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Classification and Identification of Primitive Kharif Crops using Supervised Deep Convolutional Networks

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ARTICLE INFO

ABSTRACT

Background: The severity of diseases and threats found in different crop varieties is one of the primary causes of degradation in the agricultural economy. Early detection and disease diagnosis in crops will facilitate farmers to improve their livelihood and mankind.

Objective: This study aimed to develop method for disease identification in several seasonal crops during their early stages using deep learning architectures i.e. convolutional neural networks (CNN) and compare the feasibility, accuracy and performance of the proposed network with conventional feature extraction techniques like support vector machine, k-nearest neighbor, genetic algorithm, and artificial neural networks.

Method: This study preferred a database of 600 images i.e. 200 images of individual crop varieties which are labeled with 10 kinds of crop diseases. Each crop varieties have two different kinds of classes i.e. health crop and rusty crop. The CNNs are trained in such a manner that it will be able to detect diseases from infected crop varieties.

Result: Different convolution filters and pooling types of different sizes are used in the proposed work. Max pooling with a filter size of 32*32*3 achieves the accuracy of 92%. Average pool size with a convolution filter size of 64*64*3 achieved maximum accuracy of 93.7% and gains the better results in comparison to other machine learning and feature extraction models.

Conclusions: The contribution of the proposed work could be summarized as: (i) obtained results shows improvement in the feasibility and performance of CNN over other machine learning models. (ii) High performance shows the immediate crop disease identification ability of deep learning techniques over the different feature extraction models.

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1. Introduction

In today's digitized era, as rapid growth in the agricultural economy has been seen which will surely fulfill a vision of nation food cooperates and their associates. Different individuals have different liking among several crop varieties of different genres. According to their habitat, they prefer whether the crop is edible or not. Among different crop varieties Soya, Corn, and Rice are very popular and the most consumable crops in India. But, varieties of threats like rust in crops, worm-attacks, oasis, cloudy weather degrades and affects the quality of crops. To ensure high quality and efficiency of crops, disease identification and crop prevention from damage should be identified at the preliminary stage for facilitating the farmer with help of an automated system. Due to the involvement of such systems in the field, the farmer can consult the plant biotic specialist and upload specific obtained images into a system to recognize the infected crops from the remote side.

To enhance the accuracy in disease identification and diagnosis through machine learning techniques, multifarious researchers have worked on automated disease identification which presents in plants, vegetables, and edible crops. Advanced computation techniques like pattern recognition, fuzzy based systems are also applied for identification of disease in peas, tomato, brinjal, and cabbage.

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The evolution of CNN has gained persistent research interests among researchers in the diverse field of computer science like image processing, sign language recognition, human activity pattern recognition, sound and video classification, perception driven cognitive computing etc. Zeiler and Fergus [1] preferred regularization of deep convolutional networks using stochastic pooling. Acharya et al. performed automatic identification of shockable and non-shockable life-threatening ventricular arrhythmias using a convolutional neural network. Zhang et al. [2] performed multi-task learning for food identification and analysis with CNN. Kawasaki et al. [3] proposed CNN driven system which identifies cucumber leaf diseases like mosaic and spot virus. Barbedo [4] proposed image translation and restoration techniques for detection, classification, and quantification of plant diseases. Huang et al. [5] proposed multi-modality image-based disease severity prediction study using big learning and analytics prediction. Phadikar et al. [6] preferred pattern recognition techniques for automated rice disease identification and achieved an accuracy of 70%. Zhang et al. [7] adopted supervised learning deep model for identification of rice disease and achieved higher accuracy compared to other classifiers.

In the context of machine learning, recognizing rate of disease identification and intelligent diagnosis is very crucial and plays a vital role among research communities. Although, due to the existence of lower recognition rate and convergence obtained training rate of samples is very slow and they get trapped into minimal. As of now, researchers have not explored the usage of the convolutional neural network in the identification of different crop varieties with different classes. Therefore, the key motivation for adopting this work is to automate disease recognition accuracy using different images (rotten and healthy) of distinguished crop varieties [8–10]. The proposed work could facilitate farmers to identify infected crops at an initial level before actually visiting field area and take remedial actions using CNN [11] to enhance crops disease identification accuracy. The diagnostic results obtained using CNN proved it as best classification techniques in comparison to other conventional models [12–14].

