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Soybean Plant Disease Classification using Archimedes Optimization Algorithm based Hybrid Deep Learning Model

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Abstract:

Bean which is botanically called *Phaseolus vulgaris* L belongs to the Fabaceae family. During bean disease identification, unnecessary economical losses occur due to the delay of the treatment period, incorrect treatment, and lack of knowledge. The existing deep learning and machine learning techniques met few issues such as high computational complexity, higher cost associated with the training data, more execution time, noise, feature dimensionality, lower accuracy, low speed, etc. To tackle these problems, we have proposed a hybrid deep learning model with an Archimedes optimization algorithm (HDL-AOA) for bean disease classification. In this work, there are five bean classes of which one is a healthy class whereas the remaining four classes indicate different diseases such as Bean halo blight, Pythium diseases, Rhizoctonia root rot, and Anthracnose abnormalities acquired from the Soybean (Large) Data Set. The hybrid deep learning technique is the combination of wavelet packet decomposition (WPD) and long short term memory (LSTM). Initially, the WPD decomposes the input images into four sub-series. For these sub-series, four LSTM networks were developed. During bean disease classification, an Archimedes optimization algorithm (AOA) enhances the classification accuracy for multiple single LSTM networks. MATLAB software implements the HDL-AOA model for bean disease classification. The proposed model accomplishes lower MAPE than other exiting methods. Finally, the proposed HDL-AOA model outperforms excellent classification results using different evaluation measures such as accuracy, specificity, sensitivity, precision, recall, and F-score.

Keywords: Bean disease classification; Hybrid deep learning; Archimedes optimization algorithm; LSTM; and WPD.

1. Introduction:

Agriculture is one of the major pillars in the economic sector that contribute to income, employment generation, and wealth for the country. Plant disease is the major factor to degrade agricultural products all over the world that leads to huge loss each year. The most produced and most important legume in the world is the bean (*Phaseolus vulgaris* L). On a global scale, the bean is an important legume/grain taken for consumption and was widely dispersed due to its broad adaptation [1, 28]. During the growing season, the plants grow well in about 400 mm of precipitation and moderate growing temperatures ($>10^{\circ}\text{C}$ and $<30^{\circ}\text{C}$). The growing temperatures $<30^{\circ}\text{C}$ with the tropical highlands and 60–120 days of frost-free growth are permitted by season where the ordinary bean is grown in a moderate growing region [2]. Approximately, 15% soluble fiber, 62% complex carbohydrates, several micronutrients (Ca, Fe, Mg, P, and K), and 22% protein present in the uncooked dry bean. Bean commonly provides trace nutrients, calories, and sources of protein to persons who never give additional expensive sources of nutrition. The dry edible beans are a major kind in contemporary agriculture in which the matured seed is prepared in main dishes and harvested.

Root diseases (such as Fusarium root rot, Pythium diseases, Rhizoctonia root rot, Soybean cyst nematode, and Soybean cyst nematode soil sampling), Stem and wilt diseases (including Bacterial wilt, Fusarium yellows, stem rot, and white mold), and Foliar diseases such as (Anthracnose, Bacterial brown spot, Bean common mosaic, Common bean root dust, common bacterial blight, and halo blight) are the important types of bean diseases [3, 29]. Bean disease identification and detection at an early stage is a more important one. Hence, the people quickly take suitable prevention criteria. According to the experience in observing bean disease identification, most forest producers judge a degree and disease species in traditional forestry and agricultural production in which it needs skill and knowledge to detect the symptoms of bean diseases. The unnecessary economical losses are resultant due to delay of the treatment period, incorrect treatment, and lack of knowledge to plant disease identification. It will take little time even if experts are invited to identify a disease [4]. Hence, the automatic implementation of plant diseases or bean disease identification and classification is essential [30, 31].

