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Enhance Support Vector Machine models for Cassava leaf disease variants identification and classification

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Abstract

Cassava is one of the two main staple crops grown and consumed in large quantities in Nigeria and despite its usefulness and benefits to mankind, cassava is susceptible to various diseases such as “cassava mosaic disease (CMD)”, “cassava green mottle disease (CGMD)”, “cassava bacterial blight disease (CBBD)”, and “cassava brown streak disease (CBSD)”. It is very tedious and inaccurate to identify cassava disease on its plant leaves physically, but failure to detect the disease on time affects both the quality and quantity of the product. Therefore, many researchers have developed different classification models based on machine learning techniques to detect disease on plant leaves, but many of these models are easily influenced by imbalanced datasets, the selection of irrelevant features, and fine-tuning of the hyperparameters in the classifier. Therefore, this study uses an equal number of datasets for the diseased dataset, and hybridises Binary Particle Swarm Optimisation (BPSO) with Reptile Search Algorithm (RSA) to fine-tune and select discriminating hyperparameters in the Support Vector Machine (SVM). A classification model (i.e., BPSO-RSA-SVM) was developed, trained and tested with the datasets. The results were compared with other state-of-the-art models. It was found that the BPSO-RSA-SVM achieved an accuracy of 96.73% compared with both BPSO-SVM and RSA-SVM models that achieved an accuracy of 95.51% and 94.25%, respectively. These results affirmed that hybridising two or more optimisation techniques will improve the performance of the classification model. Therefore, it is recommended that the model (BPSO-RSA-SVM) be used to detect other plant diseases on plant leaves.

Keywords: Binary Particle Swarm Optimisation, Cassava, Cassava Green Mottle Disease, Hybridises, Hyperparameter

1. Introduction

Cassava plants can grow on many continents, including Africa, Asia, and South America, because of their ability to adapt to harsh soil conditions and complex climates [1]. Cassava is the second-largest food crop in Sub-Saharan Africa after maize. More than 500 million people in Africa consume cassava daily, making it one of the continent’s most important staple foods. But numerous pests and diseases, including the “cassava bacterial blight (CBB)”, the “cassava brown streak disease (CBSD)”, the “cassava green mite (CGM)”, and the “cassava mosaic disease (CMD)”, seriously jeopardise crop yield [2]. Cassava disease can generally be diagnosed according to the shape, color, and leaf shape characteristics of the disease spots on cassava leaves [3]. However, it is challenging to recognize plant diseases by optically analyzing their signs on plant leaves. Skilled agronomists and plant pathologists frequently require help to accurately diagnose certain diseases due to the diverse array of cultivated plants and psychopathological issues, resulting in incorrect diagnoses and treatments [4].

Moreover, this study is an extended version of the paper presented at the 17th International Multi-Conference on Applications of ICT to Teaching, Research, and Administration (AICTTRA, 2024) titled “Classification and Detection of Cassava Leaf Disease Variants using Hybrid Machine Learning Technique”. However, in this extended version, three cassava diseases are considered instead of two in the conference paper, making the total dataset obtained increase from 1,248 to 1,714. Also, three classification models were developed in this extended version compared to only the hybridised classification model developed in the conference paper.

Many researchers in plant leaf disease classification have developed several classification models which utilize the combination of computer vision, image processing, and machine learning techniques. [5] Developed two classification models using 18,000 image datasets obtained from Bowen University's cassava fields in Iwo. A bag of features was used to extract the features, and principal component analysis (PCA) was used to select relevant features. The “Coarse Gaussian Support Vector Machine (CGSVM)” and the “Cubic Support Vector Machine (CSVM)” classification models were created for illness identification and were both tested using five (5) fold cross-validation.

[7] Created a machine-learning model to identify and classify diseases affecting maize using k-means clustering. 4188 photos of maize leaves were selected from the Kaggle village collection. The affected leaf region was created by image clipping, and contrast was enhanced using the histogram equalisation algorithm. While MATLAB's colour thresholder apps were used to complete the thresholding and masking processes to isolate the leaf images from their background, images with noise were subjected to median filtering. Next, the “support vector machine” was utilised in the development of the suggested classification model.

Furthermore, [8] proposed the detection of rice plant leaf disease using the Gabor wavelet and Harris Corner-based feature. The researchers used photos from the Plant Village Dataset to identify rice plant leaf diseases. The original image is resized to 300 by 450 pixels, and colour moments were used to extract two colour features (i.e., “mean” and “standard deviation”). Nonetheless, the techniques of Harris Corner and Gabor Wavelet are employed to extract textural features. The optimal features are then chosen from the collected features using the "binary particle swarm optimisation (BPSO)". Three rice diseases are identified by classifying the selected features using a Random Forest Classifier: "Brown-spot", "Bacterial Leaf Blight", and "Leaf Smut". [9] Developed an optimized support vector machine classification model for the classification of apple fruit diseases. 469 datasets were acquired by the authors from the Plant Village dataset. Numerous methods of data augmentation, including "rotation range, rescale, zoom range, horizontal flip, shear range, vertical flip, and closest fill mode", were used to obtain 3346 datasets. Subsequently, 128 X 128-pixel sizes were applied to every dataset. To extract features, "principal component analysis" was employed, and an FA+SVM classification model was produced.

