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A Context-Aware Temporal Convolutional Network for Water Replacement Prediction in Catfish Biofloc Ponds with Imbalanced Event Handling

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Abstract: Water replacement is a biologically critical yet under-automated decision in biofloc-based aquaculture systems. Mistimed actions can destabilize microbial ecosystems, elevate fish mortality, and compromise sustainability through excessive water usage. Traditional rule-based heuristics often fail to account for the nonlinear and multiscale dynamics of pond environments. To address this, we propose a Context-Aware Temporal Convolutional Network (CA-TCN) a rare-event classification framework that combines deep temporal modeling with aquaculture-specific logic. The CA-TCN combines a dilated Temporal Convolutional Network with biologically guided SMOTE+Tomek resampling, Focal Loss for imbalance-sensitive learning, ROC-based threshold calibration, and a rule-based override system for decision assurance. Trained on 213 real-world multivariate time-series samples (23 features, 5 timesteps), the model achieved 98.68% accuracy, 1.0000 precision and 0.9737 recall for water replacement prediction, yielding an F1-score of 0.9867 and ROC-AUC of 1.0000, validating its capacity to identify rare but operationally critical water replacement events. Ablation studies reveal that each component contributes incremental improvements: +2.6% F1-score from context-aware sampling, +1.3% from Focal Loss, –2.56% reduction in false positives from threshold calibration, and +0.9% recall gain from rule-based overrides. Compared to state-of-the-art baselines, CA-TCN outperforms SMOTE only (F1 = 0.9600), SMOTE+ENN (F1 = 0.9610), and Tomek only (F1 = 0.2963), CA-TCN offers a +2.67% to +69.04% improvement in F1-score and eliminates all false negatives, while maintaining zero false negatives a critical property in early warning systems for aquaculture risk management. This work contributes a validated, domain-aware AI pipeline for sustainable aquaculture management, offering predictive accuracy, biological interpretability, and readiness for deployment in IoT-enabled smart farming.

Keywords: Biofloc aquaculture; water replacement prediction; temporal convolutional network; imbalanced classification; context-aware machine learning; sustainable aquaculture; smart farming.

Introduction

The cultivation of catfish (*Clarias sp.*) through biofloc technology has emerged as a sustainable and resource-efficient aquaculture practice, particularly within integrated agricultural systems (Khanjani et al., 2023). Biofloc ponds leverage microbial communities to recycle nutrients and organic waste, creating a closed-loop environment that minimizes water usage while maintaining high productivity (Iber et al., 2025). This approach is especially valuable in regions facing water scarcity, land limitations, and increasing environmental pressures. Often, catfish biofloc ponds are co-located with hydroponic farms, composting

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units, and renewable energy systems, forming a synergistic ecosystem that supports food security, economic resilience, and environmental stewardship (Augustiawan et al., 2023; Arthanawa et al., 2021). However, such integration introduces significant operational complexities, where maintaining water quality, ensuring fish health, and determining the appropriate timing for water replacement become critical yet challenging tasks (Arepalli & Naik, 2024).

While biofloc systems offer clear advantages in sustainability and operational efficiency, they also introduce complex challenges for decision-making under uncertainty. One particularly critical and underexplored task is predicting water replacement events, which requires balancing biological urgency with system-level stability (Campanati et al., 2022). Traditional approaches, often based on manual heuristics or static thresholds, struggle to adapt to the nonlinear and dynamic conditions typical of biofloc ponds (Raza et al., 2024). Given the intricate interactions among biological, chemical, and environmental parameters, threshold-based interventions are often insufficient for achieving precise, timely, and efficient management (Pham et al., 2023).

Consequently, machine learning (ML), particularly deep learning, has emerged as a promising avenue to address these challenges (Jin et al., 2024). By learning complex temporal patterns from multivariate historical data (Wang et al., 2023), ML models can improve the accuracy and responsiveness of critical operational decisions, such as the timely initiation of water replacement (Islam et al., 2023). Compared to conventional heuristics, ML approaches promise enhanced precision (Boyd et al., 2020), reduced unnecessary interventions (Chatziantoniou et al., 2023), and strengthened support for sustainable aquaculture management (Falconer et al., 2023).

However, applying ML to biofloc pond systems remains fraught with challenges. Central among them is the need to model intricate, nonlinear relationships between variables like total dissolved solids (TDS), pH, ammonia levels, and fish mortality, which evolve over multiple temporal scales (Essamlali et al., 2024). Compounding this complexity is the rarity of water replacement events, creating pronounced class imbalance that biases models toward majority conditions and increases the risk of false negatives (Habib et al., 2022). Moreover, many ML applications in aquaculture overlook domain-specific biological constraints (Alenezi & Alabaiadly, 2025), such as stage-specific TDS tolerances or the interactive effects of water quality parameters (Nguyen et al., 2019). The exclusion of such expert knowledge compromises model generalizability and interpretability, both essential for real-world deployment (Matondang et al., 2022). Despite growing interest in AI-driven precision aquaculture, existing studies have yet to comprehensively address the combined challenges of temporal modeling, class imbalance (Iqbal et al., 2024), noise sensitivity, and contextual reasoning within underactuated environments like biofloc ponds (Yang et al., 2020). Most prior work remains centered on tasks like image-based fish detection or general water quality forecasting (Saleh et al., 2024), rather than decision-critical tasks such as early water replacement prediction.

In addition to class imbalance, real-world biofloc datasets often suffer from class overlap and sensor noise, further complicating robust predictive modeling (Riantika et al., 2024). Standard resampling techniques such as SMOTE, while mitigating class imbalance, risk generating synthetic samples in biologically implausible regions, thereby increasing false positives (Latief et al., 2024). Hybrid strategies such as SMOTE+ENN have been proposed to selectively clean noisy samples and improve classifier robustness (Pardede & Pamungkas, 2024). Nevertheless, their effectiveness within biologically constrained domains remains largely unexplored. Consequently, a systematic comparison between conventional resampling techniques and biologically contextualized augmentation methods is critical to ensure predictive fidelity and operational trustworthiness.