More computer vision methods were applied to plant disease classification with the development of computational systems in recent years. Nowadays, artificial intelligence and data mining techniques are widely used to solve the prediction and classification issues in agriculture [5]. The execution measurements and 10 fold cross-validation with Decision Tree (DT), k-Nearest Neighbors (kNN), Backing Vector Machine (SVM), and Multilayer perceptron (MLP) models were used [6]. Deep learning techniques play a vital role in plant disease classification. These machine learning and deep learning techniques met few shortcomings in terms of computational complexity, the high cost associated with training data, more execution time, noise, feature dimensionality, lower accuracy, low speed, etc [7-10]. To tackle these issues, we have proposed a hybrid deep learning model with an Archimedes optimization algorithm (HDL-AOA). The major contribution of this paper is summarized as follows:

- ❖ The combination of wavelet packet decomposition with long short-term memory is proposed as a hybrid deep learning model.
- ❖ The classification accuracy for multiple single LSTM networks during bean disease classification is boosted up using the Archimedes optimization algorithm (AOA).
- ❖ The healthy and unhealthy classes such as Bean halo blight, Pythium diseases, Rhizoctonia root rot, and Anthracnose images were collected from Soybean (Large) Data Set.

The rest of the paper is organized as: Various plant disease classifications based on deep learning techniques are delineated in section 2. Section 3 explains the proposed HDL-AOA model for bean disease classification. The experimental investigation based on the proposed model is discussed in section 4. Finally, section 5 concludes the paper.

2. Related work:

This section reviews a few of the existing works based on plant disease classification using deep learning techniques. A deep convolutional neural network (DCNN) was proposed by Uğuz et al. [7] for olive peacock spot and aculeus olearius diseases classification. There are 3400 olive leaves samples chosen in which three classes namely healthy, olive peacock spot and aculeus olearius disease were present. The VGG16 and VGG19 architectures based on the DCNN model are used. The network's performance was improved with the help of the RMS Prop optimization algorithm and Stochastic gradient descent. The multi-task system based on Convolutional Neural Networks (CNN) was suggested by Esgario et al. [8] to detect the stress severity caused by biotic agents on coffee leaves. A more accurate and robust detection system was performed using computational experiments. As a result of 86.51% severity estimation and 95.24% of biotic stress classification accuracy were obtained using multi-task system-based CNN with ResNet50 architecture. Hence, this method is appropriate for biotic stresses in coffee plantation identification and quantification.

A pre-trained Convolutional Neural Network (CNN) was proposed by Esgario et al. [9] for crop disease identification. This pre-trained CNN includes models such as DenseNet201, ResNet101, GoogLeNet, VGG19, Visual Geometry Group 16 (VGG16), and AlexNet. The author chose four kinds of crops with ten diseases such as leafhopper, yellow vein mosaic virus, citrus canker, citrus Hindu mite, brown spot, Cercospora leaf spot, two-spotted spider mite, Epilachna beetle, little leaf disease, and Tobacco Mosaic Virus TMV. For each disease class, they evaluated the prediction scores and classified images in real-time. Hernández et al. [10] proposed a Bayesian Deep Learning technique for the detection of plant diseases. When compared to the state of art methods, higher classification performance is achieved using Bayesian inference. The uncertainty of the predictions is quantified and posterior density for the plant disease detection problem was approximated.

Table 1: Literature analysis based on plant disease classification using deep learning techniques

Author	Techniques used	Name of the diseases	Advantages	Limitations
Uğuz et al. [7]	DCNN	Olive peacock spot and Aculusolearius diseases	Higher accuracy ratings	Higher computational complexities
Esgario et al. [8]	The multi-task system based CNN	Cercospora leaf, brown leaf spot, rust, and spot leaf miner in coffee leaves	Accuracy of 86.51% severity estimation and 95.24% biotic stress classification	Low representativity of the dataset
Esgario et al. [9]	Pre-trained CNN	Leafhopper, yellow vein mosaic virus, citrus canker, citrus Hindu mite, brown spot, Cercospora leaf spot, two-spotted spider mite, Epilachna beetle, little leaf disease, and TMV	97.3% best validation accuracy using GoogLeNet and cost-effective	Takes higher execution time
Hernández et al. [10]	Bayesian Deep Learning	Grape black spot and grape escass	Correct class prediction results	Data overfitting issues
Chen et al. [11]	DCNN	Maize and rice diseases	The global pooling layer reduced the dimension of feature maps	Higher-dimensional features
Li et al. [12]	CNN	Ginkgo leaf disease	Accomplished 98.44% accuracy under laboratory conditions	Data overfitting with more processing time

