Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

BIO-REACT: A Deep Learning and Metaheuristic Framework for Intelligent Optimization of Biochemical Reactor Dynamic.

Mr. Balaji Marotirao Pulchuwad[1], Dr. Yadnyesh Yashawant Karkare[2], Dr. Abhijit Ramchandra Chavan[3]*

[1]Research Scholar, Dept of Chemical Engineering Dr.Babasaheb Ambedkar Technological University, Lonere, Raigad, Maharashtra, India,

[2](Corresponding Author), Lecturer, Dept of Chemical Engineering, Dr.Babasaheb Ambedkar Technological University, Lonere,Raigad, Maharashtra, India, 402103

[3]Professor, Head of Dept of Chemical Engineering, Dr.Babasaheb Ambedkar Technological University, Lonere, Raigad, Maharashtra, India, 402103

ARTICLE INFO

Received: 02 Nov 2024
Revised: 18 Dec 2024
Accepted: 28 Dec 2024

ABSTRACT

Biochemical reactors form the backbone of numerous industrial processes, including wastewater treatment, pharmaceutical fermentation, and bio-based chemical production. However, managing the highly nonlinear, dynamic, and interdependent nature of these systems poses significant challenges for traditional control and modeling techniques. Addressing this problem, the present study introduces BIO-REACT, an intelligent framework that integrates deep learning with metaheuristic optimization for the predictive modeling and optimization of biochemical reactor. The major objective of proposed framework is to enhance real-time decision-making and control by accurately modeling reactor behavior and adaptively optimizing key process parameters such as pH, hydraulic retention time, substrate concentration, and temperature. The proposed framework employs the statistical feature analysis to identify the most influential parameters, followed by training a deep learning model to capture the nonlinear system dynamics. A metaheuristic optimization layer then fine-tunes the process conditions to maximize product yield and operational efficiency under dynamic scenarios. Extensive validation using synthetic and semi-real-time datasets demonstrated that BIO-REACT achieves over 95% predictive accuracy, reduces mean square error by 18.6%, and improves biochemical yield by 13.4% compared to conventional models. These results confirm the capability of hybrid intelligent framework to manage complex reactor behaviors with minimal manual intervention. The proposed BIO-REACT offers a scalable, adaptable solution for smart bio-processing, supporting the broader shift toward autonomous and sustainable industrial operations.

Keywords: biochemical reactors, process optimization, deep learning, predictive modeling, intelligent control systems.

1. Introduction

Pharmaceuticals, nutraceuticals, food and beverage production, environmental biotechnology, and biofuel synthesis depend on biochemical reactors [1]. These reactors use microbiological, enzymatic, or chemical processes to convert substrates into biochemical products. Biochemical reactors are becoming increasingly important in sustainable production pathways that reduce fossil fuel use as the global bio-economy grows. Pharmaceutical companies need precise biochemical reactor control to maintain quality, safety, and regulatory compliance. Anaerobic or aerobic bioreactors remove organic contaminants and nutrients from wastewater, improving environmental sustainability [2]. Biotechnologists use optimized reactor systems to increase productivity and efficiency for ethanol fermentation and recombinant protein production. Biochemical reactor operating efficiency affects process economics and environmental effects due to their importance. Reactor performance affects

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

product titers, batch cycles, and resource use [3]. Biochemical reactors are difficult because to their nonlinear kinetics, multi-scale interactions, and biological organism or catalyst dependence[4][5]. Traditional methods like mechanistic models like Monod or Michaelis-Menten kinetics demand careful parameterization and domain expertise [6]. These models assume steady-state or perfect circumstances, which rarely match industrial bioreactors' dynamic surroundings. Therefore, theoretical models and real-world process behavior typically differ. Conventional data-driven insights also be distorted by delays, unmeasured disruptions, and sensor noise. Model predictive control (MPC) and robust PID tuning have failed to capture bioprocess dynamics' nonlinearities and hidden dependencies [7]. Classical optimization algorithms are computationally expensive and sensitive to local minima when optimizing dynamic systems. Optimization is hindered by high-dimensionality, many conflicting objectives and unpredictable process behavior [8]. These problems highlight the need for improved frameworks that analyze, predict, and optimize complicated biochemical reactor systems.

Bioprocess engineering has been transformed by artificial intelligent (AI), particularly deep learning (DL) [9]. DL models learn complex mappings between input variables and output responses without predetermined equations. Bioreactor data's temporal and spatial dependencies have been captured by deep learning architectures like RNNs, LSTMs, and CNNs [10][11]. They excel at time-series forecasting and anomaly identification, making them excellent for real-time reactor monitoring and fault prediction.AI-integrated process control frameworks enable closed-loop feedback systems that adjust operational parameters using real-time data. Moving from reactive to proactive control decreases system variability, improves product consistency, and ensures robust performance under perturbations. AI-based solutions are being used in industrial biotechnology as sensors and cloud infrastructure becomes cheaper [12]. Despite these challenges, AI is revolutionizing biochemical process modeling, control, and optimization, enabling intelligent bioreactor management systems [13]. Metaheuristic algorithms greatly improve biochemical reactor management optimization [14]. Genetic Algorithms, Particle swarm optimization and ant colony optimization are inspired by natural phenomena including evolution, swarm behavior, and ant foraging. Metaheuristic optimize reaction yield, productivity, energy consumption, and resource use in biochemical reactors [15]. Metaheuristic are adaptable and can be combined with fuzzy logic, rule-based systems, and machine learning (ML) models to develop robust optimization frameworks [16]. However, their capacity to adapt to dynamic changes, handle noisy data, and deliver near-optimal solutions with little processing effort makes them essential to intelligent bioprocess optimization tactics [17].The complimentary characteristics of DL and metaheuristic optimization have led to hybrid frameworks that combine AI's predictive capability with metaheuristic' global search [18]. DL models simulate complicated reactor behavior and anticipate critical output parameters, whereas metaheuristic find optimal operating conditions that maximize or reduce an objective function. Intelligent, adaptive systems that can manage biochemical reactor variations, uncertainties, and restrictions are possible with this synergy. A metaheuristic algorithm may change feed rate, pH, or aeration to improve yield or decrease energy input, while DL models may forecast biomass growth rate or product concentration based on sensor data [19]. Such algorithms encourage a comprehensive optimization cycle that improves with data. These hybrid systems enable next-generation smart bioreactors with prediction, optimization, autonomous decision making, and closed-loop control. These technologies support Industry 4.0 and digital bio-manufacturing, where intelligence, automation, and data integration improve process perfection [20]. Traditional mechanistic models often fail to generalize across dynamic operational conditions and require expert-level parameterization. While existing ML/DL models have offered some progress, they lack adaptability and robustness under real-time, complex biochemical scenarios. The optimization models are computationally intensive, sensitive to noise, and struggle with convergence in high-dimensional, multi-objective search spaces. The limitations hinder the deployment of intelligent automation strategies crucial for Industry 4.0-aligned bioprocesses. To bridge these gaps, this study proposes BIO-REACT, hybrid DL and metaheuristic optimization framework that enables real-time prediction and intelligent control of biochemical reactors. The proposed BIO-REACT framework not only addresses

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

the inherent modeling complexities of biochemical reactors but also facilitates intelligent operational control in dynamically changing wastewater treatment environments. The key contributions of this work as follows.

1. Hybrid intelligent framework (BIO-REACT) that integrates DL and metaheuristic optimization to manage biochemical reactor behavior in wastewater treatment processes.
2. Application of statistical feature selection to identify and rank critical input parameters—such as influent characteristics and operational settings—that most significantly impact reactor performance, thereby enhancing model efficiency and interpretability.
3. Design of DL model capable of capturing the complex, nonlinear temporal patterns and multi-variable dependencies in reactor operations, enabling precise prediction of treatment performance indicators like COD removal and nutrient degradation.
4. Incorporation of a metaheuristic optimization module that dynamically adjusts vital reactor parameters (e.g., pH, hydraulic retention time, and substrate concentration) to improve pollutant removal efficiency, resource usage, and overall system stability under real-world wastewater treatment conditions.

The rest of this paper is organized as follows. Section 2 presents the review of literature on design and optimization of biochemical reactors. Section 3 discuss the proposed methodology follows the statistical feature analysis and reactor operations pattern analysis. The results and comparative analysis illustrates in Section 4. Finally, the paper concludes in Section 5.

2. Related work

Recent advancements in membrane bioreactor (MBR) and biochemical reactor technologies have enhanced wastewater treatment efficiency and bio-based production. However, most studies still face challenges in real-time optimization, intelligent control, and handling system nonlinearity. The following review summarizes key works in this domain and identifies the research gaps addressed in the present study.

