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MULTI-SCALE REGION-OF-INTEREST BASED DEEP LEARNING FOR FRUIT DISEASE IDENTIFICATION AND CLASSIFICATION

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ABSTRACT

Agricultural productivity is mainly affected by the different types of fruit diseases. To reduce such impacts, automated fruit disease identification and categorization model is vital. So, a Multi-scale Deep Learning (MDL) model was designed to identify and categorize the variety of strawberry fruit diseases. This model has an Adaptive Receptive Field Module (ARFM), a Bottleneck Block (BB), Depth-wise Residual Blocks (DRBs) and the Squeeze Excitation Residual Network (SE-ResNet) units to extract the Feature Maps (FMs) related to all disease classes. But, this model cannot partition individual fruit samples. Also, the number of fruits with multiple infections within a particular image was not easily captured. So, this article develops a Multi-scale Region-Of-Interest (ROI)-based DL model called (MRDL) to improve the accuracy of identification and categorization of a single fruit sample with a certain disease in a real-time scenario. This model is performed in 2 different phases. First, more robust features are extracted by the DRB, ARFM, and BB in the initial phase. Then, an ROI Fused (ROIF) unit, the SE-ResNet unit, a classification unit, and a mask unit are involved in the second phase. The ROIF unit obtains the FMs for all candidate ROIs using the candidate bounding boxes from the initial phase. The extracted FMs per sampled position are aggregated to get the fused FM, which is resized by integrating the attention strategy with the SE-ResNet unit. Those resized fused FMs are independently passed to the classification and mask units to classify the candidate bounding boxes and localize the infected pixels in the candidate ROIs, respectively. Finally, the test results exhibit that the MRDL model achieves 91.1%, 90.8%, and 91.6% accuracy on apple, citrus, and tomato disease databases, respectively compared to the classical models.

Keywords: segmentation, classification, multi-scale deep learning, squeeze excitation residual network, attention strategy, bounding box.

INTRODUCTION

India is ranked second in fruit production. Agriculture is the backbone of the Indian economy since it generates 18.5% of India's overall Gross Domestic Product (GDP) and offers the service to more than 52% of the population [1-2]. Owing to global warming, the varieties of fruit diseases tend to increase [3]. Such fruit infections are one of the most serious issues affecting agricultural production quality [4]. So, the identification and categorization of fruit lesions are the primary objectives to enhance agricultural productivity and quality for economic growth. It is critical to detect pathogens in fruits to supply high-quality goods. The conventional approach for fruit disease identification and categorization relies on exposed eye perception by professionals; however, in certain developing countries, counseling specialists are expensive and time-consuming due to their availability in remote places [5]. In contrast, with the broad availability of digital cameras, automated systems that process digital images of fruits and conduct a proper prognosis of fruit infections was established to increase the efficiency of identifying and categorizing the varieties of fruit diseases.

Generally, the automated systems involved many image processing and artificial intelligence algorithms to increase the quality of fruit images, obtain image characteristics and identify the infection of interest [6]. Artificial intelligence encompasses machine learning models (e.g., Support Vector Machine (SVM) [7], random forest [8], Artificial Neural Network (ANN) [9-10]), which exploit hand-crafted features for distinguishing and quantifying the diseased regions. There are many hand-crafted features [11] obtainable like texture, shape, etc. But, it is impossible to evaluate all types of features, as well as ambiguous to select suitable features. To combat these challenges, DL frameworks have been developed and outperformed the traditional algorithms in fruit disease identification and categorization [12]. Specifically, the Convolutional Neural Network (CNN) has established a significant efficiency in fruit picture classification processes.

The CNN can able to obtain visual information with no personal involvement and categorize a sample into a relevant category via a sequence of convolution and pooling procedures. Several deep learning frameworks using the CNN structure were developed for recognizing and categorizing fruit diseases. On the contrary, most prior CNN frameworks merely conduct a classification task, i.e., for a picture of fruit, it produces a unified category tag, defining whether a specified sort of illness occurs or what sort of infection it was [13]. A sample may include multiple diseased regions of one or more sorts of infections. In such a circumstance, it is preferable to localize the specific position of the diseased regions, giving detailed illness information and allowing further assessment of disease by both human specialists and automated systems.