The transfer learning of the deep convolutional neural networks (DCNN) was introduced by Chen et al. [11] for plant leaf disease identification. They selected the Inception module and VGGNet pre-trained on ImageNet for experimental investigation. According to the experimental investigation, 92.00% classification accuracy is obtained for rice plant images. For classification, the high-dimensional features are extracted and the experimental results provided better results in terms of both own dataset and public dataset. Finally, 91.83% validation accuracy is achieved during disease classification. Li et al. [12] proposed Convolutional Neural Network (CNN) for Ginkgo leaf disease detection. They combined and used Inception V3 and VGGNet- 16 models. Based on laboratory conditions, 98.44% accuracy was accomplished and the VGG model provided 92.19% accuracy. Nevertheless, data overfitting with more processing time takes place. The existing work based on the plant disease classification using deep learning techniques is delineated in Table 1.

3. Hybrid deep learning with AOA model for bean disease classification:

In this section, we have proposed hybrid deep learning with AOA (HDL-AOA) model for the bean disease classification. For this work, the normal healthy bean with four unhealthy classes such as Bean halo blight, Pythium diseases, Rhizoctonia root rot, Anthracnose were chosen. The steps involved in the proposed HDL-AOA model for bean disease classification are briefly explained in the following section.

3.1 Wavelet Packet Decomposition:

The time-frequency localization function with orthogonal wavelet packet bases and image properties are analyzed using an efficient tool called Wavelet Packet Decomposition (WPD). The original images are decomposed into sub-layers in which WPD is a kind of wavelet decomposition (WD). The low pass components of frequencies are segregated [13]. The time-frequency planes more than wavelet decomposition are divided and WPD accomplished a more precise analysis of images. When compared to WD, the WPD is more efficient for singular components, instantaneous, unbalanced, and identifying weak images. The WPD decomposes a coefficient of each layer continually. Both discrete and continuous transform are present in the WPD. The mother wavelet transform function $\phi(t)$ adopts the continuous wavelet transform for a signal $F(t)$ [14].

$$CWT_F(a, b) = \left\langle F(t), \phi_{c,d}(t) \right\rangle = \int_{-\infty}^{\infty} F(t) \phi * ((t-d)/c) \sqrt{c} dt \quad (1)$$

The scale coefficient and translation coefficient are denoted as c and d . The complex conjugates are denoted as $*$. The following equation describes a WPD process of decomposition.

$$\begin{cases} Q_j^{2k-1}(t) = PH_{j-1}^k(t) \\ Q_j^{2k}(t) = PG_{j-1}^k(t) \end{cases} \quad (2)$$

Equation (3) describes the reconstruction process of WPD.

$$Q_j^k(t) = H * Q_{j+1}^{2j-1}(t) + G * Q_{j+1}^{2j}(t) \quad (3)$$

Therefore, the time index and the wavelet packet levels are denoted as t and Q_j^k . The low and high pass filters are denoted as H and G . The single branch reconstructions reconstruct each packet at the last decomposition level to the original level. The other packet values of similar levels are expressed to be zero if the construction is an inverse of the decomposition process.

3.2 Long short-term memory networks:

Enhancement of Recurrent Neural Network (RNN) is called long short-term memory (LSTM). Instead of conventional RNN units, the LSTM accomplishes memory blocks to solve exploding

gradient and vanishing problems [15]. The network of LSTM memorizes and links the existing data to information received in the current stage [16]. Three gates such as input, forget and output gates are combined to form the LSTM. The current input is considered as x_j the new and previous cell states are denoted as y_j and y_{j-1} . The current and previous outputs are denoted as h_j and h_{j-1} . Fig 1 explains the internal architecture of LSTM. The following equations explain the input gate principle of LSTM.