However, it was observed that many researchers in plant leaf disease identification and classification used imbalanced datasets to train and test their classification models, which may lead to performance bias in favour of a specific plant illness. Also, some of these studies failed to reduce the dimensionality of the features extracted and superfluous characteristics of the dataset could lead to overfitting of the classification model, increase false positive rates, and computational complexity of the model [10]. Moreover, choosing the best feature selection method and selecting the finest features from a range of features that have been extracted can be challenging [11].

In addition, some of the researchers inappropriately split the datasets obtained into training and testing datasets, which may cause overfitting of the classification model. Support Vector Machine (SVM) is one of the machine learning techniques widely used in classification problems because of its fewer parameters (i.e., regularization parameter, penalty cost C, and kernel function), but optimising these parameters is a challenging task due to the difficulty of fine-tuning them. However, several researchers used optimisation techniques such as Binary Particle Swarm Optimisation (BPSO), Reptile Search Algorithm (RSA), and Grey Wolf Optimiser (GWO). Although optimisation algorithms have a great deal of experience in solving optimisation issues, including choosing the best feature subset (OFS) and fine-tuning the classifiers' hyperparameters. However, they sometimes experience premature convergence, population diversity, stagnation, and imbalanced exploitation and exploration search behaviour [10].

Therefore, this study resolved the issue of an imbalanced dataset by using an equal number of datasets for the diseased dataset. Also, a 10-fold cross-validation approach was used to split the datasets into training datasets and testing datasets to avoid the overfitting of the classification model. Finally, this study used BPSO, RSA and hybridised (i.e., BPSO-RSA) techniques to fine-tune the parameters of the SVM, resolve issues affecting the optimisation techniques and develop the classification models (i.e., BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM) for the classification of cassava diseases. The model won't be able to learn local features with background interference, and BPSO-RSA will stop the model from overfitting and missing significant target regions.

The main contributions of this study can be summarised as follows:

- To avoid overfitting, stagnation, and stuckness in a local optimum, the recently developed BPSO-SVM, RSA-SVM, and hybrid multiclass classification model of BPSO-RSA-SVM integrates BPSO and RSA in a parallel mechanism to eliminate redundant and unnecessary components.

- A hybrid BPSO-RSA approach enhances the hybrid model's search exploration and exploitation capabilities, promotes quicker convergence, and prevents getting stuck in a single metaheuristic algorithm in the local optimum.

- A refined Multiclass Support Vector Machine classification models (BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM) that adjusts the SVM classifier's parameters (penalty cost, C, and kernel function, γ) lowers the false positive rate and increases the system's classification accuracy for a specific set of diseases affecting the cassava were developed.

- This work advances the understanding of computer vision, particularly pattern recognition, by adding fresh findings to crop leaf disease categorisation models.

- The experimental results show that the model has low computational complexity and a minimum computational load; therefore, it can be used in real-time applications requiring high classification accuracy.

2. Materials and Methodologies

The gathered cassava dataset, preprocessing techniques, segmentation, feature extraction, and suggested models' architectures for classifying images of cassava leaves are all covered in detail in this section.

2.1 Dataset

The dataset for this study was obtained from the Kaggle village dataset because many researchers have extensively used the data obtained in this open-source data repository to train and validate their models, and the performance of their models is excellent. The datasets in the Kaggle village dataset were of high quality, making them suitable for training and testing models. As a result, the obtained dataset includes 1,714 images of cassava leaves, 466 images of cassava bacterial blight disease (CBBD), 466 images of cassava green mottle or mite disease (CGMD), 466 images of cassava mosaic disease (CMD), and 316 images of healthy cassava leaves. Figure 1 shows images of cassava leaves used in the study. The images of cassava leaves had a resolution of 512 X 512 pixels. These datasets were divided into training and testing sets using 10-fold cross-validation. For each diseased dataset, 419 images were used for training and 47 for testing. Table 1 shows that for healthy leaves, 284 images were used for training and 32 images for testing, respectively.

2.2 Preprocessing

To streamline the classification model and remove extraneous pixel information, the acquired images were first resized from 512 X 512 pixels resolution to 256 X 256 pixels resolution. After converting the RGB images to grayscale, the bi-histogram equalisation technique was applied to further improve the contrast of the images. Morphological filtering was used to sharpen the image, and adaptive median filtering was used to remove noise. The lesion was distinguished from the leaf's uninfected region using the Sobel edge detection technique. Then, colour, texture, and shape features were extracted using the Gray-Level Co-occurrence Matrix, for the texture and shape features and four colour moments for the colour features.