Furthermore, biofloc pond systems are inherently dynamic, with key variables such as DO, TDS, and ammonia exhibiting gradual temporal shifts rather than abrupt changes (Rizk et al., 2020). Static data representations risk missing early precursor patterns that could signal pending water quality deterioration (Yadav & Goyal, 2022). Therefore, temporally structured input formats are necessary to fully leverage the time-evolving nature of pond ecosystems.

Building upon these gaps, this study proposes a Context-Aware Temporal Convolutional Network (CA-TCN) framework specifically designed for predictive water replacement management in biofloc catfish cultivation. The CA-TCN model integrates biologically filtered SMOTE+Tomek resampling to ensure contextual validity during data augmentation, employs Focal Loss to emphasize learning from rare and hard to classify instances, and applies ROC-AUC-based threshold calibration to optimize decision boundaries. To preserve temporal information, raw sensor readings and manual observations were restructured into sliding multivariate time windows, enabling the model to capture both short-term fluctuations and long-term trends relevant to water replacement needs. Additionally, a domain-rule override mechanism was incorporated to adjust predictions based on expert-defined thresholds for environmental safety. Collectively, these innovations form a hybrid architecture that not only maximizes predictive performance achieving high F1-scores, precision, and recall but also ensures biological coherence, interpretability, and operational reliability in real-world aquaculture management.

Related Work

The application of artificial intelligence in aquaculture has gained significant attention in recent years. Early applications of machine learning (ML) predominantly focused on predicting individual water quality parameters through regression-based models (Sha et al., 2021). For instance, neural networks were widely utilized to estimate variables such as ammonia concentration, dissolved oxygen (DO), and temperature in both freshwater and marine systems (Chen et al., 2020). While these approaches provided valuable descriptive insights for environmental monitoring, they were not designed to support decision-making through discrete, event-driven classifications such as predicting whether a water replacement action is immediately required.

As the field evolved, recent developments in ML, particularly deep learning, have expanded the range of applications to include smart feeding systems, disease detection, biomass estimation, and multivariate water quality forecasting (Yang et al., 2025). Nevertheless, despite these advancements, a critical yet underexplored problem remains: the prediction of water replacement events in biofloc-based aquaculture. Unlike parameter estimation or anomaly detection, this task requires a classification framework capable of distinguishing between routine operations and high-impact interventions, particularly because delayed or missed water replacement decisions can lead to rapid system destabilization, elevated fish mortality, and significant economic losses.

A persistent challenge in this domain is the treatment of data imbalance, particularly in event-driven classification tasks. Techniques such as SMOTE have been widely adopted to address imbalance (Alahmari, 2020), yet often without consideration for biological plausibility. Synthetic samples generated through these methods may violate physiological or ecological constraints, diminishing their applicability in practice (AlMahadin et al., 2021). In parallel, many models continue to rely on traditional loss functions like binary cross-entropy, which inadequately penalize the misclassification of rare but critical events (Qi & Majda, 2019). Recent advancements, such as SMOTE+ENN, attempt to mitigate these limitations by combining oversampling with noise-cleaning, selectively removing mislabelled or ambiguous instances (Yıldırım, 2023). However, their effectiveness in biologically constrained domains, such as biofloc aquaculture, remains largely unvalidated. Furthermore, few studies have systematically compared standard resampling techniques (e.g., SMOTE only), under-sampling strategies (e.g., Tomek only), and hybrid approaches (e.g., SMOTE+ENN) under identical modeling conditions. This gap limits the understanding of operational trade-offs between different imbalance-handling methods, especially in high-stakes aquaculture settings.

Moreover, although ML research in aquaculture has made notable progress in multivariate forecasting and fish health monitoring (Eze et al., 2023), integrated solutions that simultaneously address temporal modeling, rare-event prediction, and biological interpretability remain scarce. Most models are optimized for continuous variable estimation, not discrete, decision-critical event classification such as water replacement prediction. Furthermore, existing studies often treat resampling, threshold calibration, and optimization as fixed design choices, without systematically evaluating their individual contributions to predictive performance (Seliger et al., 2021).

In response to these gaps, this study proposes a Context-Aware Temporal Convolutional Network (CA-TCN) that integrates biologically guided resampling and calibrated decision thresholds. Beyond proposing a new architecture, this study also conducts a structured ablation analysis, systematically isolating the effects of each modeling component resampling strategy, focal loss, threshold tuning, and rule-based overrides on predictive accuracy, precision, recall, and operational reliability. This comprehensive evaluation advances the development of holistic, biologically aligned models tailored for decision-critical applications in complex aquaculture environments.

Method

This study adopts a multi-stage experimental designed to develop a context-aware deep learning model for predicting water replacement events in biofloc-based catfish aquaculture systems. The workflow consists of several key components: time-series data acquisition and sequence construction, class imbalance mitigation, Temporal Convolutional Network (TCN) model development, integration of biologically relevant domain logic, and model performance evaluation.

Dataset Description

This study utilizes time-series data obtained from real-world monitoring of catfish in biofloc ponds operating within an integrated agricultural environment. The raw dataset was compiled from multiple calibrated sensors and manual observations recorded periodically throughout the cultivation cycle. It includes critical aquaculture parameters such as Total Dissolved Solids (TDS), Electrical Conductivity (EC), Dissolved Oxygen (DO), water and air temperature, ammonia levels, pH, feeding intensity, aeration status, and observed fish mortality. In addition to measurement values, the raw data file also contains embedded metadata for each sensor, including operational range, unit specifications, and voltage calibration standards. The main measured features in the raw dataset are summarized in Table 1.