$$I_j = \delta(W_j \bullet [h_{j-1}, x_j] + a_j) \quad (4)$$

$$\tilde{y}_j = \tanh(W_j \bullet [h_{j-1}, x_j] + a_j) \quad (5)$$

$$y_j = \tanh(W_j \bullet [h_{j-1}, x_j] + a_j) \quad (6)$$

Fig 1: Basic architecture of LSTM

The sigmoid layer is used to pass h_{j-1} and x_j . After h_{j-1} and x_j are passed via $\tanh$ layer, equation (5) is used to obtain the new information. Equation (6) combines $\tilde{y}_j$ long-term memory information y_{j-1} into y_j . The input gate bias of LSTM and weight matrices are represented as a_j and w_j . The dot product and sigmoid layer allow the selective passage of information with the help of the LSTM forget gate. Equation (7) executes the forget-based data from an existing cell

with a certain probability. The sigmoid function, offset and weight matrix are denoted as δ , a_j and w_j .

$$F_j = \sigma(W_j \bullet [h_{j-1}, y_j] + a_j) \quad (7)$$

According to equations (8) and (9), the inputs h_{j-1} are y_j determined by the LSTM output gates. The *tanh* layer passes new information y_j .

$$O_j = \sigma(W_o \bullet [h_{j-1}, y_j] + a_o) \quad (8)$$

$$F_j = O_j \tanh(y_j) \quad (9)$$

The LSTM, output gates weighted matrices are denoted as W_o and a_o .

3.3 Archimedes optimization algorithm (AOA) for multiple single LSTM networks:

In the first step, the original image is decomposed by applying WPD and various reconstruction models are taken up. The performance of bean disease classification is improved by incorporating the combined multiple single LSTM network strength [21]. The classification results are obtained from every LSTM network after inputting the decomposed images. The final classification results are obtained by summing this LSTM network. Instead of summing, apply the Archimedes optimization algorithm (AOA) to enhance the classification accuracy. The AOA is used to evaluating the weight coefficient of each model. The mean absolute percentage error (MAPE) minimization determines the optimized weight coefficient. The image series minimizing standards and the error values determines it [22]. The MAPE minimization calculates a weight coefficient of the combined classification model. The Archimedes optimization algorithm is mainly based on the Archimedes principle which is an interesting law of physics. The immersed objects are considered as a population of individuals in AOA. The accelerations, densities, random volumes with the initial population of objects are commenced in AOA [17]. Both exploitation and exploration processes are encompassed in AOA, which is considered a global optimization algorithm. The AOA updates the volume and density of every object in different iterations. The mathematical formulation of AOA stages are delineated as follows:

3.3.1 Initialization:

Equation (1) is used to initializing the position of each object.

$$OB_j = L_j + random \times (U_j - L_j); j = 1, 2, \dots, M \quad (10)$$

The j^{th} population of M objects is OB_j . The upper and lower limits of a search space are denoted as U_j and L_j . Equation (11) and (12) is used to update the density (D) and volume (V).

$$D_j = random \quad (11)$$

$$V_j = random \quad (12)$$

The D-dimensional vector creates the random interval as 0 to 1 and is denoted as *random*. Equation (13) updates the acceleration (A) of j^{th} objects [14].

$$A_j = L_j + random \times (U_j - L_j) \quad (13)$$

The best fitness value with the objects is selected there also an initial population is evaluated. Assign A_{best} , V_{best} , D_{best} and y_{best} . The fitness function of this work is optimal accuracy.

$$Fitness = 1 - Accuracy \quad (14)$$

3.3.2 Density and volume update:

Equation (15) is used to update the volume and density of j^{th} objects for the $t+1$ iteration [18].

$$D_j^{t+1} = D_j^t + random \times (D_{best} - D_j^t) \quad (15)$$

$$V_j^{t+1} = V_j^t + random \times (V_{best} - V_j^t) \quad (16)$$

Here, the best volume and density are V_j^{t+1} and D_j^{t+1} connected to the best objects.