2.3 Algorithm 3.1: Binary Particle Swarm Optimisation (BPSO) Model (Source: [17])

```
1: Initialise the particles' position ($Z_{i,j}^{f}$), the velocity constant ($Vel_c$), previous best position ($h_{i,j}^{f}$), acceleration coefficient (c1: factor of constant cognitive, c2: factor of social scaling), number of particles (N), maximum and minimum values in the continuous feature vector ($Y^{max}$, $Y^{min}$), set Iteration f=0, and maximum number of iterations (F$max$)
2: Evaluate inertial weight $\omega$ using
       $Y(t) = Y^{max} - \frac{(Y^{max} - Y^{min})\ X\ Fi}{Fmax}$
3: Evaluate maximum velocity ($v_{max}$) using
       $Vel_{max} = \left(e^{1-f/F\max}\right) Vel_c$
4: while (f < F$max$) do
5:   For all particles (i) do
6:     Using the current position $z_{i,j}^{t}$ of the i^th as a starting point, calculate each particle's performance L (L ($z_{i,j}^{f}$)) using $z_{i,j}^{(f+1)} = z_{i,j}^{f} + vel_{i,j}^{(f+1)}$
7:     Evaluate every single individual's performance with their greatest hitherto:
         If L ($z_{i,j}^{f}$) < L ($h_{i,j}^{f}$) then
           $h_{i,j}^{f} = z_{i,j}^{f}$
         End if
8:     Each particle's performance is compared to the universal best particle.
         If L ($z_{i,j}^{f}$) < L ($h_{g,j}^{f}$) then
           $h_{g,j}^{f} = z_{i,j}^{f}$
         End if
9:     Update the new velocity of particle i^th ($vel_{i,j}^{(f+1)}$) using $vel_{i,j}^{ft+1)} = \omega vel_{i,j}^{f} + c_1 r_1[h_{i,j}^{f} - z_{i,j}^{f}] + c_2 r_2[h_{g,j}^{f} - z_{i,j}^{f}]$
10:    Update the new position of particle ith ($z_{i,j}^{(t+1)}$) using
         If rnd() < P($vel_{i,j}$), then $z_{i,j} = 1$; else $z_{i,j} = 0$;

         where
           $P(\upsilon) = \frac{1}{1 + e^{-\upsilon el(i,j)}}$
           $z_{i,j}^{(f+1)} = z_{i,j}^{f} + vel_{i,j}^{(f+1)}$
   End for
11:  If ($vel_{(i,j)} > vel_{max}$)
```

```
        $vel_{(i,j)} = vel_{max}$
        Endif
12  If ($vel_{(i,j)} < -vel_{max}$)
        $vel_{(i,j)} = -vel_{max}$
        Endif
13: Increase the number of iterations f= f + 1
14: If f > Fmax, then move to step 15; otherwise
        step 5
    End while
15: Return gbest ($h_{g,j}^{f}$)
```

2.3 Algorithm 3.2: Reptile Search Algorithm (RSA) Model (Source:[17])

1. Initialise the RSA parameters, number of features (M), minimum and maximum features boundaries (Lw, Up), a sentient specification that governs the global optimum performance (δ), two parameters factors that contribute to the quality of the classification model (θ and μ), number of population (Po), set iteration f=0, and the highest number of repetitions (F)

2. Generate an initial population randomly using $Z_{i,j} = random \times (Up - Lw) + L_b$, for $a \,\varepsilon\, \{1,\dots,P)$ and $k \in \{1,\dots, M)$

3: while f < F) do

4: For all populations (Po) do

5: Update RSA parameters using

$$\Psi_{i,}^{f} = B_j^{f} \, X \, P_{i,k}$$

$$P(t) = \delta + \frac{z_{(i,k)} - M(z_i)}{B_k(t) \times \left(U_{(k)} - L_{(k)}\right) + \varepsilon}$$

$$M(z_i) = \frac{1}{i} \sum_{k=1}^{i} z_{(i,k)}$$

$$R_{(i,k)}(t) = \frac{B_j(t) - z_{(r2,k)}}{B_k(g) + \varepsilon}$$

$$ES(f) = 2 \times r_3 \times \left(1 - \frac{1}{F}\right)$$

where, $\Psi_{i,j}{}^{t}$ represents the operator for hunting for kth place in the i^{th} solution, the reducing function $R_{i,k}$, is used to decrease the search region. ES(f) was used for the probability ratio reducing from 2 to-2 over iterations. ε is a modest floor value, δ represents a sensitive parameter controlling exploration performance, and $M(z_i)$ signifies the average solution.

6: Perform Exploration Mechanisms (i.e., global search) using

$$Z_{i,k}^{(f+1)} = B_k^{f} \; X \; \Psi_{i,k}^{f} \; X \; \beta \text{ - } R_{i,k}^{f} \; X \; random, \quad f \leq F^{*}.25 \quad Z_{i,k}^{(f+1)} = B_k^{f} \; X \; Z_{(random \;\varepsilon\; [1,Po],,k)} \; X \; ES^{f} \; X \; random \quad f \leq 2(F^{*}.25) \; and \; f > F^{*}.25$$

7: Perform Exploitation Mechanisms (i.e. local search) using

$$Z_{i,k}^{(f+1)} = B_k^{f} - \Psi_{i,k}^{f} \; X \; \varepsilon \text{ - } P_{i,k}{}^{f} \; X \; random, \quad f \leq 3(F^{*}.25) \; and \; f > 2(F^{*}.25)$$

$$Z_{i,k}^{(f+1)} = B_k^{f} - \Psi_{i,K}^{f} \; X \; \varepsilon \text{ - } P_{i,k}{}^{f} \; X \; random, \quad f \leq F \; and \; f > 3(F^{*}.25)$$

