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Fusion Driven Apple leaf Disease Classification using a Siamese Squeeze and Excitation Residual Network with Feature Pyramid Learning

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Abstract

The classification of apple leaf diseases is a complex task that requires specialized expertise and is a major contributor to crop losses in agriculture worldwide. The effective earlier diagnosis of automatic apple leaf disease classification model is crucial to maintain the crop's healthy growth. The existing research cannot provide adequate classification results for apple leaf diseases due to the sophisticated classification models. This research proposed the novel Feature pyramid Siamese Squeeze and Excitation Residual neural network (FPS2ENet) model for precise categorization of apple leaf diseases. Initially, the proposed research employed the bilateral guided filter (BGF) which is composed of median and fast guided filter to clean up the apple leaf images. Furthermore, the color, textural and neighboring pixel relationship features are extracted from the apple leaf image with aid of windmill graph-based feature extraction technique. After that, the proposed model is employed with two blocks namely Feature pyramid neural network block (FPNN) for deep feature selection as well as Squeeze and Excitation Residual neural network block for disease classification. Moreover, the Siamese layer and fully connected layer are employed for fusion and classifying process respectively. In experimental analysis, there are four datasets are utilized including Kashmiri Apple Plant Disease Dataset (KAPD), New Plant Diseases Dataset (NPD), Plant Pathology Apple (PPA) dataset, plant village-apple-color (PVAC) dataset. In the performance analysis scenario, the various kinds of analysis are evaluated with different existing methods such as Bi-GRU, Bi-LSTM, DenseNet, and ResNet for accessing the proposed model effectiveness. The numerous effective analyses are performance metric analysis, loss and accuracy curve analysis, ROC curve analysis and confusion matrix analysis. In addition to this, the proposed method can attain 98.81 %, 99.43%, 99.88% and 99.61 % accuracy in KAPD, NPD, PPA and PVAC dataset correspondingly.

1. Introduction

The botanical name of apple is *Malus domestica* under the family of Rosaceae [1], which has sweet and fleshly fruit. The apple is cultivated in many countries and has no restriction on

climate. That is, it could bloom even in hot and cold areas and bear bunch of fruits [2]. Apple trees are one of the fruits bearing trees with high cultivar diversity [3, 4]. The annual production of fruit from apple tree is more than several billion pound with annual value more than 500-dollar millions at united states of America. However, due to the climatic and environmental factors [5], the three affected several diseases, which directly affect the production of apples [6]. Most of the fruit bearing trees are invasive to pathogens and so like apple trees [7]. The fungus of plants will affect both leaf's and fruits, which results in low yield [8] of fruits. Some of the most common diseases in apple leaf and trees are scab, bitter rot and black rot [9, 10] that could be manually identified by the symptoms of blemishes, spotting, patches, etc., [11]. The disease weakens the tree and makes leaves and pre-matures bloom to fall, which affects the fruiting behavior of apple trees.

The early prediction of apple tree disease makes it easy to find the fungus that has been affecting apple leaf. This makes easy prediction of cause of disease and remedy for effect is easily solved. To have early diagnosis, computer aided diagnosis systems are performed that reduce the errors in manual findings. The identification at the earlier stage is performed by machine learning algorithm. The machine learning methods such as support vector machine, multi-class support vector machine, and multi label k-nearest neighbor methods [12] adopted at the initial stages, which could only classify the health of apple trees. These classifiers are used with different feature extraction and segmentation algorithms such as Gray Level Co-occurrence Matrix, K-means clustering etc., [13]. By using those methods, the detection time of the system increases hence deep learning concept has been utilized to solve the issue.

Deep learning architecture has been used with IoT based agricultural [14] data; however, the IoT data has high level of noise and reduced image quality. Hence to reconstruct that a pre-processing step is used before classification. The input image data is normalized and augmented using rotation technique, different noise levelling, and image enhancement models [15]. However, based on intensity variation in images the classifier makes use of poor features for classification. Hence a contrast stretching based preprocessing is applied in [16], which highlights the affected area of apple leaf. By using real time apple leaf data, a classification model concerning deep neural network has been used in [17]. However, the performance of different classes of convolutional neural networks such as ResNet, Inception V3, MobileNet, DenseNet etc., [18] are also used for classification of apple leaf disease. But the problem of increasing hyper parameters of these networks, the precise classification is still a research topic. To overcome these problems, this research proposed a novel automatic apple leaf disease classification model with different classes. The major contribution of the proposed method is described below.

- To develop an effective model for precise classification of various apple leaf disease.
- To develop a bilateral guided filter (BGF) for eliminating unwanted noises from the apple images.

- To implement a windmill graph-based feature extraction technique (WGFE) that could extract the three different kinds of features from apple leaf images.
- To design a novel classifier namely Feature pyramid Siamese Squeeze and Excitation Residual neural network (FPS2ENet) that aimed to classify different types of images simultaneously.
- To compare the performance of proposed classification model in terms of accuracy precision, recall etc., with state-of-art-techniques.

The entire research flow of the proposed method is discussed as follows: the section (2) describes the relevant research based on the apple leaf disease classification. From section (3), the proposed method and these fundamental concepts are covered. Furthermore, the various kinds of experimental analysis are defined in section (4). Finally, the proposed method is concluded in section (5).

2. Literature survey

To detect the healthy and diseased state of apple leaf disease, Tian et al. [19] proposed a multi-scale dense network. The diagnosis model makes use of 11 types of images for prediction, however, the processing using these data is insufficient to detect. Hence image augmentation has been performed. The dataset expansion was achieved by using cycle general adversarial network for the disease of ring rot and anthracose at fruit surface. Then the disease of apple has been predicted by using dense neural network with convolution-based descriptor and ResNet based transformation.

The sub-class of apple leaf disease was recognized by Luo et al. [20] using deep network-based architecture. The problem of apple production was solved by using multi-scale feature fusion process. In that model, the architecture of ResNet is improved by incorporating batch normalization and rectified linear units. Then the system loss was reduced through down-sampling of channel and spatial projection. Finally, the pyramid convolution functions were replaced by 3x3 convolutional block of ResNet. Before subjecting the classifier model, the data was pre-processed for data augmentation by involving the changes of Gaussian noise, rotation, and changing brightness.

For the detection of peculiar disease in apple plants on plant pathology dataset, a multi classification model was adopted by Yadav et al. [21]. In that model, the author adopted apple foliar disease neural network that automatically classified foliar disease in apple leaf. Initially, the duplicate data from the database is removed followed by that data augmentation is performed by random flipping, random cropping, resizing and changing the shape of image. To do predefined objective, the author utilized hybrid efficient net model that has lambda layers B3 and B4 along with the dropout layer. At the final stage of classifier four dense layers are formed along with SoftMax function.

The leaf blotch and rust are common type of apple disease, which affect major production from apple plant, hence, to solve that Bi et al. [22] adopted a deep learning model for agriculture dataset from China. The adopted model is a mobile version of convolutional neural network with high stability and low cost. The adopted model has 3x3 depth wise convolution function and 1x1 pointwise convolution function. These two layers sandwich batch normalization and rectified linear unit for accurate detection.

For the detection of apple leaf disease, Hasan et al. [23] reported a color segmentation and improved discrete wavelet transformation. To segment the infected region of apple leaf L*a*b space color segmentation approach is used in which average color marker and nearest neighbor method classify the information based on each pixel. The model evaluates two different features such as histogram feature and wavelet transform based feature. These features are used to identify the type of disease using random forest classifier. By using these two-feature extraction model a total of 128 features are used for further identification.

3. Methodology

In the field of agriculture, the quality of plant yield is the major problem. Since the environmental factors regarding pollution rate is increasing, the photosynthesis mechanism of plants is affected. Also, geographical change increases the rate of pests in environment, which further affects the plants' yield. However, to improve yielding it is necessary to predict plant disease so that adequate or proper pesticide and fertilizers are suggested. In literature, most models bring separate models for prediction, however, separate models would increase the time and memory of processing. This degrades the efficiency of detection process.

Hence to cope with that issue a leaf disease prediction model is performed for apple plants. The images are acquired through camera imaging, hence the noise in the images will be high also the intensity at each pixel will vary, which would reduce the detection procedure accuracy. Hence a filtering technique is adopted that aimed to equalize the intensity of images. The noise at the images is filtered by using BGF that make use of fast guided filter and median filter. Then the features from the intensity normalized images are extracted by using WGFE technique, which extracts the color and texture features from apple leaf images. Since diseased apple leaf images have number of spots, the graph-based method would provide improved extraction process. Based on obtained features, the feature selection and classification is made by using deep learning method known as FPS²ENet. Here, the feature pyramid neural network (FPNN) is used for selecting the features through sampling, then the feature sets are given to Squeeze and Excitation Residual neural network (SERNN). Furthermore, the Siamese layer is utilized for fusion operation and fully connected layer is employed to classify the apple leaf images. This classifier model can diagnose various types of diseases associated with apple leaf images. Furthermore, the overall workflow of the proposed model is illustrated in Figure (1).