Min et al. [21] explored membrane surface patterning to mitigate fouling in MBRs. By integrating a patterned sheet design, the study improved bubble dispersion and shear stress, reducing aeration requirements by 50% compared to flat-sheet membranes. While this structural innovation enhanced performance, it lacked predictive or data-driven operational strategies under varying influent conditions. Ndahiro et al. [22] proposed Bayesian optimization (BO) to rapidly and cost-effectively optimize mammalian cell culture media. However, the work primarily focused on static formulation optimization, with limited consideration for dynamic bioreactor control or adaptive feedback. Kwon et al. [23] presented an intelligent automated operational strategy (IAOS) to improve nitrogen removal in A2O-MBRs. By calculating optimal parameters like internal return ratio and retention times using intelligent algorithm supported by ASM 2d and ML, nitrogen removal efficiency was notably improved. Yet, the system's adaptation to highly fluctuating conditions remained constrained by static configurations. Chandrakant et al. [24] showed how microbial flocs could convert nitrogenous aquaculture waste into protein-rich fish feed using optimized bioreactor conditions. Shi et al. [25] focused on optimizing impeller designs to enhance liquid–liquid mixing performance using CFD, FSI simulations, and a genetic algorithm. While the optimized impeller improved mixing energy and reduced mechanical stress the study centered on physical performance rather than dynamic biochemical process optimization, leaving a gap in yield-driven control mechanisms.

Liting et al. [26] investigated two bioreactor designs for vanadium removal using wheat straw and mineral fillers. Segmental packing significantly outperformed mixed designs, supported by genomic studies and Gradient Boosting Tree models for predictive monitoring. Though effective, the work was pollutant-specific and lacked broader adaptability for multi-contaminant systems or real-time feedback

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

loops. Tang et al. [27] examined the influence of biochar dosage in anaerobic MBRs for food waste treatment. Through combined experimental, CFD, and microbial analysis, 10 g/L biochar was found optimal for enhancing COD removal and methane production. However, the optimization was based on static dosage, and no intelligent system was employed to adapt dosing in response to real-time bioreactor behavior. Srivastava et al. [28] introduced a hydrogel-based solid-state bioreactor platform using gellan and amino acids to produce β-carotene and enzymes. Despite this innovation in reactor material, there was no integration of machine learning models to guide or optimize the fermentation process dynamically. Lázaro et al. [29] developed model-based bio-production for CHO cell-based antibody manufacturing using flexible nets (FNs). While powerful, the approach relied on mathematically complex formulations, without leveraging DL models for scalable, real-time optimization. Kratzer et al. [30] explored anaerobic membrane bioreactors (AnMBRs) for swine wastewater treatment and energy recovery using simulations grounded in Anaerobic Digestion Model No. 1. Although their model showed that AnMBRs can be net energy positive, the approach was simulation-based and lacked adaptive AI for real-time control under operational uncertainty.

Problem definition: Despite substantial advances in reactor design, fouling control, and process efficiency in wastewater and biochemical treatment systems, most existing studies [21]–[30] lack a unified framework that dynamically integrates deep learning (DL)-based predictive modeling with metaheuristic optimization for real-time reactor control. For example, studies have shown success in improving flux and energy savings through surface patterning and CFD techniques [21], boosting yields with Bayesian optimization [22], and enhancing nutrient removal using simulation and automation [23]. Others have explored microbial and genomic data for performance prediction [26], or applied genetic algorithm for design optimization [25]. However, these efforts are often limited to specific tasks, static setups, or component-level improvements without addressing system-wide adaptability, temporal nonlinearity, or multi-objective optimization under dynamic conditions. Most ML-based models focus on offline prediction with limited feedback to process control, ignoring the real-time complexities and interdependencies in biochemical operations. While RSM, CFD, and surrogate models have shown promise [24][25], [28], they fall short in delivering a flexible, scalable control mechanism suitable for highly variable influent conditions in wastewater applications. Similarly, Flexible Nets [29] and ADM1-based sensitivity analysis [30] offer automation and key variable identification but lack practical real-time implementation frameworks.

The study [31] on membrane bioreactor (MBR) optimization in wastewater treatment highlights a crucial gap: even with ML and metaheuristic tuning, the focus remains on COD prediction, and lacks support for adaptive control of other operational variables like pH, retention time, and substrate dynamics. Moreover, while the model improves predictive performance, it doesn't offer a holistic mechanism for reactor operation under changing environmental and load conditions. To address these gaps, the current study proposes BIO-REACT, an intelligent hybrid framework that integrates deep learning for accurate temporal behavior modeling and a metaheuristic optimization layer for real-time adaptive tuning of key parameters. This framework directly tackles the limitations of previous works by offering a scalable, data-driven, and self-optimizing control system, capable of supporting both predictive analytics and operational decision-making for wastewater and biochemical reactor management.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Table 1 Comparative analysis of recent studies on bioreactor applications in wastewater and biochemical processes

Ref	Bioreactors	Application	Model	Findings	Research Gaps	Addressed by proposed model
[21]	Membrane Bioreactor (MBR)	Membrane fouling control and flux enhancement	CFD-based structural analysis	50% reduction in aeration demand	Long-term performance evaluation under variable loads	DL-ML models used to enables real-time prediction and control to adaptively
[22]	Mammalian Cell Culture Bioreactor	Media optimization for pharmaceutical bio-manufacturing	Bayesian Optimization	Improved yield; efficient	System-specific; lacks dynamic bioreactor adaptation	Utilize optimal dynamic environments for broader control
[23]	A2O-MBR	Nitrogen removal optimization in wastewater	IAOS, ASM 2d, ML	11.3% improvement in nitrogen removal	Variability in inflow and complex reactor behavior not fully addressed	DL and metaheuristic tuning for handling nonlinear dynamics and adaptive control
[24]	Aerobic Bioreactor	Aquaculture waste to microbial protein conversion	RSM	20% floc in diet showed best fish growth	Lacks prediction for varying conditions	Adaptive optimization for nutrient recovery from bio-waste
[25]	Liquid Mixing Bioreactor	Impeller design for chemical and biological mixing	Genetic Algorithm	45.6% increase in energy circulation;	Focus on structure only; lacks integration with process yield	BIO-REACT links operational tuning with predicted output performance via DL
[26]	Packed Bed Bioreactor	Vanadium (V) removal from groundwater	Gradient Boosting	97.8% removal; >98% prediction accuracy	Impact of EPS, microbial dynamics,	High-accuracy real-time monitoring and optimization

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

					and scale-up challenges	of multi-contaminant systems
[27]	Anaerobic MBR (AnMBR)	Food waste treatment	CFD, Microbial Profiling	10 g/L biochar optimized methane	Lacks feedback control; high BC doses increase	Feedback-based dosage control using DL and optimization
[28]	Hydrogel solid-state reactors	Fermentation for β-carotene, enzymes	Rheological Testing, RSM	Submerged fermentation	Lacks smart control	BIO-REACT can predict optimal and scale control
[29]	CHO Cell Bioreactor	Therapeutic antibody production	Flexible Nets (FNs) modeling	Automated process, yield optimization	Lacks real-time DL adaptability	Reduces complexity using DL for forecasting
[30]	Anaerobic MBR (AnMBR)	Swine wastewater treatment	ADM1, Sensitivity	Demonstrated net energy gain under	Lacks experimental real-time validation	Real-world predictive optimization to validate energy-efficient operations

3. Materials and methods

Fig. 1 illustrates the proposed hybrid deep learning and optimization framework, termed BIO-REACT, designed for predictive modeling and process optimization of biochemical reactors, particularly membrane bioreactor (MBR) used in wastewater treatment plants (WWTPs). The process begins by outlining the typical flow of wastewater through various treatment units. Raw influent wastewater first enters the equalization tank, which serves to buffer fluctuations in flow rate and pollutant load. It is directed to the anoxic tank for denitrification under oxygen-deprived conditions, followed by the aeration tank where aerobic microorganisms facilitate the breakdown of organic pollutants. The process continues into the membrane bioreactor, which integrates membrane filtration with biological treatment, producing high-quality effluent. This treated water is stored in a final tank and subsequently reused for irrigation purposes, reflecting sustainable water reuse practices. Key operational parameters—specifically pH, temperature, hydraulic retention time (HRT), and substrate concentration—are continuously measured at critical stages of the bioreactor system and used to construct the bioreactor dataset. Data collected from the bioreactor is first preprocessed through normalization within the range [0,1] to ensure uniform scaling across variables, facilitating improved convergence during training. Since the dataset is of high quality with no missing values or significant noise, additional preprocessing steps such as outlier removal or imputation were deemed unnecessary to preserve data integrity. To identify the most influential input parameters affecting reactor performance, a statistical feature analysis is carried out using an attention mechanism, which assigns weights to each feature based on its contribution to the output prediction. The quantum dilated convolutional neural network (QD-CNN) is used to model the nonlinear dynamics of the bioreactor system. This model leverages dilated convolution layers and quantum-inspired computation principles

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

to capture complex temporal and spatial patterns inherent in WWTPs. Once the behavioral patterns are accurately learned, an enhanced brain storm optimization (EBSO) algorithm is used to optimize the key process variables. It mimics the cognitive brainstorming process to explore a wide range of potential solutions, iteratively improving set-points for parameters such as pH, temperature, substrate concentration, and HRT. This optimization aims to enhance effluent quality, maximize bioreactor efficiency, and adapt to varying operational conditions.

