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A FRILLED-LIZARD ALGORITHM-BASED HYPERPARAMETER OPTIMIZATION FRAMEWORK FOR SUPPORT VECTOR MACHINE IN AUTOMATED POULTRY FECAL IMAGE CLASSIFICATION

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ABSTRACT

Coccidiosis and Newcastle Disease(NCD) are among the most disastrous poultry illnesses generally, responsible for enormous profitable losses and pitfalls to food security. Accurate, timely, and computationally effective discovery of these conditions remains a persistent challenge for both marketable and smallholder poultry operations. This research showcases the development of a Frilled-Lizard Optimization-based Support Vector Machine (FLO-SVM) for the automated detection and classification of Coccidiosis and Newcastle Disease in poultry using fecal image datasets. The FLO algorithm, a novel bio-inspired metaheuristic, was applied to automatically tune three critical SVM hyperparameters: kernel coefficient (γ), the penalty factor (C), and kernel function type. The utilized dataset sourced from kaggle consist 1,400 poultry images, with Coccidiosis represented by 304 images and Newcastle Disease by 376 images. Pre-processing involved conversion, of grayscale discrepancy improvement via CLAHE, image normalization, and principal component analysis (PCA) for feature extraction. The study employed Model evaluation of 10-fold cross-validation across threshold values of 0.3, 0.4, 0.5, and 0.51. The FLO algorithm converged to an optimal configuration of RBF kernel with C = 5.7242 and γ = 0.7922 after 30 iterations, leading to an achievement of a fitness value of 0.9829. The FLO-SVM resulted to peak accuracy of 97.50% for Newcastle Disease and 97.21% for Coccidiosis, respectively, at threshold 0.51, The outcome outperforms the SVM baseline by over 1.5%. Sensitivity exceeded 94%, and false positive rates were reduced to approximately 1.56–1.64% at threshold 0.51. Execution time was greatly decreased, ranging from 30.63 to 38.26 seconds compared to over 58 seconds for the conventional SVM. The output of the result indicate that FLO-SVM provides an accurate, reliable, and computationally efficient framework for poultry disease detection, with significant practical applicability for on-farm diagnostic systems.

Keywords: *Coccidiosis, Frilled-Lizard Optimization, Hyperparameter Tuning, Newcastle Disease, Poultry Disease Detection, Support Vector Machine*.

1.0 INTRODUCTION

Generally, the poultry industry sustains the livelihoods of hundreds of millions of smallholder growers and constitutes one of the swift growing parts of the domestic animal sector, with world flesh meat product transcending 130 million tonnes annually (FAO, 2021). Yet this productive capacity is constantly endangered by contagious conditions. Coccidiosis is a complaint caused by protozoan spongers, which is estimated to regard for a substantial bit of total chemotherapeutic complaint control expenditure in ferocious poultry systems worldwide alone (Ahmad *et al.*, 2024). Traditional individual approaches for these conditions are frequently time- consuming, expensive, and require technical laboratory installations, making them impracticable for large-scale ranch monitoring (Liebhart *et al.*, 2023). Accordingly, machine literacy- grounded

individual approaches, particularly Support Vector Machines (SVMs), have attracted considerable attention due to their capability to handle high- dimensional data, on-linear decision boundaries, and limited training samples. SVMs identify an optimal hyperplane that maximizes the periphery between complication classes, making them especially suitable for double and multi-class poultry complication category tasks and multi-class (Cervantes *et al.,* 2020).

