Introducing the Mutated Binary Whale Optimization Algorithm for Rice Leaf Disease Classification

Sutikno
Department of Informatics, Faculty of Science and Mathematics, Diponegoro University, Indonesia
sutikno@lecturer.undip.ac.id (corresponding author)

Helmie Arif Wibawa
Department of Informatics, Faculty of Science and Mathematics, Diponegoro University, Indonesia
helmie@lecturer.undip.ac.id

Indra Waspada
Department of Informatics, Faculty of Science and Mathematics, Diponegoro University, Indonesia
indrawaspada@lecturer.undip.ac.id

Received: 7 August 2025 | Revised: 26 September 2025 | Accepted: 5 October 2025

 DOI: https://doi.org/10.48084/etasr.13915

ABSTRACT

Rice leaf diseases can reduce yields, making early detection crucial. Machine learning has played a significant role in identifying and classifying these diseases. Combining appropriate descriptors for feature extraction has been shown to improve accuracy but increases classification time. Reducing classification time can be achieved through feature selection. One wrapper feature selection method that has exploration and exploitation capabilities to solve optimization problems is the Binary Whale Optimization Algorithm (BWOA). However, this feature selection method is prone to get stuck in local solutions when facing high-dimensional search spaces. This study proposes a new feature selection algorithm, an improvement on BWOA, to address this problem by incorporating a mutation process. The proposed method is called the Mutated Binary Whale Optimization Algorithm (MBWOA). Based on experimental evidence, the proposed method can reduce both fitness and classification time without compromising accuracy, but even improving it. Additionally, the proposed method exhibits faster convergence than BWOA. The proposed method achieves 100% accuracy on the RLD1 dataset and 99.41% accuracy on the RLD2 dataset. Therefore, the proposed method is relatively suitable for classifying or detecting rice leaf diseases.

Keywords-improvement of BWOA; mutation algorithm; MBWOA; rice leaf disease classification

I. INTRODUCTION

Rice is a crucial commodity for Indonesia's food security and economy, supporting millions of farmers. By 2025, Indonesia is projected to be the fourth-largest rice producer in the world [1]. However, leaf diseases such as bacterial blight, brown spot, leaf scald, and narrow brown spot can reduce yields by up to 50% if not detected early [2]. Thus, timely detection is essential to prevent significant crop losses.

Machine learning has great potential in image analysis for plant disease detection, especially rice leaves, providing faster, more accurate, and more efficient identification compared to traditional methods. Research in this area has grown significantly over the last decade, with two primary approaches to feature extraction: handcrafted and non-handcrafted. Non-handcrafted approaches utilize deep learning models such as VGG-16 [3], InceptionResNetV2 [4], GoogleNet [5], AlexNet [6, 7], and YOLO [8] to automatically extract features. In [9], an enhanced sea horse optimization algorithm was proposed for deep learning-based multimodal fusion. Handcrafted approaches extract visual features such as color, texture, and shape. In [10], it was shown that the Histogram of Oriented Gradients (HOG) was superior to the Local Binary Pattern (LBP). Several studies combined several descriptors to improve accuracy. In [11], color extraction, Gray Level Co-occurrence Matrix (GLCM), and shape features (centroid, eccentricity, and axis length) were combined, while in [12], GLCM and Pearson correlation analysis were combined. Combining several appropriate descriptors has been shown to improve accuracy [13] but results in a larger number of features, which in turn increases the computation time. Feature selection can reduce the number of features without reducing accuracy [14]. Wrapper feature selection can increase accuracy by selecting the optimal feature subset [15].

Optimization problems can be addressed using wrapper feature selection methods such as the Binary Whale Optimization Algorithm (BWOA), which combines exploration and exploitation [16]. However, this feature selection approach is prone to getting stuck in local solutions when faced with a highly dimensional and non-linear search space. In [17], this issue was addressed by introducing two mutation phases. The first mutation phase serves to reduce the features while maintaining accuracy, while the second adds features to improve accuracy. However, the application of the second mutation requires a very significant computational time [18]. This study proposes improvements to the BWOA algorithm using a single mutation process to enhance exploration capabilities, ensuring that the optimal feature subset can be selected consistently and efficiently. The proposed algorithm is named Mutated Binary Whale Optimization Algorithm (MBWOA) and was used for the feature selection process in the detection of rice leaf diseases to improve accuracy and reduce classification time.