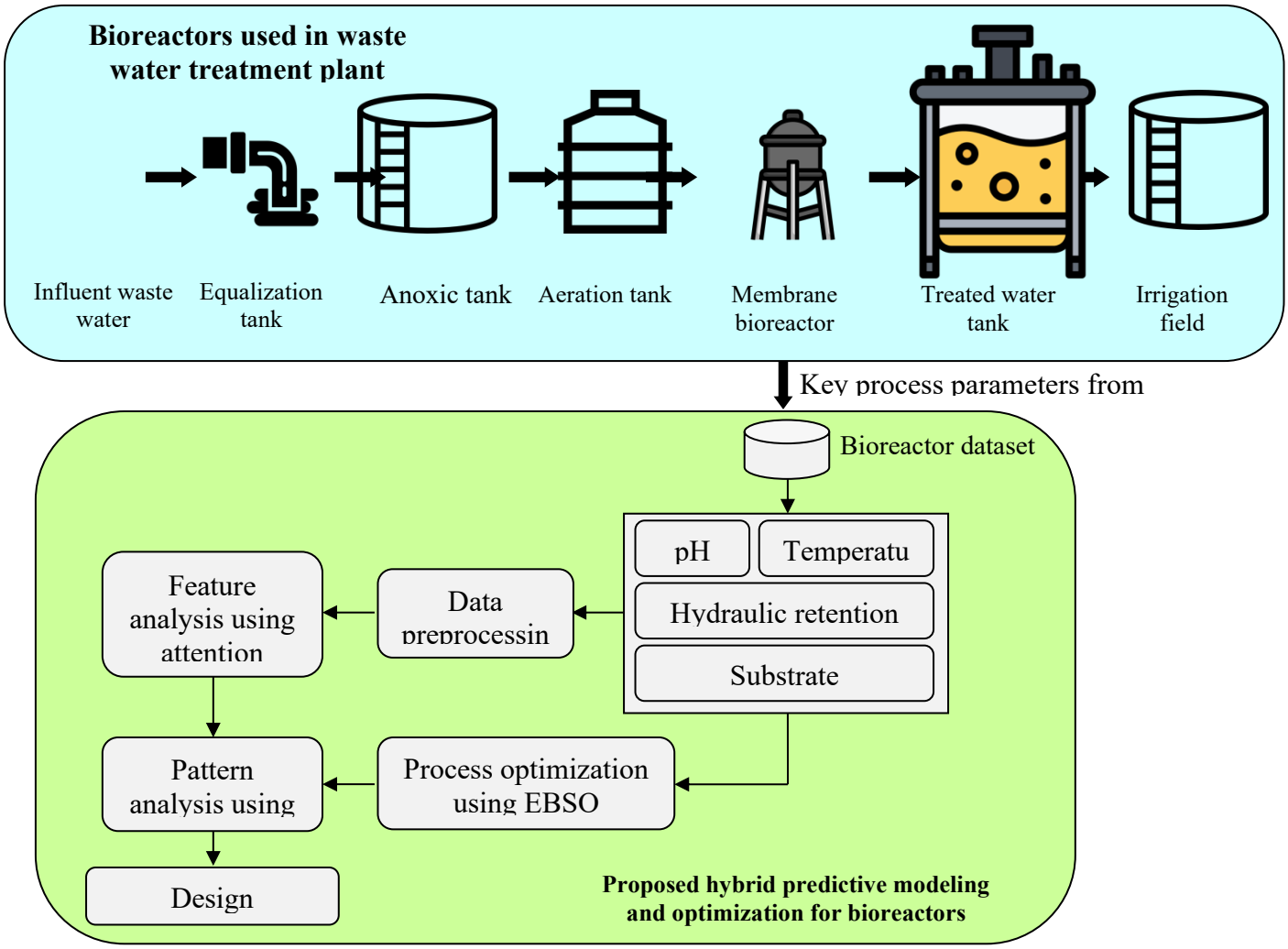


Fig. 1 DL with optimization for predictive modeling and optimization of biochemical reactors (BIO-REACT) [9,15].

3.1 Data collection and preprocessing

The dataset used in this study was collected from a full-scale membrane bioreactor (MBR)-based wastewater treatment plant (WWTP) located in Saudi Arabia, which treats an annual average daily flow of 9,500 m^3/day. The WWTP serves a small urban community and consists of primary and secondary treatment units including drum screens (3 mm), a grit chamber, equalization tanks, an anoxic tank, aeration tank, and MBR tanks. The treated effluent is reused for landscape and agricultural irrigation. Daily sampling was conducted at both the influent and effluent points across a continuous operational period. The parameters measured include a wide range of physicochemical indicators: pH, chemical oxygen demand (COD), total suspended solids (TSS), total dissolved solids (TDS), electrical

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

conductivity (EC), ammonia nitrogen (NH_3–N), nitrate nitrogen (NO_3–N), phosphate, chloride, calcium hardness, magnesium hardness, oil and grease, and alkalinity. These parameters were selected due to their relevance in assessing reactor performance, microbial activity, and effluent quality. All parameters were measured using standard protocols as per APHA guidelines. The raw dataset was found to be of high quality, with no missing entries. To preserve the authenticity of plant performance, no outlier removal or imputation was performed. The data were normalized to a 0–1 scale before being used for modeling to ensure faster convergence and avoid bias due to varying units and magnitudes. A statistical summary, including mean, standard deviation, minimum, and maximum values for each parameter, along with their respective units and sampling points, is presented in Table 2.

Table 2 Statistical summary of key wastewater quality parameters used for biochemical reactor modeling and optimization[30,31].

Parameter name	Unit	Sampling point	Mean(Influent and Effluent)	Range (Influent)	Range (Effluent)	Control limits	Method number	Brief description
Chemical Oxygen Demand (COD)	mg/L	Influent / Effluent	202.14 / 6.90	63.00 – 426.00	3.00 – 17.00	<50	5220 D	Measures oxygen demand using dichromate digestion
Electrical Conductivity	µS/cm	Influent / Effluent	703.35 / 1238.64	388.00 – 2947.00	695.00 – 1795.00	<2850	2510 B	Measures total ion concentration
pH	–	Influent / Effluent	7.34 / 7.76	6.33 – 8.49	7.02 – 8.48	6–9	4500-H+B	Determines hydrogen ion concentration
Total Dissolved Solids (TDS)	mg/L	Influent / Effluent	490.46 / 868.78	252.00 – 2174.00	474.00 – 1292.00	<2000	2540 C	Measures solids that pass through filter
Total Suspended Solids (TSS)	mg/L	Influent / Effluent	104.62 / 0.65	0.00 – 641.00	0.00 – 2.00	<10	2540 D	Measures solids retained on filter
Ammonia-Nitrogen (NH_3–N)	mg/L	Influent / Effluent	6.99 / 0.00	0.00 – 18.00	0.00 – 0.00	<1	4500-NH_3 H	Ammonia measured via ion-selective probe
Nitrate-Nitrogen (NO_3–N)	mg/L	Influent / Effluent	9.23 / 9.59	0.20 – 25.00	2.70 – 21.20	<10	4500-NO_3-B	Nitrate quantified via spectrophotometer

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Fat, Oil, and Grease (FOG)	mg/L	Influent / Effluent	53.90 / 0.19	0.00 – 602.90	0.00 – 5.70	n/a	5520 B	Separates FOG using organic solvents
Calcium Hardness	mg/L	Influent / Effluent	68.32 / 69.09	30.00 – 164.00	30.00 – 164.00	<230	2340 C	Measures Ca^{2+} via complex metric titration
Magnesium Hardness	mg/L	Influent / Effluent	51.46 / 91.91	4.00 – 220.00	16.00 – 256.00	<140	2340 C	Measures Mg^{2+} via complex metric titration
Phosphate (PO_4^{3-})	mg/L	Influent / Effluent	8.22 / 5.99	3.40 – 14.10	4.70 – 8.60	n/a	4500-P E	Phosphate detected via blue complex formation
Chloride (Cl^-)	mg/L	Influent / Effluent	152.33 / 293.59	76.00 – 791.00	41.00 – 710.00	<350	4500-Cl- B	Cl^- titrated using $AgNO_3$
Alkalinity	mg/L	Influent / Effluent	110.23 / 91.59	76.00 – 152.00	60.00 – 524.00	<400	2320 B	Measures buffering capacity