This research work presents novel deep learning driven CNN based approach for the identification of different crop diseases. The CNN model has been trained using stochastic gradient descent algorithm and Adam optimizer by varying different parameters like batch_size, optimizer, activation, epoch_size, and hidden layer units. We have considered a total of 270 crop varieties images for pre-processing and then individual crops varieties processed images i.e. 90 are utilized to train CNNs. The advantage of applying CNN is that it overcomes the recognition accuracy obtained by conventional model and achieves higher and faster convergence compared to other linear and non-linear models like Support Vector Machine (SVM), K-Nearest Neighbor (KNN) and Back Propagation (BP) [15,16]. In proposed CNN, images are entered directly into model after their scaling and normalization. Then images are classified from the scaled dataset using convolution 2D and pooling techniques. We have applied three different kinds of pooling like Max-pooling and Average-pooling in which maximum and average probabilistic values always chosen from the given set [17]. The pool filter size varies from 2*2 to 4*4 which enhances model generalizability. For differentiating 3 categories of crops multiclassification learning algorithm SoftMax is preferred in proposed work.

The rest of the paper is organized as follows: Section 2 describes the proposed architecture of convolutional neural network with details of various parameters used in network training. Section 3 focuses on image processing of crop disease identification. Section 4 introduces the experimental sample with results and discussion. Finally, the conclusion is given in Section 5.

2. Proposed architecture of deep convolutional neural network

The convolutional neural network is a class of deep feed-forward neural network models that can process multidimensional data as multiple images which include different layers of neurons connected between layers [18]. CNN is an improved version of Artificial Neural Network (ANN) which also comprised of input, hidden and output layers. Our multistage CNN based model includes an input layer, convolution layer, max pooling, average pooling, fully connected unit, and softmax layer. The architecture is explained in Fig. 1 depicted below as:

2.1. Convolutional layer

In the proposed architecture we preferred three convolutional layers. The purpose of these layers is to perform feature extraction and selection on the input image. In individual layers, filter slides over the input to produce a rectified activation map on the identification of features obtained through edges, corners etc. The obtained output feature map combines multiple convolutions which are denoted by the expressed formula shown in 0. Eq. 1 as:

$$p_i^l = f(\sum_{j \in R_i} p_j^{l-1} * q_{ij}^l + b_i^l) \tag{1}$$

Where q_{ij} represents kernel, layer represented by l, b_i represents bias and R_i represents set of input maps to be used for generating output p_i.

2.2. Max pooling and Average pooling layer

These are sub-sampling layers which reduce the variance and computed the maximum and average feature value over identified features of the image. It helps to manage the problem of over-fitting and identified the disease in infected crops.

The pooling layer accepts input volume of size $W_1 * H_1 * D_1$ which requires two parameters Spatial extent (F) and Stride (S), which produces output volume of size $W_2 * H_2 * D_2$.

Here $W_2 = (W_1 - F)/S + 1$, $H_2 = (H_1 - F)/S + 1$ and $D_2 = D_1$.

The advantage of this type of distribution using max and average pooling not only makes CNN convergence faster but improves generalization ability of network.

2.3. Fully connected layer

The neuron present in this layer has a full connection to all activations in the previous layer. Their obtained activations can be computed with matrix multiplications followed by bias if present in the network.