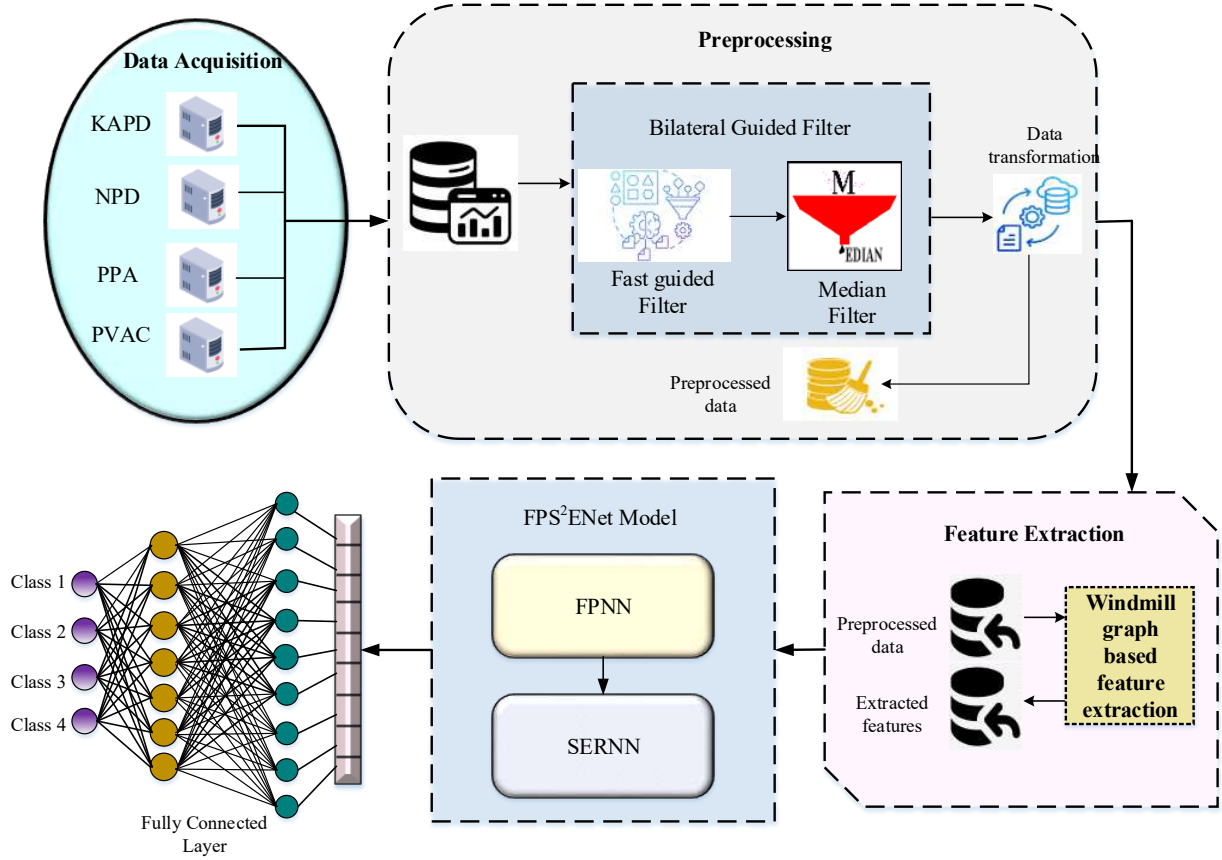


Figure (1) Overall workflow of the proposed model

3.1 Bilateral Guided Filter

In order to remove the unwanted noise from the ALI, the bilateral guided filter (BGF) techniques are utilized which combines the capabilities of median filter and fast guided filter (FGF). Initially, the input image is passed through the FGF model then the FGF filtered image is fed into the median filter. Compared to the input image, the FGF filtered image becomes less blurry and more coordinated. In the beginning, the input image and the guidance image are sub sampled and the local linear coefficients are computed in FGF. To create the FGF filtered image, these coefficients are subsequently sampled and applied to the guiding image. Furthermore, the mathematical representation of FGF is illustrated in Eqn (1).

$$FGF_x = L_{C1_j} + G_x L_{C2_j} \quad \forall x \in SW_j \quad (1)$$

Here, the SW_j and G_x are specified as square window and guidance image correspondingly. Furthermore, x and j are represented as pixel index and window index respectively. L_{C1_j} and L_{C2_j} are indicated as local linear coefficients, which are calculated using Eqn (2) and (3) respectively.

$$L_{C1j} = \frac{1}{SW} \frac{\sum_{x \in SW_j} G_x \text{Im}_x - m_j p_j'}{\gamma_j^2 + \nu} \quad (2)$$

$$L_{C2j} = p_j' - L_{C1j} m_j \quad (3)$$

Here, $p_j' = \frac{1}{SW} \sum_{x \in SW_j} p_j$. The mean, variance and regularization parameter are indicated as m , γ and ν respectively.

When using median filtering, each of the neighboring pixel values are sorted through a numerical sequence, and the middle pixel value is taken into consideration when replacing a pixel. Normally, median filters operate on the moving window concept. After calculating median values of each pixel inside the window, these values are substituted or changed to image pixel values. The mathematical representation of the median filter is derived in Eqn (4).

$$M(p) = \text{median}\{FGF(p)\} \quad (4)$$

Where, p is denoted the 8 neighboring pixels.

3.2 Windmill Graph based feature extraction

For feature extraction, this research presents unique graph-based techniques called Windmill Graph based Feature Extraction (WGFE). The windmill graph $WG(x, y)$ is known as undirected graph, which is created for $x \geq 2$ and $y \geq 2$ by connecting N duplicates of the entire graph at a common global vertex. Normally, $WG(x, y)$ contains radius, diameter, girth, and network connectivity values as 1, 2, 3 and 1 correspondingly. Additionally, the $WG(x, y)$ comprises $y * x * ((x - 1/2))$ edges and $((x - 1) * y) + 1$ vertices. There are numerous Windmill graph variations accessible including butterfly, star and friendship graphs. In order to efficiently capture the relationship between nearby pixels in a specific region, this research is composed of two WGFE variants namely WGFEH and WGFEV. In a 5×5 region, the apple leaf image (ALI) pattern normally composed with 24 pixels and encompassing the center pixel (c_p). Among the 24 surrounding pixels, 8 define the rook $r_1, r_2, r_3, \dots, r_8$, 8 indicate the bishop $h_1, h_2, h_3, \dots, h_8$, and the remaining eight represent the knight $s_1, s_2, s_3, \dots, s_8$.

WGFE_H feature extraction utilized for collecting the interaction among neighboring and nearby pixels along with the relationship among individual pixels in horizontal direction. In an adjacent region, WGFE_H obtains two feature codes including WGFE_{H1} and WGFE_{H2}. Let assume, four pixel positions including r_8 , b_1 , c_p and b_4 can take into consideration in order to extract features for WGFE_{H1}. In the beginning, the pixels r_8 , b_1 , c_p and b_4 are contrasted against the pixels r_8 , b_1 , c_p and b_4 in order to capture the relationship between the adjacent pixels. Similarly, the pixels r_8 , b_1 , c_p and b_4 are contrasted sequentially with r_4 in order to capture the relationship between the

surrounding pixels which is mathematically illustrated in Eqn (5). The mathematical evaluation of feature extraction using $WGFE_{H1}$ method is depicted in Eqn (6).

$$WGFE'_{H1} = \{\gamma(r_8, b_1), \gamma(b_1, c_p), \gamma(c_p, b_4), \gamma(b_4, r_8), \gamma(r_8, r_4), \gamma(b_1, r_4), \gamma(c_p, r_4), \gamma(b_4, r_4)\} \quad (5)$$

$$WGFE_{H1} = \sum_{n=1}^8 (WGFE'_{H1} \cdot K_{G_n}) \quad (6)$$

Where, $\gamma(a, b) = \begin{cases} 1, & \text{if } a \geq b \\ 0, & \text{otherwise} \end{cases}$ and $K_{G_n} = [Squares, odd, prime, natural, binary, fibonacci]$