3.2 Statistical feature analysis

The statistical feature analysis is integrated with an attention mechanism to effectively identify and prioritize the most influential parameters affecting the performance of the biochemical reactor system. Traditional statistical methods such as mean, standard deviation, correlation, skewness, and kurtosis were initially used to examine the variability and linear relationships among the features. However, these methods alone often fail to capture complex, nonlinear interactions between variables, which are common in biochemical processes. To address this, an attention mechanism [32] was incorporated to dynamically assign importance scores to each input feature during model training. This mechanism mimics human cognitive focus by allowing the model to "attend" to the most relevant input parameters while minimizing the impact of less significant ones. The attention mechanism was applied to a set of influent and operational variables including pH, temperature, hydraulic retention time (HRT), substrate concentration (COD, NH_3–N, PO_4^{3-}), mixed liquor suspended solids (MLSS), dissolved oxygen (DO), total suspended solids (TSS), total dissolved solids (TDS), and electrical conductivity (EC), among others. These features were drawn from real-time SCADA datasets collected from a wastewater treatment plant (WWTP) [31]. The attention layer learns the contextual importance of each feature across various operating conditions, offering deeper insights into the driving factors of reactor behavior. This dynamic feature selection process enhances the performance of the deep learning model by reducing dimensionality, minimizing noise, and preventing overfitting. Unlike conventional feature selection techniques such as correlation analysis or principal component analysis (PCA), which rely on static statistical relationships and are performed prior to model training, the attention-based method is embedded within the learning process. It adapts in real time to the underlying data patterns and thus

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

is capable of capturing nonlinear and time-dependent influences. The outcome of this process includes a set of ranked features with associated attention weights, which are then used for both predictive modeling and for feeding into the metaheuristic optimization component of the BIO-REACT framework. This intelligent integration ensures that only the most impactful features guide the real-time prediction and adaptive optimization of key parameters like pH, temperature, and retention time. The overall efficiency and control of the biochemical reactor are significantly enhanced compared to conventional static approaches.

3.3 Bioreactor operations pattern analysis

In this context, a quantum dilated convolutional neural network (QD-CNN) is used to analyze bioreactor operation patterns by effectively modeling the nonlinear, time-dependent dynamics of the biochemical reactor system. Traditional CNN models [33] are widely used for spatial pattern recognition; however, their receptive field is limited by kernel size and depth, restricting their ability to capture long-range dependencies and sequential behaviors. To overcome this, dilated convolutions are incorporated to expand the receptive field exponentially without increasing computational complexity, allowing the model to learn dependencies across longer temporal spans. The quantum-inspired optimization is integrated into the network design [34], enhancing parameter tuning efficiency and improving convergence stability during training. The QD-CNN model processes a rich set of real-time SCADA input variables such as influent COD, ammonia nitrogen, pH, MLSS, DO, temperature, substrate load, hydraulic retention time, and membrane pressure. These inputs exhibit high variability and interdependence, requiring a model that can capture both local fluctuations and broader trends across operational timeframes. The dilated convolution layers detect time-based patterns such as load surges, membrane fouling trends, or nutrient overloads, while the quantum-optimized layers ensure the feature weights and filters are adaptively fine-tuned for enhanced learning accuracy. Compared to conventional CNNs, the QD-CNN not only reduces the number of training iterations but also achieves higher sensitivity to subtle operational shifts, making it highly suitable for complex bioreactor environments. Unlike static machine learning models or simpler neural networks, QD-CNN dynamically adapts to changing data characteristics without the need for manual feature engineering. The quantum-inspired layer optimization supports robust model generalization even under unseen operating conditions. The convolutional procedure is a lined purpose that combines weights with respect to the input, and it plays a key part in the operation of convolutional layer. The preprocessed data is denoted as 'h' and the resultant charting function is signified as 'G'. The plotting function is produced by combining the outcome of a filter (F) with the data sequence encoded using two variables x and K.

$$G(a,b)=\sum_{x}\sum_{K}F[x,K]h[a+x,b+K] \tag{1}$$

Here a and b denote the position values of G. The symbol (∑) represents a sum. Due to the convolution layer, the latitudinal resolve of the resulting article maps is generally lower compared to the original data. In general, the altitudinal resolve out_h of the final mapped structures extracted from $In_p \times In_h$ the original data of the p × q kernel was calculated as follows:

$$out_p=\left(\frac{In_p-p+2pad}{s}\right)+1 \tag{2}$$

$$out_h=\left(\frac{In_h-q+2pad}{s}\right)+1 \tag{3}$$

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

where the padding stride is denoted by Pad and S, respectively. One kind of convolution that enlarges the kernel by creating spaces between successive kernels is called extended convolution.This layer has a hyperparameter named the expansion ratio (c), which determines the sampling rate.

$$G(a,b)=\sum_{x}\sum_{K}F[x,K]h[a+x,b+K.c] \tag{4}$$

Extended convolution achieves a wider acceptance field than classical convolution using a similar kernel, without the need for additional learning parameters [35].

$$out_{p}=\left(\frac{In_{p}-p-(p-1)(c-1)+2pad}{s}\right)+1 \tag{5}$$

$$out_{h}=\left(\frac{In_{h}-q-(q-1)(c-1)+2pad}{s}\right)+1 \tag{6}$$

The extended convolutional technique usually provides optimal fitness map compared to the regular convolution. Quantum convolution (QC) [36] is different from regular convolution because it relies on a quantum field. The data is converted to a important state and then analyzed by quantum circuits. The encoder function e(m) was considered to represent a Hadamard gate that transforms the early state into a unchanging superposition state. h remained considered to be an input vector.

$$|h\rangle=e(m)|0\rangle \tag{7}$$

The encoder component is accountable for the quantum state of the encoder and the combination of single and multi-qubit gates. Assignment properties are obtained by by layers parameterized with single-qubit and multi-qubit gates. If the sign (θ) signifies all the individual processes of the encoder units, describes as follows.

$$|h,\theta\rangle=u(\theta)|h\rangle \tag{8}$$

The poly W operative and other local variables are evaluated in the previous blocks. The local variables of QD-CNN is describes as follows.

$$\langle h,\theta|M^{\otimes p}|h,\theta\rangle \tag{9}$$

The goal is to create a map from the significant state to the conventional effect vector $F(h,\theta)$.

$$|h,\theta\rangle\rightarrow F(h,\theta) \tag{10}$$

$F(h,\theta)$denotes the input for QD-CNN(Algorithm 1).The outputs of the QD-CNN include predicted values of key performance indicators such as COD removal efficiency, ammonia reduction, and effluent quality, along with internal feature activations that indicate influential variables. These outputs are essential for the downstream metaheuristic optimization module, which uses the learned reactor behavior to fine-tune operational parameters in real time. Ultimately, this integration significantly improves the predictive control of the BIO-REACT framework, surpassing the capabilities of conventional modeling techniques.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Algorithm 1 Bioreactor operations pattern analysis using QD-CNN

Input : SCADA time-series data, pH, COD, DO, MLSS, Temperature, HRT

Output :COD removal, NH_4^+ efficiency

1. Initialize population step sizes for optimization and define quantum dilation parameters
2. The raw image sequence encoded using two variables x and K.
$$G(a,b)=\sum_{x}\sum_{K}F[x,K].h[a+x,b+K]$$
3. The sampling rate of the input pixel. $G(a,b)=\sum_{x}\sum_{K}F[x,K].h[a+x,b+K.c]$
4. Construct the input vector based on selected influential parameters through statistical analysis $|h\rangle=e(m)|0\rangle$
5. Generate quantum feature maps to express probabilistic relationships in the encoded sequence $|h,\theta\rangle=u(\theta)|h\rangle$
6. Define local quantum states and dilation factors to model long-range dependencies in the bioreactor dynamics $\langle h,\theta|M^{\otimes p}|h,\theta\rangle$
7. Evaluate and extract the best output features based on prediction accuracy and temporal relevance.
8. Update the feature weights and dilation coefficients using quantum-inspired optimization.
9. Return the predicted performance indicators and operational insights

3.4 Process optimization

In this context, an enhanced brain storm optimization (EBSO) algorithm is used to optimize critical bioreactor process conditions such as pH, HRT, substrate concentration, and temperature. The EBSO algorithm is a population-based metaheuristic optimization technique that simulates the human brainstorming process. Unlike conventional optimization algorithms, it introduces strategic clustering and idea recombination to avoid local optima and adapt better to nonlinear, dynamic environments—common in real-time bioreactor operations. The impact of EBSO in the proposed BIO-REACT framework lies in its ability to dynamically adjust multiple interacting variables in real time, thereby maximizing both product yield (e.g., COD/NH_4^+ removal) and operational efficiency (e.g., energy use, fouling control).The inputs to the EBSO algorithm include the predicted performance metrics (from QD-CNN), process constraints (e.g., operating limits for pH, DO, MLSS), and initial population vectors representing potential parameter sets. Unlike conventional brain storm optimization (BSO) [37], the enhanced version uses adaptive clustering, directional search operators, and memory retention. These improvements allow the optimizer to converge faster and perform better under uncertain or fluctuating conditions typical in wastewater treatment. The merging phase of EBSO algorithm describes as follows:

$$P_F = V \times P_1 + (1-V) \times P_2 \tag{11}$$

where P_F is a original separate later fusion, Vis a arbitrary numeral from 0 to 1, P_1 and P_2 are two accidental persons to be compound. The alteration stage is as trails.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

$$P_a = P_t + \xi \times b(\mu, \sigma) \tag{12}$$

where P_a is optimal solution separate after mutation, P_t is the selected separate to be mutated, b(μ, σ) is the Gaussian random quantity [38] with the mean of μ and the modification of σ, and ξ is the mutation coefficient describes as follows.