2.4. Softmax layer

Softmax regression is the generalization of logistic regression used to handle multiple classes. The hypothesis function takes the form as
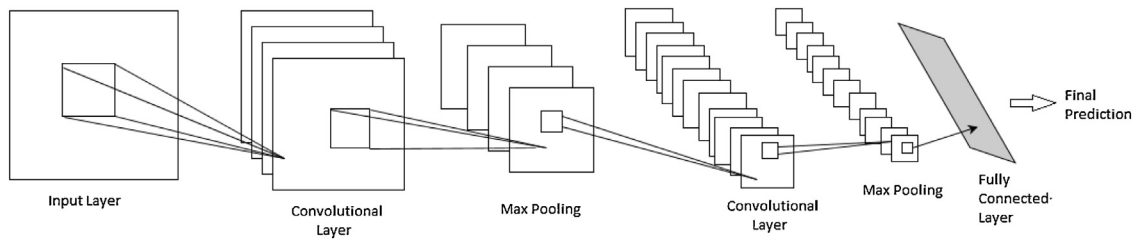
$$h_\theta(x) = \frac{1}{1 + \exp(-\theta^T x)} \tag{2}$$

Fig. 1. Architecture of CNN.

The goal is to train model parameter θ so that cost function $J(\theta)$ get minimized.

$$J(\theta) = - \left[\sum_{i=1}^{m} y^{(i)} \log h_\theta \left(x^{(i)} \right) + (1 - y^{(i)}) \log(1 - h_\theta \left(x^{(i)} \right)) \right] \quad (3)$$

The probability of classifying x as the category of j is for different training dataset ranges from $\left\{ x^{(1)}, y^{(1)}, \ldots .(x^{(m)}, y^{(m)}) \right\}$ is:

$$p\left(x^{(i)} = j y^{(i), \theta} \right) = \frac{e^{\theta_j^T y^{(i)}}}{\sum_{l=1}^{k} e^{\theta_l^T y^{(i)}}} \quad (4)$$

Backpropagation gradient descent approach has been used to train the network for identification and classification of different crop varieties. Out of all excitatory neurons present in convolution layers high and efficient, activated neurons will be responsible for identification of disease in crops of distinguished varieties. The next section describes the training performed to train CNNs.

2.5. Back propagation gradient descent training algorithm

The backpropagation gradient algorithm is used to train CNN which usually works in feedforward and backpropagation pass. A multiclass problem with m classes has been considered to minimize the mean squared error function over P training samples.

$$E = \frac{1}{P} \sum_{p=1}^{P} \sum_{k=1}^{m} (t_k^p - y_k^p)^2 \quad (5)$$

Where t_k^p is the kth dimension of the pth pattern label and y_k^p is the value of the kth output layer unit in response to the pth input pattern.

The output vector of the current layer j using input layer h is denoted as

$$x^j = f(W^j x^{j-h} + b^j) \quad (6)$$

Here $w^j x^{j-h}$ is the summing junction output and b^j is the generated bias.

The backward phase uses given relation below to propagate the error back from higher to lower layers.

$$\delta^j = (W^{j+1})^T \delta^{j+1} \bigodot f'(W^j x^{j-h} + b^j) \quad (7)$$

The weight updation represented by ΔW^j has been performed according to the formula listed below as:

$$\frac{\partial E}{\partial W^j} = x^{j-h} (\delta^j)^T \quad (8)$$

$$\Delta W^j = -\eta \frac{\partial E}{\partial W^j} \quad (9)$$

The following parameters are also tuned during training of disease identification based convolutional Neural Network.

- Epoch: It determines the completion of single pass of training dataset through the CNN network. We have used 5 epochs and steps per epoch would be 160.
- Batch Size: It indicates after how many segments the algorithm will update the weights of network. We have set the size of batch to 32 which will proceed after next iterations.
- Learning rate, shear and zoom range: The learning rate of network is 0.001 and shear & zoom range set to 0.2
- Momentum and Linear unit: The rectified linear unit (ReLU) is used and momentum set to 0.7.
- Cross validation: In proposed work 10-fold cross validation is performed to assess CNN ability for disease identification of soya, rice and corn crops.