The $WGFE_{H1}$ feature extraction procedure is followed in the $WGFE_{H2}$ feature extraction with 4 pixel positions namely r_6, b_2, c_p, r_2 and b_3 that is evaluated in Eqn (7). The mathematical representation of the feature extraction using $WGFE_{H2}$ method is shown in Eqn (8).

$$WGFE'_{H2} = \{\gamma(c_p, b_2), \gamma(b_2, e_6), \gamma(r_6, b_3), \gamma(b_3, c_p), \gamma(c_p, r_2), \gamma(r_6, r_2), \gamma(b_2, r_2), \gamma(b_3, r_2)\} \quad (7)$$

$$WGFE_{H2} = \sum_{n=1}^8 (WGFE'_{H2} \cdot K_{G_n}) \quad (8)$$

After that, the histogram features are extracted from both $WGFE_{H1}$ and $WGFE_{H2}$ with help of Eqn (9) and (10) respectively.

$$His_{WGFE_{H1}} = Histogram(WGFE_{H1}) \quad (9)$$

$$His_{WGFE_{H2}} = Histogram(WGFE_{H2}) \quad (10)$$

Finally, the $WGFE_H$ value is calculated with aid of Eqn (11) and the mathematical equation for calculating the size of $WGFE_H$ with $M \times M$ image dimension is represented in Eqn (12).

$$WGFE_H = His_{WGFE_{H1}} \cup His_{WGFE_{H2}} \quad (11)$$

$$Size_{WGFE_H} = \lceil (M-4)/l \rceil * \lceil (M-4)/l \rceil * 2 * length \quad (12)$$

Furthermore, the relationships between nearby and neighboring pixels as well as the relationship between individual pixels in a vertical direction are collected using the $WGFE_V$ feature extraction technique. The $WGFE_H$ feature extraction process carried out to the $WGFE_V$ feature extraction procedure in order get the $WGFE_V$ feature.

Additionally, the handcrafted features such as color and textural features are extracted from the ALI. Using RGB and HIS techniques, the color features of the ALI are retrieved. The ALI colors are represented by R, G, B, r, g and b in RGB model as well as hue (H), intensity (I) and saturation (S) in HIS model. In order to get the color features, a specific region color image can be processed in several color spaces such as RGB and HIS. In this color image, nine values such as R, G, B, r, g, b, H, I and S are gathered. Additionally, the five statistical features are

extracted such as entropy En , energy E , variance V , skewness S and peak value P_v with help of Eqn (13-16) respectively.

$$En = \sum_{p=1} [G(p)]^2 \quad (13)$$

$$E = \sum_{p=1} G(p) \log[G(p)] \quad (14)$$

$$S = 1/\alpha^3 \sum_{p=1} (p - \bar{p})^3 G(p) \quad (15)$$

$$P_v = 1/\alpha^4 \sum_{p=1} (p - \bar{p})^4 G(p) - 3 \quad (16)$$

Where, $G(p) = \text{Histogram}(p) / \text{Area}$ is denoted as grey level and mean value is represented as $\bar{p}$. One of the most crucial features for ALI disease identification is textural features. In textural features, there are six features such as autocorrelation A_c , dissimilarity D_s , cluster shade C_s , cluster prominence C_p , contrast C_t and correlation C_l are extracted with aid of Eqn (17-22).

$$A_c = \frac{\sum_{l=0}^n \sum_{m=0}^n L(x, y) L(l+x, m+y)}{\sum_{l=0}^{I-1} \sum_{m=0}^{I-1} L(l, m)} \quad (17)$$

$$D_s = \sum_s \sum_r |s - r| p(s, r) \quad (18)$$

$$C_s = \sum_{s=0}^{I-1} \sum_{r=0}^{I-1} (s + r - l_x - l_y)^3 p(s, r) \quad (19)$$

$$C_p = \sum_{s=0}^{I-1} \sum_{r=0}^{I-1} (s + r - l_x - l_y)^4 p(s, r) \quad (20)$$

$$C_t = \sum_s \sum_r |s - r|^2 p(s, r) \quad (21)$$

$$C_l = \sum_s \sum_r \frac{(s - m_x)(r - m_y) p(s, r)}{\gamma_x \gamma_y} \quad (22)$$

Where, the gray level occurrence matrix is represented as $p(s, r)$ and the gray pixel values are denoted as s and r correspondingly. The mean value is specified as m_x and m_y as well as variance are indicated as γ_x and γ_y . Furthermore, I is represented as gray level image.

3.3 Feature pyramid Siamese Squeeze and Excitation Residual neural network (FPS²ENet).

In this research, FPS²ENet model is utilized for ALI disease classification. The proposed model is composed of two blocks namely pyramid neural network (FPNN) and Squeeze and excitation residual neural network (SERNN) with two layers. In each layer, the features are selected via sampling by employing the FPNN afterwards, these deep features are fed into SERNN. Finally, the two layers are fused using Siamese layer and then fully connected layer is utilized for ALI classification. The in-depth description of each layer is illustrated in upcoming section. Furthermore, the entire framework of the proposed model is demonstrated in Figure (2)

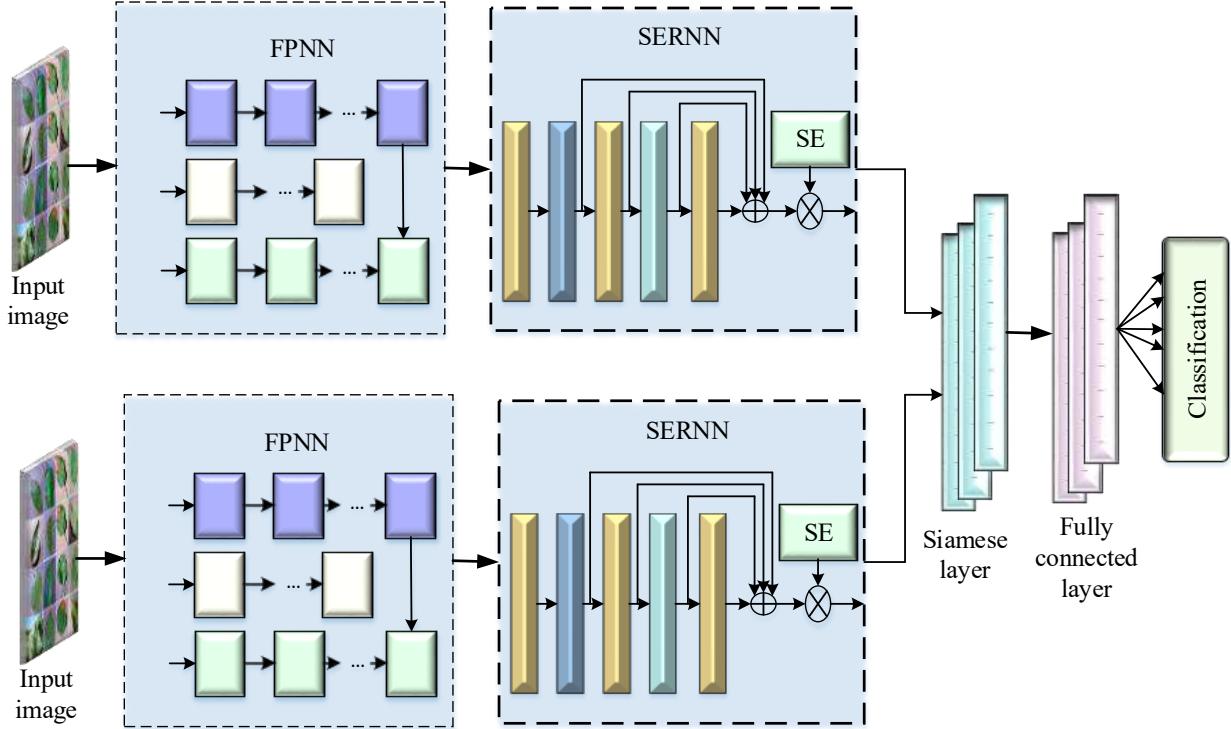


Figure (2) Framework of the proposed model

3.3.1 Feature pyramid Neural Network

The FPNN is composed of multi-scale feature layers and can produce results feature layers on the same dimensions. The general view of the FPNN is depicted in Figure (3). Furthermore, several image and semantic data must be described by cross-fusing features to construct an advanced linguistic feature pyramid system. Here, Cross-fusion feature maps are produced by merging feature maps of various scales that result in feature maps with more semantic data.

