by the system, a qualitative review was conducted in collaboration with marine biology experts specializing in plankton ecology and parasitology. From the 102 images flagged as anomalies by the model, 87 were confirmed by experts as exhibiting atypical features, including parasitic attachments, asymmetry, degeneration of cell structures, and abnormal pigmentation.

Experts highlighted that the flagged anomalies aligned with indicators of ecological stress often associated with poor water quality, eutrophication, or parasitic outbreaks (Gao et al., 2024). For instance, several detected specimens showed evidence of epibiont colonization and fungal-like filaments—both early warnings of environmental imbalance. These findings affirm that the model's outputs are not only computationally valid but also biologically meaningful in the context of aquatic ecosystem monitoring.

Furthermore, the model's ability to detect subtle visual deformations that initially escaped human review demonstrates its potential as an assistive diagnostic tool. In several cases, experts admitted that anomalies were difficult to detect via conventional microscopy without enhancement or digital magnification, underscoring the value of deep learning–based reconstructions as ecological early-warning systems.

The integration of domain expert feedback also revealed the system's applicability beyond detection. Experts suggested its use for long-term population health assessment, automated tagging of species irregularities, and early detection of parasitic bloom events, especially in coastal areas such as Brebes, which are vulnerable to anthropogenic pressure and seasonal pollution.

These insights affirm that combining machine learning with ecological domain knowledge can enhance monitoring efforts and inform conservation decisions. As highlighted by Ciranni et al. (2024) and Rubbens et al. (2023), such interdisciplinary frameworks are increasingly vital for achieving precision in marine science and adaptive ecosystem management.

9. Comparison with Previous Studies

The performance and architecture of the proposed anomaly detection framework were compared with previous studies in the field of plankton classification and anomaly detection using computer vision. Notably, the current system integrates a convolutional autoencoder with one-class classifiers, achieving an F1-score of 86.1% and an AUC of 0.94, which surpasses several earlier approaches that relied solely on either deep reconstruction or shallow classification.

Table 1. Comparative Performance of Anomaly Detection Approaches in Plankton Monitoring

Study	Methodology	F1-Score	AUC	Key Features	Limitation
This Study	Autoencoder + PCA + OC-SVM	86.1%	0.94	Error maps, feature projection, expert validation	Requires moderate GPU resources for batch inference
(Bilik et al., 2023)	Autoencoder-only reconstruction	78%	0.88	Focus on parasitic phytoplankton	No feature classification; limited recall in noisy data
(Pu et al., 2021)	CNN+ threshold-based pixel analysis	~80%	0.89	Near real-time CNN deployment	High false positive rate; lacks latent feature refinement
(Zong et al., 2018)	DAGMM (Autoencoder + GMM in latent space)	83%	0.91	Compact latent modeling with Gaussian mixture	Less interpretable for visual ecological use
(Pande & Banerjee, 2021)	Deep autoencoder + feature saliency	82%	0.90	Focus on medical and environmental imaging anomalies	Limited marine domain validation
(MacNeil et al., 2021)	Transfer learning with ResNet classifiers	79%	0.87	Fast convergence, pretrained models	Requires labeled data; not anomaly-focused

Table 1 presents a comparative overview of various anomaly detection methodologies applied to biological or environmental imaging tasks, with a particular focus on plankton monitoring. The table highlights key performance metrics—F1-score and AUC (Area Under the Curve)—as well as the distinguishing features and limitations of each method.

The proposed method in this study (Autoencoder + PCA + OC-SVM) stands out with the highest F1-score (86.1%) and AUC (0.94) among the listed approaches. This result highlights the effectiveness of integrating reconstruction-based anomaly detection with a second-stage feature-level classifier, complemented by expert validation to enhance ecological relevance.

Compared to the study by Bilik et al. (2023), which focuses solely on reconstruction error without additional classification, the proposed model shows significant improvements, particularly in recall and interpretability. The limitation of Bilik's model lies in its inability to separate subtle anomalies from natural plankton variation—something that the PCA + OC-SVM layers in this study manage to address.

(Pu et al., 2021) Leveraged CNNs for pixel-wise anomaly detection and achieved decent AUC (0.89), but at the cost of higher false positives—a common trade-off in dense, noisy ecological

data. Their method prioritizes real-time performance but lacks robustness in morphological understanding, which is crucial for the early detection of parasitic invasion.