3.3.3 Density factor and transfer operator:

The collision between objects occurs at first and the objects try to reach an equilibrium state after some time. The transfer operator *Tf* with AOA implements this. Equation (17) transforms search space from exploration to exploitation.

$$Tf = \exp\left(\frac{t - t_{\max}}{t_{\max}}\right) \quad (17)$$

Here, the number of iteration and the maximum number of iteration are denoted as t and $t_{\max}$. Where Dd is denoted as the density decreasing factor.

$$Dd^{t+1} = \exp\left(\frac{t - t_{\max}}{t_{\max}}\right) - \left(\frac{t}{t_{\max}}\right) \quad (18)$$

3.3.4 Exploration stage:

The collision between objects occurs if $Tf \leq 0.5$, then selects the random material *RM*. Equation (19) updates the acceleration of the object for the $t+1$ iteration.

$$A^{t+1} = \frac{D_{Rm} + V_{Rm} \times A_{Rm}}{D_j^{j+1} \times V_j^{j+1}} \quad (19)$$

Hence, the volume, density, and acceleration of random material are expressed as V_{Rm} , D_{Rm} and A_{Rm} . During one-third of iterations, the Tf guarantees an exploration.

3.3.5 Exploitation stage:

There is no collision between the objects if $Tf > 0.5$. Equation (20) updates the acceleration of the object for the $t+1$ iteration.

$$A_j^{t+1} = \frac{D_{best} + V_{best} \times A_{best}}{D_j^{j+1} \times V_j^{j+1}} \quad (20)$$

Here, the best object acceleration is A_{best} .

3.3.6 Acceleration normalizing:

Equation (21) calculates the percentage of normalizing acceleration.

$$A_{j-acceleration}^{t+1} = \alpha \times \frac{A_j^{t+1} - \min(A)}{\max(A) - \min(A)} + \beta \quad (21)$$

Where the normalization range is denoted as α and β .

3.3.7 Updating position:

Equation (22) updates the position of the object if $Tf \leq 0.5$ (exploration stage).

$$y_j^{j+1} = y_j^t + D_2 \times random \times A_{j-normalization}^{t+1} \times Dd \times (y_{random} - y_j^t) \quad (22)$$

The constant term is denoted as D . Equation (23) updates the position of the object if $Tf > 0.5$ (exploitation stage).

$$y_j^{j+1} = y_{best}^t + E \times D_2 \times random \times A_{j-normalization}^{t+1} \times Dd \times (T \times y_{random} - y_j^t) \quad (23)$$

Equation (23) is used to change the flag F to the direction of motion.

$$F = \begin{cases} 1 & \text{if } P \leq 0.5 \\ -1 & \text{if } P > 0.5 \end{cases} \quad (24)$$

Where, $P = 2 \times random - D_4$.

3.3.8 Validation:

The objective function evaluates each object. Assign A_{best} , V_{best} , D_{best} and y_{best} . The steps involved in AOA for multiple single LSTM networks are depicted in algorithm 1.

Algorithm 1: AOA steps for multiple single LSTM networks

```

Initialization of AOA population, D, input, forget, and output gates of LSTM with the maximum
number of iterations  $t_{max}$ 
Initialize AOA acceleration, density, and volume with random position
Compute the fitness function using equation (14) and choose the excellent fitness
Set  $t=1$ 
While  $t \leq t_{max}$  do
  For every  $j$  object do
    Equation (15) and (16) is used to update the volume and density
    Use equation (17) and (18) to update transfer and density decreasing factor
    If  $Tf \leq 0.5$  then
      Use equation (20) and (21) to update the acceleration and normalization
      Use equation (22) to update the position
    else
      If  $Tf \leq 0.5$  then
        Use equation (21) and (22) to update the acceleration and normalization
        Use equation (24) to update the direction flag
      End If
    End If
  End for
  Select the best fitness and compute each object
  Set  $t=t+1$ 
End While
Obtain the optimal classification accuracy
Return to object with the optimal fitness value
End

```

3.4 Hybrid deep learning model (WPD-LSTM) for classification model:

The WPD is used to decompose the image series in the proposed model. Mother wavelet utilizes a frequency-based third-order Daubechies type wavelet function (db3). In the classification image series, different frequency bands regularly exist simultaneously. The classification image series are separated in to high and low-frequency components after decomposition through WPD [23]. Some random output and fast varying image output are represented using high-frequency components and the low-frequency components denote the image output trend. The historical image output is an input model used in the proposed hybrid learning model [24, 25]. the relationship among bean image disease classification will be considered in this way. Fig 2 explains the hybrid deep learning with the AOA model for bean disease classification.