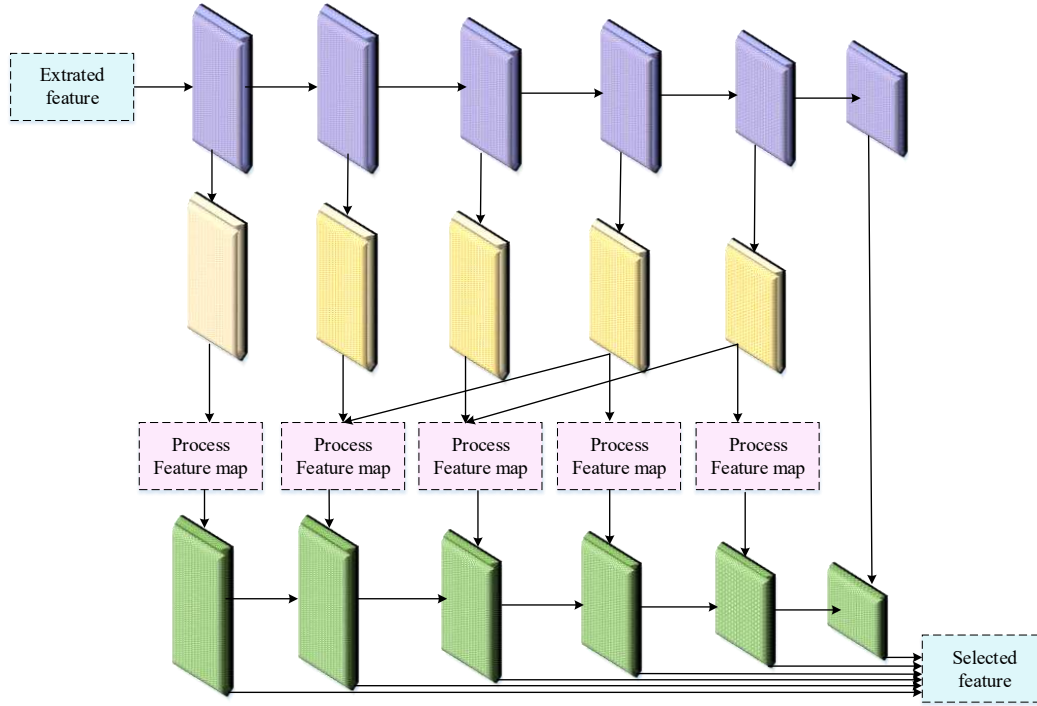


Figure (3) Architectural view of the FPNN

To obtain superior and better accurate results in ALI disease classification, feature pyramids collaborate with core networks to deliver excellent feature maps. The input for the subsequent pyramid network can use the outcome of the preceding pyramid network. To aid in cross-fusion, each ascending input feature map channel initially gets modified to 256 channels. After that, additional processing such as batch norm, sum, Conv, and ReLU occur via the cross-fusion channel. Finally, the FPNN can produce output chart as $\{C_2, C_3, C_4, C_5, C_6\}$ with appropriate proportions as $\{39, 19, 10, 5, 3\}$ a 256 number of channels.

3.3.2 Squeeze and excitation residual neural network (SERNN)

This SNN consists of three main modules, namely convolution layer via max pooling layer (CMP) and Residual neural Network (ResNet) and squeeze and excitation layer (SE) which are illustrated in Figure (4).

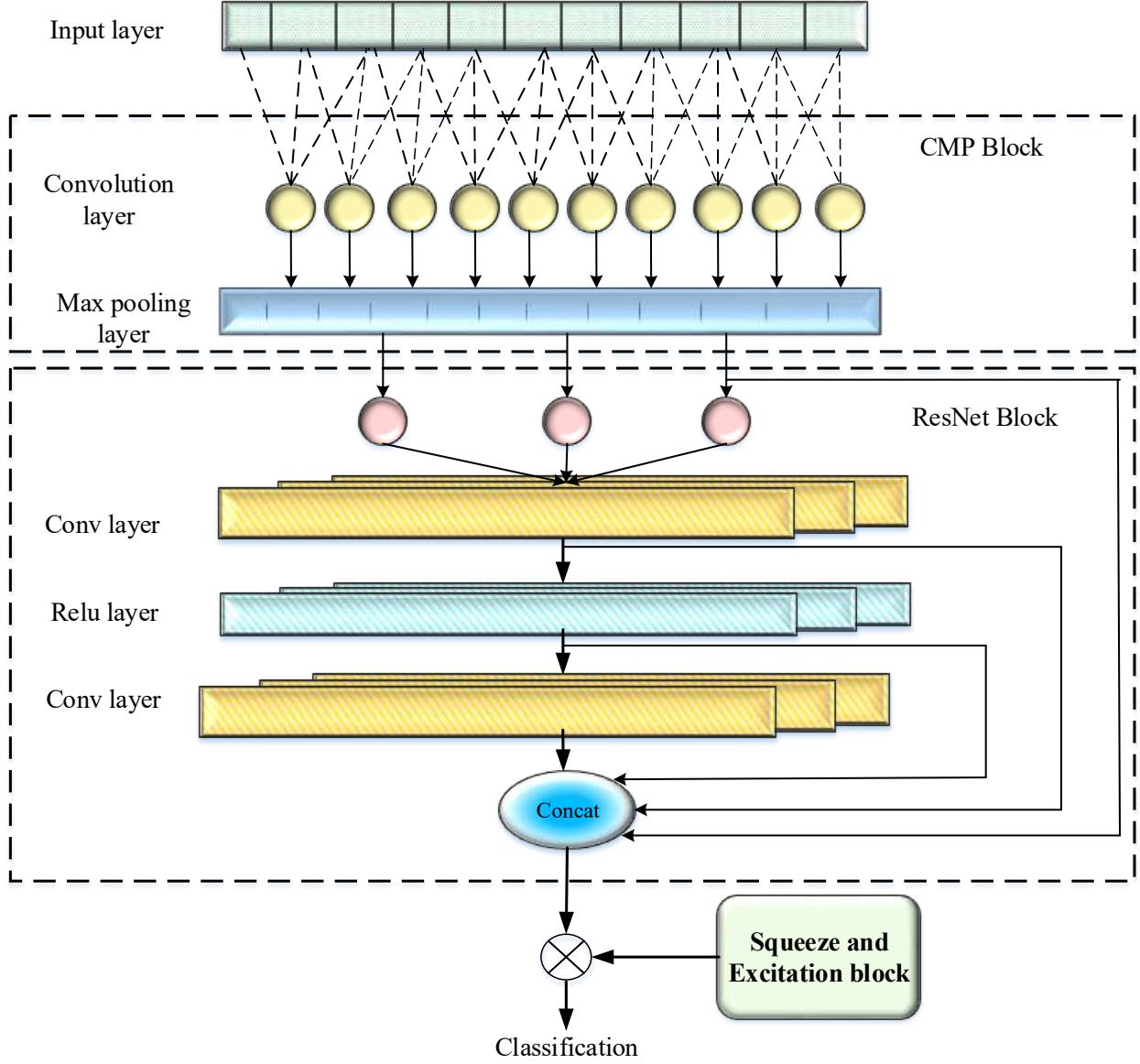


Figure (4) Layout of the SERNN

$F = [f_1, f_2, \dots, f_n]$ is indicated as input features in the CMP after that the corresponding outcome of the CMP is preceding to the upcoming layers. Furthermore, the weight shared kernel value $K_v = \Re^{K \times \rho}$ is applied to the Convolutional block in order to get the N dimension latent vector V_t^1 of the input feature that can depicted in Eqn (23).

$$V_t^1 = K_v i_{t:t+\rho-1} B_v \quad (23)$$

Here, kernel size and bias vector are specified as ρ and B_v respectively. Also, the window for the input sequence is denoted as $i_{t:t+\rho-1}$. To generate a series of latent vectors $V^1 = V_1^1, V_2^1, \dots, V_{n-\rho+1}^1$, this kernel procedure is applied in every feature. Furthermore, each successive N -length

subsequence of the convolution block outcomes is subjected to the N max-pooling block. The mathematical representation of the max pooling layer is depicted in Eqn (24).

$$V_{i,j}^2 = \max(V_{i:N+i-1,j}^1) \quad (24)$$

The objective of max-pooling block is to maintain the most important features across every N stride while separating the convolution outputs. In short, this technique reduces the quantity of analyzed features by N . Moreover, the outcome of the CMP block is fed forward to the input of the next layer, namely ResNet. In ResNet block, the convolutional layer is utilized initially to obtain the shallow feature that can mathematically expressed as Eqn (25).

$$F_s = \text{Conv}(V_{i,j}^2) \quad (25)$$

After that, F_s is continues to be used for deep feature extraction process with help of ReLU layer. To regulate the resultant data automatically, further a 1×1 convolutional layer is also added which can be derived as below.

$$F_C = \text{Conv}([F_s; F_r; F_a]) \quad (26)$$

Where, the first convolutional, ReLU layer and attention layer outcome are denoted as F_s , F_r and F_a correspondingly. Furthermore, the SE block is further introduced to reduce the feature quantity, which can briefly be discussed in following sub section.