II. MATERIALS AND METHODS

A. Datasets

This study utilized two publicly available datasets: Leaf Rice Disease (RLD1) [19] and Rice Leaf Diseases (RLD2) [20]. Figure 1 displays selected instances of each dataset. Figure 1(a) is an example of an image in RLD1 containing rice leaf images from Southeast Sulawesi, Indonesia, and includes three disease classes: blast, blight, and tungro, each with 80 images. Figure 1(b) illustrates an example of RLD2, which comprises 2254 images categorized into five classes: bacterial, brown, healthy, leaf scald, and narrow. Both datasets were divided into 85% for training and 15% for testing. To obtain optimal parameter values, the data was divided into five folds as part of the cross-validation process during training.

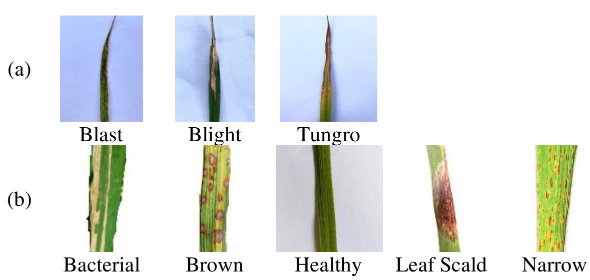

Fig. 1. Examples from the datasets.

B. Developed System

Figure 2 shows the system developed in this study. In the preprocessing stage, the images from the dataset were resized to 128×128 px. The feature extraction process combined three descriptors: GLCM, LBP, and Color Histogram (CL). The GLCM descriptor was used to detect rough texture patterns, such as spots or damage to leaf tissue. LBP was used to recognize wrinkled or spotted leaf surfaces, while CL functions to identify color changes due to disease in the leaves. The GLCM descriptor [21] is a popular method for texture feature extraction and can calculate statistical features such as contrast, homogeneity, energy, and correlation [22].

LBP is a texture descriptor that compares the intensity of neighboring pixels with the center pixel to produce a binary code that represents local patterns [23]. CH is a statistical method that represents the distribution of colors in digital images by calculating the frequency of each color value [24]. The features of these three descriptors are then combined using the concatenation method. A detailed explanation of the descriptors and their combinations can be found in [25].

The following process was feature selection using the proposed algorithm, MBWOA. The final process was classification using RF. This classifier employed an effective ensemble learning method for classification [26]. In [27], RF, Decision Tree (DT), Gradient Boosting, and Naïve Bayes (NB) were compared. The test results showed that RF produces the best accuracy [27]. In [28], several algorithms were also compared, including RF, NB, DT, Logistic Regression (LR), KNN, and Support Vector Machine (SVM), showing that RF achieved the best accuracy.

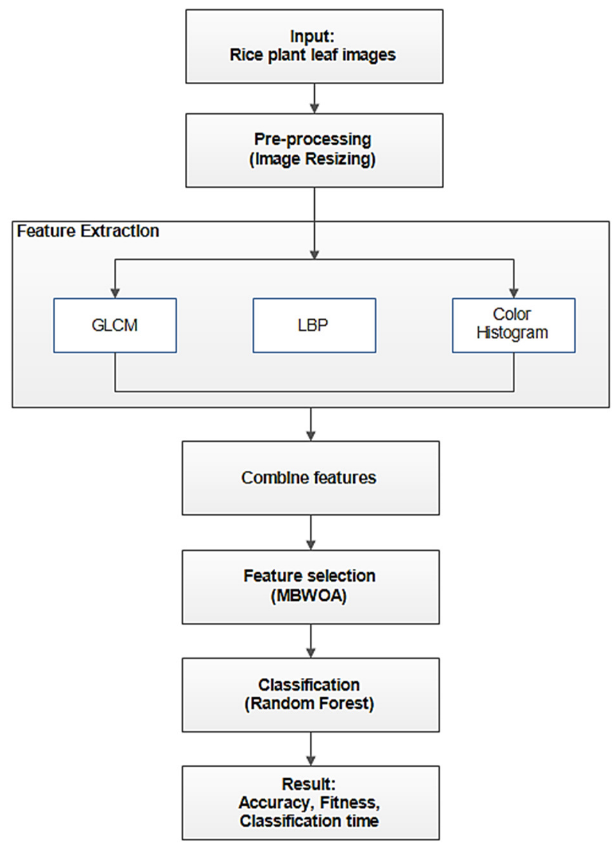

Fig. 2. Proposed system for classification of rice leaf diseases.