According to the DL principle, Ilyas *et al.* [14] developed a Multi-scale Deep Learning (MDL) model-based semantic partition, which comprises a deep convolutional-based encoder-decoder structure to recognize and categorize the different strawberry fruit diseases, including the class of overgrown or infected strawberries. In the encoder network unit, an ARFM was utilized to adaptively modify the Receptive Field (RF) dimension of neurons for multi-scale context fusion. Also, a BB was designed to train channel and spatial interdependencies enabling the model to capture highly vigorous characteristics. Moreover, DRBs were applied to decrease the computation burden and memory usage of the network. In the decoder unit, the SE-ResNet modules were applied for the partition task, which obtains the FMs related to all disease classes. On the other hand, this network model was not able to segregate individual fruit samples. Additionally, the number of fruits with multiple infections within a particular image was not easily captured. So, this work focuses on enhancing the identification and categorization of a single fruit sample with a specified infection in a complex background, i.e., in a real-time atmosphere where lighting, varying background and occlusion exist.

In this paper, a MRDL model is developed, which enhances the efficiency of fruit disease identification and categorization. The objective of this study is to introduce a novel attention strategy and enhance the representational features of fruit disease images. It performs both categorization and localization processes. This novel attention strategy can adaptively fine-tune its RF dimension to deal with the picture characteristics at various sizes from a given picture having various resolutions. As well, it can dynamically prioritize or suppress the features based on their significance. The major difference between the MDL and MRDL is that the SE-ResNet is applied to find the ROI of diseased regions, whereas this is applied to find the fruits phenotype, i.e., fruit shape in the MDL model. The major contributions of this MRDL model involve two phases.

In the first phase, the DRB, ARFM and BB are performed to extract more robust features by learning channel and spatial interdependencies. The second phase comprises an ROIF unit, the SE-ResNet unit, a categorization unit and a mask unit. The ROI unit extracts the FMs for every candidate ROI by using the candidate bounding boxes from the primary phase. To tackle the problem of quantization, a bilinear interpolation is employed to determine the accurate characteristics per sampled position and those are concatenated by the max function to get the final FMs. Because of retrieving FMs, this model shares the candidate bounding boxes with another stage of the network, extracts FMs from all stages and concatenates the FMs using aggregation.

After aggregation, the SE-ResNet unit is included to resize the fused FMs, i.e. integrating attention strategy. Moreover, the resized fused FMs are independently passed to the classification unit and the mask unit.The classification unit categorizes the candidate bounding boxes and bounding box regression, whereas the mask unit performs the pixel-to-pixel localization of all bounding boxes, i.e. partition and localize the infected areas.Finally, this model is analyzed by using images of multiple fruits with various diseases. The test outcomes imply that the MRDL can able to categorize and localize the diseased regions from the fruit images with better accuracy.

The remaining sections of this article are structured as follows: Section II surveys the work associated with the different fruit disease identification and categorization models. Section III describes the presented MRDL model whereas Section IV displays its efficiency. Section V summarizes the entire work and discusses the upcoming enhancement.

LITERATURE SURVEY

Ilic *et al.* [15] suggested various data mining techniques for predicting cherry fruit pathogen disease. First, the raw dataset was supplied to the Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) to discard the outliers. Afterward, the discriminant classification analysis and compact classification tree were performed to create the prediction model, which helps to predict cherry fruit diseases. But, the accuracy was not efficient due to the limited number of data.

Zhang *et al.* [16] designed a characteristic waveband selection scheme depending on the mixture of the Ant Colony Optimization (ACO) and variable selection principles. In this scheme, 6 characteristic wavebands for all categories of citrus blemishes were computed. Then, a simple layer of SVM and tree-type SVM classifiers were developed to categorize the citrus fruit blemishes. But, the number of images collected was not adequate, which influences the classifier's efficiency.