3.3.3 Squeeze and excitation block (SE)

The SE modules utilize the benefits of channel dependencies to improve network modeling capabilities that can be diagrammatically represented as Figure (5). This module eliminates unnecessary features and highlights crucial aspects within the channels. Initially, the SE model is to squeeze the global spatial information into a channel description with aid of global pooling layer. The mathematical equation for the squeeze process is expressed in Eqn (27).

$$S_q = F_{S_q}(I_C) = \frac{1}{h \times w} \sum_{p=1}^h \sum_{q=1}^w I_c(p, q) \quad (27)$$

Here, the squeeze function is specified as F_{S_q} and the height and weight are represented as h and w respectively. Moreover, the input of the c^{th} channel is indicated as I_c . After that, an excitation function is then followed by a squeeze process that attempts to entirely express the channel-wise correlations. The mathematical evaluation of the excitation process is illustrated in Eqn (28).

$$Ex = F_{EX}(I_{S_q}, S) = \sigma(S_U \mu(S_D I_{S_q})) \quad (28)$$

Where, the preceding layer's squeezed input is indicated as I_{S_q} and the excitation function and ReLU activation function are represented as F_{EX} and μ correspondingly. The sigmoid function

is denoted as σ . Furthermore, the channel upscaling and down-scaling are denoted as $S_U \in \mathbb{R}^{c \times \frac{c}{r}}$ and $S_D \in \mathbb{R}^{\frac{c}{r} \times c}$ respectively.

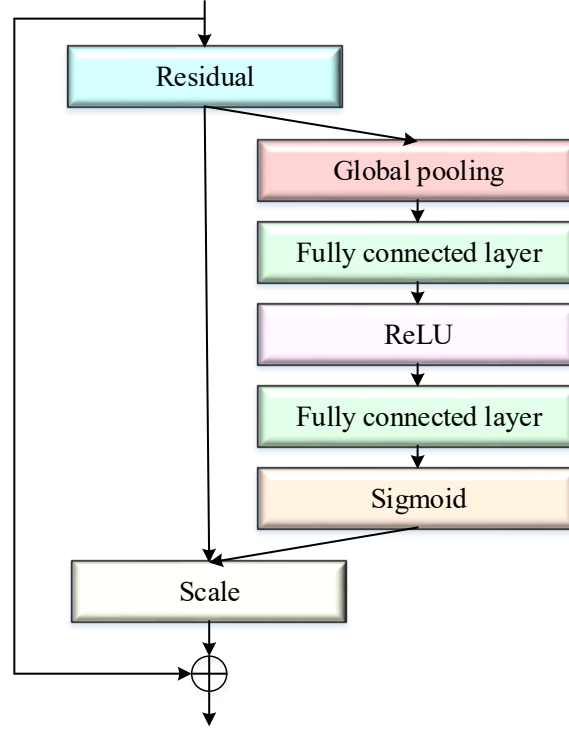


Figure (5) Structural view of SE block

Finally, this research utilized Siamese layer for fusing the two layers. After that, the fully connected layer is employed to classify the AVL disease with different classes. According to the dataset, the number of classes may vary.

4 Result and Discussion

To ensure the efficacy of the proposed model, this research conducted several evaluation analyses. Furthermore, the effectiveness of the proposed approach can be implemented using Python programming language to assess the precise of the ALI disease categorization model's process. Moreover, the performance evaluation is fully based on accuracy, precision, recall and F1-score. Additionally, the ROC curve analysis and confusion matrix analysis are employed for evaluating the effectiveness of the ALI disease categorization model. Furthermore, this analysis is performing four types of datasets, and the brief description of each dataset is illustrated in upcoming section. Moreover, overall analysis of the proposed AVL disease categorization is evaluated with existing models including Bi-LSTM, Bi-GRU, ResNet, and DenseNet. The subsequent sections can present four types of analysis such as performance metrics analysis, loss and accuracy curve analysis, ROC curve analysis and confusion matrix analysis.

4.1 Dataset description

In performance analysis, the four types of dataset are utilized namely Kashmiri Apple Plant Disease Dataset (KAPD), New Plant Diseases Dataset (NPD), Plant Pathology Apple (PPA) dataset, plant village-apple-color (PVAC). The short overview of each dataset is explained below.

KAPD: Regarding informative and scientific purposes, most of the images in this dataset are gathered through the orchards in the region of Kashmir. Furthermore, approximately 419 images of both healthy and diseased apple leaves are gathered. Although the diseases only affect most apple leaves in the months of May, June, and July. This duration is utilized for collecting the apple image samples to create real time datasets. Each image was taken manually with a variety of trademarked mobile phones and digital cameras. After that, every photograph sample has been placed in a distinctive marked folder. Additionally, this dataset normally consists of four classes such as apple rot, healthy, leaf blotch, scab leaves. Moreover, the pictorial representation of this dataset's sample images is depicted in Figure (6).



Figure (6) Sample image of KAPD dataset

NPD: The offline enhancement is used to generate this dataset via the source dataset. Furthermore, the source dataset is termed as Plant village, and the sample images are presented in Figure (7). This dataset includes approximately 87K RGB images of both normal and diseased farm apple leaves. Furthermore, these dataset images are classified into four types of image classes namely scab, black rot, cedar- apple-rust and healthy. Additionally, the entire dataset is divided into two subsets including 80% for training and 20% for validation process.



Figure (7) Sample image of NPD dataset

PPA: This dataset contains 18,633 RGB images with both healthy and unhealthy apple leaves images. Additionally, the overall dataset is classified into four categories such as healthy, rust, scab and multiple diseases. Furthermore, the sample images of this dataset is illustrated in Figure (8).



Figure (8) Sample image of PPA dataset

PVAC: The four primary classes of apple leaves are contained in this dataset including apple-scab, apple-rot, apple-rust, and apple-healthy which are demonstrated in Figure (9). For each class in the dataset, the entire apple leaves images are categorized into 630 number of apple-scab images, 621 number of apple-rot images, 275 number of apple-rust images and 1645 number of healthy images. Furthermore, the model is trained on the training images to identify similarities and differentiate between healthy and unhealthy leaves. After that, the efficiency and precision of the trained models on unobserved data are assessed using the testing images. The proposed model uses this extensive data to properly identify apple leaves as healthy or afflicted with diseases. Depending on the structure of the dataset, the system can gather information from a variety of leaf states, which enhances its capacity to extrapolate and precisely diagnose plant illnesses.



Figure (9) Sample image of PAVC dataset

4.2 Performance metrics analysis

The effectiveness of the proposed AVI disease classification model is assessed in this demonstration. Furthermore, this section can access the success rate of the proposed model in

terms of accuracy, recall, precision, f1-score, completion time and true positive rate (TPR). Furthermore, the success rate and effectiveness of the proposed model is compared to the various existing models namely, ResNet, DenseNet, Bi-LSTM and Bi-GRU. Additionally, the comparison analysis of the proposed model with this existing model via four dataset is demonstrated in Figure (10).