C. Binary Whale Optimization Algorithm (BWOA)

As an adaptation of WOA, BWOA operates within a binary search space by transforming continuous values into binary ones. Since WOA functions in a continuous domain, a threshold of 0.5 is applied during conversion: values exceeding 0.5 are assigned 1, and values at or below the threshold are assigned 0. Figure 3 presents the algorithm for BWOA [16].

```
Initialize the whales population X_i (i = 1, 2, ..., n)
Calculate the fitness of each search agent
X*= the best search agent
while (t < t_max)
    for each search agent
    Update a, A, C, l, and p
        if (p<0.5)
            if (|A| < 1)
                Update the position of the current search agent by Eq. (2)
            else if (|A|≥1)
                Select a random search agent (X_rand)
                Update the position of the current search agent by Eq. (9)
            end if
        else if (p ≥ 0.5)
            Update the position of the current search by Eq. (6)
        end if
    end for
    Check if any search agent goes beyond the search space, and amend it
    Calculate the fitness of each search agent
    Update X* if there is a better solution
    t=t+1
end while
return X*
```

Fig. 3. The standard BWOA algorithm.

BWOA is inspired by the natural foraging behavior of whale pods in the ocean [29]. The development of this algorithm has been advanced, including improving it for dynamic optimal power flow by integrating fuzzy logic control [30]. The algorithm operates through two primary phases: exploration and exploitation. During the exploitation stage, solution updates are governed in (1) and (2), where t denotes the current iteration, X^* represents the best solution found so far, and X indicates the current solution. The vectors A and C, which influence the position updates, are determined in (3) and (4), respectively, with the parameter a calculated in (5), and r being a randomly generated vector within the range [0, 1]. The variable t_{max} refers to the total number of iterations. To model the spiral movement of whales, a logarithmic spiral equation is applied as shown in (6), where $\overrightarrow{D'}$ is the absolute distance between the current and optimal solution vectors. The parameter l is randomly selected from the interval $[-1, 1]$, and b defines the shape of the spiral. Finally, the new whale position is updated according to (7).

$$\vec{D} = \left|\vec{C}.\overrightarrow{X^*}(t) - \vec{X}(t)\right| \tag{1}$$

$$\vec{X}(t+1) = \overrightarrow{X^*}(t) - \vec{A}.\vec{D} \tag{2}$$

$$\vec{A} = 2\vec{a}.\vec{r} - \vec{a} \tag{3}$$

$$\vec{C} = 2.\vec{r} \tag{4}$$

$$a = 2 - t\frac{2}{t_{max}} \tag{5}$$

$$\vec{X}(t+1) = \overrightarrow{D'}.e^{bl}.\cos(2\pi l) + \overrightarrow{X^*}(t) \tag{6}$$

$$\vec{X}(t+1) = \begin{cases} \overrightarrow{X^*}(t) - \vec{A}.\vec{D}, & if\ p < 0.5 \\ \overrightarrow{D'}.e^{bl}.\cos(2\pi l) + \overrightarrow{X^*}(t), & if\ p \geq 0.5 \end{cases} \tag{7}$$

The second phase of BWOA enhances the exploration capability of the algorithm. In this phase, the vector A plays a key role by employing random values greater than 1 or less than 1 to encourage the search agents to diverge from the currently known optimal solutions. This mechanism allows the algorithm to explore new regions of the search space. The corresponding mathematical representation of this process is provided in (8) and (9). The variable of $\overrightarrow{X_{rand}}$ represents a random positional vector.