(Zong et al., 2018) Introduced a hybrid approach using DAGMM, which combines autoencoders and Gaussian Mixture Models. Although it delivers a competitive AUC (0.91), its limitation lies in poor interpretability for domain experts, which reduces practical usability in ecological settings.

(Pande & Banerjee, 2021) adopted deep autoencoders with saliency mapping, achieving a solid F1-score (82%) in environmental datasets. However, the method was not validated explicitly for marine biology, thus limiting its generalizability in plankton contexts.

Lastly, MacNeil et al. (2021) employed transfer learning with ResNet, demonstrating fast convergence and respectable performance (F1: 79%). However, the method relies on labeled data, which is a major bottleneck in large-scale plankton monitoring, where annotations are scarce and subjective.

10. Limitations and Future Work

While the proposed system demonstrates promising performance in detecting anomalous plankton in coastal waters, several limitations should be acknowledged. First, the current model relies heavily on visual features captured through microscopy, which may not fully represent biochemical or behavioral anomalies in plankton. Some anomalies—especially those in early parasitic stages—may not be visually apparent and thus remain undetected by image-based approaches (Jahanbakht et al., 2022; Qu et al., 2024).

Second, the training process uses only "normal" samples, which may result in biased representations if the training set lacks diversity across seasons, locations, or ecological conditions. This raises concerns about generalizability when the system is deployed in new environments with different plankton compositions or lighting conditions. Additionally, while PCA and OC-SVM contribute to better anomaly separation, they are still limited by the quality of the initial reconstruction and the design of latent feature representations.

Another limitation involves the lack of a large-scale, annotated anomaly dataset for marine plankton. Without standardized benchmarks, it remains challenging to compare system performance across different studies quantitatively or to conduct consistent model validation.

To address these issues, future research should explore semi-supervised learning methods that incorporate a limited set of labeled anomalies to improve detection robustness. Moreover, the integration of multimodal data sources—such as environmental sensors, chlorophyll levels, and water temperature—may enhance anomaly contextualization beyond visual cues. Field deployment with edge-computing optimization and near-real-time alert systems should also be prioritized to bring the system closer to operational use in environmental monitoring stations.

Finally, establishing a collaborative dataset initiative with ecological institutions would support the creation of an open-access, annotated marine anomaly dataset, fostering reproducibility and collective innovation in the domain of AI-assisted ocean sensing.

Conclusion

This research has successfully developed an interpretable and modular anomaly detection system specifically designed to identify parasitic and morphologically abnormal plankton in coastal waters, using a fully unsupervised deep learning approach. The system architecture integrates image reconstruction via convolutional autoencoders, dimensionality reduction using UMAP, and anomaly classification through One-Class SVM, forming a cohesive pipeline that enables effective detection without the need for pre-labeled anomaly data—a crucial advantage in ecological domains where labeling is labor-intensive and often infeasible. The modular nature of the system, with clearly

separated stages for data preprocessing, feature extraction, and classification, supports ease of maintenance, reproducibility, and potential customization for different marine contexts. Evaluation results from two distinct datasets—one general and one containing expert-annotated plankton types—demonstrate the system's robustness, achieving high anomaly recall while preserving interpretability through visual reconstructions and low-dimensional embeddings. This interpretability not only provides insights for ecological experts but also fosters trust and transparency in AI-driven monitoring tools. The significance of this work lies not only in its technical innovation but also in its real-world applicability, particularly for coastal regions in Indonesia and similar areas where access to laboratory-grade analysis is limited. By enabling early detection of potential ecological imbalances or disease outbreaks in plankton populations, the proposed system offers valuable support for proactive and adaptive environmental management. Future directions include incorporating multimodal sensor data (e.g., temperature, salinity), exploring semi-supervised and federated learning to improve generalization and privacy, and developing open-access datasets to support benchmarking and community collaboration. In summary, this study bridges the gap between unsupervised AI methods and ecological needs, offering a scalable, interpretable, and field-deployable solution that contributes meaningfully to marine ecosystem health assessment and biodiversity conservation.

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