8. End for

9. Increase the iteration f=f+1

10 If f>F, move to step 11; otherwise, step 4

11. End while

12. Return the best position

2.4 Formulation of the Hybrid Model (BPSO-RSA) Model

[18], [19], and [20] claim that while BPSO is reliable for handling challenging optimization problems, its quick convergence can easily trap the swarm inside certain local optima. Recently, the reptile search algorithm was developed as a novel optimization technique; however, it still has certain drawbacks, including highly complex computations, sluggish convergence, as well as

neighbourhood minimum trapping [21]. Multiple local optima may arise in the large solution space due to the presence of unnecessary and redundant features [22].

However, these local optimum points can seriously impede the RSA and BPSO algorithms' ability to reach the global optimum, which could result in feature subsets that are not optimal. The hybrid optimiser successfully exploits the strengths of both BPSO and RSA techniques to provide promising candidate solutions and realise global optima efficiency. In this study, the BPSO and RSA work together in a parallel manner to address the problems of early convergence, stagnation, and population diversity, as well as to maintain a harmony between the capabilities of local and global search behaviours of both algorithms. The primary objective of the parallel mechanism is to shift the existing potential solutions to a different seeking zone if one of the algorithms is unable to enhance the potential solutions or gets trapped in the local optimal region. Algorithm 3.1 provides the pseudo-code for the BPSO-RSA Hybrid model.

2.4.1 Algorithm 3.3: Binary Particle Swarm Optimisation-Reptile Search Algorithm (BPSO-RSA) Model

1. Initialise BPSO parameters POP (number of particles), $w_{i,j}^{f}$ (particle position), h_a previous best position), vl_c (velocity constant), p (initial

   iteration), P (permitted number of iterations)

2. Assign the RSA parameters their initial values.: ϕ (sensitive parameter that governs the performance of the exploration), POP (population number), Y (number of features), Upp (upper feature boundaries), Low (lower feature boundaries), p (first iteration), and P (maximum iteration).

3. Set the shared parameters POP (population number), YY (feature number), and p (maximum number of iterations) to their initial values.

4. For p = 1 to P do

5. Split candidate solutions for BPSO and RSA using

$$W_{i\,(BPSO-RSA)} = \begin{cases} z_i^{BPSO} & 1 \le i \le POP/2 \\ z_{i\,RSA} & POP/2 < i \le POP \end{cases} \quad (3.1)$$

6. Update the potential candidate solutions (z_i,) for BPSO using the BPSO Algorithm and RSA
   Algorithm
7. Assess the updated candidate solutions from both algorithms using the fitness function below

$$FitFun = \eta \times \left(1 - \frac{POP_c}{POP}\right) + \mu \times \frac{da_i}{Y} \quad (3.2)$$

8. Update the BPSO and RSA solutions for the upcoming iteration using

$$W_a^{BPSO}(p+1) = w_i^{RSA}(p+1) = w\hat{}a(p) \quad 1 \le i \le POP/2 \quad (3.3)$$

where $w\hat{}_i(p) = w_{argmin(pi(t))}{}^{(g)}$

9. Determine the entire candidate solution for the subsequent iteration. Using

if dimension (argminimum fitness$_i$ ≤ X/2) > dimension (argminimum fitness$_i$ ≤ Z/2) then BPSO dominate (a + 1) iteration

if dimension (argminimum fitness ≤ Z/2) < dimension (argminimum fitness$_i$ ≤ Z/2) then RSA dominate (a + 1) iteration

if dimension (argminimum fitness$_i$ ≤ Z/2) = dimension (argminimum fitness$_i$ ≤ Z/2) then BPSO & RSA dominate (a +1) iteration

(3.4)

10. end for
11. Provide the optimal contender solution with the lowest Fitness Function.

3. Results

The BPSO-RSA-SVM classifiers are used to classify leaves in the trained and tested datasets for cassava mosaic disease (CMD), cassava green mottle or mite disease (CGMD), and all cassava disease datasets.

3.1 Result of Performance Evaluation Metrics of the Classification Model on the Cassava Datasets

The outcomes displayed in Table 2 showed that there is a higher rate of misclassification in All cassava diseased datasets than in other cassava datasets. For instance, 33,36, and 27 were misclassified as healthy cassava leaves rather than diseased by BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM models, respectively. Similarly, 40, 45, and 33 were misclassified as disease rather than healthy cassava leaves by BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM models, respectively. Also, when comparing all three diseased datasets (i.e., CBBD, CGMD, and CMD). There is a higher rate of misclassification in CGMD datasets than in other datasets. Likewise, when comparing all three models, there is a higher rate of misclassification by the RSA-SVM model than the others.