3. Crop disease identification

3.1. Image data acquisition of crop diseases

An image database comprised of disease infected several crop varieties like soya, rice and corn which are 270 in total. These images of different crop varieties are collected or taken from northern cultivated land of India. The image database depicted mainly 10 kind of crop diseases like soya diseases includes soya downy mildew (SDM), soyabean wilt disease (SWD), soya sheath blight (SSB), soya acne disease (SAD), soya stem blight (SSB), soya anthracnose (SA), soya sclerotinia (SS), soya dodder (SD), soya nuclear disease (SND) and soya powdery mildew (SPM). Similarly rice diseases includes Rice blast (RB), Rice lodging (RL), Rice powdery mildew (RPM), Verticillium wilt (VW), watery wilt disease (WWD), Rice Bakana disease (RBD), Rice flax spot (RFS), Rice dwarf disease (RDD), Rice leaf blight (RLB) and Rice blight (RB). Another category of corn disease includes corn smut (CS), corn blight (CB), corn stalk rot (CSR), corn round spot (CRS), corn spot blight (CSB), corn stalk rot (CSR), corn black beam disease (CBBD), corn anthracnose (CA), corn eclipse disease (CED) and fusarium head blight (FHB). These crop images of high resolution are captured by canon DSLR EOX 1300D and canon SX 430 which provides sharpen and good quality image. Some of the images are collected from online image repository of Anhui Academy of Agricultural Sciences, Hefei. This database contains high end quality images of crops, vegetables, fruits and beverages.

The collected images are processed and analyzed using Python Library called Keras and Adam Optimizer with support of Tensor Flow in back end. Experimentation is performed in Spyder (Python GUI) with support of numpy and sci-kit learn.

3.2. Image data pre-processing of crop diseases

In order to fit CNN to the images Keras module, Image Generator has been used through which all the nodes generated through max pooling and flattening would connect to all the hidden layers and generates training and testing data. The entire workflow procedure in form of graphical abstract is shown in Fig. 2. The crops images considered are color images so due to the absence of stationary
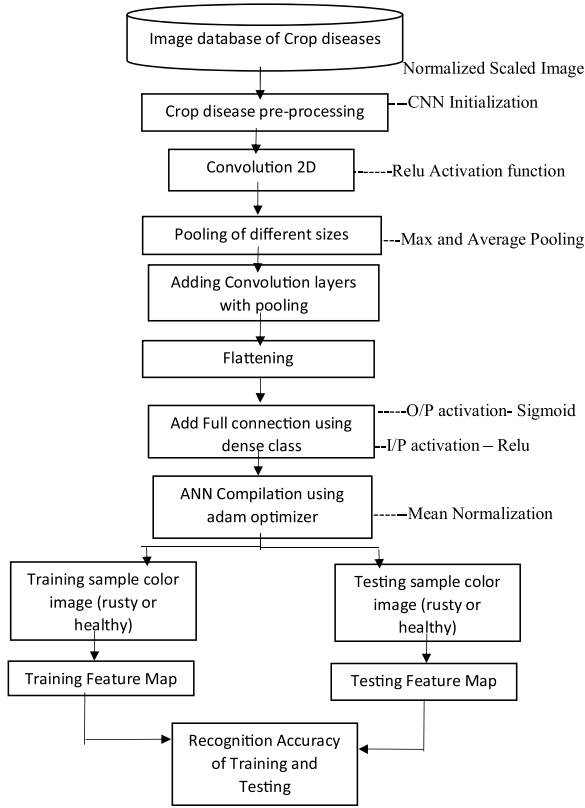
Fig. 2. Workflow Procedure.

property rescaling of color images date are done to [0,[1]] as shown in form of code snippet for soyabean image in Fig. 3.