$$\vec{D} = |\vec{C}.\overrightarrow{X_{rand}} - \vec{X}| \tag{8}$$

$$\vec{X}(t+1) = \overrightarrow{X_{rand}} - \vec{A}.\vec{D} \tag{9}$$

In BWOA-based feature selection, a solution is represented by a binary vector consisting of N elements, where N corresponds to the total number of features in the original dataset. Each element in the vector takes a value of either 0 or 1, with a value of 1 indicating that the corresponding feature is selected, and 0 indicating exclusion. The fitness of each solution is assessed using the function defined in (10). In this function, $\gamma_R(D)$ denotes the classification error, $|R|$ refers to the number of selected features, and $|C|$ is the total number of available features. The parameters α and β represent the weights assigned to classification error and feature subset size, respectively. Although most previous works have adopted the KNN classifier, this study utilizes the RF classifier. In this implementation, α is set to 0.99 and β to 0.01 [31].

$$Fitness = a\gamma_R(D) + \beta\frac{|R|}{|C|} \tag{10}$$

```
Initialize the whales population X_i (i = 1, 2, ..., n)
Initialize the mutation probability vector M_p
Calculate the fitness of each search agent
X*=the best search agent
while (t < t_max)
    for each search agent
    Update a, A, C, l, and p
        if (p<0.5)
            if (|A| < 1)
                Update the position of the current search agent by Eq. (2)
            else if (|A|≥1)
                Select a random search agent (X_rand)
                Update the position of the current search agent by Eq. (9)
            end if
        else if (p ≥ 0.5)
                Update the position of the current search by Eq. (6)
        end if
    end for
    Check if any search agent goes beyond the search space, and amend it
    Calculate the fitness of each search agent
    Update X* if there is a better solution
    //Mutation process
    Define vector one_positions to store the locations of the selected features in X*
    Define X_mut= X*
    For i=1 to the length of one_positions
        idx= one_positions(i)
        Generate a random number r
        If (r < M_p(idx))
            X_mut(idx)= 0 while keeping the other features
            Fitness_mutated= the fitness of X_mut
            If (Fitness_mutated < Fitness)
                Fitness= Fitness_mutated
                X*= X_mut
            End if
        End if
    End for
    t=t+1
end while
return X*
```

Fig. 4. The proposed feature selection: MBWOA algorithm.

D. The Proposed Mutated Binary Whale Optimization Algorithm (MBWOA)

MBWOA was developed from BWOA by adding a mutation process, and Figure 4 shows its pseudocode. The mutation process was applied after the best search agent update process, with the hope that this process could increase exploration, resulting in a better subset of features in the feature selection results. The mutation process begins by determining the $one\_position$ and X_{mut} vectors. The $one\_position$ vector is employed to record the indices of selected features in the best solution vector (X^*). The mutated vector, denoted as X_{mut}, is derived from X^*. The mutation process is performed by comparing a randomly generated value r with the corresponding mutation probability value from the vector M_p. If r is less than the i-th element of M_p, the mutation is applied to the corresponding position in the solution vector. The value of r is a randomly generated value ranging from 0 to 1. M_p is a vector defined as in (11), where mp_i is the i-th mutation probability, which has a value between 0 and 1.

$$M_p = (mp_{1,}, mp_2, \dots, mp_n) \quad (11)$$

E. Performance Evaluation

The evaluation process involved several performance metrics, including accuracy (Acc), the number of selected features (NF), fitness value, and Time of Classification (TC). Accuracy was computed using (12) [32], while the fitness value was obtained through (10). In the context of multiclass classification, TP_i (True Positive) denotes the number of correctly predicted instances belonging to class i. Conversely, TN_i (True Negative) represents the number of instances accurately identified as not belonging to class i. FP_i (False Positive) corresponds to instances from other classes that were incorrectly classified as class i, whereas FN_i (False Negative) refers to instances from class i that were wrongly assigned to other classes.

$$Accuracy = \frac{\sum_{i=1}^{K} TP_i + TN_i}{\sum_{i=1}^{K} TP_i + TN_i + FP_i + FN_i} \quad (12)$$

III. RESULTS AND DISCUSSION

The testing of the proposed feature selection, namely MBWOA, was carried out with variations in mp_i values. This study tested mp_i values of 0.1 to 0.9 with an increment of 0.1. The test outcomes for both datasets are summarized in Table I.