Despite their strong theoretical framework, conventional SVMs are highly sensitive to the choice of hyperparameters, including the penalty factor (C), kernel coefficient (γ), and kernel function. Improper hyperparameter selection can lead to overfitting or poor generalization, limiting classification performance (Syarif *et al.,* 2016). Meta-heuristic optimization algorithms provide an effective remedy by automating hyperparameter search. The Frilled-Lizard Optimization (FLO) algorithm, inspired by the predatory hunting strategy and tree-retreat exploitation behavior of the frilled lizard (Chlamydosaurus kingii), has demonstrated strong exploration-exploitation balance, fast convergence, and robust performance in complex search spaces (Falahah *et al.,* 2024). Several prior studies have proposed SVM-based classifiers for poultry disease detection. Okinda *et al.* (2019) achieved 97% classification accuracy for Newcastle Disease detection using RBF-kernel SVM with spatial-temporal mobility features, though only a single SVM parameter was optimized. Khatun *et al.* (2016) applied SVM to poultry sound signals but reported sensitivity to environmental noise. These studies demonstrate the potential of SVM while highlighting the critical limitation of suboptimal hyperparameter tuning. The integration of FLO with SVM addresses this limitation by providing a fully automated, adaptive, and efficient optimization mechanism. Therefore, this study develops a FLO-SVM model specifically targeting Coccidiosis and Newcastle Disease detection, evaluating its performance under variable decision threshold conditions to provide a robust diagnostic framework suitable for real-world poultry farming environments.

2.0 MATERIALS AND METHODOLOGY

The study followed a systematic machine learning pipeline encompassing data acquisition, preprocessing, FLO-based hyperparameter optimization, SVM classification, and performance evaluation using a developed graphical user interface (GUI) implemented in MATLAB R2023a.

2.1 Dataset

The dataset was sourced from the Kaggle open repository comprising of 1,400 poultry fecal images. For the purpose of this research, the Coccidiosis class and Newcastle Disease class which are 304 images and 376 images respectively, were used alongside the Healthy and Salmonella classes, comprising 320 images and 400 images classes respectively for model

training. All images utilized were resized to a uniform dimension of 224×224 pixels to ensure consistency across the dataset. A 70 ratio 30 training-testing split was applied within a 10-fold cross-validation

scheme to ensure there is an unbiased performance estimation and improved model generalization.

2.2 Data Pre-processing

The pre-processing pipeline start with the conversion of RGB images to grayscale using the weighted channel formula:

$$Gray(x) = \alpha R + \beta G + \gamma B \quad \text{..... (i)}$$

Where $\alpha, \beta, and\ \gamma$ are the coefficient factor of Red, Green and Blue of the images respectively. This reduced computational complexity while preserving essential structural and texture features relevant for disease detection. Subsequently, contrast enhancement was performed using Contrast Limited Adaptive Histogram Equalization (CLAHE) to amplify disease-related features such as lesions and discolorations. Image normalization was then applied to standardize pixel intensity distributions:

$$I_{norm}(x, y) = \frac{I(x, y) - I_{min}}{I_{max} - I_{min}} \quad \text{..... (ii)}$$

Finally, Principal Component Analysis (PCA) was employed for feature extraction, reducing dimensionality while retaining the most discriminative features.

2.3 Frilled-Lizard Optimization (FLO)

The FLO algorithm was applied to optimize three SVM hyperparameters: the penalty factor C, kernel coefficient γ, and kernel function type. FLO initializes a population of N candidate solutions (frilled lizards), each representing a hyperparameter configuration. The algorithm operates in two phases: (1) Phase 1 - Hunting Strategy (Exploration), where lizards move toward candidate prey with better objective function values using the equation:

$$X^{PI}_{i,d} = X_{i,d} + r\,(SP_{i,d} - I \,.\, X_{i,d}),\ i = 1, 2, \ldots . N, and\ \ d = 1,2, \ldots m \quad \text{---------- (iii)}$$

and (2) Phase 2 - Moving Up the Tree (Exploitation), where refined local search is performed:

$$X^{P2} = X + (1 - 2r)\ \frac{(ub_d - Ib_d)}{}, i = 1, 2 \ldots N, d = 1,2 \ldots m, and\ t = 1, 2, \ldots, T - (iv)$$

The fitness function used was SVM classification accuracy:

$$F(Xi) = \frac{(TP+TN)}{(TP+TN+FP+FN)} \quad \text{.....(v)}$$

The algorithm was executed over 30 iterations with a population size N = 10.