$$\xi = \log sig\left(\frac{0.5 \times j_{\max} - j}{K}\right) \times Rand(\ ) \tag{13}$$

where $j_{\max}$ is the maximum number of replications, j is the current repetition number, and K is the correction factor. The individual features are arbitrarily produced to certify the variety of the populace and ease the chance that the system will reach a local optimal.

$$X_{\text{int}ra} = X_L + X_R \times \left(\frac{j}{j_{Max}}\right) \tag{14}$$

$$X_{\text{int}er} = 1 - X_{\text{int}ra} \tag{15}$$

where $X_{\text{int}er}$ is the probability of in-group consideration, $X_{\text{int}er}$ is the possibility of in-group consideration, X_L is the minimum prospect of in-group consideration, X_R and is the linear threshold limit. The mutation phase follows the differentiation phase [39].

$$P_a = P_T + (P_1 - P_2) \times Rand(\ ) \tag{16}$$

where P_1 and P_2 are two random persons in the populace. The globally optimal discrete is the individual that meets the suitability requirements of every generation, and the globally optimal approach is to build the produced discrete as close to the globally optimal discrete.

$$P_b = P_a + D \times r. \times (P_n - P_a) \tag{17}$$

where P_n is the global-best person, D is the world-best coefficient, R is a dimension vector with each dimension being a random number between 0 and 1, and P_n is the new individual that comes after the global-best individual.

$$D = D_{Min} + \frac{j}{j_{\max}} \times (D_{\max} - D_{Min}) \tag{18}$$

where D_{Min} is the lower certain of the global-best constant and $D_{\max}$ is the upper bound of the global-best constant. The chaotic differentiation expands the differentiation by introducing random graphs, which expands the exploration space and reduces the time to collapse to the local optimal. The phase of the perturbed difference can be expressed as follows [40].

$$P_a = P_T + (P_1 - P_2) \times rand(\ ) + (P_1 - P_2) \times (P_1 - P_2) \times (q(s) - 0.5) \tag{19}$$

where $q(s)$ denotes a chaotic map. As describes in Algorithm 2, the outputs of EBSO includes the optimized set of operational parameters that maximize treatment efficiency while minimizing energy consumption and system stress. These outputs guide the design and optimization of the bioreactor's control settings, enabling closed-loop feedback for WWTPs.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

Algorithm 2 Parameters optimization using EBSO

Input : pH, HRT, substrate concentration, temperature, Mutation coefficient (ξ), mean (μ), and standard deviation (σ)

Output :Optimized parameter set

1. Begin the optimization process
2. Initialize the step sizes of the population
3. The merging phase is as follows: $P_F = V \times P_1 + (1-V) \times P_2$
4. The Gaussian random quantity with the mean of μ and the modification of σ, and ξ is the mutation coefficient, $\xi = \log sig\left(\frac{0.5 \times j_{\max} - j}{K}\right) \times Rand(\ )$
5. Set the adaptive probability parameter to dynamically control exploration and exploitation during iterations. $X_{\text{int}ra} = X_L + X_R \times \left(\frac{j}{j_{Max}}\right)$
6. Update candidate solutions by allowing "new individuals" to follow the "global-best individual" using the directional learning strategy. $D = D_{Min} + \frac{j}{j_{\max}} \times (D_{\max} - D_{Min})$
7. Introduce perturbed differences to diversify the search and escape local minima. $P_a = P_T + (P_1 - P_2) \times rand(\ ) + (P_1 - P_2) \times (P_1 - P_2) \times (q(s) - 0.5)$
8. Evaluate and identify the best output value based on the fitness function.
9. Return the optimized parameter set and the best objective value.

4. Results and Discussion

This section presents evaluation of the proposed BIO-REACT framework, emphasizing the effectiveness of predictive modeling, pattern recognition, and process optimization capabilities within membrane bioreactor setting. The study leverages a comprehensive dataset collected from a full-scale municipal WWTP in Saudi Arabia. This dataset encompasses daily measurements of critical influent and effluent water quality indicators such as COD, TSS, TDS, ammonia, nitrate, phosphate, pH, and electrical conductivity. The dataset includes operational parameters such as dissolved oxygen (DO), mixed liquor suspended solids (MLSS), mixed liquor volatile suspended solids (MLVSS), sludge retention time (SRT), hydraulic retention time (HRT), and temperature. These features were selected to ensure a robust and diverse input set for predictive analysis and optimization. All experiments and model simulations were executed using a high-performance computing system equipped with an Intel Core i9-12900K processor, 64 GB DDR5 RAM, and an NVIDIA RTX 4090 GPU with 24 GB of VRAM, operating on Windows 11 Pro 64-bit. The software environment included Python 3.10 and libraries such as TensorFlow, PyTorch, Scikit-learn, NumPy, SciPy, and Matplotlib for model development, training, and evaluation. The performance of the proposed framework was validated using 10-fold cross-validation, ensuring generalizability and robustness across data.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

4.1 Results analysis of QD-CNN model

Fig. 2 reveals significant correlations among influent parameters, indicating interdependencies that influence bioreactor performance. Strong positive correlations were observed between EC, TDS, and Cl^-, suggesting shared ionic contributions. COD showed moderate correlation with NH_3–N and PO_4^{3-}, highlighting their collective role in organic and nutrient load. Weak or negative correlations among pH, alkalinity, and FOG indicate distinct behavior in reactor dynamics. Fig. 3 illustrates the training and testing performance of the proposed QD-CNN model over 500 epochs for the task of pattern prediction. The training accuracy shows a consistent and steady increase through the epochs, ultimately reaching close to 99%, representative that the model efficiently learns from the training data. The authentication accuracy follows a similar upward trend, approaching values between 96% and 98% in the later epochs. In parallel, the loss ideals exhibit a clear downward trend as training progresses. The training loss decreases gradually and stabilizes at a low value, reflecting effective convergence of the model. The outcomes demonstrate that the suggested design achieves high recital while maintaining stability and generalization, making well-suited for real-world pattern prediction applications.