(a)

(b)

(c)

Figure 1: Samples of the Cassava Dataset used for the study (a) Cassava Mosaic Disease (CMD), (b) Cassava Bacterial Blight Disease (CBBD), (c) Cassava Green Mottle/Mite Disease (CGMD), (d) Healthy Cassava Leaf (Source: Kaggle Village Dataset)

Table 1: Distribution of the Cassava dataset acquired from Kaggle Village Datasets

Class	Content	Number of Images per Class	No. of Train Data	No. of Test Data
1	Cassava Bacterial Blight Disease (CBBD)	466	419	47
2	Cassava Mosaic Disease (CMD)	466	419	47
3	Cassava Green Mite/ Mottle Disease (CGMD)	466	419	47
4	Healthy Cassava Leaves	316	284	32
	TOTAL	**1,714**	**1,532**	**173**

Moreover, results in Table 3 show that the BPSO-RSA-SVM model outperforms both BPSO-SVM and RSA-SVM with 5.22%, 94.78%, 97.27%, 97.63%, 96.73%, and 59.57 sec of false positive rate, specificity, sensitivity, precision, accuracy, and computation time, respectively. Also, the BPSO-SVM model outperforms the RSA-SVM in terms of all performance evaluation metrics except computation time. BPSO-SVM achieved 7.04%, 92.96%, 96.30%, 96.64%, 95.51%, and 82.31 seconds of false positive rate, specificity, sensitivity, precision, accuracy, and computation time, respectively. However, the RSA-SVM model achieved a false positive rate of 8.86%, specificity of 91.14%, sensitivity of 95.28%, precision of 95.58%, and accuracy of 94.25% at 68.78 seconds

Furthermore, results in Table 4, Table 7, and Table 9 show that the BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM classification models are statistically significant since the p-values for all the performance evaluation metrics used to evaluate the classification model are less than 0.05.

Table 2: Outcomes of the Misclassification of the Models' Performance on the Cassava Datasets

	All Cassava Disease Datasets	Cassava Bacterial Blight Disease (CBBD)	Cassava Green Mottle Disease (CGMD)	Cassava Mosaic Disease (CMD)
TP				
BPSO-SVM	1365	448	445	447
RSA-SVM	1362	441	442	439
BPSO-RSA-SVM	1371	452	451	453
FN				
BPSO-SVM	33	18	21	19
RSA-SVM	36	25	24	27
BPSO-RSA-SVM	27	14	15	13
FP				
BPSO-SVM	40	15	18	16
RSA-SVM	45	22	21	24
BPSO-RSA-SVM	33	11	12	10
TN				
BPSO-SVM	276	301	298	300
RSA-SVM	271	294	295	292
BPSO-RSA-SVM	283	305	304	306

Table 3: Outcomes of the Classification Models' Performance Evaluation Metrics on the Cassava Datasets

	Cassava Bacterial Blight Disease (CBBD)	Cassava Green Mottle Disease (CGMD)	Cassava Mosaic Disease (CMD)	All Cassava Disease Datasets	Average
FPR (%)					
BPSO-SVM	4.75	5.70	5.06	12.66	7.04
RSA-SVM	6.96	6.65	7.59	14.24	8.86
BPSO-RSA-SVM	3.48	3.80	3.16	10.44	5.22
Specificity (%)					
BPSO-SVM	95.25	94.30	94.94	87.34	92.96
RSA-SVM	93.04	93.35	92.41	85.76	91.14
BPSO-RSA-SVM	96.52	96.20	96.84	89.56	94.78
Sensitivity (%)					
BPSO-SVM	96.14	95.49	95.92	97.64	96.30
RSA-SVM	94.64	94.85	94.21	97.42	95.28

BPSO-RSA-SVM	97.00	96.78	97.21	98.07	97.27
Precision (%)					
BPSO-SVM	96.76	96.11	96.54	97.15	96.64
RSA-SVM	95.25	95.46	94.82	96.80	95.58
BPSO-RSA-SVM	97.62	97.41	97.84	97.65	97.63
Accuracy (%)					
BPSO-SVM	95.78	95.01	95.52	95.74	95.51
RSA-SVM	93.99	94.25	93.48	95.27	94.25
BPSO-RSA-SVM	96.80	96.55	97.06	96.50	96.73
Computation Time (sec)					
BPSO-SVM	51.86	51.80	50.12	175.46	82.31
RSA-SVM	52.92	50.70	52.40	137.07	68.78
BPSO-RSA-SVM	40.27	40.34	41.01	116.66	59.57

Table 4: One Sample Statistics (BPSO-SVM Model)

Performance Metrics	N	Mean	Std. Deviation	Std. Error Mean
Accuracy	16	95.44	0.54	0.14
False Positive Rate	16	7.99	3.51	0.88
Specificity	16	92.01	3.51	0.88
Sensitivity	16	96.53	0.80	0.20
Precision	16	96.33	1.01	0.25
Computational Time	16	82.24	56.31	14.01

Table 5: One Sample Statistics (BPSO-SVM Model)