Wang *et al.* [17] developed a tomato disease identification technique using the deep CNN and object recognition framework. In this technique, faster Residual CNN (R-CNN) was utilized to recognize the categories of tomato infections, whereas mask R-CNN was utilized to identify and segregate the positions and contours of the diseased regions. But the accuracy was degraded due to the low-resolution images and the number of images was not sufficient.

Yang *et al.* [18] developed a model to classify the apricot cultivator depending on the shape features of apricots. In this model, a successive projection method and PCA were applied to minimize the number of features. Also, various machine learning algorithms were employed to identify apricot cultivators. But it needs additional features like color and firmness to achieve higher efficiency.

Ji *et al.* [19] designed a categorization model to choose the potato diseases depending on the mixture of hyperspectral imaging techniques and Multi-class SVM (MSVM). First, the potato images were gathered and the background noise was eliminated by masking. After that, K-means grouping was employed to split the image and the mean spectral within the potato area was extracted and the LDA was applied to minimize the data size. Further, the SVM was used to categorize the potatoes into healthy and unhealthy. But the training period was high while increasing the number of images.

Tian *et al.* [20] developed a new multi-scale dense categorization model to recognize the infected and non-infected apple fruits and leaves. First, Cycle-GAN was employed to create the anthracnose and ring rot lesions on the shell of non-infected apple fruits by learning the image features. Then, DenseNet and multi-scale link have been applied to classify the apple diseases. But, the images of various categories of apple diseases for training were not adequate.

Septiarini *et al.* [21] developed a technique to categorize the maturity range of oil palm fresh fruit bunch into raw, ripe and half-ripe. First, the feature extraction process was employed depending on the color and texture. Then, the PCA was applied to choose the most substantial features. Moreover, an ANN with a back-propagation scheme was used to find the prediction class. But, the misclassification of half-ripe fruit as ripe fruit occurred because of uneven fruit color alterations.

James & Sujatha [22] designed a Hybrid Neural Clustering (HNC) classifier to categorize the apple fruit diseases. First, the feature vectors were extracted and the K means clustering was applied to group the vector points. After that, the Feed Forward Back Propagation (FFBP) neural network was used to classify the apple fruit diseases into different categories. But, the database considered for training was limited.

Yao *et al.* [23] designed an improved Xception network called L2MXception, which ensembles normalization terms of L2-norm and mean to classify the peach diseases. On the other hand, the accuracy was not effective because the number of samples gathered for training was less. Khan *et al.* [24] developed an automated model to identify and categorize fruit diseases. First, the diseased fruit images were pre-processed by the contrast stretching method. Then, the diseased areas were obtained by the adaptive and quartile variance-based partition method. The obtained binary images were merged by the weighted coefficient of correlation. Moreover, the most relevant features were chosen by the entropy and rank-based correlation. The chosen features were categorized by the MSVM into different disease classes. But it has a high computation burden while increasing the number of features.

PROPOSED METHODOLOGY

In this section, the MRDL model is described briefly for fruit disease identification and categorization. Figure-1 shows the schematic representation of this study. First, different fruit images with varieties of diseases are collected from the available websites to create training and testing sets. Then, the learning images are considered to train the MRDL model and the trained model is employed to classify the test samples into different classes of fruit diseases.

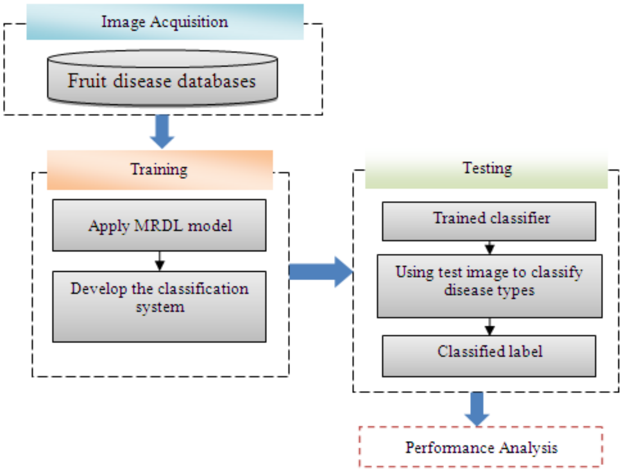

Figure-1. Schematic representation of presented fruit disease identification and categorization system.