TABLE I. TEST RESULTS OF THE PROPOSED METHOD

mp_i	RLD1 Dataset			RLD2 Dataset		
	Acc (%)	**NF**	**Fitness**	**Acc (%)**	**NF**	**Fitness**
0.1	94.44	36	0.0375	97.62	23	0.0251
0.2	94.44	22	0.0489	98.21	29	0.0249
0.3	88.89	25	0.0349	98.81	29	0.0259
0.4	94.44	24	0.0398	97.62	28	0.0272
0.5	88.89	21	0.0535	98.81	24	0.0222
0.6	88.89	22	0.0444	**99.41**	**29**	**0.0249**
0.7	**100.00**	**23**	**0.0345**	97.62	28	0.0241
0.8	94.44	15	0.0422	98.51	19	0.0248
0.9	88.89	14	0.0330	97.32	9	0.0236

In RLD1, the highest accuracy of 100% was achieved with 23 features and a fitness value of 0.0345, while in RLD2, the highest accuracy value reached 99.41% with 29 features and a fitness value of 0.0249. The smallest number of features is 14 in RLD1 and 9 in RLD2, at an mp_i value of 0.9 in both, but the accuracy was also the lowest.

MBWOA was compared with the BWOA feature selection, and Table II presents the results of this comparison. In RLD1, both BWOA and MBWOA achieved the same accuracy; however, MBWOA produced fewer features, smaller fitness values, and faster classification times. In RLD2, MBWOA produced higher accuracy, smaller fitness values, and shorter classification time, although the number of features was the same. Thus, the integration of a mutation algorithm into BWOA demonstrates a reduction in both fitness and classification time while maintaining classification accuracy or even increasing it. Figure 5 shows a comparison of the convergence of these two feature selection methods. Figure 5(a,b) shows that MBWOA (blue) exhibits faster convergence and lower fitness values than BWOA (red), indicating superior optimization performance. However, integrating the mutation mechanism into BWOA nearly doubled the Time of Feature Selection (TFS).

To assess its effectiveness, the proposed method was benchmarked against previous studies, as detailed in Table III. In [10], several stages were proposed, namely the segmentation process using the Otsu method, the feature extraction process comparing HOG and LBP descriptors, and the classification process using SVM with a Polynomial kernel. In [33], a CNN was used for the feature extraction process, comparing four classifiers: DT, SVM, KNN, and LR. In [25], three descriptors were combined: GLCM, LBP, and CH. The classification process uses RF, and no feature selection process was employed [25]. According to the results in the table, the proposed method consistently outperformed previous studies in accuracy on the RLD1 dataset, while in the RLD2 dataset, a clear advantage is shown over the methods in [10, 33].

TABLE II. COMPARISON OF MBWOA (PROPOSED METHOD) AND BWOA

	RLD1 Dataset		RLD2 Dataset	
	BWOA	**MBWOA**	**BWOA**	**MBWOA**
Acc (%)	**100.00**	**100.00**	98.81	**99.41**
NF	36	**23**	**29**	**29**
Fitness	0.0426	**0.0345**	0.0264	**0.0249**
TFS (s)	**1017.4536**	1955.9922	**2720.9870**	5247.7559
TC (s)	0.0823	**0.0809**	0.1081	**0.1015**

TABLE III. COMPARISON OF THE PROPOSED APPROACH AND PRIOR RESEARCH

Method	Acc (%)	
	RLD1 Dataset	**RLD2 Dataset**
HOG+SVM [10]	69.44	84.52
LBP+SVM [10]	72.22	89.58
CNN+DT [33]	83.33	91.96
CNN+SVM [33]	80.56	93.45
CNN+KNN [33]	86.11	93.45
CNN+LR [33]	58.33	50.89
(GLCM+LBP+CH)+RF [25]	97.22	**99.41**
Proposed	**100.00**	**99.41**

(a)

(b)