- (i) The original image is decomposed using WPD. The original image output series is denoted as $Y = (I_{j-M+1}, I_{j-M+2}, \dots, I_j)^T$. Here, the bean image at time t is I_j and time

horizon is M . The decomposed into a range of series with WPD is Y . The image output time series is decomposed into four series to consider the decomposition effect and computational efficiency. The WPD with y_j decomposed series is rebuilt into four series.

Where, $R_j = (I_{j,t-M+1}, I_{j,t-M+2}, \dots, I_{j,t})^T$ describes a sub-series j .

- (ii) From step (i), develop an independent LSM network for each sub-series. The inputs of each LSTM network consider the image data $R_j = (I_{j,t-M+1}, I_{j,t-M+2}, \dots, I_{j,t})^T$. Where, $IV_j = (I_j, b_1, b_2, \dots, b_k)$ are the input variables of each LSTM. The deep learning model adopts four independent well trained three-layer LSTM networks. The classification result provided these independent LSTM networks.
- (iii) A final classification result of bean disease classification is acquired by adopting an Archimedes optimization algorithm (AOA).

(iv) **Table 2:** Parameter settings for HDL-AOA

Parameters	Ranges
Type of transformation function	Mother wavelet
Decomposition level	4
LSTM batch size	60
Halving factor	0.9
Momentum	0.8
Learning rate	0.00002
Objective number	30
D ₁	2
D ₂	6
D ₃	2
D ₄	0.5
Number of iteration	Maximum

4. Experimental Analysis:

In this work, we have proposed hybrid deep learning with the AOA (HDL-AOA) model for bean disease classification in which the proposed model performances are evaluated using various types of performance evaluation metrics and comparative analysis. The tensorflow2 on an Intel(R) Core(TM) 17-2.2GHz processor with Python and Keras package implement the proposed HDL-AOA for bean disease classification. Additionally, the 4G and 16 GB RAM with graphical processing unit (GPU) NVIDIA GTX 1050 execute the experiments. [26] The experimental investigation in terms of classification performance analysis and comparative

analysis are delineated in the following section. Table 2 delineates the parameter used for bean disease classification.

Fig 2: Proposed hybrid deep learning with AOA model for bean disease classification

4.1 Dataset explanation:

In this work, the dataset images were taken from Soybean (Large) Data Set [19] and [20] (<https://www.ag.ndsu.edu/publications/crops/dry-edible-bean-disease-diagnostic-series#section-12>). This dataset consists of 19 classes of attributes. From this, we have selected a single healthy

class with four unhealthy classes such as Bean halo blight, Pythium diseases, Rhizoctonia root rot, and Anthracnose (Fig 3). The training and testing image details based on the dataset are delineated in Table 3. Table 4 explains the bean disease symptoms.

Table 3: Dataset description

Name of the class	Training set	Testing set	Total set
Healthy	820	230	1050
Bean halo blight	670	150	820
Pythium diseases	690	200	890
Rhizoctonia root rot	1200	250	1450
Anthracnose	795	300	1095

Fig 3: Sample data description, (a) Healthybean and (e) Bean halo blight, (b) Healthybean root and (f) Pythium disease affected root, (c) Healthy bean leaf and (g) Anthracnose disease affected bean leaf, (d) Healthy bean root and (h) Rhizoctonia root rot

4.2 Evaluation measures:

The performance efficiency of the proposed model is evaluated using different kinds of evaluation metrics such as accuracy, specificity, sensitivity, precision, recall, F-score, and MAPE. Each measure is delineated as follows:

$$Accuracy = \frac{True\ positive + True\ negative}{True\ positive + True\ negative + False\ positive + False\ negative} \quad (25)$$

The specificity, sensitivity, precision, and recall equations are delineated in equations (26) to (29).