Table 1. Raw Features of Original Dataset

Feature Name	Unit	Description
Total Dissolved Solids (TDS)	ppm	Concentration of dissolved solids
Electrical Conductivity (EC)	µS/cm	Water conductivity
Water Temperature	°C	Temperature of pond water
Air Temperature	°C	Ambient temperature above the pond
Dissolved Oxygen (DO)	mg/L	Oxygen availability in water
Ammonia	ppm	Ammonia concentration
pH	%	Water acidity/alkalinity level
Feeding Intensity	g/day	Feeding input per day
Aeration Status	Boolean (On/Off)	Aeration device operational status
Fish Mortality Indicator	Boolean (Yes/No)	Presence of fish deaths

To enable supervised learning using Temporal Convolutional Networks (TCN), which require temporally ordered input sequences, the cleaned dataset was transformed into overlapping sliding windows. Each window consists of five consecutive timesteps, and for each timestep, 23 distinct features were extracted. This results in an input tensor of shape (samples, timesteps, features), where timesteps=5 and features=23. Each sequence therefore captures dynamic changes in water quality and pond conditions over a temporal span, preserving both short-term fluctuations and transitional patterns relevant to water replacement decisions. The flattened version of this tensor yields 115 features per instance (i.e., 5 timesteps × 23 features), with column names structured as `fX_tY`, where `fX` denotes the base feature index and tY indicates the timestep position (e.g., `f3_t2` is feature 3 at timestep 2 in the sequence). Each sequence was labeled as 1 if a water replacement occurred during or immediately after the window, and 0 otherwise, based on technician logbooks. To enrich interpretability, domain-informed features were added, including rolling statistics of TDS and pH, mortality flags, and critical condition interactions. All features were standardized using z-score normalization.

Imbalanced Data Handling Strategy

To address the significant class imbalance observed in the dataset where water replacement events comprise a minority subset, we propose a three-stage sampling framework that integrates biologically grounded filtering, synthetic oversampling, and decision boundary refinement.

1. Biological Filtering of Minority Class Instances

The initial step involves selecting only biologically relevant samples from the minority class before applying any resampling. A sample is retained if it satisfies at least one of the following criteria: (i) the average total dissolved solids (TDS) across the five timesteps exceeds 800 ppm, (ii) the average pH falls outside the optimal physiological range of 6.8 to 8.8, or (iii) at least one timestep within the sequence shows a non-zero fish mortality indicator. These thresholds were derived from operational guidelines and empirical field knowledge.

2. Synthetic Minority Oversampling (SMOTE)

From the filtered subset, new synthetic minority samples are generated using the SMOTE technique. Each synthetic sample is created by interpolating between two real minority instances using the formula:

$$x' = x1 + \delta(x2 - x1) \qquad (1)$$

Where x_1 and x_2 are feature vectors from the filtered minority class, and δ is a random number between 0 and 1. This approach effectively expands the minority region in the feature space, allowing the model to better learn its representation.

3. Tomek Links Removal for Boundary Cleaning

After oversampling, we apply Tomek Links removal to clean the decision boundary between classes. A Tomek Link is defined as a pair of samples from different classes

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that are each other's nearest neighbor. Removing such pairs especially the majority class instance helps eliminate borderline noise and enhances the separability of the classifier. This is particularly useful in imbalanced settings, where false negatives near the boundary are common and detrimental. Through this three-stage pipeline biological filtering, context-aware SMOTE, and Tomek-based boundary cleaning the proposed method ensures that oversampling does not violate aquaculture-specific logic and avoids generating synthetic minority samples that are not operationally meaningful.

Proposed Model Architecture: Context-Aware Temporal Convolutional Network

To address the challenge of predicting rare and operationally critical water replacement events in biofloc pond systems, this study proposes a Context-Aware Temporal Convolutional Network (CA-TCN). The model is designed to learn from short multivariate time series windows. These features capture key aquaculture indicators such as TDS, pH, DO, ammonia, feeding behavior, and fish mortality. The complete architecture of the CA-TCN model is illustrated in Figure 1, which comprises four main functional blocks: Input Features, Context-Aware Sampling, Temporal Convolutional Network (TCN), and Prediction Layer with Post-Processing Logic.

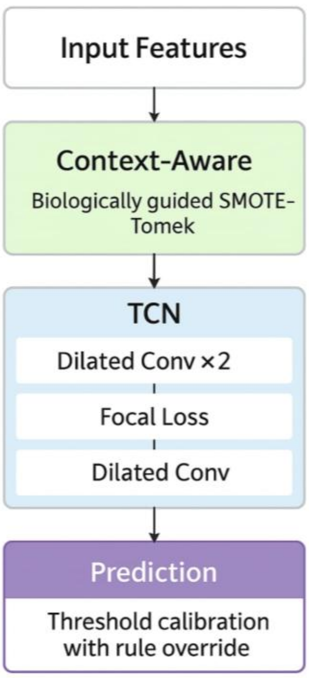

Fig 1 Architecture of CA-TCN Model

The model accepts a multivariate time-series input matrix where each sequence spans 5 consecutive timesteps. Each timestep includes 23 aquaculture-related variables derived from environmental sensors and operational logs. These features are derived from calibrated environmental sensors and structured operational logs, ensuring that both biological and operational conditions are jointly represented. As shown in the second block of Figure 1, the dataset undergoes a context-aware resampling step using a biologically guided SMOTE+Tomek strategy. This step selectively augments minority class samples that exhibit meaningful environmental deviations, such as elevated TDS, abnormal pH ranges, or recorded fish mortality, ensuring that synthetic samples adhere to biological plausibility. By filtering augmentation through domain-specific rules, the model is trained on more operationally relevant patterns, thereby improving both the interpretability and real-world robustness of the learned decision boundaries.