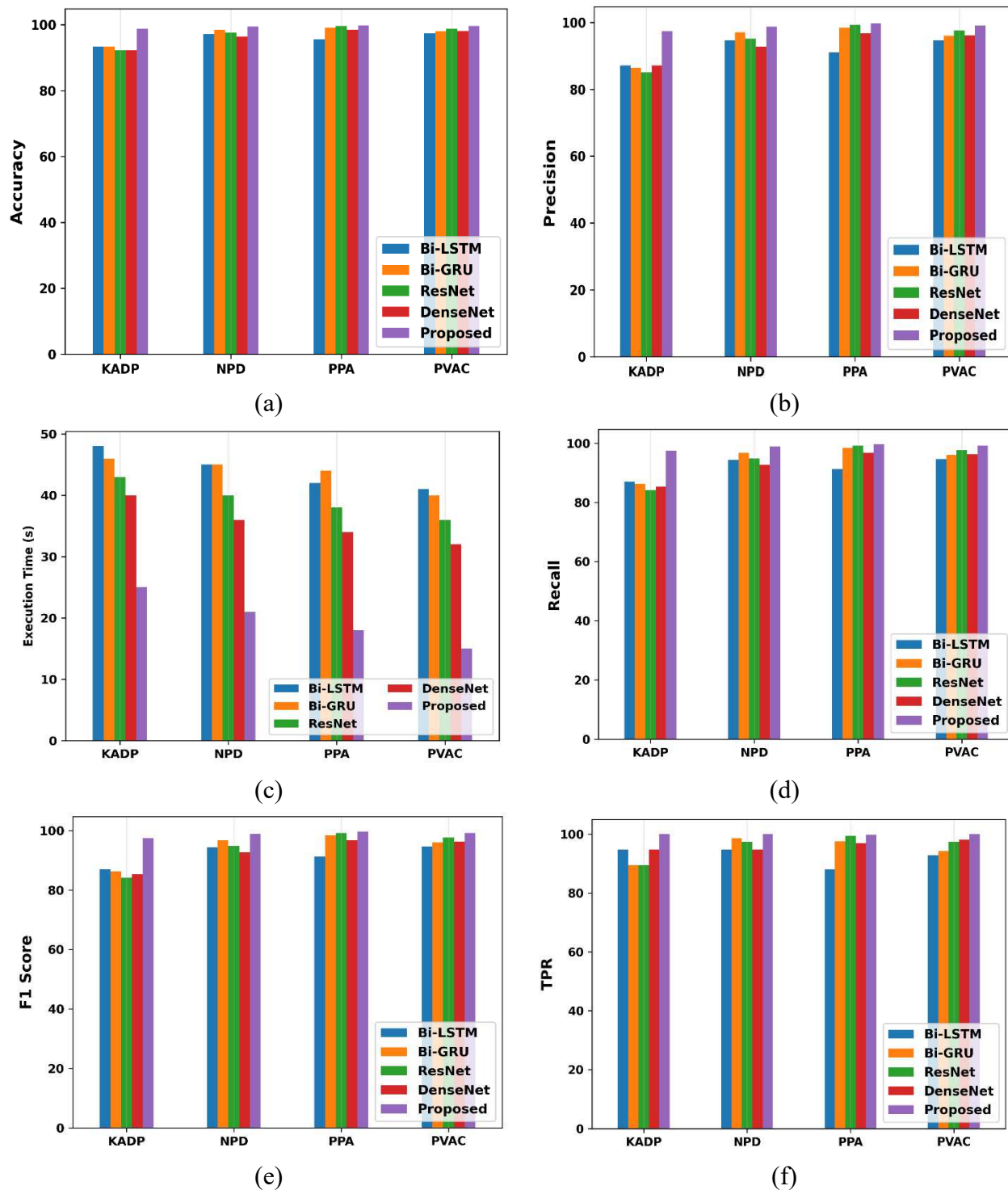


Figure (10) Performance metrics analysis

In Figure 10 (a), the proposed model can attain huge accuracy values compared to another existing model. Furthermore, the existing model gets almost similar accuracy values in four classes, but they attain less accuracy values in the KADP dataset. From Figure 10 (b), it can be seen that, compared to the proposed model, the existing model can obtain less than 90% precision in the KADP dataset. Furthermore, the proposed method can get above 90 % in precision. The Bi-LSTM model can attain lower precision values in three datasets namely, NPD, PPA and PVAC. Additionally, both Bi-GRU and ResNet achieve similar outcomes. From Figure 10 (c), it can observe that the proposed method only utilized less time for completing execution in all the datasets. But Bi-LSTM can consume large amounts of time for execution in the four dataset and Bi-GRU also utilizes high time consumption. Furthermore, DenseNet and ResNet can consume moderate amount of time for completing the execution. From Figure 10 (d), it can be evident that the proposed model can achieves high recall results compared to other existing models. Furthermore, the proposed and existing models can obtain near to equivalent recall values in the PVAC dataset. In Figure 10 (e), the existing model obtains F1-score values as low compared to the proposed model. From Figure 10 (f), the proposed method can achieve above 95% of TPR in four datasets. But the Bi-LSTM models get less TPR in PPA dataset.

4.3 Loss and accuracy curve analysis

The loss curve summarizes the entire amount of the error in the proposed model which gauges if the proposed model is classified as apple leaf effectively or poorly. A high error rate can result in a significant loss which indicates poor performance from the model. When the error rate is less than model indicates huge effectiveness. Furthermore, the loss or cost function is utilized for evaluating the error rate. The accuracy curve is used for analyzing the success rate of the proposed model. When the model has low accuracy yet a huge loss rate then it indicates that the model has significant mistakes in most of the data. However, low accuracy and loss indicate that the model produces humble errors in most of the data. On other hand, when both accuracy and loss rate are huge then that results in large mistakes in some of the data. Finally, if the model attains high accuracy and less loss then that is indicated as the ideal situation for the ALI disease classification. Furthermore, the training accuracy and loss curve analysis of both proposed and existing models in the four types of datasets are illustrated in Figure (11).

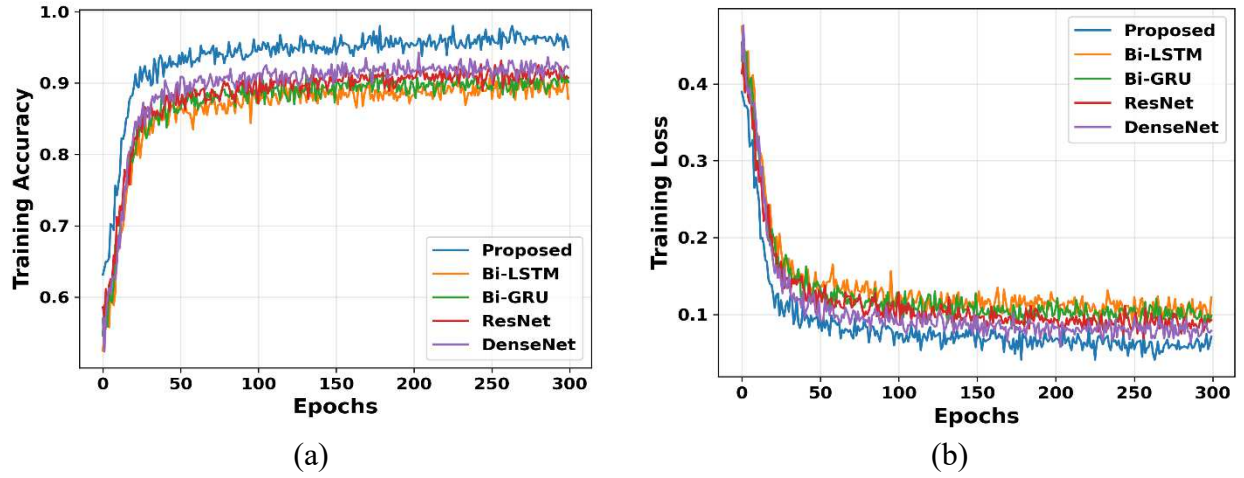


Figure (11) Training (a) accuracy and (b) loss of the KAPD

From Figure 11), it clear that the proposed method attains huge accuracy and less loss in KAPD dataset, which means that the suggested method obtains huge performance. Furthermore, the Bi-LSTM model can attain less accuracy and huge loss compared to other models. Moreover, the bi-GRU and ResNet can obtain moderate results.

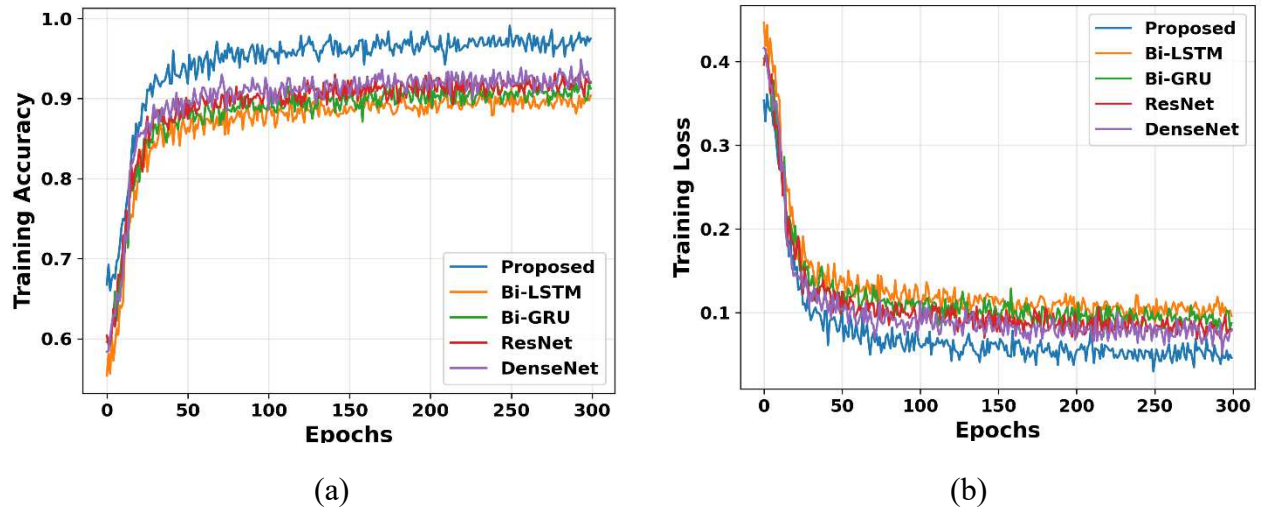


Figure (12) Training (a) accuracy and (b) loss of the NPD

In Figure (12), the proposed model in NPD dataset is increased gradually the accuracy in the range of 0 to 50 epochs. After that, the proposed model can be stable at a high accuracy rate. Likewise, the proposed method can gradually decrease the loss curve in the range of 0 to 45 then it can be stable at a lower loss rate. But the existing methods attain moderate accuracy and loss rate in NPD dataset.