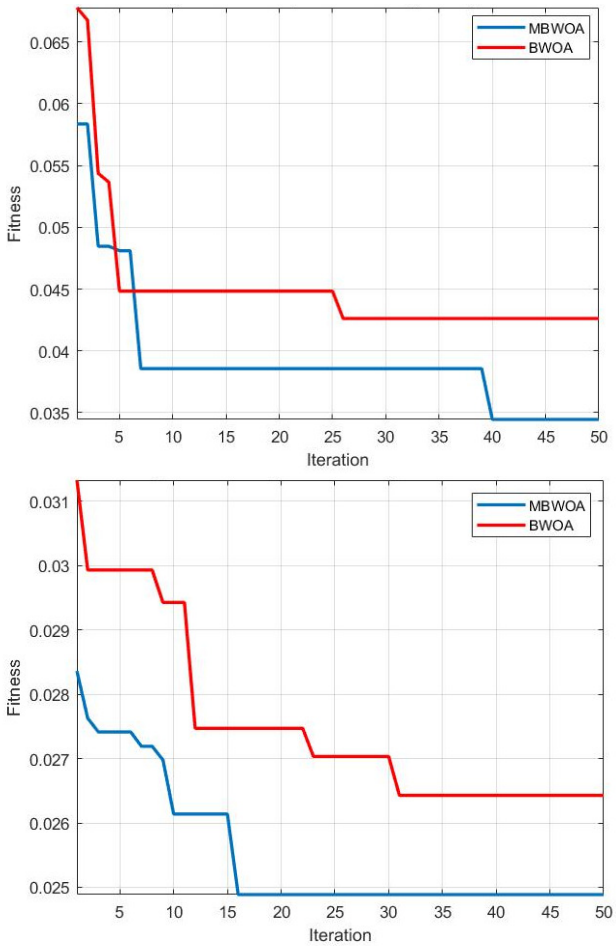

Fig. 5. Comparison of convergence between MBWOA and BWOA: (a) RLD1 dataset, (b) RLD2 dataset.

IV. CONCLUSION

This study presented a new feature selection algorithm that improves BWOA by adding a mutation process. The proposed method was named the Mutated Binary Whale Optimization Algorithm (MBWOA). BWOA tends to become stuck in local solutions when confronted with large-dimensional search spaces. The addition of a mutation process improves exploration capabilities and ensures that the best feature subset can be selected efficiently. Test results showed that adding a mutation algorithm to the BWOA feature selection can reduce fitness while increasing classification time, without decreasing accuracy. In addition, the proposed method yields higher accuracy compared to previous studies, such as those using the LBP+SVM and CNN+KNN methods. Even when applied to larger datasets, the proposed method demonstrates improved classification accuracy, achieving 100% on RLD1 and 99.41% on RLD2. However, integrating the mutation mechanism into BWOA nearly doubled the training time. Despite this, the method remains well-suited for tasks involving the classification or detection of rice leaf diseases.

REFERENCES

[1] "Rice." *USDA Foreign Agricultural Service* https://www.fas.usda.gov/data/production/commodity/0422110.

[2] N. Jiang *et al.*, "Resistance Genes and their Interactions with Bacterial Blight/Leaf Streak Pathogens (Xanthomonas oryzae) in Rice (Oryza sativa L.)—an Updated Review," *Rice*, vol. 13, no. 1, Dec. 2020, Art. no. 3, https://doi.org/10.1186/s12284-019-0358-y.

[3] B. S. Anami, N. N. Malvade, and S. Palaiah, "Deep learning approach for recognition and classification of yield affecting paddy crop stresses using field images," *Artificial Intelligence in Agriculture*, vol. 4, pp. 12–20, 2020, https://doi.org/10.1016/j.aiia.2020.03.001.

[4] N. Krishnamoorthy, L. V. N. Prasad, C. S. P. Kumar, B. Subedi, H. B. Abraha, and V. E. Sathushjunar, "Rice leaf diseases prediction using deep neural networks with transfer learning," *Environmental Research*, vol. 198, Jul. 2021, Art. no. 111275, https://doi.org/10.1016/j.envres.2021.111275.

[5] R. Yakkundimath, G. Saunshi, B. Anami, and S. Palaiah, "Classification of Rice Diseases using Convolutional Neural Network Models," *Journal of The Institution of Engineers (India): Series B*, vol. 103, no. 4, pp. 1047–1059, Aug. 2022, https://doi.org/10.1007/s40031-021-00704-4.