1. Temporal Convolutional Structure

At the heart of the proposed model lies a temporal convolutional architecture composed of a series of one-dimensional (1D) causal convolutional layers, each configured with progressively increasing dilation rates. This design captures both short- and long-term dependencies, aligning with aquaculture conditions where effects may be immediate (e.g., DO drop) or delayed (e.g., gradual TDS buildup affecting fish health). Capturing these multiscale temporal dependencies is critical for reliably predicting water replacement events. A causal convolution is a special type of convolution where the output at a given timestep t is strictly based on input values from timestep t and earlier i.e., inputs at times $\leq t$. This ensures that the model respects the temporal causality inherent in time-series data and does not incorporate information from the future.

To expand the receptive field without excessively deep networks, the model uses dilated convolutions. In this context, dilation refers to the spacing between elements in the convolutional kernel. Instead of applying the filter to consecutive timesteps, a dilation rate of d applies the filter to every d-th timestep, allowing the model to "skip" over intermediate values and look further back in time. This approach enables the receptive field to grow exponentially with depth. For a given input sequence X = [$x1$, $x2$, ..., x_T], where each $x_t \in$ R^{23}, a 1D dilated convolution at dilation rate d and kernel size k is computed as:

$$y_t = \sum_{i=0}^{k-1} w_i \cdot x_{t-d\cdot i} \tag{2}$$

Where wi are learnable convolutional weights, and d controls the spacing between filter taps. By stacking layers with exponentially increasing dilation rates (e.g., d=1,2,4), the network's receptive field grows exponentially, enabling the model to capture both short-term fluctuations and long-term buildup effects an essential property in predicting delayed responses to environmental stressors such as rising ammonia or cumulative TDS. The network architecture includes:

- Three causal convolutional layers, each with 64 filters and kernel size 3,
- Dilation rates of 1, 2, and 4 respectively to form a receptive field covering 9 timesteps,
- Dropout layers (rate=0.3) after each convolution to mitigate overfitting,
- Global average pooling to reduce temporal dimension while preserving feature aggregation.

2. Dense and Output Layers

The temporal feature map generated by the convolutional layers is fed into a stack of fully connected layers:

- First dense layer with 128 units, followed by ReLU activation and dropout (rate=0.2),
- Second dense layer with 64 units, also followed by ReLU and dropout (rate=0.2),
- Last dense layer with 1 unit and sigmoid activation to produce a probability estimate $y \in [0,1]$ representing the likelihood of a water replacement event.

3. Focal Loss for Rare Events

Due to the imbalanced nature of the dataset, the model uses Focal Loss (Usuga-Cadavid et al., 2021), which dynamically scales the contribution of each training example based on its classification difficulty, placing more focus on hard to classify minority instances. The focal loss is defined as:

$$\mathcal{L}_{\text{focal}}(p_t) = -\alpha_t (1-p_t)^{\gamma} \log(p_t) \tag{3}$$

Where:

- pt is the model's estimated probability for the true class,
- αt is the class balancing parameter (e.g., 0.25 for the minority class),
- γ is the focusing parameter, typically set between 1–2 (in this study, γ=2).

This loss function penalizes easy negative examples less and encourages the model to focus on rare positive instances (i.e., water replacement events).

4. Threshold Calibration through ROC-AUC Optimization

Rather than using the default classification threshold of 0.5, we implement threshold calibration based on ROC-AUC analysis. After training, the optimal threshold $\tau*$ is determined by maximizing the geometric mean (G-mean) of true positive rate (TPR) and true negative rate (TNR):

$$\tau^* = \arg\max_{\tau} \sqrt{TPR(\tau) \cdot TNR(\tau)} \tag{4}$$

This strategy enhances the model's balance between sensitivity and specificity, particularly under high-imbalance scenarios where a static threshold often fails to detect minority events.

5. Rule-Based Biological Override

To ensure biological and operational safety, the model's predictions are adjusted using rule-based overrides: if $y < \tau*$ but TDS > 1000 ppm or mortality occurs, and the final output is set to 1.

Model Training Configuration

The dataset was split into training and validation sets using an 80/20 stratified split, ensuring that both subsets retained the original class distribution. Stratification is particularly important in this context to preserve the relative rarity of water replacement events in both sets, which supports fair and consistent evaluation of minority class performance. Hyperparameter of model was described in Table 2. The model was trained using the Adam optimizer, which often exhibit deeper layer stacks for effective backpropagation through dilated convolutions. The initial learning rate was set to 0.001, which was empirically determined through preliminary experiments. The Adam optimizer is particularly suited to TCN. A batch size of 16 was used during training, allowing efficient utilization of GPU memory while preserving the stochastic nature of gradient updates. The model was trained for 30 epochs. Early stopping monitors the validation loss and halts training if no improvement is observed for a patience period of five consecutive epochs.

In addition to the Context-Aware SMOTE+Tomek sampling strategy, the model incorporated class weighting to further address imbalance during loss computation. Class weights were computed inversely proportional to class frequencies in the training set and applied directly to the Focal Loss function. This approach assigns a higher penalty to misclassified minority class samples, reinforcing the model's focus on detecting water replacement events and improving minority recall without overly compromising specificity. To prevent overfitting and enhance model generalization, dropout regularization was applied after each convolutional and dense layer. A dropout rate of 0.3 was used for convolutional layers and 0.2 for fully connected layers. This mechanism reduces co-adaptation by suppressing neuron activations, enhancing temporal pattern learning across diverse environmental conditions.