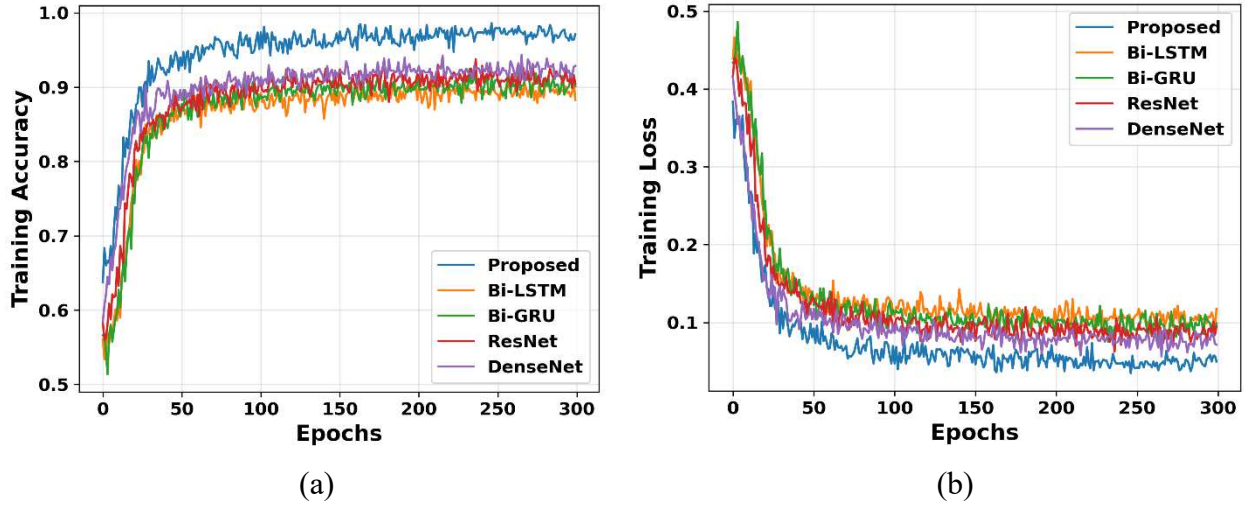


Figure (13) Training (a) accuracy and (b) loss of the PAP

From Figure (13), it can be seen that, in the 45 epochs onwards, the proposed method can start to obtain huge accuracy rate and lower loss rate in PAP dataset. The existing methods are obtaining similar results but compared to the proposed method, which can obtain less performance.

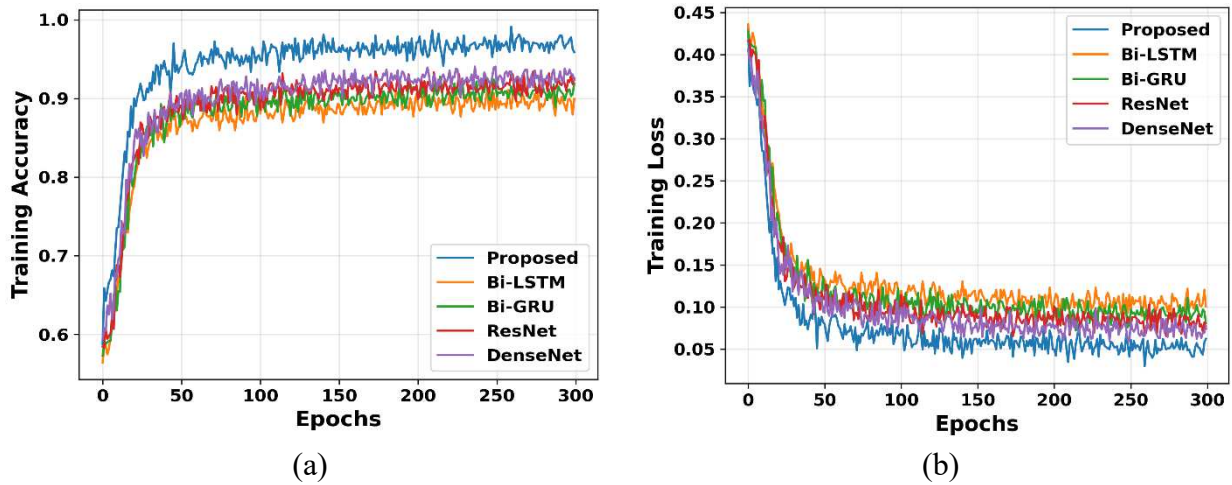


Figure (14) Training (a) accuracy and (b) loss of the PVAC

In Figure (14), the accuracy curve of the existing models gradually increases on 0 epochs onward after that it can stable in 50 epochs onwards in the PVAC dataset. Furthermore, all the existing methods produces nearby outcomes. But comparing the proposed model with existing model in PVAC dataset, the proposed model can obtain high performance rate.

4.4 ROC curve analysis

This section employs the Receiver Operating Characteristic Curve (ROC) to validate the ALI disease classification effectiveness. By calculating the true positive rate (TPR) over the false

positive rate (FPR) with different threshold levels, the ROC curve is constructed. The ROC curve is utilized for determining the effectiveness of the proposed model with various existing methods. Furthermore, the Roc curve analysis of the four datasets with both existing and proposed model is demonstrated in Figure (15).