[6] C. J. N. Canlas *et al.*, "Camera Radial Distance-Based Accuracy of a Bacterial Blight, Brown Spot, and Rice Blast Plant Disease Identification System for Remote Communications," *Journal of Image and Graphics*, vol. 10, no. 4, 2022, https://doi.org/10.18178/joig.10.4.158-165.

[7] C. G. Simhadri and H. K. Kondaveeti, "Automatic Recognition of Rice Leaf Diseases Using Transfer Learning," *Agronomy*, vol. 13, no. 4, Mar. 2023, Art. no. 961, https://doi.org/10.3390/agronomy13040961.

[8] J. Deng *et al.*, "Deep-Learning-Based Rice Disease and Insect Pest Detection on a Mobile Phone," *Agronomy*, vol. 13, no. 8, Aug. 2023, Art. no. 2139, https://doi.org/10.3390/agronomy13082139.

[9] D. R. F. R. Anandhi and S. Sathiamoorthy, "Enhanced Sea Horse Optimization with Deep Learning-based Multimodal Fusion Technique for Rice Plant Disease Segmentation and Classification," *Engineering, Technology & Applied Science Research*, vol. 13, no. 5, pp. 11959–11964, Oct. 2023, https://doi.org/10.48084/etasr.6324.

[10] M. E. Pothen and M. L. Pai, "Detection of Rice Leaf Diseases Using Image Processing," in *2020 Fourth International Conference on Computing Methodologies and Communication (ICCMC)*, Erode, India, Mar. 2020, pp. 424–430, https://doi.org/10.1109/ICCMC48092.2020.ICCMC-00080.

[11] D. R. Sulistyaningrum, A. Rasyida, and B. Setiyono, "Rice disease classification based on leaf image using multilevel Support Vector Machine (SVM)," *Journal of Physics: Conference Series*, vol. 1490, no. 1, Mar. 2020, Art. no. 012053, https://doi.org/10.1088/1742-6596/1490/1/012053.

[12] D. Zhao *et al.*, "Study on the Classification Method of Rice Leaf Blast Levels Based on Fusion Features and Adaptive-Weight Immune Particle Swarm Optimization Extreme Learning Machine Algorithm," *Frontiers in Plant Science*, vol. 13, May 2022, Art. no. 879668, https://doi.org/10.3389/fpls.2022.879668.

[13] Sutikno, A. Harjoko, and Afiahayati, "Improving Detection Performance of Helmetless Motorcyclists Using the Combination of HOG, HOP, and LDB Descriptors," *International Journal of Intelligent Engineering & Systems*, vol. 15, no. 1, pp. 428–441, 2022.

[14] B. Remeseiro and V. Bolon-Canedo, "A review of feature selection methods in medical applications," *Computers in Biology and Medicine*, vol. 112, Sep. 2019, Art. no. 103375, https://doi.org/10.1016/j.compbiomed.2019.103375.

[15] J. Zhang, Y. Xiong, and S. Min, "A new hybrid filter/wrapper algorithm for feature selection in classification," *Analytica Chimica Acta*, vol. 1080, pp. 43–54, Nov. 2019, https://doi.org/10.1016/j.aca.2019.06.054.

[16] S. Mirjalili and A. Lewis, "The Whale Optimization Algorithm," *Advances in Engineering Software*, vol. 95, pp. 51–67, May 2016, https://doi.org/10.1016/j.advengsoft.2016.01.008.

[17] M. Abdel-Basset, D. El-Shahat, I. El-henawy, V. H. C. de Albuquerque, and S. Mirjalili, "A new fusion of grey wolf optimizer algorithm with a two-phase mutation for feature selection," *Expert Systems with*

Applications, vol. 139, Jan. 2020, Art. no. 112824, https://doi.org/10.1016/j.eswa.2019.112824.

[18] Sutikno, A. Harjoko, and Afiahayati, "Fusion of BIFFOA and Adaptive Two-Phase Mutation for Helmetless Motorcyclist Detection," *International Journal of Advanced Computer Science and Applications*, vol. 13, no. 1, 2022, https://doi.org/10.14569/IJACSA.2022.0130170.

[19] T. Setiady, "Leaf Rice Disease." Kaggle, [Online]. Available: https://www.kaggle.com/datasets/tedisetiady/leaf-rice-disease-indonesia.