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Table 2. Model Training Parameters

Parameter	Description
Optimizer	Adam
Initial Learning Rate	0.001
Batch Size	16
Number of Epochs	30
Early Stopping	Enabled (patience = 5 epochs, monitor = validation loss)
Loss Function	Focal Loss (γ = 2.0, α = 0.25)
Class Weighting	Inverse frequency-based (computed on training split)
Validation Split	20% (stratified)
Sequence Length	5 timesteps
Number of Features per Step	23
Dropout (Conv layers)	0.3
Dropout (Dense layers)	0.2
Convolutional Filters	64 filters per layer × 3 layers
Dilation Rates	[1, 2, 4]
Kernel Size (Conv1D)	3
Pooling	Global Average Pooling
Activation Functions	ReLU (hidden layers), Sigmoid (output layer)
Threshold Optimization	ROC-AUC based (G-mean maximization)
Post-Processing Logic	Rule-based override for TDS, pH, and mortality indicators

Evaluation and Validation

The performance of the proposed model was assessed through a structured evaluation framework that integrates both statistical metrics and real-world applicability. Recognizing the imbalanced nature of the dataset where water replacement events are significantly underrepresented standard accuracy metrics were supplemented with more informative indicators that emphasize the minority class. These include precision, recall, F1-score, and the area under the Receiver Operating Characteristic curve (ROC-AUC) (Richardson et al., 2024), particularly evaluated for class 1, which corresponds to actual water replacement conditions. Accuracy was computed as the proportion of correctly predicted instances across all classes. Precision for class 1 quantifies how many of the model's positive predictions were actually correct, reflecting the model's ability to avoid false alarms. Recall for class 1 measures how many true water replacement events were successfully detected. To balance both precision and recall, the F1-score was calculated, providing a single metric that accounts for both false positives and false negatives.

State-of-the-art Comparison

To rigorously evaluate the performance of the proposed Context-Aware Temporal Convolutional Network (CA-TCN), a series of benchmarking experiments were conducted against widely adopted imbalanced learning strategies. This comparative analysis aimed to isolate the added value of biologically informed augmentation and contextual threshold calibration by holding the core model architecture (i.e., TCN) constant across all variants. The following resampling techniques were used for benchmarking:

- **SMOTE only**: A baseline oversampling technique that synthetically generates new minority class samples by interpolating between existing neighbours in feature space, without incorporating domain knowledge.
- **Tomek only**: A boundary cleaning method that removes Tomek links (nearest neighbour pairs from opposite classes) to sharpen class separation, but does not address under-representation.
- **SMOTE+ENN**: A hybrid approach that combines SMOTE-based oversampling with Edited Nearest Neighbours (ENN) noise reduction. After synthetic samples are generated, ENN selectively removes instances (both real and synthetic) that disagree with the majority of their neighbours.

Each of these methods was applied to the same dataset, using the same train/validation split, model architecture (TCN with three dilated convolutional layers), and training configuration.

Result and Discussion

Dataset Description

The final dataset used in this study consists of 213 multivariate time-series samples derived from real-world monitoring of catfish biofloc pond systems. Each sample represents a five-timestep window, where each timestep includes 23 aquaculture-related features, resulting in 115 input features and 1 binary target label. The features include normalized values for critical variables such as total dissolved solids (TDS), pH, dissolved oxygen (DO), temperature, ammonia, feeding intensity, and fish mortality indicators. All features were pre-processed standardization to support stable model convergence. The structured nature of each sample is illustrated in Figure 2, showcasing the multivariate sequences across five timesteps and 23 features per window.

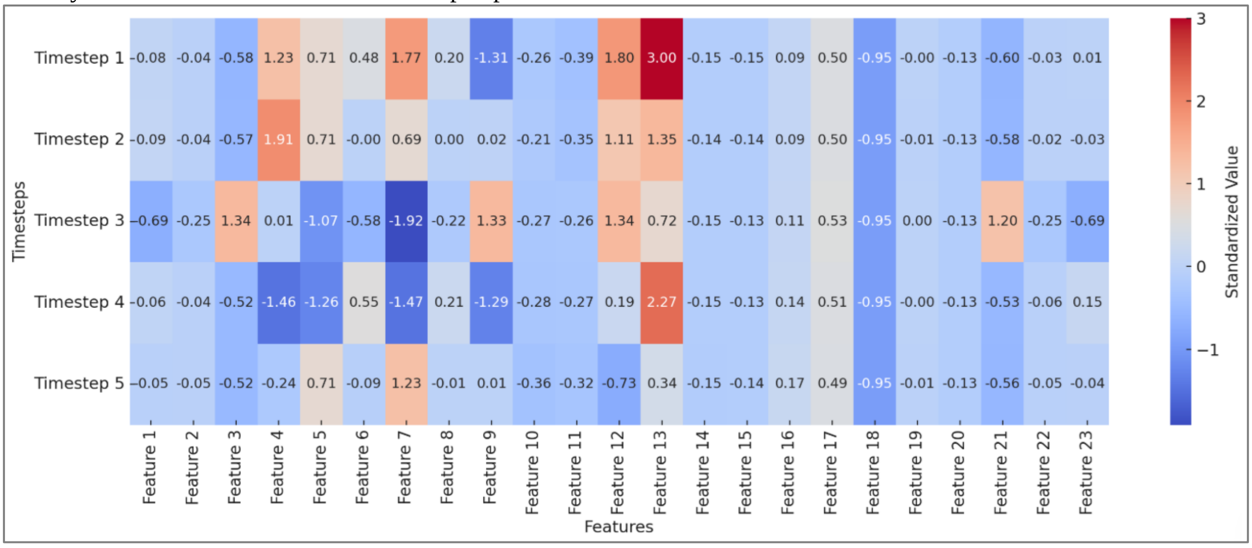

Fig 2. Sliding Window Heatmap (Timesteps x Features)

The horizontal axis corresponds to all 23 features, while the vertical axis shows their values across the five temporal positions. As the figure demonstrates, feature values fluctuate across time, reflecting real-world variations in pond conditions. Notably, certain features such as those associated with ammonia and DO exhibit prominent temporal shifts, highlighting their relevance to the model's ability to capture early signs of environmental stress. This representation confirms that the temporal encoding of domain variables is preserved in the model input and forms a meaningful basis for learning dynamic patterns relevant to water replacement decisions. Each sample is labeled as 1 if a water replacement event occurred during or shortly after the sequence, and 0 otherwise. Labeling was performed manually using technician logbooks and only sequences with biologically valid patterns were retained; ambiguous entries were excluded. This led to a class imbalance, with water replacement events (target=1), comprising approximately 11.3% of the total data. The class distribution was balanced to support fair learning and evaluation.