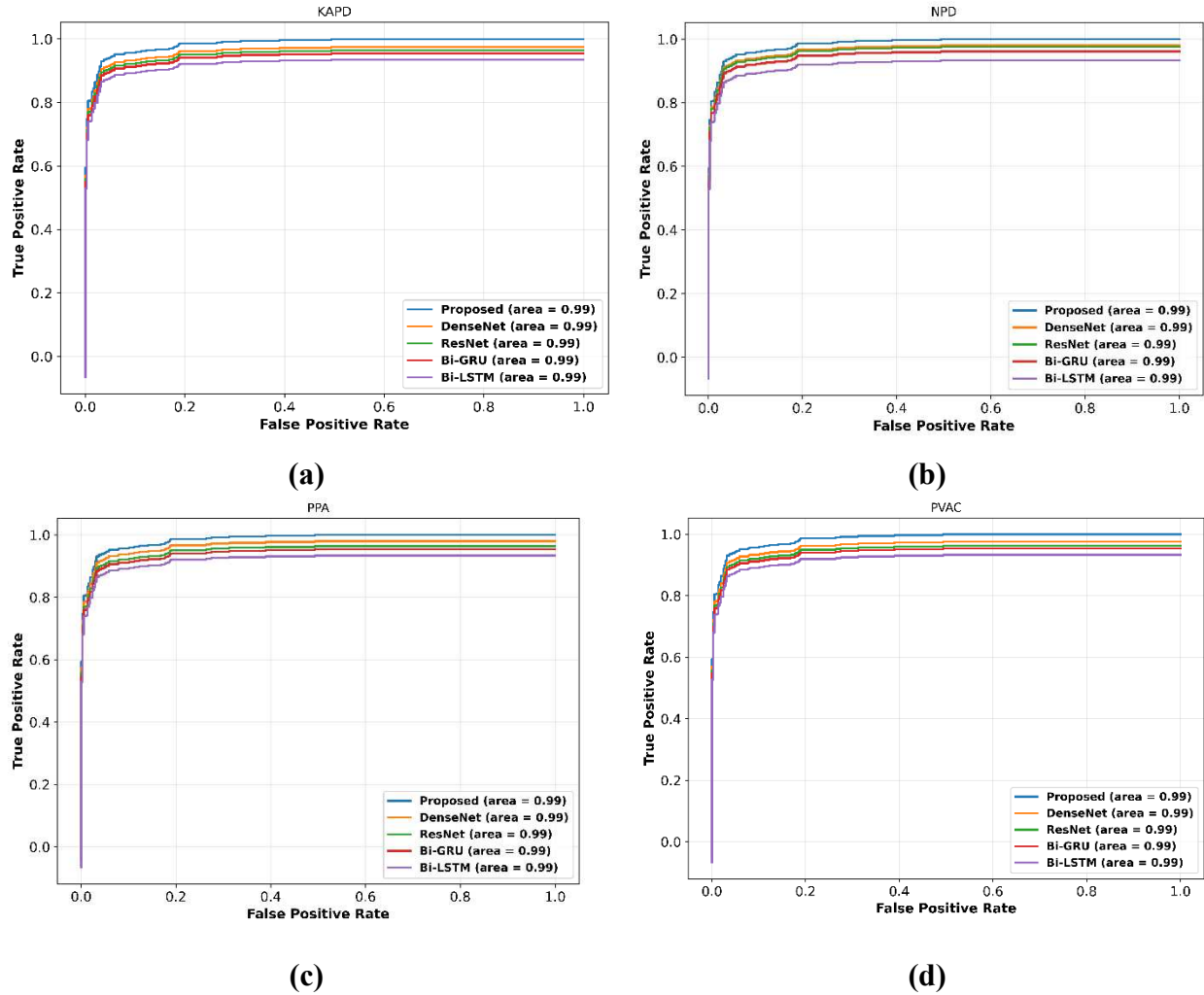


Figure (15) ROC curve analysis of the four-dataset including (a) KAPD, (b)NPD, (c) PPA and (d) PVAC

From Figure (15), it obviously declares that the proposed model for ALI disease classification can obtain huge ROC curve rate in all the four datasets. Here, the Bi-LSTM can attain at least ROC values in four datasets. In PPA dataset, both proposed and existing models for AVL disease classification can achieve nearby values. In the four datasets, all the models are constant up to 0.8 at a true positive rate then they increase gradually. In both KAPD and PVAC, the Bi-GRU, ResNet, DenseNet gets moderate results.

4.5 Confusion matrix analysis

The anticipated result of the ALI disease classification with matrix format is referred to as confusion matrix. The confusion matrix is also used for evaluating the effectiveness of the proposed model. Furthermore, the effectiveness of the proposed and various existing models in the four dataset is evaluated in the matrix form which is depicted in Figure (16).

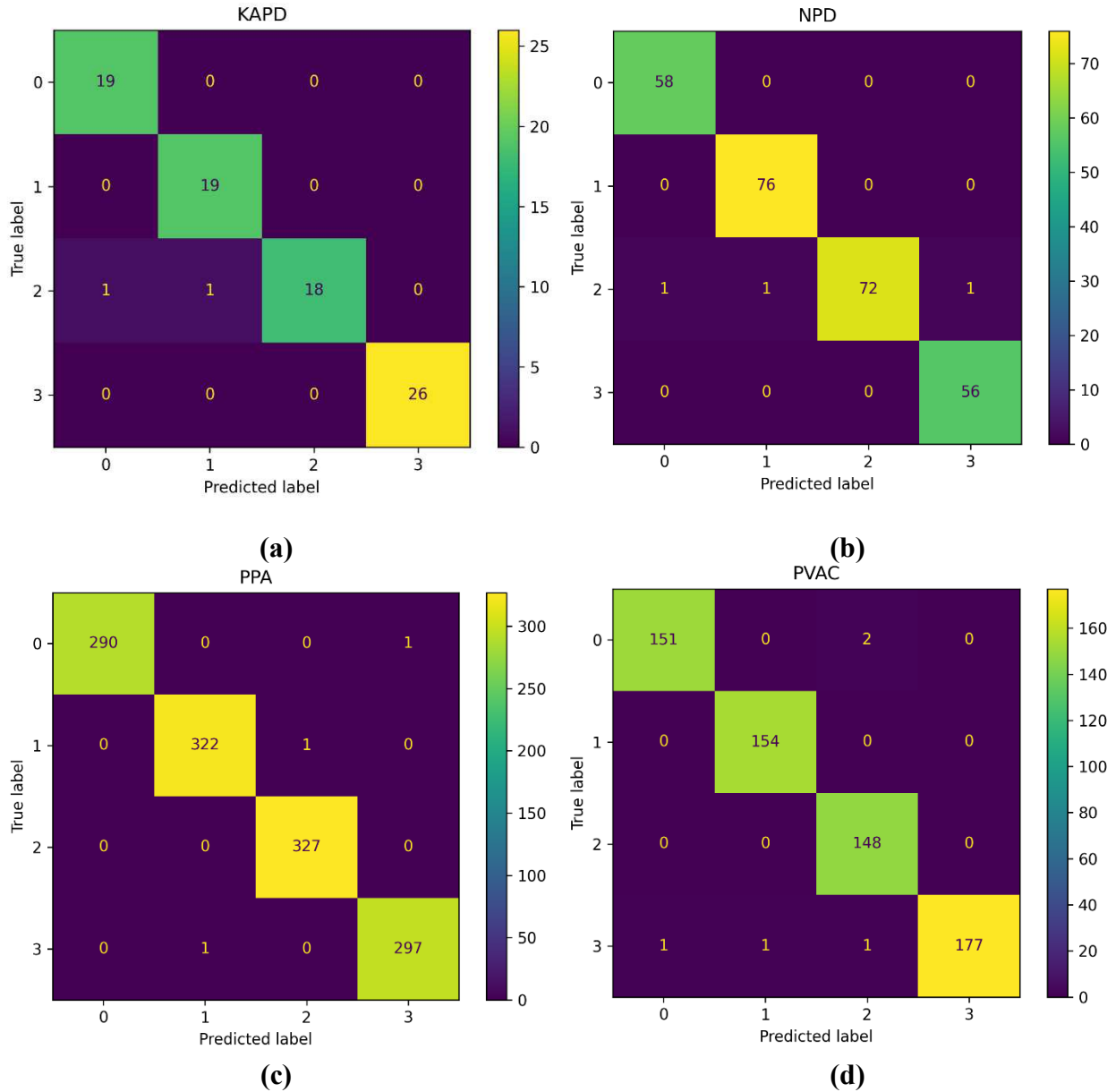


Figure (16) confusion matrix analysis of the four dataset such (a) KAPD, (b) NPD, (c) PPA and (d) PAVC.

From Figure (16), it can understand that the proposed model can effectively predict the apple leaf with four different classes and few of them only mislead. In KAPD dataset, the proposed method can classify all four classes accurately yet only 2 images are classified as erroneous. Furthermore, the 58, 76, 72 and 56 sample images in the NPD dataset is precisely predicted as class 0, 1, 2 and 3 respectively. The remaining 3 sample apple images of the NPD dataset are

classified as inaccurate. Moreover, the 3 sample images with class 1, 2 and 3 in the PPA dataset are inaccurate as class 3, 1 and 0 respectively. The remaining sample apple images of the PPA dataset are accurately classified as corresponding classes respectively. In PAVC dataset, the 5 apple image samples are classified as mistakenly, and remaining images are classified as exact.

5. Conclusion

The various diseases of apple leaves are hard to identify due to the limitations imposed by biological growth regulations and the season. To precisely diagnose of apple leaf diseases, a novel FPS2ENet model has been proposed in this research. This model is capable of automatically identifying the distinctive characteristics of leaf diseases and enabling an extremely accurate entirety learning process. The proposed model mainly consists of blocks namely deep feature selection via FPNN block and classification through SERNN block. To increase effectiveness, the BGF and WGFE techniques are employed for the process of preprocessing and feature extraction respectively. In performance evaluation stage, the processed methods obtain adequate results that can exceed the results of existing models in terms of classification effectiveness. Additionally, the python programming language is utilized for implementation, and four different types of apple leaf dataset are used for evaluating effectiveness. Furthermore, the four types of performance analysis are performed including performance metrics analysis, loss and accuracy curve analysis, ROC curve analysis and confusion matrix analysis. These analysis of results demonstrated that the proposed model could classify the four prevalent classes of apple leaf diseases accurately. In future, we focus on accurate classification in furthermore classes.

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Author Contribution

Conceptualization, Writing Review and Editing, A.P.K., S.K.R.; Methodology, A.P.K., K.V.R.; Formal analysis, A.P.K., S.K.R.; Investigation and Supervision, S.K.R.,

Data availability

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations:

Ethics approval

This study uses publicly available Apple leaf image datasets. No experiments involving human participants or animals were performed by the authors; therefore, ethical approval was not required.

Consent to participate

Not applicable, as the research does not involve human participants.

Consent for publication

All authors have read and approved the final manuscript and consent to its publication.

Competing interests

The authors declare no competing interests.

Reference

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