We reduce the image dimension so that training time will not become very long. Let us assume p dimensional vector y represents any image and z is the product of height and weight (kernel size). The convolution 2D comprised of (y as filter and z as kernel size) i.e. 32*3*3. The preprocessing on N images in crop diseases database is computed using given formula for individual pixel value.

$$y^i = \frac{y^{\tilde{i}} - \mu}{\sqrt{S}} \tag{10}$$

Here

$$\mu = \frac{1}{N}\sum_{j=1}^{N} y_j$$

$$S = \frac{1}{N}\sum_{k=1}^{N}(y_k - \mu)(y_k + \mu)^T$$

3.3. Pseudocode for forward and backward convolutions

defconv_fwd(P, W)

P – Previous layers output activations defined by P_prev and W_prev.
W – Weights and array size would be z * z
Returns:
Q – conv output,
cache – cache of values needed for conv_backward() function
do Retrieve dimensions from P's shape using P_prev and W_prev) = P.shape
do Retrieve dimensions from W's shape
Now, Compute the dimensions using stride and no padding

P = P_prev-z + 1

W = W_prev-z + 1

Perform Looping over vertical(c) and horizontal(d) axis of output volume
for c in range(H):
for d in range(W):

x_slice = X[c : c + d, w : w + c]

H[c, d] = sumof(x_slice * W)

Restore the information for backpropagation using cache = (P, W)
return H, cache
def conv_bwd(dH, cache) // Performing backward computation
Arguments:
dH – cost gradient wrt to H.
dP – cost gradient wrt to conv layer P.
dW – cost gradient wrt to conv layer W for shape (f,f)
// Store the information from cache using (P, W) = cache
Do Retrieve P dimensions using P_prev and W_prev
Do Retrieve W's dimension for (f, f)
Do retrieve dH dimensions using P and W
Initiate dP and dW using P and W shapes
Iterate over vertical(c) and horizontal(d)
for c in range(P):

```
from keras.preprocessing.image import ImageDataGenerator

train_datagen = ImageDataGenerator(rescale = 1./255, shear_range = 0.2, zoom_range = 0.2,
                                    horizontal_flip = True)

test_datagen = ImageDataGenerator(rescale = 1./255)

training_set = train_datagen.flow_from_directory ('F:\Machine
Learning\Soybean_Images_MachineLearning-master\Soybean_Images_MachineLearning-
master/training_set', target_size = (128, 128), batch_size = 32, class_mode = 'binary')

test_set = test_datagen.flow_from_directory('F:\Machine
Learning\Soybean_Images_MachineLearning-master\Soybean_Images_MachineLearning-
master/testing_set',  target_size = (128, 128), batch_size = 32, class_mode = 'binary')

classifier.fit_generator (training_set, steps_per_epoch = 160, epochs = 5, validation_data =
test_set validation_steps = 20)
```

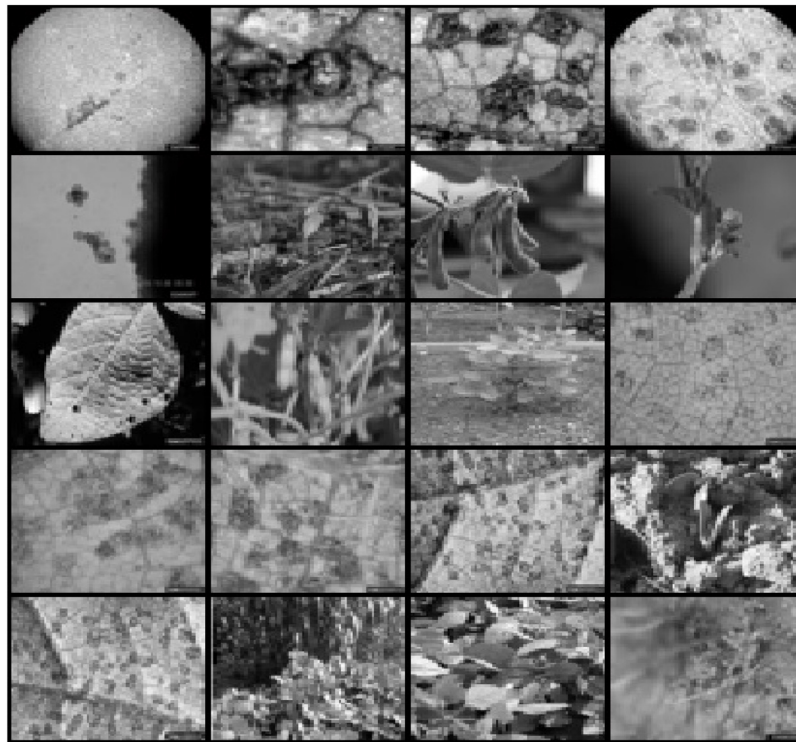**Fig. 3.** Code Snippet for Soyabean Image.