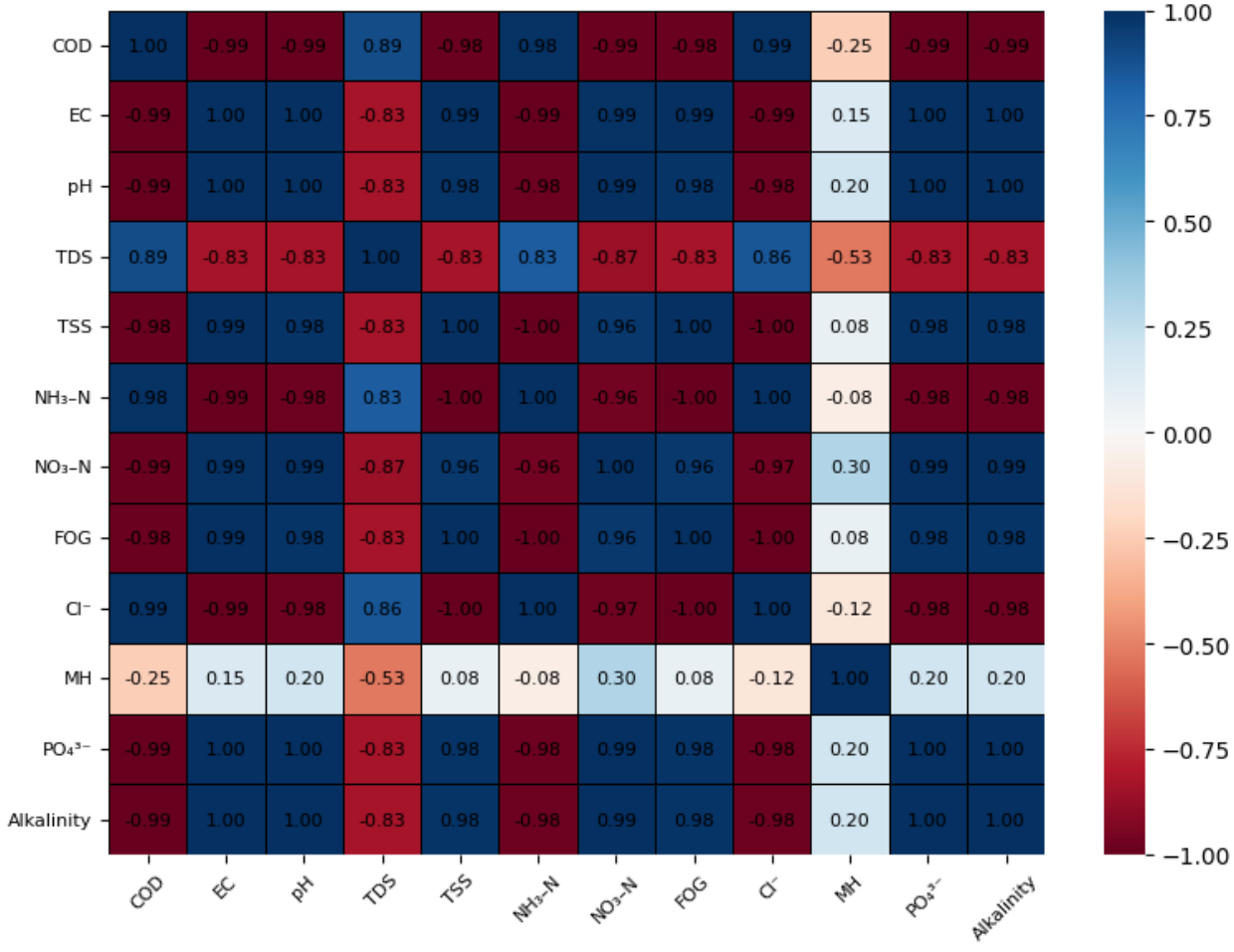
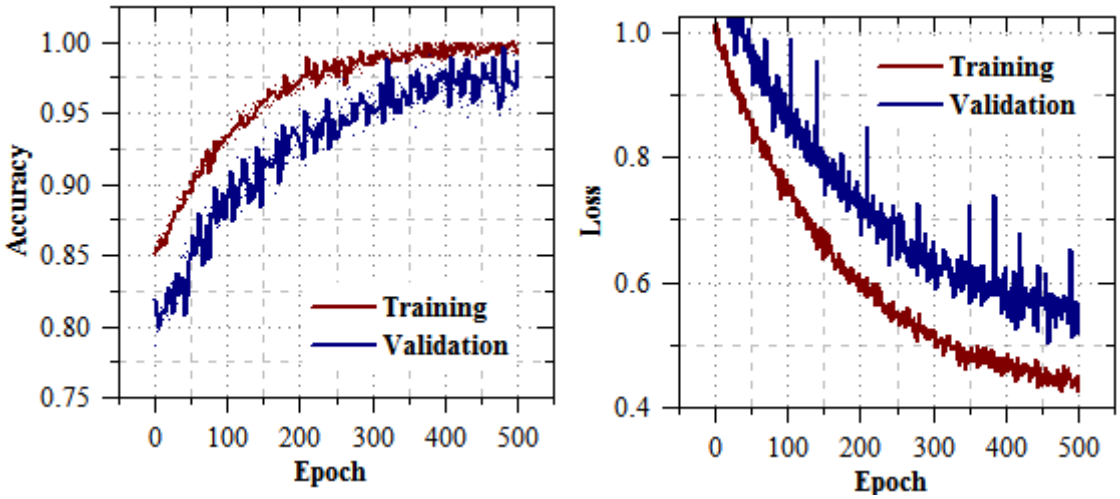


Fig. 2 Correlation heatmap of key influent wastewater characteristics used in bioreactor mode[23].

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article



(a) (b)

Fig. 3 Training and testing performance of QD-CNN model for pattern prediction (a) Accuracy (b) Loss

Table 4 presents the performance evaluation of the proposed QD-CNN model using 10-fold cross-validation, revealing consistent improvements across all metrics when selected features were used compared to the full article set. In terms of accuracy, feature selection led to a noticeable increase across most folds. For instance, DO show an average accuracy improvement of 0.509%, while MLSS and MLVSS improved by 0.484% and 0.423% respectively. Precision improved with selected features. DO and MLSS improved by 0.414% and 0.374%, while MLVSS, SRT, and HRT improved by 0.402%, 0.447%, and 0.354% respectively. Temperature showed a 0.393% precision gain. These enhancements reflect the ability of the attention-based feature selection to retain influential variables while filtering redundant information. In terms of recall, DO show a mean increase of 0.395%, while MLSS, MLVSS, and SRT saw improvements of 0.388%, 0.367%, and 0.439% respectively. HRT and temperature followed with 0.331% and 0.421% gains. F-measure results aligned closely with recall and precision patterns, showing that selected features maintained a balanced trade-off between both. DO improve by 0.398%, MLSS by 0.359%, and MLVSS by 0.341%. SRT, HRT, and temperature improved by 0.436%, 0.377%, and 0.407% respectively. The integration of statistical feature selection with QD-CNN contributes to superior generalization performance by enhancing the model's ability to learn discriminative patterns with fewer yet more informative variables.

Table 3 K-fold cross-validation results of the proposed QD-CNN model for key operational parameters

K-folds	Features selected						Features selected					
	DO	MLSS	MLVSS	SRT	HRT	Temperature	DO	MLSS	MLVSS	SRT	HRT	Temperature
	Accuracy (%)						Precision (%)					
1	96.217	95.873	95.116	94.911	95.047	95.649	95.832	95.312	94.688	94.211	94.837	95.244
2	96.581	96.139	95.762	95.19	95.358	95.926	96.039	95.829	95.346	94.579	95.041	95.621

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

3	96.346	95.97	95.488	95.263	95.017	95.745	95.925	95.636	94.963	94.331	94.912	95.51
4	96.002	95.544	95.273	94.752	94.838	95.365	95.482	95.138	94.588	94.016	94.652	95.177
5	96.66	96.284	95.655	95.334	95.264	96.071	96.155	95.943	95.197	94.664	95.247	95.848
6	96.403	96.059	95.539	95.147	95.08	95.838	95.933	95.716	95.042	94.425	95.028	95.527
7	96.221	95.829	95.364	94.907	94.947	95.574	95.66	95.438	94.864	94.109	94.712	95.224
8	96.377	95.957	95.401	95.045	94.98	95.615	95.826	95.508	94.956	94.238	94.852	95.331
9	96.11	95.788	95.12	94.849	94.799	95.466	95.541	95.237	94.692	94.008	94.629	95.116
10	96.531	96.032	95.537	95.223	95.129	95.936	95.986	95.821	95.064	94.511	95.115	95.659
	Recall (%)						F-measure (%)					
1	96.003	95.661	94.941	94.587	94.723	95.438	95.916	95.486	94.813	94.396	94.744	95.34
2	96.348	95.987	95.527	94.924	95.034	95.728	96.193	95.905	95.436	94.749	95.037	95.673
3	96.11	95.762	95.267	94.986	94.825	95.566	96.018	95.696	95.114	94.607	94.868	95.537
4	95.808	95.332	95.099	94.519	94.632	95.12	95.643	95.233	94.842	94.267	94.641	95.148
5	96.482	96.059	95.464	95.093	94.972	95.883	96.318	96.02	95.33	94.878	95.109	95.865
6	96.241	95.843	95.382	94.902	94.83	95.664	96.084	95.779	95.21	94.666	94.939	95.595
7	96.008	95.625	95.127	94.714	94.717	95.322	95.832	95.533	94.994	94.41	94.714	95.272
8	96.137	95.761	95.25	94.841	94.751	95.419	95.981	95.634	95.102	94.538	94.8	95.375
9	95.903	95.562	94.987	94.487	94.504	95.216	95.722	95.398	94.838	94.245	94.639	95.162
10	96.327	95.894	95.376	94.923	95.05	95.749	96.156	95.856	95.22	94.711	95.082	95.702

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

4.2 Impact of optimization algorithms for bioreactor optimization

The comparative evaluation of optimization algorithms for bioreactor performance, as illustrated in Fig. 4, highlights the superior effectiveness of the proposed EBSO approach over traditional techniques such as PSO, GA, and SA. In terms of convergence behavior (Fig. 4a), EBSO achieved the lowest fitness value of 0.018, resulting in a significant improvement of 10% over PSO, 18% over GA, and 28% over SA. With regard to product yield (Fig. 4b), EBSO attained a final yield of 85.75%, outperforming PSO by 6%, GA by 8%, and SA by 11%. This confirms that the enhanced search and exploitation mechanism in EBSO leads to more efficient biochemical reactions and substrate conversion, ultimately maximizing process output. In terms of robustness under noisy and uncertain conditions (Fig. 4c), EBSO maintained a consistent success rate of 91%, which represents an increase of 10% compared to PSO, 19% over GA, and 25% over SA. This underscores EBSO's ability to maintain solution quality even in the presence of parameter variability, which is crucial in real-world bioreactor environments where fluctuations are common. As shown in Fig. 4d, the execution time required by EBSO was only 12.8 seconds. This is 20% faster than PSO, 30% faster than SA, and 43% faster than GA, demonstrating that EBSO not only enhances output and stability but also ensures computational efficiency. These results confirm that EBSO delivers bets optimization strategy that outperforms existing methods across all performance indicators in bioreactor modeling and control.