					95% Confidence Interval of the Difference	
Performance Metrics	**T**	**Df**	**Sig. (2-tailed)**	**Mean Difference**	**Lower**	**Upper**
Accuracy	703.66	15	0.00	95.44	95.15	95.73
False Positive Rate	9.11	15	0.00	7.99	6.12	9.86
Specificity	104.96	15	0.00	92.01	90.14	93.88
Sensitivity	482.64	15	0.00	96.53	96.10	96.96
Precision	381.12	15	0.00	96.3	95.79	96.87
Computational Time	5.84	15	0.00	82.24	52.23	112.24

Table 6: One Sample Statistics (RSA-SVM Model)

Performance Metrics	N	Mean	Std. Deviation	Std. Error Mean
Accuracy	16	94.15	0.95	0.24
False Positive Rate	16	9.89	3.33	0.83
Specificity	16	90.11	3.33	0.83
Sensitivity	16	95.50	1.23	0.31
Precision	16	95.25	1.38	0.35
Computational Time	16	72.73	37.46	9.37

Table 7: One Sample Statistics (RSA-SVM Model)

					95% Confidence Interval of the Difference	
Performance Metrics	**T**	**Df**	**Sig. (2-tailed)**	**Mean Difference**	**Lower**	**Upper**
Accuracy	396.48	15	0.00	94.15	93.64	94.65
False Positive Rate	11.88	15	0.00	9.89	8.11	11.66
Specificity	108.26	15	0.00	90.11	88.34	91.89
Sensitivity	309.95	15	0.00	95.50	94.84	96.15
Precision	275.44	15	0.00	95.25	94.52	95.99
Computational Time	7.77	15	0.00	72.73	52.77	92.69

Table 8: One Sample Statistics (BPSO-RSA-SVM Model)

Performance Metrics	N	Mean	Std. Deviation	Std. Error Mean
Accuracy	16	96.62	0.30	0.07
False Positive Rate	16	6.17	3.27	0.82
Specificity	16	93.83	3.27	0.82
Sensitivity	16	97.48	0.47	0.12
Precision	16	97.27	0.75	0.19
Computational Time	16	60.04	34.14	8.54

Table 9: One Sample Statistics (BPSO-RSA-SVM Model)

					95% Confidence Interval of the Difference	

Performance Metrics	T	Df	Sig. (2-tailed)	Mean Difference	Lower	Upper
Accuracy	1279.92	15	0.00	96.62	96.46	96.78
False Positive Rate	7.54	15	0.00	6.17	4.42	7.91
Specificity	114.70	15	0.00	93.83	92.09	95.57
Sensitivity	830.95	15	0.00	97.48	97.23	97.73
Precision	522.24	15	0.00	97.27	96.88	97.67
Computational Time	7.03	15	0.00	60.04	41.84	78.23

3.2 Comparison Results of the Classification Model with the Existing Cassava and Some Other Crops Classification Models

The developed classification model's comparison results with those of other existing classification models are shown in Table 10. The methodology of this study is comparable to that of [6], [23], and [9] that optimise the support vector machine with Flower Pollination Algorithm (FPA), Particle Swarm Optimisation (PSO), and Firefly Algorithm (FA), respectively. The BPSO-RSA-SVM model outperformed the Random Forest model developed by [12] regarding specificity, sensitivity, accuracy, and computational time. Also, the BPSO-RSA-SVM outperformed (KNN, SVM & DT), FPA-KNN, T-RNet*, (VGG16 & EfficientNet with Transfer Learning), and FA-SVM models developed by [26], [23], [16], [13], and [9], respectively, in terms of sensitivity, precision and accuracy.

Moreover, the BPSO-RSA-SVM model outperformed the SVM model developed by [7] in terms of specificity and sensitivity. In addition, the BPSO-RSA-SVM outperformed the CSVM & CGSVM and PSO-SVM models developed by [5] and [6] in terms of accuracy. Similarly, MKSVM, FPA-SVM, and ECNN models developed by [24], [23], and [15], respectively, outperformed the BPSO-RSA-SVM model. However, the EKNN model developed by [25] outperformed the BPSO-RSA-SVM in terms of specificity, sensitivity, precision, and accuracy. Also, the AlexNet, FPA-CNN, and CNN models developed by [26], [23], and [14], respectively, outperformed the BPSO-RSA-SVM in terms of sensitivity, precision, and accuracy. Moreover, the SVM and BPNN models developed by [12] outperformed the BPSO-RSA-SVM model in terms of specificity, sensitivity, and accuracy. Furthermore, the MKSVM model developed by [24] outperformed the BPSO-RSA-SVM model in terms of specificity and accuracy, while the FPA-SVM model developed by [23] outperformed the BPSO-RSA-SVM in terms of precision and accuracy. Finally, the SVM and ECNN models developed by [7] and [15] outperformed the BPSO-RSA-SVM model in terms of accuracy.

4. Discussion of the Findings

Table 2 shows that the All-diseased and CGMD datasets have higher misclassification rates than both the CMD and CBBD datasets. The All-diseased dataset has a higher misclassification rate than the other datasets because it includes both the CGMD and the CMD datasets. Furthermore, similarity in early characteristics of two or more diseases may confuse the classifier [27], crop-specific lesion phenotype patterns or features that differ between one diseased type and another [28], and similarities in geometric features between the disease type

[29], and multiple disease symptoms and altered symptoms features [30].