Fig. 4. Different image patches of infected crop diseases.

```
for d in range(W):

dP[c : c + f, d : d + f]+ = W * dH(c, d)


dW+ = P[c : c + f, d : d + f] * dH(c, d)

    return dP, dW
    from keras.preprocessing.image import ImageDataGenerator
    train_datagen = ImageDataGenerator(rescale = 1./255,
shear_range = 0.2, zoom_range = 0.2, horizontal_flip = True)
    test_datagen = ImageDataGenerator(rescale = 1./255)
    training_set = train_datagen.flow_from_directory
('F:\Machine        Learning\Soybean_Images_MachineLearning-
master\Soybean_Images_MachineLearning-master/training_set',
target_size = (128, 128), batch_size = 32, class_mode = 'binary')
    test_set = test_datagen.flow_from_directory('F:\Machine
Learning\Soybean_Images_MachineLearning-
master\Soybean_Images_MachineLearning-master/testing_set',
target_size = (128, 128), batch_size = 32, class_mode = 'binary')
    classifier.fit_generator    (training_set,   steps_per_epoch = 160,
epochs = 5, validation_data = test_set validation_steps = 20)
```

4. Experimental samples

In the present study, the convolutional based deep learning model is applied for disease identification in different crops varieties like soya, rice and corn. We have used a database of 600 images i.e. 200 images for individual crop varieties which are labeled with 10 kinds of crop diseases. Each crop varieties have two kinds of classes i.e. health crop and rusty crop. After preprocessing, random selection of crops patches with size 8*8 and corresponding feature maps of crops diseases is shown in Figs. 4 and 5 respectively.

We have compared the disease recognition performance of different crop varieties on various parameters like pool size 2D (Max and Average), convolution filter & kernel size and tensor input shapes.

Fig. 5. Feature maps of crop diseases with image patches.

For training and test samples 10-fold cross validation strategy is used. Training set consists of 160 images whereas testing and validation set consists of 20 images for individual crop varieties. We compared convolutional filter size of 16*16, 32*32 and 64*64 with kernel size of 3*3, 6*6 and 9*9. The accuracy results obtained after taking different filter size is shown in Tables 1 and 2 respectively. Also, it can be seen that we have chosen input tensor shape of size 32*32*3, 64*64*3 and 128*128*3. The crop disease recognition accuracy has been compared with different pooling size as shown in Tables 1 and 2 and among them average pool size with filter size of 64*64 achieved maximum accuracy of 93.7 and gain better results in comparison to max pool size. Table 3 denotes the result comparison of proposed CNN model in comparison with other machine learning and feature extraction models.

6 *A. Khamparia et al. / Sustainable Computing: Informatics and Systems xxx (2019) xxx–xxx*

Table 1
Recognition accuracy obtained using different convolutional filter and Max pool size.

No of Epochs = 5, Batch Size = 32	Convolution filter size	Tensor Shape	Max pool Size	Recognition accuracy (Training)	Recognition accuracy (Testing)	Recognition accuracy (Validation)
Filter 1 (filter*size)	16*3*3	32*32*3	2*2	0.895	0.65	0.63
	16*6*6	64*64*3	3*3	0.896	0.79	0.78
	16*9*9	128*128*3	4*4	0.915	0.83	0.84
Filter 2 (filter*size)	32*3*3	32*32*3	2*2	0.92	0.67	0.66
	32*6*6	64*64*3	3*3	0.919	0.776	0.78
	32*9*9	128*128*3	4*4	0.886	0.822	0.819
Filter 3 (filter*size)	64*3*3	32*32*3	2*2	0.91	0.67	0.67
	64*6*6	64*64*3	3*3	0.911	0.83	0.85
	64*9*9	128*128*3	4*4	0.885	0.876	0.86

Table 2
Recognition accuracy obtained using different convolutional filter and Average pool size.