$$Specificity = \frac{True\ positive}{True\ positive + False\ negative} \quad (26)$$

$$Sensitivity = \frac{True\ negative}{True\ negative + False\ positive} \quad (27)$$

$$Precision = \frac{True\ positive}{True\ positive + False\ positive} \quad (28)$$

$$Recall = \frac{True\ positive}{True\ positive + False\ negative} \quad (29)$$

Table 4: Disease symptoms

Name of the diseases	Symptoms
Bean halo blight	Broad yellow-green halo may develop around necrotic spots, which may infect the infect pods and seeds
Pythium disease	Water-soaked necrotic areas on roots or hypocotyls and initial root rot symptoms appear as elongated
Anthracnose	Dark and slender leaf vein and petiole lesions
Rhizoctonia root rot	Internal brick-red discoloration of pith

Where the number of instances that belong to the correctly identified class is True Positive (TP). The number of instances that belong to the incorrectly identified class is False Negative (FN). The number of instances that do not tend to the class, which are incorrectly identified is called False Positive (FP). Similarly, the number of instances not tends to the class, which are correctly identified are called True Negative (TN). Equation (30) and (31) explains the F-score value and the mean absolute percentage error (MAPE).

$$F - score = 2 * \frac{P_{recision} * R_{ecall}}{P_{recision} + R_{ecall}} \quad (30)$$

$$MAPE = \frac{1}{M} \sum_{t=1}^M \frac{|R_j - \hat{R}_j|}{R_j} \times 100\% \quad (31)$$

Where, the true and forecasted values are defined as R_j and $\hat{R}_j$. The classification horizon is M at time t .

4.2 Performance Analysis:

The performance analysis with respect to accuracy and loss is depicted in Fig 4. According to the ratio of 70/30 divides both training and testing set. The input images were resized into 224×224 pixels. The training and testing performance in terms of accuracy and loss are depicted in Fig 4 (a) and (b). There are 30 epochs chosen for this experiment. Fig 4 (a) takes 30 epochs with 100% accuracy in which the accuracy levels varying from 0.65% to 0.98% training accuracy and the testing accuracy varies from 0.83% to 0.92%. According to Fig 4 (b), the training loss varies from 0.82% to 1.0%. Similarly, the testing loss varies from 0.45% to 0.23%. The proposed HDL-AOA takes better training accuracy and testing accuracy as well as training loss and testing loss in terms of bean disease classification.

Fig 4: Performance analysis, (a) Accuracy and (b) Loss

Fig 5 depicts the proposed HDL-AOA performance analysis with respect to each class. We have selected a healthy bean plant with four unhealthy images belongs to Bean halo blight, Pythium diseases, Rhizoctonia root rot, Anthracnose diseases. The accuracy, specificity, and

sensitivity performance of each class are evaluated. For a healthy class, we have obtained 84% accuracy, 89% specificity, and 91% sensitivity results. We have obtained 89% accuracy, 81% specificity, and 90% sensitivity results for the bean halo blight class. The Pythium class provided 91% accuracy, 84% specificity, and 81% sensitivity outcomes. For Rhizoctonia root rot, we have attained 91% accuracy, 95% specificity, and 84% sensitivity results. Similarly, 92% accuracy, 88% specificity, and 95% sensitivity results are obtained for Anthracnose. The Confusion matrix with respect to each class is delineated in Fig 6.

Fig 5: Proposed HDL-AOA performance analysis with respect to each class

	Healthy	Bean halo blight	Pythium	Rhizoctonia root rot	Anthracnose
Healthy	84%	4.5%	8.12%	2.12%	1.26%
Bean halo blight	0%	89%	2.68%	3.56%	4.76%
Pythium diseases	4.15%	1.66%	91%	3.19%	0%
Rhizoctonia root rot	4.65%	0%	3.89%	91%	0.46%
Anthracnose	3.78%	1.12%	3.01%	0%	92%

Fig 6: Confusion matrix with respect to each class

Fig 7 illustrates the proposed HDL-AOA performance analysis with respect to ROC. When analyzing the overall performance, the ROC curves plotted among true positive rate (TPR) and false-positive rate (FPR) respectively. Each class varies from 0.1 to 1.0. The area under ROC (AUC) is computed to be 9.9% for HDL-AOA models. Based on the ROC curve, we have obtained better true positive rates in terms of the healthy class, Bean halo blight, Pythium disease class, Rhizoctonia root rot class, Anthracnose class.