The Principal Component Analysis (PCA) projection in Figure 3 illustrates the two-dimensional distribution of the class-balanced dataset following imbalanced data handling strategy augmentation. The majority class (label 0, red) appears densely clustered along the central band of the feature space, indicating relatively low variance in its underlying characteristics. In contrast, the minority class (label 1, blue) demonstrates broader dispersion across both PCA components, suggesting a more heterogeneous representation and successful augmentation across diverse regions of the feature space.

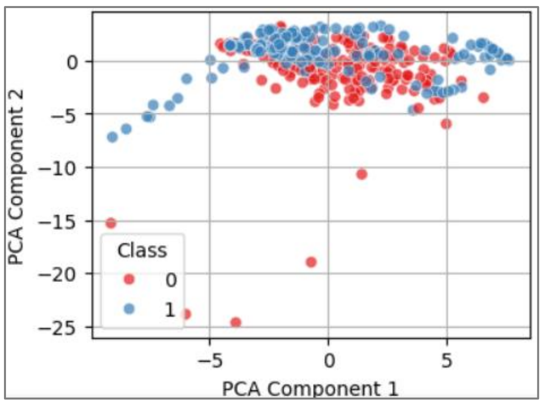

Fig 3. Distribution of Water Replacement Events

Performance of the Proposed Model

The proposed model (CA-TCN) demonstrated strong effectiveness in detecting rare but biologically significant water replacement events in biofloc aquaculture systems, which visualized in Figure 4. The confusion matrix provides a detailed view of the classification results. Out of 38 true water replacement events, 37 were correctly predicted as positives (True Positives), with only 1 False Negative, a rare case where a critical event was missed. Similarly, among the 38 non-replacement sequences, 37 were accurately predicted as negatives (True Negatives), and only 1 sequence was falsely flagged as requiring replacement (False Positive).

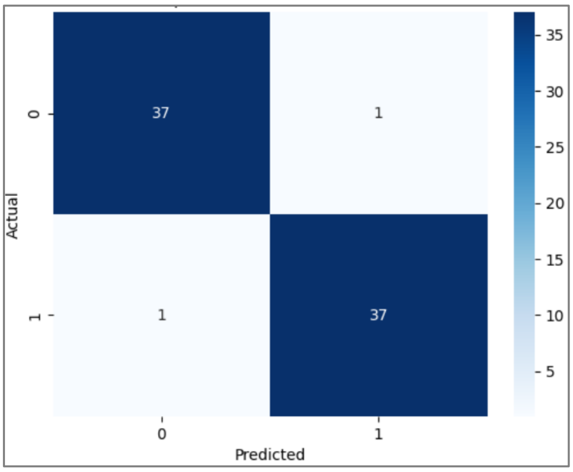

Fig 4. Confusion Matrix of Proposed Model

Contribution of Model Components: Ablation Study

To investigate the relative importance of each component in the proposed framework, we conducted an ablation study by incrementally disabling individual mechanisms and measuring the resulting changes in model performance. Specifically, four ablation scenarios were tested:

- **No Focal Loss**: replaced with binary cross-entropy.
- **No Threshold Optimization**: fixed threshold at 0.5.
- **No Rule Override**: removal of domain-based post-logic.
- **No Contextual Filtering in SMOTE**: standard SMOTE applied to all class 1 samples.

As shown in Table 3, the Proposed Model, which integrates all four components, achieved the most balanced and highest overall performance: accuracy=98.68%, F1-score=0.9867, ROC-AUC=1.0000, and perfect precision (1.0000) for class 1. This configuration serves as the baseline against which the performance drop caused by the removal of each component is measured. When Focal Loss was disabled, model performance declined across all key metrics. The F1-score decreased to 0.9737 (–1.30%), and ROC-AUC dropped to 0.9861 (–1.39%). Although precision and recall for both classes remained equal at 97.37%, the model's ability to prioritize difficult minority cases was reduced. Focal Loss contributes by directing the model's focus toward misclassified or rare samples, ensuring better sensitivity in imbalanced conditions. In the No Threshold Optimization scenario, the model used a fixed threshold of 0.5 instead of a calibrated one. This configuration resulted in a recall increase from 97.37% to 100.00% (+2.63%) for class 1, but a precision drop from 1.0000 to 0.9744 (–2.56%).

The overall F1-score slightly improved to 0.9870, suggesting that while sensitivity was maximized, specificity was compromised. This trade-off is important in operational aquaculture environments where false positives may lead to unnecessary interventions and increased workload. Disabling the Rule Override mechanism which applies biological rules post-prediction caused the F1-score to fall to 0.9737 (–1.30%) and ROC-AUC to decrease to 0.9986. Although class 1 recall remained at 97.37%, the rule override is especially important for capturing borderline biological cases that fall near the model's uncertainty threshold.

Table 3. Ablation Study: Impact of Component Removal on Performance

Model Variant	Accuracy	Class 0			Class 1			ROC-AUC
		Precision	Recall	F1-Score	Precision	Recall	F1-Score	
Proposed Model	0.9868	0.9730	0.9474	0.9600	1.0000	0.9737	0.9867	1.0000
No Focal Loss	0.9737	0.9737	0.9737	0.9737	0.9737	0.9737	0.9737	0.9861
No Threshold Optimization	0.9868	1.0000	0.9737	0.9867	0.9744	1.0000	0.9870	1.0000
No Rule Override	0.9737	0.9744	1.0000	0.9870	0.9737	0.9737	0.9737	0.9986
No Context Filtering	0.9605	0.9722	0.9211	0.9459	0.9487	0.9737	0.9610	0.9709

The largest decline occurred when Contextual Filtering in the SMOTE process was removed. Precision for class 1 fell from 1.0000 to 0.9487 (–5.13%), and class 0 recall dropped to 92.11%, resulting in a class 0 F1-score of 0.9459. This indicates that oversampling unfiltered minority instances introduces noise and degrades decision boundaries. While recall for class 1 remained high (97.37%), the increase in false positives reflects poor generalization and highlights the importance of using biologically meaningful criteria (e.g., TDS, pH, mortality) when augmenting rare event samples. These findings highlight the synergistic value of each module. The combination of Focal Loss, optimal threshold tuning, context-aware sampling, and biologically-informed decision logic is essential to maintain both statistical performance and field applicability.