Image Acquisition

In this study, benchmark databases retrieved from Kaggle databases for apples, Mendeley databases for citrus fruits and tomato disease databases are considered.

- **Apple disease database:** This database comprises [25] an image gallery of healthy and diseased apple fruits. The diseases targeted in this database are Blotch_Apple, Normal_Apple, Rot_Apple, and Scab_Apple. There are 116 Blotch_Apple images, 67 Normal_Apple images, 114 Rot_Apple images and 85 Scab_Apple images available for training. Similarly, 30 Blotch_Apple images, 24 Normal_Apple images, 38 Rot_Apple images and 28 Scab_Apple images available for testing.
- **Citrus disease database:** This database contains [26] the pictures of non-diseased and diseased citrus fruits. The diseases involved in this database are the Blackspot, Canker, Scab, Greening and Melanosis. Every picture was tagged by the field specialist Dr. BasharatALiSaleem for defining all categories like black spot, canker, greening, scab and non-diseased pictures.
- **Tomato disease database:** Photos from the web pages are considered and projected for guaranteeing the accurate associations between pictures and pathogen categories. Then, pictures of 10 tomato infections are chosen such as tomato malformed fruit, tomato blotchy ripening, tomato puffy fruit, tomato dehiscent fruit, tomato blossom-end rot, tomato sunscald, tomato virus disease, tomato gray mold, tomato ulcer disease and tomato anthracnose. Additionally, pictures of non-diseased tomatoes, a database of 11 categories of, with an overall of 286, tomato pictures are considered. This database is partitioned into the learning, validation and test collections in a fraction of 6:2:2.

Multi-scale Region-Of-Interest (ROI)-based Deep Learning

The collected databases are fed to the MRDL mode, which performs 2 phases for identifying and categorizing the fruit diseases. Figure-2 portrays the entire structure of the MRDL model using a convolutional encoder-decoder network.