4.3 Comparative Analysis:

Performance evaluation of MAPE with respect to various methods and each class are depicted in Fig 8. Different methods such as long short-term memory (LSTM), Recurrent neural network (RNN), Multiple layer perceptron (MLP), Convolutional neural network (CNN), and proposed HDL-AOA model were chosen to validate the performance of MAPE. The MAPE value of the proposed HDL-AOA model is averagely minimized compared with other methods such as LSTM, MLP, CNN, and RNN. Based on Fig 8, the proposed HDL-AOA achieves 2% MAPE for healthy class, 2.1% for bean halo blight, 3% for Pythium, 5% for Rhizoctonia, and 2% for Anthracnose. However, the proposed HDL-AOA model accomplishes low errors during bean disease classification.

Fig 7: Proposed HDL-AOA performance analysis with respect to ROC

Table 5: State-of-comparison of classification

Evaluation measures	Name of the methods				
	RNN	DCNN	CNN	LSTM	HDL-AOA
Accuracy	89.01%	98.01%	96.89%	97.13%	98.23%
Specificity	76.89%	95.12%	93.14%	95.09%	97.13%
Sensitivity	91.89%	93.12%	89.92%	97.92%	98.01%
Precision	81.89%	82.56%	94.78%	97.82%	98.45%
Recall	92.45%	97.23%	82.66%	98.41%	99.12%
F-score	78.85%	98.67%	98.25%	98.14%	99.45%

Table 5 illustrates the state-of-art comparison of bean disease classification. In this experiment, we have chosen five state-of-art methods including Recurrent Neural Network

(RNN) [27], Deep Convolutional Neural Network (DCNN) [7], Convolutional Neural Network (CNN) [9], Long Short Term Memory (LSTM) [26] and proposed HDL-AOA. The proposed HDL-AOA demonstrates 98.23% accuracy, 97.13% specificity, 98.01% sensitivity, 98.45% precision, 99.12% recall, and 99.45% F-score values than other existing techniques.

Fig 8: Performance evaluation of MAPE with respect to various methods and each class

5. Conclusion:

This paper proposed a hybrid deep learning model with Archimedes optimization algorithm (HDL-AOA) for bean disease classification. The four unhealthy image classes (Bean halo blight, Pythium diseases, Rhizoctonia root rot, and Anthracnose) along with the healthy class images were collected from Soybean (Large) Data Set. The HDL-AOA model for bean disease classification is implemented in MATLAB software. The proposed HDL-AOA achieves the MAPE values such as 2% for healthy class, 2.1% for bean halo blight, 3% for Pythium, 5% for Rhizoctonia, and 2% for Anthracnose than other existing methods such as LSTM, MLP, CNN, and RNN. The proposed HDL-AOA demonstrates 98.23% accuracy, 97.13% specificity, 98.01% sensitivity, 98.45% precision, 99.12% recall, and 99.45% F-score values than other existing techniques including RNN, DCNN, LSTM, and CNN.

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Conflict of interest

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Human and Animal Rights

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Figures

Figure 1

Basic architecture of LSTM

Figure 2

Proposed hybrid deep learning with AOA model for bean disease classification

Figure 3

Sample data description, (a) Healthybean and (e) Bean halo blight, (b) Healthybean root and (f) Pythium disease affected root, (c) Healthy bean leaf and (g) Anthracnose disease affected bean leaf, (d) Healthy bean root and (h) Rhizoctonia root rot

(a)

(b)

Figure 4

Performance analysis, (a) Accuracy and (b) Loss

Figure 5

Proposed HDL-AOA performance analysis with respect to each class

	Healthy	Bean halo blight	Pythium	Rhizoctonia root rot	Anthracnose
Healthy	84%	4.5%	8.12%	2.12%	1.26%
Bean halo blight	0%	89%	2.68%	3.56%	4.76%
Pythium diseases	4.15%	1.66%	91%	3.19%	0%
Rhizoctonia root rot	4.65%	0%	3.89%	91%	0.46%
Anthracnose	3.78%	1.12%	3.01%	0%	92%

Figure 6

Confusion matrix with respect to each class

Figure 7

Proposed HDL-AOA performance analysis with respect to ROC

Figure 8

Performance evaluation of MAPE with respect to various methods and each class