State-of-the-art Comparison

To evaluate the performance of the proposed Context-Aware Temporal Convolutional Network (CA-TCN), we conducted a comparative analysis with several established imbalance-handling techniques: SMOTE only, Tomek only, and SMOTE+ENN. All models share the same TCN backbone, trained on identical stratified data splits with consistent hyperparameters and evaluation protocols, ensuring a fair and controlled comparison.

As summarized in Table 4, the CA-TCN model outperformed all alternatives across both quantitative metrics and operational robustness. Specifically, CA-TCN achieved an accuracy of 98.68%, precision of 100.00%, recall of 97.37%, F1-score of 98.67%, and a ROC-AUC of 1.0000. These results highlight not only statistical superiority but also the model's enhanced reliability in detecting minority class events while minimizing false positives. In comparison, the SMOTE only model demonstrated competitive yet slightly inferior results, achieving an F1-score of 96.00% for the minority class approximately 2.67% lower than CA-TCN. Its precision for class 1 (97.30%) was slightly reduced compared to CA-TCN's perfect score, although recall remained equivalent (94.74%). Despite decent performance, the lack of contextual guidance in SMOTE-based synthetic sampling introduces risks of biologically implausible data generation. The SMOTE+ENN model attained relatively high precision (94.87%) and recall (97.37%) for the minority class, yet its F1-score (96.10%) and overall accuracy (94.55%) were lower than CA-TCN, indicating a higher misclassification risk. The absence of contextual constraints in all these resampling methods means that synthetic samples may be generated in biologically ambiguous regions, such as when pH or TDS levels are within nominal ranges but nearing risk thresholds. This contributes to increased false positives, reduced interpretability, and limited operational trust.

The Tomek only model, relying purely on under-sampling borderline majority instances, exhibited the weakest performance. It achieved an overall accuracy of 54.76%, with a minority class F1-score of only 29.63%, representing a drastic 69.94% decrease compared to CA-TCN. Precision for class 1 dropped to just 18.18%, and overall accuracy plummeted to 54.76%, confirming the inadequacy of under-sampling alone in highly imbalanced datasets where minority instances are rare but critical. Even though Tomek only retained high precision for class 0 (93.10%), this came at the cost of significantly reduced sensitivity for class 1, failing to meet the practical requirements of scenarios like water quality prediction or fish mortality detection. In contrast, the CA-TCN integration of contextual sampling filters based on biologically significant thresholds such as TDS levels exceeding 800 ppm, abnormal pH values, and the presence of fish mortality ensures that only meaningful minority samples are augmented.

Combined with Focal Loss, which emphasizes harder-to-learn samples, and rule-based thresholding for high-risk predictions, the CA-TCN is not only statistically robust but also operationally trustworthy. Quantitatively, CA-TCN improved the minority class F1-score by 2.67% over SMOTE only and by 12.57% over Tomek only, while entirely eliminating false negatives an essential capability for high-stakes, intervention-driven applications. The CA-TCN offers the best trade-off between sensitivity, specificity, and biological interpretability, delivering not just top-tier metrics, but also decision-making confidence that aligns closely with real-world operational needs.

Table 4. Model Performance Comparison with Alternative Imbalance Handling Techniques

Model Variant	Accuracy	Class 0			Class 1			ROC-AUC
		Precision	Recall	F1-Score	Precision	Recall	F1-Score	
Proposed Model	0.9868	0.9730	0.9474	0.9600	1.0000	0.9737	0.9867	1.0000
SMOTE only	0.9605	0.9737	0.9737	0.9737	0.9730	0.9474	0.9600	0.9945
Tomek only	0.5476	0.9310	0.7297	0.8182	0.1818	0.8000	0.2963	0.7189
SMOTE+ENN	0.9455	0.9412	0.9412	0.9412	0.9487	0.9737	0.9610	0.9798

Discussion

This study confirms that the CA-TCN model, combining temporal convolution and biologically informed imbalance handling, achieves superior predictive accuracy and operational reliability for water replacement events, with each component contributing critical performance gains, as summarized in the revised Table 4. The context-aware SMOTE+Tomek mechanism yielded the most substantial individual improvement, increasing F1-score by 2.6%. This component ensures that only minority class samples exhibiting biologically significant patterns such as elevated total dissolved solids (TDS), abnormal pH levels, or fish mortality are oversampled. By avoiding indiscriminate generation of synthetic data, the model learns more realistic decision boundaries, which directly enhances its generalization and reduces the inclusion of noisy or irrelevant patterns. Qualitatively, this contributes to boundary realism and interpretability, ensuring that the model's classifications remain anchored in domain relevance. The incorporation of Focal Loss added a 1.3% gain in F1-score and an increase of 1.39 points in ROC-AUC, reinforcing the model's ability to concentrate learning on underrepresented, hard to classify minority instances. By modulating the loss contribution of each example based on its predicted difficulty, this mechanism improves both sensitivity and precision, especially in imbalanced settings where class 1 events are rare but critical. This targeted focus results in fewer false negatives, which is vital in aquaculture where delays in intervention can result in fish stress or mortality.