No of Epochs = 5, Batch Size = 32	Convolution filter size	Input Tensor Shape	Average pool Size	Recognition accuracy (Training)	Recognition accuracy (Testing)	Recognition accuracy (Validation)
Filter 1 (filter*size)	16*3*3	32*32*3	2*2	0.914	0.67	0.66
	16*6*6	64*64*3	3*3	0.916	0.81	0.83
	16*9*9	128*128*3	4*4	0.918	0.85	0.84
Filter 2 (filter*size)	32*3*3	32*32*3	2*2	0.935	0.68	0.68
	32*6*6	64*64*3	3*3	0.922	0.782	0.78
	32*9*9	128*128*3	4*4	0.89	0.834	0.82
Filter 3 (filter*size)	64*3*3	32*32*3	2*2	0.937	0.69	0.71
	64*6*6	64*64*3	3*3	0.932	0.86	0.88
	64*9*9	128*128*3	4*4	0.901	0.885	0.89

Table 3
Comparative performance of CNN over other models.

Algorithm	CNN	ANN (BP)	KNN	SVM	Genetic Optimization
Accuracy	93.7%	89.4%	90.12%	91.33%	91.78%
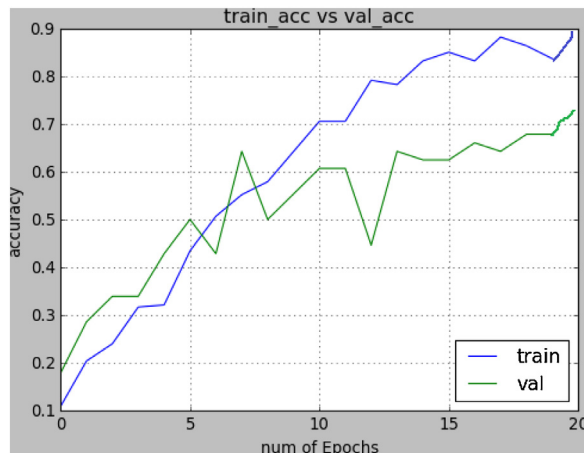
Fig. 6. Train vs Validation.

CNN training is done with two activations functions; Tanh and ReLU. Tanh activation function is similar to the logistic sigmoid activation function but its performance is better. The main advantage of using Tanh function was due to its capability to map negative inputs to a strongly negative region and all the nearby zero inputs are mapped near zero. ReLU activation function performed best in the experiment because of its half-rectified nature. To prevent data over-fitting, drop out technique is adopted as it is best regularization technique which able to makes some of the neurons '0', hence the complexity of the network is decreased and enable our model to get best fitted. As shown in Fig. 6, early stopping criterion is applied after 20 epochs where the model accuracy stops improving on val-idation set. The monitor arguments in Early stopping allowed to specify the performance measure to monitor in order to end training. The model check point saves the best model state observed during training with help of hdf5 mechanism as shown in Eq. 11 as:

$$sp = ModelCheckpoint(\text{'our\_model.h5'}, monitor = \text{'valloss'}) \quad (11)$$

As shown in Fig. 6, the training accuracy is increasing with number of epochs going up. The system was tested with multiple segments of the datasets. CNN was performing better with more data provided in the training. Curve shown in Fig. 6 was plotted using 160 samples drawn from the image data set with training stopped after 20 epochs.

5. Conclusions

In the proposed work, CNN based model effectively recognize and identifies the different crop diseases using visual computing and deep learning networks. The proposed model achieves better recognition accuracy, faster generalization, convergence ability and performance in the comparison to other machine learning and feature extraction models. Although, a lot of research challenges are still open to address in deep convolutional models as they require a large number of layers and neurons associated with them in each iteration which is not fixed. It also requires a large image database and parameter tuning is one of the optimal challenges that occurred while training and testing of deep convolutional models. Our future work focuses on the involvement of deep stack and belief networks which uses tensor driven training algorithms in different areas like medical diagnosis, remote sensing, and automobile exhaust emission driven systems.