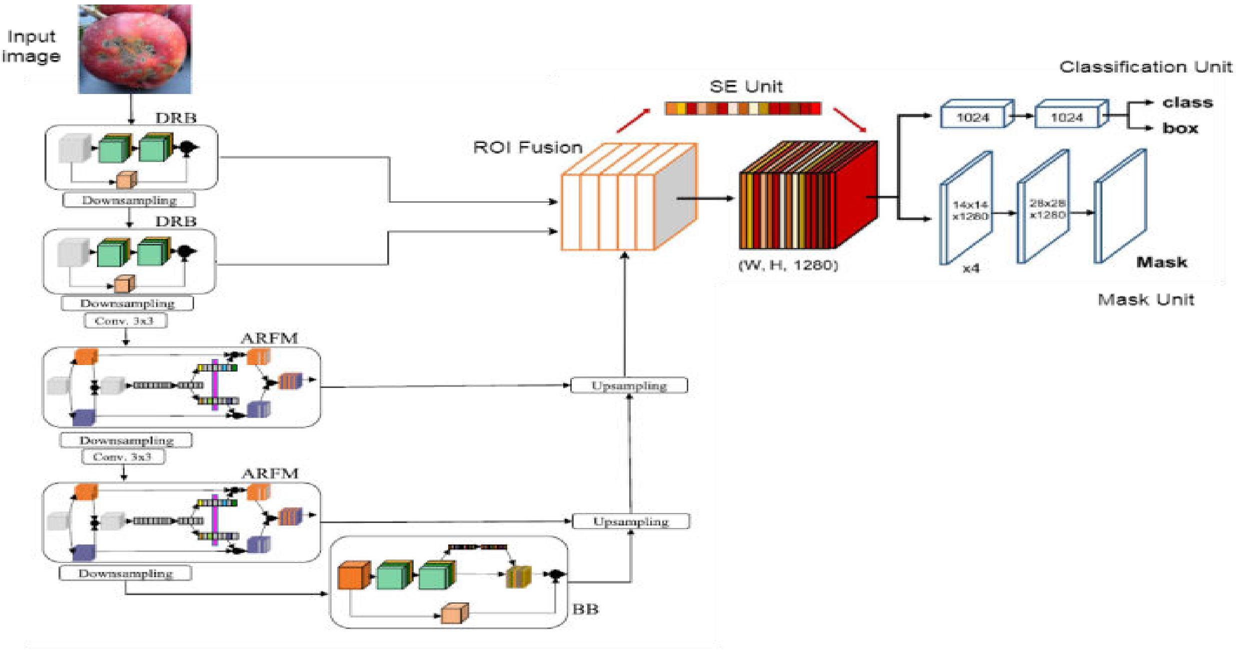

Figure-2. Entire structure of MRDL model using convolutional encoder-decoder network.

Initial Phase

The initial phase is called an encoder segment comprising DRB, ARFM and BB. In each level in the encoder segment, the spatial scale equals the scale of the respected level and the FMs of every level are aggregated.

The initial 2 levels in the encoder, DRBs are utilized rather than the standard convolution to obtain the spatially improved FMs. In this structure, DRBs are used with 2 depth-wise convolution functions in all blocks in the encoder to obtain the distinctive FM with fewer floating-point processes. Then, the resultant FM is added to the input FM to determine the outcome. Also, ARFM is used rather than utilizing modifying kernels with their linear concatenation of FMs. The key goal of this ARFM is to fine-tune the RF depending on the stimuli obtained.

The ARFM accepts deep tensors as input and results in a FM that comprises many distinctive characteristics chosen by a dynamic strategy. Initially, the FMs are split by various kernels. Then, those determined FMs are linearly aggregated and a global mean pooling is applied, which converts the FMs into Fully Connected (FC) neurons. Such initial FC unit links to the other FC dense unit that contains more neurons similar to the percentage of the initial unit.

After that, the BB is applied to transfer the affluent characteristics from the initial phase to the second phase. It determines the distinctive characteristics from the encoder segment and doesn't down sample any auxiliary. It distributes such features, which contain less correlation with every other. The BB comprises 2 end-to-end depth-wise convolutions, which helps to determine the features depend on the corresponding filters and do not point to the characteristics that exist in the deepness. Thus, this encoder segment captures a low-dimensional FM per spatial position and recognizes the candidate bounding boxes.

Second Phase

The second phase called the decoder segment comprises SE and ROI fusion, which captures FMs per candidate box and conducts the categorization and partition of the presented candidate boxes. The second phase involves a ROIF unit, a categorization unit and a mask unit. The ROIF unit captures the FMs of dimension $k \times k$ per candidate area by using the candidate bounding boxes from the initial phase. A bilinear interpolation is applied rather than the quantization to determine accurate characteristics per sampled position and those are concatenated by the max function to get $k \times k$ FMs. Because capturing FMs, the candidate bounding boxes with each another stage of encoder segment are shared, FMs from all levels are extracted and the FMs are fused by the aggregation. After the aggregation, the SE unit is included to recreate the fused FMs, i.e., integrating attention strategy.

The recreated, fused FMs are independently provided to the classification unit and the mask unit. The dimension of the input FMs is assigned to 7×7 $(k = 7)$ and 14×14 $(k = 14)$ for the classification and mask units, correspondingly. The classification unit has 2 convolutions with 7×7 kernel and 1×1 kernel, executing a classification of all bounding boxes. The mask unit includes 4 convolutions with 3×3 kernel after that the up sampling with a stride 2 and 1×1 convolution. The mask unit conducts a pixel-to-pixel localization of all bounding boxes.