Moreover, the results in Table 3 showed that BPSO-RSA-SVM outperforms both the BPSO-SVM and RSA-SVM models in terms of all the performance evaluation metrics. One of the reasons why BPSO-RSA-SVM outperforms the other two models is that BPSO-RSA select discriminating parameters of the SVM and lesions of the disease features that are better than either BPSO or RSA. Also, BPSO-RSA operates in parallel, allowing one algorithm to push the other, which might be stuck in the local optimum, to a better search region to reach the global optimum. Similarly, BPSO-RSA resolves issues affecting both the algorithms' performances, such as premature convergence, getting stuck in local optimum, population diversity and high computation complexity.

Furthermore, the results in Table III showed that the BPSO-SVM model outperforms the RSA-SVM model in terms of all performance evaluation metrics except computation time. The reason for these results is that all the parameters (i.e., maximum velocity, inertia weight, acceleration coefficient, C1-cognitive factors, and C2–social factors) that affect the performance of BPSO were carefully chosen based on the literature. Linear decreasing inertia weight (LDIW) was used to compute the inertia weight (w), which maintains a balance between the exploration and exploitation capabilities of the BPSO. This process improves the BPSO's searching behaviour and keeps it from becoming stuck in the local optimum, as demonstrated by the use of chaotic dynamic adaptive adjustment techniques in studies by [31] and [32].

Table 10: Comparison of the Developed Multiclass Classification Model (i.e., BPSO-RSA-SVM) With Existing Cassava and Some Other Crops (Source: Ayoade et al., 2024b)

Authors & Model	No of Dataset	Classifier Optimized	Methodology	Specificity (%)	Sensitivity (%)	Precision (%)	Accuracy (%)	Time (Sec.)
Ibrahim *et al*. (2022)								
SVM	6,004	No	LBP-HOG, SVM	98.48	98.88	-	98.74	100.11
BPNN	6,004	No	LBP-HOG, BPNN	97.16	98.17	-	97.82	135.58
Random Forest	6,004	No	LBP-HOG, Random Forest	95.27	97.15	-	96.49	156.79
Jayanthi and Shashikumar (2020) MKSM	-	No	GLCM, MKSVM	99.02	97.34	-	97.34	-
Noola and Bassavaraju (2022) EKNN	3,820	No	HOG, EKNN	99.88	99.60	99.71	99.86	-
Emuoyibofarhe *et al.* (2019)								
CSVM	18,000	No	Bag of Features, PCA, CSVM				83.90	179.00
CGSVM	18,000	No	Bag of Features, PCA, CGSVM				61.60	175.00

Mohd Yusof and Nazari (2021) SVM	4,188	No	GLCM, K-Means Clustering Colour Thresholder Apps Features,SVM	85.05	90.64	-	97.33	-
Yag and Altan (2022)								
FPA-SVM	4,800	Yes	2D-DWT, FPA-SVM	-	96.44	97.58	97.54	-
FPA-CNN	4,800	Yes	2D-DWT, FPA-CNN	-	99.60	99.52	99.55	-
FPA-KNN	4,800	Yes	2D-DWT, FPA-KNN	-	93.82	94.25	93.97	-
Kour and Arora (2019) PSO-SVM	1,813	Yes	LBP, K-Mean Clustering, Histogram Equalization, PSO-SVM	-	-	-	95.23	-
KNN	90,483	No	LBP, PCA, KNN	-	95.96	96.33	96.33	-
SVM	90,483	No	LBP, PCA, SVM	-	90.40	92.29	90.40	-
DT	90,483	No	LBP, PCA, DT	-	NAN	87.00	88.58	-
AlexNet	90,483	No	LBP, PCA, AlexNet	-	99.86	99.92	99.85	-
Sufuoglu and Birant (2024) CNN	2152	No	CNN	-	97.84	97.94	98.28	-
Zhong *et al*. (2022) T-RNet*	21,397	N0	FAMP-Softmax, Grad_CAM, 2D T-SNE, T-RNet*	-	91.10	91.10	91.12	-
Lilhore *et* al. (2022) ECNN	6256	No	GAEPL, BNL, DBP, CLAHE, SMOTE, ECNN	-	87.85	96.09	99.30	-
Kalyani *et al*. (2023)								
VGG16	10,000	No	EfficientNet, Transfer Learning	-	87.94	88.01	91.11	-
EfficientNet with Transfer Learning	10,000	No	EfficientNet, Transfer Learning	-	80.60	80.40	89.00	-
Makrufi and Almaki (2022) FA-SVM	3346	Yes	PCA, FA-SVM	-	87.50	91.00	94.00	-
BPSO-RSA-SVM	1,248	Yes	GLCM, Colour Moment, Sobel Edge Detection, Adaptive Median Filtering, Bi-Histogram Equalization, Morphological	94.78	97.27	97.63	96.73	59.57

	Filtering, BPSO-RSA-SVM

More so, the results in Table X showed that the BPSO-RSA-SVM model outperformed the Random Forest model developed by [12], the (KNN, SVM, and DT) models developed by [26], and the SVM model developed by [7]. The reason for this is that the BPSO-RSA-SVM model had fewer datasets and classes than these models did. Additionally, the classifiers used in these models were not optimised. For example, [12], [26], and [7] used 6,004, 90,483, and 4,188 datasets, respectively, whereas the BPSO-RSA-SVM used only 1,248. Furthermore, the SVM classifier used in the developed model was optimised using two optimisation techniques (BPSO and RSA), resulting in a robust optimiser that selects discriminating classifier parameters and disease lesions that outperform these models.