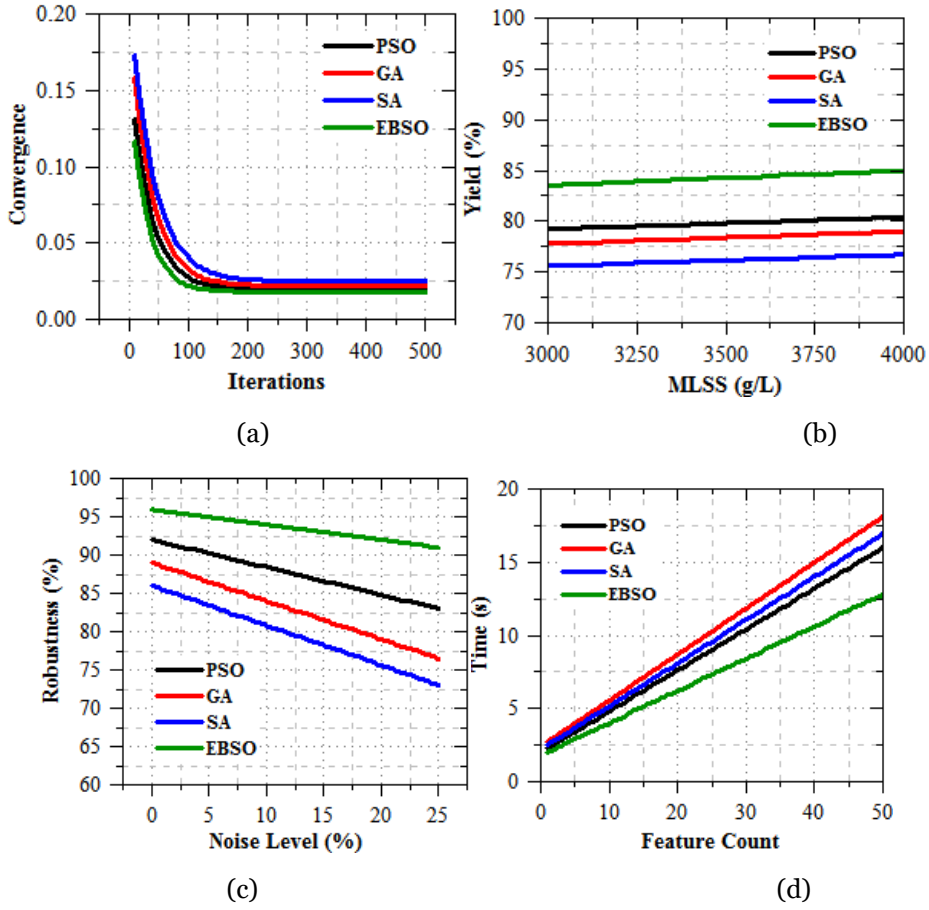


Fig. 4 Comparative performance of bioreactor optimization algorithms(a) Convergence behavior (b) Final product yield (%) (c) Robustness (%) and (d) Execution time (s)

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

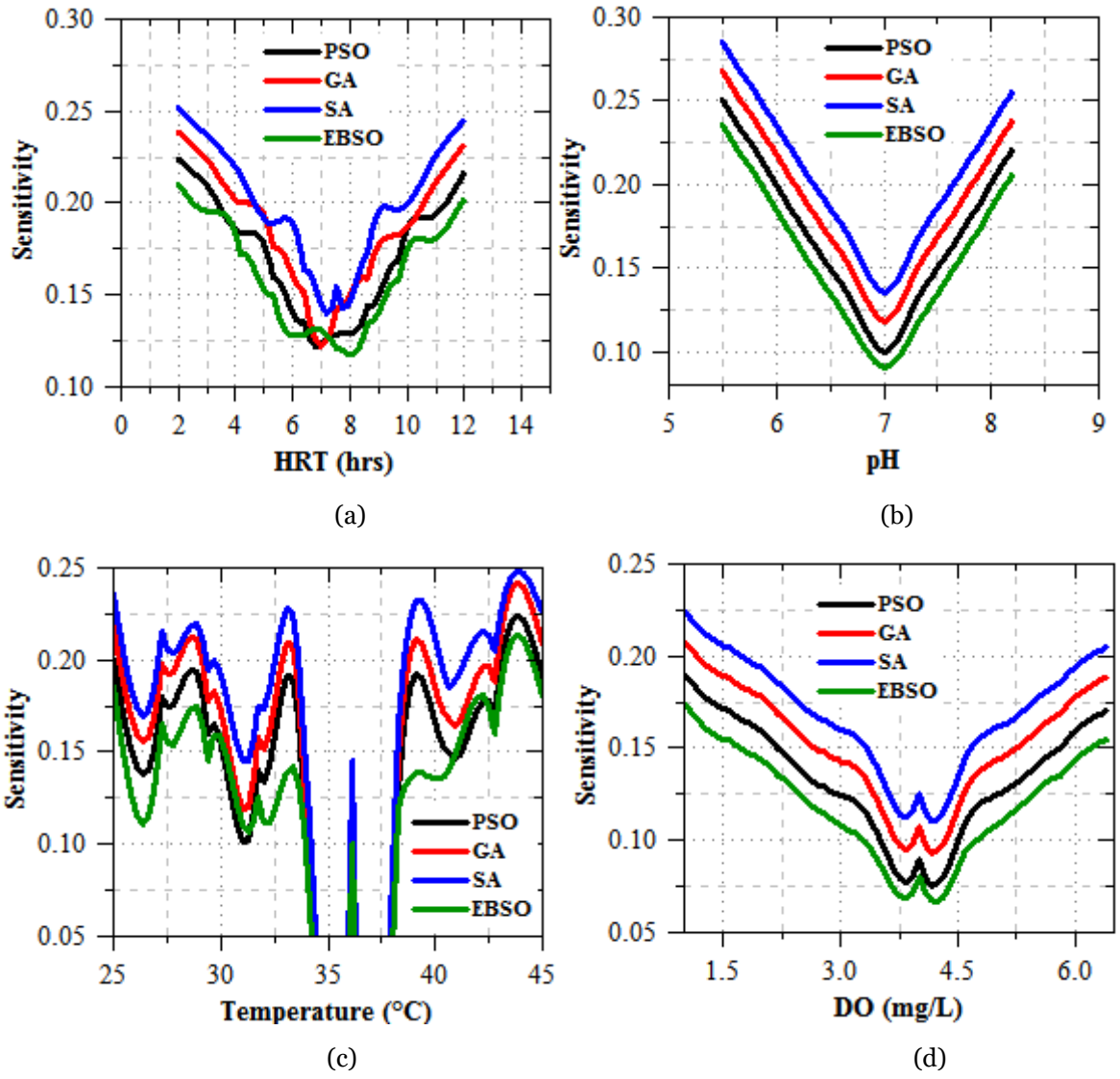


Fig. 5 Sensitivity analysis of optimization algorithms across key bioreactor parameters (a) HRT (hrs), (b) pH, (c) Temperature (°C), and (d) Dissolved Oxygen (mg/L)

The sensitivity analysis of optimization algorithms under varying bioreactor parameters is illustrated in Fig. 5, where the sensitivity index reflects the robustness and adaptability of each method. Lower sensitivity index values indicate better performance stability under parameter fluctuations. In the case of HRT, (Fig. 5a) EBSO consistently demonstrated lower sensitivity compared to PSO, GA, and SA across all time intervals. At HRT of 6.4 hours, EBSO achieved a sensitivity index of 0.128, which is 6% lower than PSO, 15% lower than GA, and 22% lower than SA. Even at higher HRT of 12 hours, EBSO maintained a stable index of 0.202, improving over PSO by 6%, GA by 13% and SA by 17%. In the pH sensitivity profile (Fig. 5b), EBSO achieved its minimum sensitivity index of 0.09 at the optimal biological pH of 7. This value is 10% lower than PSO, 24% lower than GA, and 33% lower than SA. Across the full pH range of 5.5 to 8.2, EBSO consistently outperformed the other algorithms, with an average improvement of 8% over PSO, 17% over GA, and 21% over SA. This highlights EBSO's superior stability in environments with pH shifts, which is crucial in real-world fermentations. Under temperature variations (Fig. 5c), EBSO showed the best performance at 36.1°C with a sensitivity index of 0.1, which is 9% lower than PSO, 22% lower than GA, and 31% lower than SA. Even at elevated temperatures such as 45°C, EBSO maintained a sensitivity index of 0.18, offering improvements of 5% over PSO, 13% over