Attention Strategy in SE Unit

An attention strategy is integrated into the SE unit. The SE unit conducts 2 processes such as compression and transformation. For a FM $f \in \mathbb{R}^{H \times W \times C}$, the compression function performs global mean pooling to sum up the global spatial data of all channels c by

$$z_c = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} f_c(i,j) \tag{1}$$

In Equation (1), f_c defines c^{th} channel and H, W and C are the height, width and the number of channels, correspondingly. This compression process offers channel-wise statistics. During the transformation process, the channel descriptor $z \in \mathbb{R}^C$ exits via a chain of functions to give an altered channel descriptor z' by

$$z' = \rho_2\left(\varphi\left(\rho_1\left(\sigma(z)\right)\right)\right) \tag{2}$$

In Equation (2), σ, ρ and φ are the sigmoid factor, a FC unit and a Rectified Linear Unit (ReLU), correspondingly. Here, ρ_1 minimizes the dimensionality and ρ_2 maximizes the dimensionality, i.e. a bottleneck structure. After that, a channel-wise multiplication is applied between z' and the FM f, producing the absolute outcome $\tilde{f} = f \cdot z'$.

Thus, this MRDL is trained and applied for the segregation and categorization of diseased regions and their classes from the test fruit images, respectively

RESULTS AND DISCUSSIONS

The efficiency of the MRDL model is assessed by implementing it in MATLAB 2019a using the different fruit disease databases (discussed in Section 3.1). Also, a comparative analysis is conducted to summarize the effectiveness of the MRDL in contrast to the existing models, including MDL [14], Mask R-CNN [17], MSVM [19], HNC [22] and L2MXception [23]. The considered metrics for comparing the efficiency of the proposed and existing models are precision, recall, f-measure and accuracy. Figure 3 demonstrates some examples of the diseased fruit images from the considered databases

Apple disease database			
Apple _Normal			
Apple_Blotch			
Apple_Rot			
Apple_Scab			
Citrus disease database			
Citrus_Normal			
Citrus_Blackspot			
Citrus_Canker			

Citrus_Greening			
Citrus_Scab			
Tomato disease database			
Tomato_Normal			
Tomato_Anthracnose			
Tomato_Blossomendrot			
Tomato_Blotchyripening			
Tomato_Deformed			

Tomato_Graymold			
Tomato_Lateblight			
Tomato_Sunscald			
Tomato_Virusdisease			

Figure-3. Examples of the diseased fruit images from the considered databases.

Accuracy

It is the fraction of proper partition and categorization of diseased fruit samples over the total samples tested.

$$\text{Accuracy} = \frac{\text{TruePositive(TP)+TrueNegative (TN)}}{\text{TP+TN+FalsePositive(FP)+FalseNegative (FN)}} \quad (3)$$

In Equation (3) TP is the number of healthy fruit samples correctly categorized as healthy, whereas TN is the number of diseased fruit samples correctly categorized as corresponding diseased classes. Similarly, FP is the number of diseased fruit samples categorized as healthy and FN is the number of healthy fruit samples categorized as diseased classes.

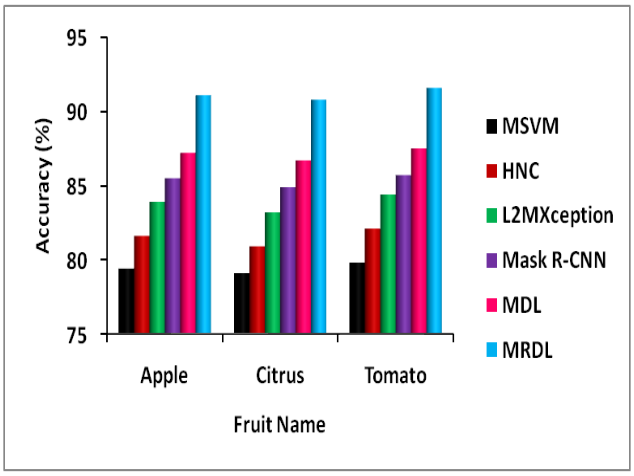

Figure-4. Comparison of accuracy.