2.4 SVM Classification Model

The SVM classifier employed a kernel-based decision function:

$$F(\mathrm{X}) = \sum \alpha_i \, y_i \, K(x_i, X) + b \quad \text{.....(vi)}$$

where Lagrange multipliers are represented as (α_i), class labels (y), and a kernel function (K (x_i, X)) is the kernel function. Four kernel types were evaluated: linear, polynomial (poly), Radial Basis Function (RBF), and sigmoid. The optimization objective minimized classification error subject to regularization constraints: $0 \leq \alpha_i \leq C$ and $\Sigma \, \alpha_i \, y_i = 0$. Classification decisions were evaluated across four threshold values (0.3, 0.4, 0.5, and 0.51) to analyze threshold sensitivity.

2.4 Performance Evaluation Metrics

Model performance was evaluated using Accuracy (ACC), Sensitivity (SEN), Specificity (SPEC), Precision (PREC), False Positive Rate (FPR), and detection time. The confusion matrix elements are True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN) formed the basis for all metric calculations. Sensitivity measures the ability to detect true positive disease cases, while specificity measures the correct identification of healthy cases. A 10-fold cross-validation scheme was used throughout to ensure robust, unbiased performance estimation.

3.0 RESULTS AND DISCUSSION

3.1 FLO Hyperparameter Optimization

The FLO algorithm was executed over 30 iterations to identify the optimal SVM hyperparameter configuration. Selected results from the optimization process are presented in Table 1. Initial iterations exhibited variable fitness values as the algorithm explored the search space. By iteration 8, a linear kernel configuration with C = 8.0385 achieved a fitness of 0.9591. Continued optimization led to further improvement; by iteration 19, an RBF configuration achieved 0.9757. Final convergence at iteration 30 yielded the optimal configuration: RBF kernel with C = 5.7242 and γ = 0.7922, achieving the highest fitness value of 0.9829. This progressive improvement demonstrates FLO's effective exploration-exploitation balance and its ability to systematically refine hyperparameter selection toward globally optimal configurations.

Table 1: Selected Iterations of SVM Hyperparameter Optimization with FLO

Iteration	C	Gamma	Kernel	Fitness
1	1.996	0.8693	Sigmoid	0.9500
8	8.0385	0.9249	Linear	0.9591
13	6.8663	0.0483	RBF	0.9155
19	7.7510	0.3303	RBF	0.9757
30	5.7242	0.7922	RBF	0.9829

3.2 FLO-SVM Classification Performance for Coccidiosis and Newcastle Disease

Table 2 presents the classification performance of FLO-SVM for Coccidiosis and Newcastle Disease classes across decision thresholds of 0.3 to 0.51. At threshold 0.3, FLO-SVM achieved sensitivity values of 94.08% for Coccidiosis and 95.74% for Newcastle Disease, with precision values of 91.67% and 93.75% respectively. False positive rates were reduced to 2.37% and 2.34%, demonstrating markedly improved class discrimination compared to conventional SVM. As the threshold increased to 0.5, specificity values improved to 98.18% for Coccidiosis and 98.24% for Newcastle Disease, while sensitivity and precision remained above 93% and 95%, respectively. This behaviour reflects the FLO algorithm's exploitation phase convergence toward optimal hyper parameter configurations that refine the SVM decision boundary. At the highest threshold of 0.51, FLO-SVM achieved its best accuracy values of 97.21% for Coccidiosis and 97.50% for Newcastle Disease. The false positive rates were further reduced to 1.64% and 1.56% respectively, while execution times ranged from 31.43 to 38.26 seconds—substantially lower than the baseline SVM's 58–70 seconds. These improvements confirm the effectiveness of FLO in automatically tuning SVM parameters to deliver superior diagnostic performance.