Declaration of Competing Interest

The authors acknowledge that they have no competing and conflict of interest.

References

[1] M. Zeiler, R. Fergus, Stochastic pooling for regularization of deep convolutional neural networks, arXiv preprint (2013), arXiv:1301.3557.

[2] L.N. Zhang, B. Yang, Research on recognition of maize disease based on mobile internet and support vector machine technique, Trans. Tech. Publ. 108 (13) (2014) 659–662.

[3] R. Kawasaki, H. Uga, S. Kagiwada, H. Iyatomi, Basic study of automated diagnosis of viral plant diseases using convolutional neural networks, Proceedings of the International Symposium on Visual Computing (ISVC) (2015) 638–645.

[4] J.G.A. Barbedo, Digital image processing techniques for detecting, quantifying and classifying plant diseases, SpringerPlus 2 (1) (2013) 660–672.

[5] W. Huang, S. Zeng, M. Wan, G. Chen, Medical media analytics via ranking and big learning: a multi-modality image-based disease severity prediction study, Neurocomputing 204 (2016) 125–134.

[6] S. Phadikar, J. Sil, Rice disease identification using pattern recognition techniques, Proceedings of the IEEE International Conference on Computer and Information Technology (ICCIT) (2008) 420–423.

[7] Y. Lu, S. Yi, N. Zeng, Y. Liu, Y. Zhang, Identification of Rice diseases using deep convolutional neural networks, Neurocomputing 67 (2017) 378–384.

[8] Z. Shicha, M. Hanping, H. Bo, Z. Yancheng, Morphological feature extraction for cotton disease recognition by machine vision, Microcomput 23 (4) (2007) 290–292, Inf.

[9] D. Silver, A. Huang, C.J. Maddison, A. Guez, L. Sifre, et al., Mastering the game of go with deep neural networks and tree search, Nature 529 (7587) (2016) 484–489.

[10] K. Simonyan, A. Zisserman, Very deep convolutional networks for large-scale image recognition, arXiv preprint (2014), arXiv:1409.1556.

[11] F.Y. Wang, Lets go: from AlphaGo to parallel intelligence, Oil Gas Sci. Technol. 34 (7) (2016) 72–74.

[12] X. Zhang, Y. Lu, S. Zhang, Multi-task learning for food identification and analysis with deep convolutional neural networks, J. Comput. Sci. Technol. 31 (3) (2016) 489–500.

[13] K. Khairnar, R. Dagade, Disease detection and diagnosis on plant using image processing - a review, Int. J. Comput. Appl. 108 (13) (2014) 36–39.

[14] A. Krizhevsky, I. Sutskever, G.E. Hinton, Imagenet classification with deep convolutional neural networks, Adv. Neural Inf. Process. Syst. (2012) 1097–1105, Lake Tahoe, Nevada, USA.

[15] Z. Jian, Z. Wei, Support vector machine for recognition of cucumber leaf diseases, Proceedings of the International Conference on Advanced Computer Control (ICACC) (2010) 264–266.

[16] H.C. Shin, H.R. Roth, M. Gao, L. Lu, Deep convolutional neural networks for computer-aided detection: CNN architectures, dataset characteristics and transfer learning, IEEE Trans. Med. Imaging 35 (5) (2016) 1285–1298.

[17] M. Anthimopoulos, S. Christodoulidis, L. Ebner, A. Christe, S. Mougiakakou, Lung pattern classification for interstitial lung diseases using a deep convolutional neural network, IEEE Trans. Med. Imaging 35 (2016) 1207–1216.

[18] W. Huang, S. Zeng, M. Wan, G. Chen, Medical media analytics via ranking and big learning: a multi-modality image-based disease severity prediction study, Neurocomputing 204 (2016) 125–134.