Figure-4 displays the accuracy (in %) realized by the different fruit disease classification models applied to 3 different databases. It addresses that the accuracy of the MRDL model on the Apple disease database is 14.74% greater than the MSVM, 11.6% greater than the HNC, 8.58% greater than the L2MXception, 6.55% greater than the mask R-CNN and 4.47% greater than the MDL models. Similarly, the accuracy of the MRDL model on the citrus disease database is 14.79% greater than the

MSVM, 12.24% greater than the HNC, 9.13% greater than the L2MXception, 6.95% greater than the mask R-CNN and 4.73% greater than the MDL models. For the tomato disease database, the accuracy of the MRDL model is 14.79% greater than the MSVM, 11.57% greater than the HNC, 8.53% greater than the L2MXception, 6.88% greater than the mask R-CNN and 4.69% greater than the MDL models. This is because of enhancing the segregation and localization of diseased regions from the fruit images to classify their corresponding disease classes.

Precision

It is calculated as:

$$\text{Precision} = \frac{\text{No.ofproperlyclassifieddiseasedfruits}}{\text{No.ofproperlyclassifieddiseasedfruits+} \\ \text{No.ofimproperlyclassifieddiseasedfruits}} \quad (4)$$

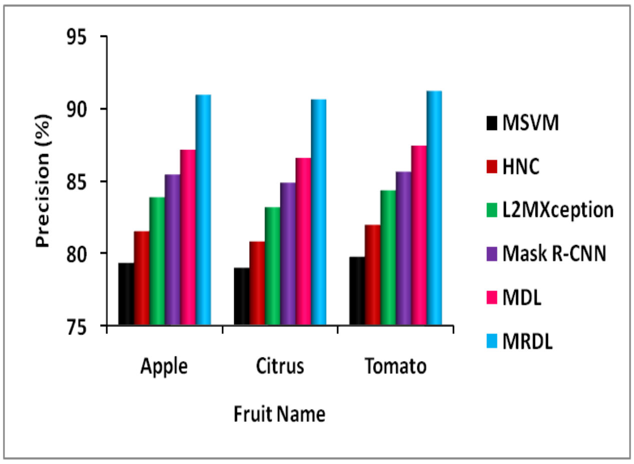

Figure-5. Comparison of precision.

In Figure-5, the precision (in %) of the MRDL compared with various fruit disease classification models applied to apple, citrus and tomato disease databases is shown. It observes that the precision of the MRDL model on the apple disease database is 14.66% larger than the MSVM, 11.58% larger than the HNC, 8.47% larger than the L2MXception, 6.46% larger than the mask R-CNN and 4.36% larger than the MDL models. Similarly, the precision of the MRDL model on the citrus disease database is 14.75% larger than the MSVM, 12.16% larger than the HNC, 8.98% larger than the L2MXception, 6.8% larger than the mask R-CNN and 4.69% larger than the MDL models. For the tomato disease database, the precision of the MRDL model is 14.38% larger than the MSVM, 11.3% larger than the HNC, 8.14% larger than the L2MXception, 6.53% larger than the mask R-CNN and 4.33% larger than the MDL models because of enhancing the partitioning and localizing the diseased pixels in the candidate regions from the fruit images during the classification of their corresponding disease classes.

Recall

Recall is calculated as:

$$\text{Recall} = \frac{\text{No.ofproperlyclassifieddiseasedfruits}}{\text{No.ofproperlyclassifieddiseasedfruits+} \\ \text{No.ofimproperlyclassifiedhealthyfruits}} \quad (5)$$

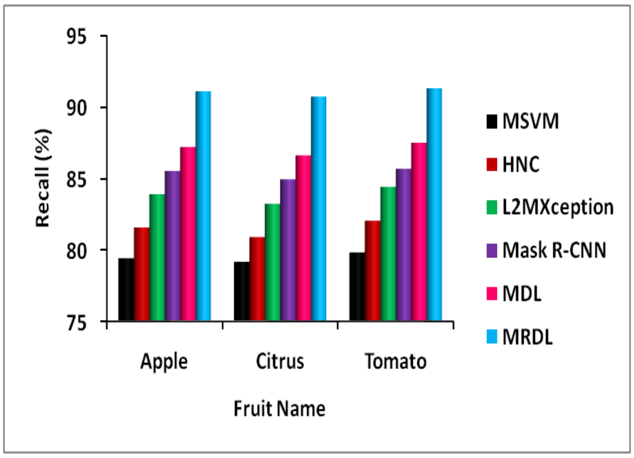

Figure-6. Comparison of recall.