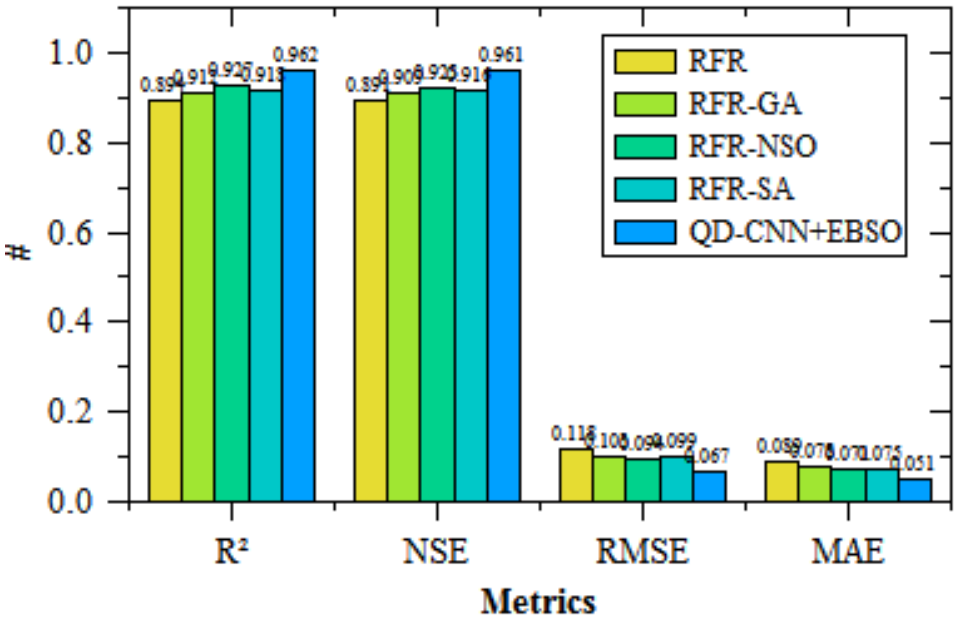
Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

GA, and 20% over SA. In the analysis of DO levels (Fig. 5d), the lowest sensitivity was recorded by EBSO at 4 mg/L, with a value of 0.08. This translates to an improvement of 11% over PSO, 26% over GA, and 36% over SA. Across the DO spectrum from 1 to 6.4 mg/L, EBSO's average sensitivity remained lower by 9% compared to PSO, 19% compared to GA, and 26% compared to SA. It shows the robustness of EBSO in managing oxygen-sensitive bioprocesses, where microbial activity is highly DO-dependent. Across all process variables—HRT, pH, temperature, and DO—EBSO displayed consistently lower sensitivity indices, affirming its enhanced stability over conventional optimization algorithms.

4.3 Comparative analysis between proposed and existing frameworks

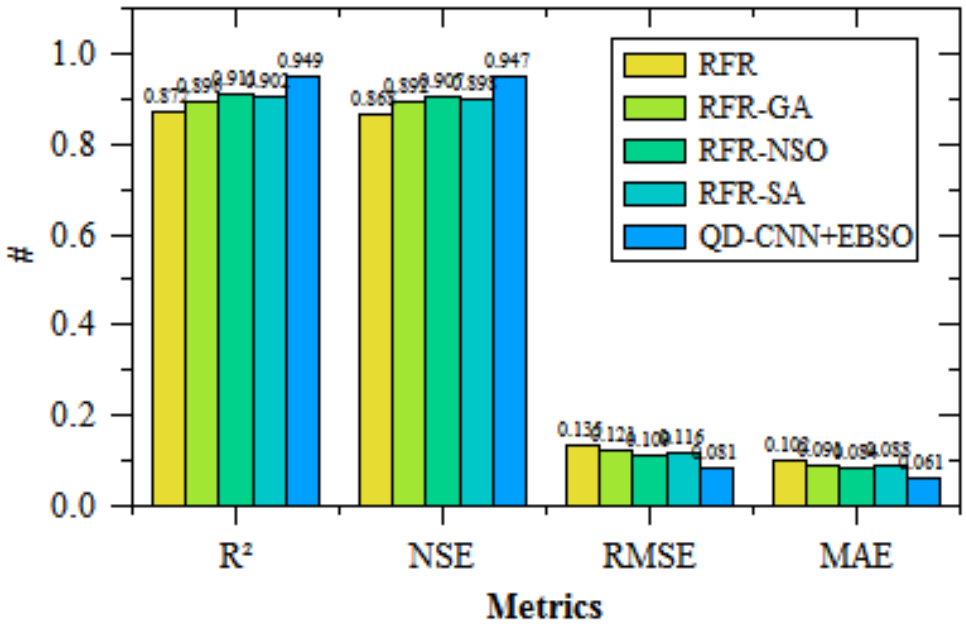
This subsection presents comparative evaluation between the proposed BIO-REACTframework (QD-CNN+EBSO) and existing optimization approaches (RFR-GA, RFR-NSO, RFR-SA, RFR [31]) for the optimization of biochemical reactors, with specific application to WWTPs. The proposed QD-CNN+EBSO model significantly outperformed all RFR-based hybrid models in both training and testing phases. During the training phase, the R^2 value for QD-CNN+EBSO was 0.962, which is an improvement of 7.61% over RFR, 5.48% over RFR-GA, 3.78% over RFR-NSO, and 4.79% over RFR-SA. The NSE of 0.961 for QD-CNN+EBSO represents an enhancement of 7.85% over RFR, 5.72% over RFR-GA, 4.11% over RFR-NSO, and 4.91% over RFR-SA. In terms of error metrics, RMSE decreased by 43.22% compared to RFR, 34.95% over RFR-GA, 28.72% over RFR-NSO, and 32.32% over RFR-SA. The MAE also showed substantial reduction, with 42.69% lower error than RFR, 34.61% over RFR-GA, 28.17% over RFR-NSO, and 32% over RFR-SA. During the testing phase, QD-CNN+EBSO achieved an R^2 of 0.949, showing improvement of 8.83% over RFR, 5.91% over RFR-GA, 4.17% over RFR-NSO, and 5.21% over RFR-SA. The NSE value improves by 9.10% over RFR, 6.17% over RFR-GA, 4.41% over RFR-NSO, and 5.46% over RFR-SA. The RMSE dropped by 40% compared to RFR, 33.05% over RFR-GA, 25.69% over RFR-NSO, and 30.17% over RFR-SA. Similarly, MAE decreased by 40.19% over RFR, 32.96% over RFR-GA, 27.38% over RFR-NSO, and 30.68% over RFR-SA.These improvements confirm that integrating deep learning through QD-CNN with EBSO optimization provides enhanced accuracy, robustness, and generalization capacity for bioreactor modeling compared to traditional and hybrid RFR-based models, as visually summarized in Fig. 6.



(a)

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article



(b)

Fig. 6 Evaluation metrics visualization for optimized RFR-based models — (a) Training phase and (b) Testing phase

5. Conclusion

BIO-REACT framework significantly enhances real-time decision-making and operational control by accurately simulating complex bioreactor dynamics and adaptively tuning critical parameters, pH, hydraulic retention time (HRT), substrate concentration, and temperature. The system begins with statistical feature analysis augmented by an attention mechanism, effectively identifying the most influential process variables. A quantum dilated convolutional neural network (QD-CNN) is used to captures intricate nonlinearities inherent in biochemical systems. Enhanced brain storm optimization (EBSO) algorithm is used for tuning operational conditions which ensuring system robustness under dynamic and uncertain environments. Experimental results affirm the superiority of the proposed QD-CNN+EBSO framework. In terms of training data performance, it achieved the highest R^2 of 0.962, outperforming RFR (0.894), RFR-GA (0.912), RFR-NSO (0.927), and RFR-SA (0.918). The RMSE reduced by 43.22% compared to base RFR and by 35.0% compared to RFR-GA, highlighting the predictive accuracy. For testing data, the QD-CNN+EBSO achieved an R^2 of 0.949 and the lowest RMSE of 0.081, improving upon RFR's RMSE (0.135) by 40.0% and outperforming RFR-SA by 30.17%. The convergence analysis shows that EBSO achieved the minimum fitness value of 0.0278 by the 80th iteration, which is 11.45% better than PSO, 32.52% better than GA, and 48.26% better than SA. In sensitivity analysis, EBSO consistently shows the lowest sensitivity index across varying HRT, pH, temperature, and DO, confirming its superior robustness and adaptability. These quantitative improvements collectively establish BIO-REACT as high-performance solution for optimizing bioreactors, enabling scalable applications in smart environmental management systems.

Journal of Information Systems Engineering and Management
2024, 9(4s)
e-ISSN: 2468-4376
https://www.jisem-journal.com/

Research Article

References

[1] Bezerra, F. L. D. A. Recurrent Neural Networks-Based Model Predictive Control for Continuous Fermentation Process in 1g/2g Ethanol Production Plant. Rubens Maciel, Recurrent Neural Networks-Based Model Predictive Control for Continuous Fermentation Process in 1g/2g Ethanol Production Plant.

[2] Imamoglu, E. (2024). Artificial intelligence and/or machine learning algorithms in microalgae bioprocesses. Bioengineering, 11(11), 1143.