Also, the results in Table 10 show that the BPSO-RSA-SVM model outperforms the CSVM and CGSVM models developed by [5]. For instance, the number of datasets used in their study is 18,000, which is significantly higher than the 1,248 used in BPSO-RSA-SVM. However, the reason why the performances of these two models are low compared with the BPSO-RSA-SVM is that, despite its strong theoretical foundations and high classification accuracy, normal SVM is unsuitable for classifying large data sets because SVM's training complexity is highly dependent on data set size [33].

In addition, the performance of the BPSO-RSA-SVM model outperformed the PSO-SVM model developed by [6] and the FPA-KNN model developed by [23]. The reason for this is that all of the optimisation techniques that can be used to optimise the classifier have issues that affect their performance, such as premature convergence, getting stuck in local optimal, population diversity, stagnation, and maintaining a balance between the exploration and exploitation capabilities of the optimization techniques is extremely difficult. However, many researchers overcome this problem by introducing some factors to improve the performance of the optimization technique, such as chaotic search and adaptive inertia weight factor used by [31] and [32] to improve BPSO, and some researchers combine two optimization techniques to resolve their issues, such as [34] that combine Cuckoo Search Algorithm (CS) with Particle Swarm Optimization (PSO) and [35] that combine Aquila Optimizer (AO) with the Whale Optimization Algorithm (WOA).

Moreover, the BPSO-RSA-SVM model outperforms the (VGG16 & EfficientNet with Transfer learning) and T-RNet* deep learning models created by [13] and [16]. The BPSO-RSA-SVM model outperforms T-RNet* because the T-RNet* model setup is too complex [36]-[37] or the data quality is low (Khang, 2023) because it was collected manually by the authors using a camera.

Similarly, the BPSO-RSA-SVM model outperforms VGG16 and EfficientNet with Transfer learning because these models used insufficient training data [37], and there is no evidence that learning parameters were carefully selected [36]. However, the performance of the EKNN, MKSVM, and SVM & BPNN models developed by [25], [24] and [12], respectively, was better than BPSO-RSA-SVM, although the classifiers used in their models were not optimised, as opposed to the developed model, which was optimised using two optimisation methods (BPSO & RSA).

These findings suggest that optimising the classifier in a classification model does not guarantee that the model's performance will be superior to that of non-optimised models.

Finally, the FPA-SVM model developed by [23] outperforms the BPSO-RSA-SVM model due to the Flower Pollination Algorithm‘s simplicity, flexibility, derivation-free mechanism, and avoidance of local optima [39]. Similarly, the deep learning models AlexNet, CNN ECNN, and FPA-CNN developed by [26], [14], [15], and [23] outperformed the BPSO-RSA-SVM model. One of the reasons is that deep learning models outperform machine learning models in terms of robustness, scalability, and generalisation [40]. Likewise, "In numerous fields, such as cybersecurity, natural language processing, bioinformatics, robotics and control, and medical information processing, among many others, the deep learning model has been shown to outperform popular machine learning techniques" [41]. Also, if the model setup is not complex [36]-[37], if the dataset is of good quality [38], if there is a sufficient training dataset [37], and if the learning parameters were carefully selected [36]. However, the use of a recently developed classification model (BPSO-SVM, RSA-SVM, and BPSO-RSA-SVM) in crop pathology will make early disease detection easier and less expensive. This new development will benefit many farmers and agriculturalists by preventing the spread of disease from sick to healthy crops. The proposed models will also prevent crop losses, such as a reduction in yield quantity and quality or a loss of agricultural fields and increase the efficacy of disease control strategies.

5. Conclusion and Future work

The detection and classification of diseases affecting cassava has become a primary research focus for many researchers due to its higher financial value than other staple crops and significant contribution to national income. To fine-tune the parameter in the support vector machine (SVM), this study developed a hybrid model that produced a dependable optimiser. The reptile search algorithm is used in tandem with binary particle swarm optimisation to address issues that affect each algorithm independently. As shown in Tables 3 and 6, the hybridisation of the two algorithms improves the performance of the BPSO-RSA-SVM classification model, explaining why it outperforms the previous models, even though they were deep learning models.

Future Work

Despite being optimised with two techniques, the majority of deep learning models outperformed the BPSO-RSA-SVM model. As a result, future work will collect large datasets or augment existing datasets, replace the support vector machine with a convolutional neural network (CNN), optimise it using two optimisation techniques (BPSO and RSA), and compare the results to the machine learning model developed. For the experimental analysis, a real-time environment with additional performance measurement parameters will be used.

6. References

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