Figure-6 displays the recall obtained by the different fruit disease classification models applied to 3 different databases. It analyzes that the recall of the MRDL model on the Apple disease database is 14.73% higher than the MSVM, 11.7% higher than the HNC, 8.58% higher than the L2MXception, 6.52% higher than the mask R-CNN and 4.48% higher than the MDL models. Similarly, the recall of the MRDL model on the citrus disease database is 14.64% higher than the MSVM, 12.19% higher than the HNC, 9.04% higher than the L2MXception, 6.84% higher than the mask R-CNN and 4.77% higher than the MDL models. For the tomato disease database, the recall of the MRDL model is 14.41% higher than the MSVM, 11.31% higher than the HNC, 8.17% higher than the L2MXception, 6.57% higher than the mask R-CNN and 4.35% higher than the MDL models. This concludes that the MRDL enhances the recall for identifying and classifying the fruit disease classes compared to the other models.

F-measure

It is computed as:

$$\text{F} - \text{measure} = 2 \times \frac{\text{Precision}\cdot\text{Recall}}{\text{Precision+Recall}} \quad (6)$$

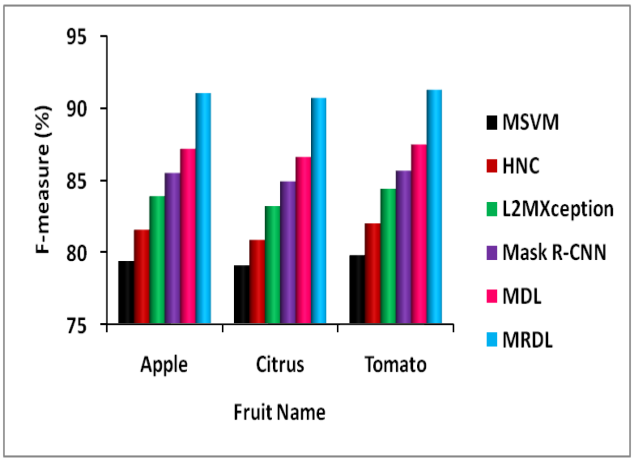

Figure-7. Comparison of F-measure.

Figure-7 portrays the f-measure for the different fruit disease classification models applied to 3 different databases. It indicates that the f-measure of the MRDL model on the Apple disease database is 14.7% better than the MSVM, 11.64% better than the HNC, 8.52% better than the L2MXception, 6.49% better than the mask R-CNN and 4.43% better than the MDL models. Similarly, the f-measure of the MRDL model on the citrus disease database is 14.69% better than the MSVM, 12.18% better than the HNC, 9.01% better than the L2MXception, 6.82% better than the mask R-CNN and 4.73% better than the MDL models. For the tomato disease database, the f-measure of the MRDL model is 14.39% better than the MSVM, 11.3% better than the HNC, 8.15% better than the L2MXception, 6.55% better than the mask R-CNN and 4.34% better than the MDL models. This concludes that the MRDL increases the f-measure to identify and categorize the varieties of fruit diseases compared to the other models.

CONCLUSIONS

In this study, the MRDL model was presented for identifying and classifying a single fruit sample with a certain disease. During the initial phase, DRB, ARFM and BB were performed to capture more robust characteristics from the fruit images and obtain the candidate bounding boxes for classification. Afterward, the FMs for each candidate's ROIs were extracted and fused into the ROIF unit by considering the candidate bounding boxes. Those fused FMs were provided to the SE-ResNet integrated with the attention strategy to resize them. Moreover, the resized fused FMs were fed to the classification and mask units in parallel for disease classification and diseased pixel localization, accordingly. At last, the findings proved that the MRDL model on apple disease, citrus disease and tomato disease databases has an accuracy of 91.1%, 90.8% and 91.6%, respectively compared to the classical models

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