[20] "Rice Leaf Diseases." Kaggle, [Online]. Available: https://www.kaggle.com/datasets/esc2023/rice-leaf-diseases.

[21] R. M. Haralick, K. Shanmugam, and I. Dinstein, "Textural Features for Image Classification," *IEEE Transactions on Systems, Man, and Cybernetics*, vol. SMC-3, no. 6, pp. 610–621, Nov. 1973, https://doi.org/10.1109/TSMC.1973.4309314.

[22] L. K. Soh and C. Tsatsoulis, "Texture analysis of SAR sea ice imagery using gray level co-occurrence matrices," *IEEE Transactions on Geoscience and Remote Sensing*, vol. 37, no. 2, pp. 780–795, Mar. 1999, https://doi.org/10.1109/36.752194.

[23] T. Ojala, M. Pietikäinen, and D. Harwood, "A comparative study of texture measures with classification based on featured distributions," *Pattern Recognition*, vol. 29, no. 1, pp. 51–59, Jan. 1996, https://doi.org/10.1016/0031-3203(95)00067-4.

[24] M. J. Swain and D. H. Ballard, "Color indexing," *International Journal of Computer Vision*, vol. 7, no. 1, pp. 11–32, Nov. 1991, https://doi.org/10.1007/BF00130487.

[25] Sutikno, H. A. Wibawa, and D. H. Ballard, "Improving Classification Performance of Rice Leaf Diseases using the Combination of GLCM, LBP, and CH Descriptors." 2025.

[26] L. Breiman, "Random Forests," *Machine Learning*, vol. 45, no. 1, pp. 5–32, Oct. 2001, https://doi.org/10.1023/A:1010933404324.

[27] P. Mekha and N. Teeyasuksaet, "Image Classification of Rice Leaf Diseases Using Random Forest Algorithm," in *2021 Joint International Conference on Digital Arts, Media and Technology with ECTI Northern Section Conference on Electrical, Electronics, Computer and Telecommunication Engineering*, Cha-am, Thailand, Mar. 2021, pp. 165–169, https://doi.org/10.1109/ECTIDAMTNCON51128.2021.9425696.

[28] S. M. Shahidur Harun Rumy, Md. I. Arefin Hossain, F. Jahan, and T. Tanvin, "An IoT based System with Edge Intelligence for Rice Leaf Disease Detection using Machine Learning," in *2021 IEEE International IOT, Electronics and Mechatronics Conference (IEMTRONICS)*, Toronto, Canada, Apr. 2021, pp. 1–6, https://doi.org/10.1109/IEMTRONICS52119.2021.9422499.

[29] M. Mafarja and S. Mirjalili, "Whale optimization approaches for wrapper feature selection," *Applied Soft Computing*, vol. 62, pp. 441–453, Jan. 2018, https://doi.org/10.1016/j.asoc.2017.11.006.

[30] K. Widarsono, A. Soeprijanto, and R. S. Wibowo, "Improved Whale Optimization Algorithm for Dynamic Optimal Power Flow with Renewable Energy Penetration," *Engineering, Technology & Applied Science Research*, vol. 15, no. 1, pp. 20379–20387, Feb. 2025, https://doi.org/10.48084/etasr.9662.

[31] Y. Hou, J. Li, H. Yu, and Z. Li, "BIFFOA: A Novel Binary Improved Fruit Fly Algorithm for Feature Selection," *IEEE Access*, vol. 7, pp. 81177–81194, 2019, https://doi.org/10.1109/ACCESS.2019.2917502.

[32] M. Paliwal and U. A. Kumar, "Neural networks and statistical techniques: A review of applications," *Expert Systems with Applications*, vol. 36, no. 1, pp. 2–17, Jan. 2009, https://doi.org/10.1016/j.eswa.2007.10.005.

[33] S. S. Pandi, K. D. Kumar, K. Raja, and A. Senthilselvi, "Rice Plant Leaf Disease Classification using Machine Learning Algorithm," in *2024 2nd International Conference on Advancement in Computation & Computer Technologies (InCACCT)*, Gharuan, India, May 2024, pp. 59–63, https://doi.org/10.1109/InCACCT61598.2024.10551249.