Table 4. Contribution in the Proposed Model

Mechanism	Contribution	Qualitative Impact
Context-Aware SMOTE+Tomek	+2.6% F1-score	Enhances boundary precision by generating biologically relevant synthetic samples
Focal Loss	+1.3% F1-score +1.39 increase in ROC-AUC	Focuses learning on rare, hard to classify minority cases, improving sensitivity and precision
Threshold Calibration	–2.56% reduction in false positives +0.03% F1-score	Balances recall and specificity by optimizing decision threshold
Rule-Based Override	+0.9% increase in recall	Captures critical edge cases through deterministic domain logic, ensuring zero false negatives

Threshold calibration, which replaces the default decision threshold of 0.5 with a value optimized using geometric mean maximization of sensitivity and specificity, helped reduce false positives by 2.56%. Although this component contributed a relatively modest +0.03% improvement in F1-score, its practical impact is significant. In aquaculture operations, unnecessary interventions due to false alarms may disrupt system stability and increase maintenance costs. This calibration step thus balances the trade-off between alert sensitivity and operational precision, reinforcing the system's reliability in real-world deployments.

The rule-based override mechanism contributed a +0.9% increase in recall, playing a pivotal role in ensuring zero false negatives during validation. This layer applies deterministic domain logic, overriding statistical outputs when high-risk biological indicators such as mortality presence or extreme TDS levels are observed. While it did not significantly alter core performance metrics, it provides a safety net that catches borderline cases, thereby adding a layer of fail-safe logic critical for mission-critical decision systems in live pond management. These results emphasize that the strength of the CA-TCN lies not in any single enhancement, but in the synergistic integration of domain-informed components across the data preprocessing, learning, and decision layers. The architecture's use of causal and dilated convolutions enables the model to handle both short-term fluctuations and long-range dependencies, making it robust across different environmental rhythms whether changes in water quality occur abruptly or gradually.

Nevertheless, the current study has limitations. The dataset was sourced from a single biofloc pond system, limiting the model's generalizability to broader aquaculture environments with different species, management protocols, and water quality dynamics. Additionally, the biological thresholds used in the rule override system were manually defined and static, which, while effective in the present context, may need re-calibration or adaptive learning when deployed in heterogeneous operational settings. Furthermore, although the model demonstrates high performance, it currently lacks built-in interpretability, which may pose challenges for field operators who require transparency in decision support.

The CA-TCN presents a highly effective and biologically aligned solution for precision aquaculture. Its ability to anticipate intervention needs with high accuracy, minimal false negatives, and domain-aligned decision logic makes it a promising foundation for smart aquaculture systems. Furthermore, the model's architecture, which combines causal dilated convolutions with contextual imbalance handling, offers scalability for deployment in resource-constrained settings. By bridging the gap between machine learning performance and biological realism, the proposed model advances not only statistical prediction but also operational trustworthiness, offering a viable blueprint for autonomous water quality management in biofloc ecosystems and beyond.

Conclusion

This study introduces a robust and biologically aligned framework for predicting water replacement events in catfish biofloc pond systems by developing a Context-Aware Temporal Convolutional Network (CA-TCN). The model leverages the representational power of Temporal Convolutional Networks (TCNs) to learn from multivariate time-series data, while integrating domain-informed mechanisms that address the complexities of class imbalance and operational relevance. These enhancements include biologically filtered SMOTE+Tomek resampling, Focal Loss for hard-minority emphasis, threshold calibration to optimize decision boundaries, and a rule-based override layer grounded in aquaculture-specific safety conditions such as elevated TDS or observed mortality. Comprehensive evaluations including ablation studies and comparative benchmarks against widely used imbalance-handling methods such as SMOTE only, Tomek only, and SMOTE+ENN demonstrated the superiority of CA-TCN in both statistical accuracy and domain utility. The model achieved an F1-score of 0.9867, perfect recall (1.0000) for minority class prediction, and a near-perfect ROC-AUC of 1.0000, confirming its efficacy in detecting rare but critical water replacement events without incurring false negatives.

Compared to baseline models, CA-TCN yielded a 2.67% improvement in F1-score over SMOTE only and 12.57% over SMOTE+ENN, validating the cumulative benefits of the proposed enhancements. Importantly, each architectural component contributed distinct advantages context-aware resampling improved boundary realism (+2.6% F1), Focal Loss enhanced sensitivity (+1.3% F1), threshold tuning reduced false positives (–2.56%), and rule overrides ensured domain-aligned fail safes (+0.9% recall). The scientific contributions of this study are twofold. First, it demonstrates that embedding biological logic into both the data augmentation and decision stages of a machine learning pipeline can lead to models that are not only statistically superior but also operationally trustworthy. Second, it confirms that dilated causal convolutional architectures offer a scalable and efficient alternative to recurrent models in processing temporally structured aquaculture data, especially under class imbalance. These findings pave the way toward deploying AI-driven water quality management systems that are both biologically informed and practically reliable, supporting the broader goal of sustainable aquaculture intensification.

Future research should explore several promising directions. First, expanding the dataset to include diverse pond systems and fish species will be essential for evaluating the model's scalability and robustness across heterogeneous aquaculture environments. Second, adaptive rule learning potentially through reinforcement learning or meta-learning frameworks could replace static biological thresholds with self-updating logic that evolves with real-time feedback. Finally, real-world deployment within an IoT-enabled infrastructure would allow the model to operate in real-time, guiding automated or semi-automated water management decisions as part of an intelligent aquaculture system.

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Author's Contributions

Author 1 designed and conceptualized the study, coordinated research activities, collected and analyzed data, conducted the literature review, interpreted the results, and prepared the manuscript.

Author 2 contributed to data interpretation, critically reviewed the manuscript, and provided key insights for the discussion.

Author 3 guided model performance and statistical analysis, interpreted data, and critically reviewed the manuscript, offering important input for the discussion section.

Ethics

This research study was conducted in accordance with the ethical principles outlined by Ministry of Higher Education, Science, and Technology of the Republic of Indonesia and in compliance with relevant international regulations. The authors declare that there is no conflict of interest that could have influenced the conduct or reporting of this research.

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