Table 2: FLO-SVM Performance Metrics for Coccidiosis and Newcastle Disease

Class	Threshold	TP	FN	FP	TN	FPR(%)	SPEC(%)	SEN(%)	PREC(%)	ACC(%)	Time(s)
Cocci	0.3	286	18	26	1070	2.37	97.63	94.08	91.67	96.86	37.83
NCD	0.3	360	16	24	1000	2.34	97.66	95.74	93.75	97.14	32.49
Cocci	0.4	285	19	23	1073	2.10	97.90	93.75	92.53	97.00	37.79
NCD	0.4	359	17	21	1003	2.05	97.95	95.48	94.47	97.29	31.17
Cocci	0.5	284	20	20	1076	1.82	98.18	93.42	93.42	97.14	38.12
NCD	0.5	358	18	18	1006	1.76	98.24	95.21	95.21	97.43	30.63
Cocci	0.51	283	21	18	1078	1.64	98.36	93.09	94.02	97.21	38.26
NCD	0.51	357	19	16	1008	1.56	98.44	94.95	95.71	97.50	31.43

3.3 Comparative Analysis with Baseline SVM

Table 3 presents the baseline SVM performance for Coccidiosis and Newcastle Disease at selected thresholds. At threshold 0.3, the SVM achieved sensitivity of 91.12% for Coccidiosis and 92.02% for Newcastle Disease. Comparing with FLO-SVM results, the introduction of FLO optimization yielded average sensitivity gains of approximately 2.96% for Coccidiosis and 3.72% for Newcastle Disease. False positive rates were reduced by approximately 0.73–1.27 percentage points. These

improvements are clinically meaningful in poultry disease management: a reduction in false positives translates directly to fewer unnecessary treatment interventions, reduced costs, and lower antimicrobial resistance risks.

Table 3: Baseline SVM Performance for Coccidiosis and Newcastle Disease

Class	Threshold	TP	FN	FP	TN	FPR(%)	SPEC(%)	SEN(%)	PREC(%)	ACC(%)	Time(s)
Cocci	0.3	277	27	34	1062	3.10	96.90	91.12	89.07	95.64	61.47
NCD	0.3	346	30	37	987	3.61	96.39	92.02	90.34	95.21	70.55
Cocci	0.5	275	29	30	1066	2.74	97.26	90.46	90.16	95.79	62.13
NCD	0.5	344	32	33	991	3.22	96.78	91.49	91.25	95.36	69.84
Cocci	0.51	274	30	27	1069	2.46	97.54	90.13	91.03	95.93	58.56
NCD	0.51	343	33	30	994	2.93	97.07	91.22	91.96	95.50	70.38

The progressive improvement from SVM to FLO-SVM is consistent with empirical evidence that bio-inspired metaheuristic algorithms significantly enhance SVM hyperparameter tuning by automatically navigating complex, multi-dimensional search spaces [6]. The superior performance of FLO-SVM for Newcastle Disease compared to Coccidiosis across all metrics may be attributed to the larger class size of NCD (376 images vs. 304), providing more training examples and enabling the SVM to learn more discriminative decision boundaries. These findings align with related studies in multi-class disease classification, where optimized SVM models with RBF kernels consistently outperform manually tuned counterparts by 2–5% in accuracy [9].

4.0 CONCLUSION

This study successfully developed and evaluated a Frilled-Lizard Optimization-based Support Vector Machine (FLO-SVM) for automated detection of Coccidiosis and Newcastle Disease in poultry. The FLO algorithm effectively optimized the SVM penalty factor, kernel measure, and kernel function through a 30- replication search process, clustering to an optimal RBF kernel configuration with fitness value 0.9829. The FLO- SVM achieved a rigor of 97.21 for Coccidiosis and 97.50 for Newcastle Disease at a threshold of 0.51, representing advancements of over 1.5 over the conventional SVM. sensitivity exceeded 94 while false positive rates were reduced below 2, attesting the model's trustability for accurate complication discovery with minimum false alerts. execution time was reduced by roughly 45 compared to the SVM baseline. The findings establish FLO-SVM as a practical, efficient, and accurate diagnostic framework for poultry disease management, with strong potential for integration into real-time, farm-level monitoring systems.

Competing Interests

Authors declare no conflict of interest.

Authors' Contributions

Author 1 designed the study, developed the MATLAB implementation, Author 3 contributed to data collection and validation. Author 2 supervised the study and reviewed the manuscript. Author 4 and 5 wrote the manuscript.

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