

Image Classification for Silkworm using Deep Neural Network-VGG 19

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ABSTRACT—Sericulture is the technique of agronomy of silkworms to harvest high quality silk. Application of sericulture method needs further ecological approaches such as claim of enzymes for the improved and high product harvests. This project is to categorize or recognize the silk worm using Deep Neural Network that advances the seed production of silkworms, which upsurges silk production by making a desired high precision model for silkworm classification and also to identify the diseased and healthy silkworm to improve the production of silk. To extracts general features and then categorizes them under multiple tags based upon features perceived and to recognize the diseased and healthy silk worm so that the quality and quantity production of seed cocoon and revolving cocoons with pecuniary support for building of nurture house cocooning shed, and rearing equipment's progresses. This project is very useful for the farmers as it helps them financially.

Keywords: VGG-19, CNN, Deep Learning, Image Classification

LINTRODUCTION

Sericulture is an agro-based trade. It comprises agronomy of host plants and nurture of silkworms for the creation of cocoon to yield raw silk. The key events of sericulture include of foodplant gardening to feed the silkworms which turn silk cocoons and spinning the cocoons for unwinding the silk thread for processing and interlacing to harvest the treasured products. Sericulture plays a major role in rural employment, poverty mitigation and making foreign exchange. A lot of commercial openings are offered in various arenas of sericulture. It is essential to upgrade the skills of the sericulturists to use the complete capabilities of sericulture to harvest qualitatively larger cocoons and to gross profitable income.

Silkworm suffers from numerous diseases and the silk cocoon crop failure or low yield is due

_____ to the diseases in silkworm. Silkworm diseases are caused by microbes and are highly infectious. The growth of diseases in silkworm is inclined by environmental and nutritious aspects such as temperature, humidity and mulberry leaf content. The common diseases in silkworm are 1. Grasserie, Nuclear polyhedrosis commonly known as 'Grasserie or Milky disease'. It is a main viral disease in silkworm. The disease is caused by Bombyx mori Nuclear Polyhedrosis Virus (BmNPV).2 Flacherie is a flaccid disease common in silkworm. It is a disorder caused by either viruses, bacteria or by an association of both. The disease is caused by Bombyx mori infectious flacherie virus (Infectious Flacherie) and Bombyx mori densonucleosis virus (Densonucleosis) and in connotation with bacteria or bacteria alone such as Streptococci / Staphylococci / Bacillus sp. / Serratia bacteria. 3. Muscardine is a disease instigated via fungus in silkworm. White muscardine is the common fungal disease and it is instigated by a fungus i.e Beauveria bassiana. There is also an rare but hazardous disease i.e. Pebrine is a chronic disease silkworm. Causative in agent areAmicrosporidian, Nosema bombycis and strains of Nosema sp. The disease is predictable to occur at any time of the year and is not controlled to any season. The occurrence of diseases not only indemnities the crop but also cause financial loss to the farmers.

Silk is also known as the "Queen of Textiles" and is recognized for its qualities like luxury, elegance, class and comfort. It has overcome the tasks from other natural and artificial fibres and persisted the certain "Queen of Textiles" for eras. The silkworms feed on the certain food plants and spin cocoons as per a 'protective shell' with silk fibre. Silkworm has four phases in its life cycle they are viz., egg, caterpillar, pupa and moth. Man restricts in this life cycle at the cocoon stage to obtain the silk, used in interlacing of the dream fabric.High worth silkworm and flawed silkworm

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are identified mainly by manual selection, this identification process is inefficient. In recent years, deep learning especially the convolution neural network (CNN) has achieved high success and gradually become the main method in the area of image classification.

In this paper, we have developed a deep neural network that is VGG 19 model, that obtain accurate search results in a short time on the user side. We address these challenges by our proposed VGG 19 model for efficient and accurate results.

II. LITERATURE SURVEY

In the beginning of sericulture, people used to work manually to classify the silkworm. In this paper we have used VGG19 model to classify the image of silkworm. For the last few years, a lot of research has been working in the field of image classification as it is the most basic application and implementation of deep learning. With the advancement of artificial neural networks and deep learning architectures are used for image classification. These convolutional neural networks are based on artificial neural networks are used in the application of multiclass image classification. The VGG19 model can be used as multiclass image classification using Deep Convolutional Network. The classification accuracy of the VGG-19 model will be visualized the classification performance on test data using confusion matrices. The model has given a minimum accuracy of 72% and a maximum accuracy of 95% [1]. Images of dogs and cats are the most popular example to train image classifiers, The image classifier to recognize various breeds of dogs and cats using fine-tuned using VGG models. Two common models are VGG16 and VGG19. Using this model VGG19 has obtained training accuracy of 98.59%. The validation accuracy of 98.56%, and testing accuracy of 84.07% [2]. A recent revolution in deep learning techniques have given an opportunity for automated classification of diseases. Six pre-trained Convolutional Neural Network (CNN) have been used namely AlexNet, VGG16, Visual Geometry Group 19 (VGG19), GoogLeNet, ResNet101 and DenseNet201 with its corresponding resultsexplored. The images are classified based on prediction scores have been evaluated for each disease classes [3]. For agricultural purposes, multiple methods have been proposed toidentify the plant diseases. But, detecting plant diseases with high accuracy was a challenge in computer vision. The deep learning context where a pre-trained VGG-19 model is used for feature extraction. A dataset consisting of two classes diseased and undiseased. From the model VGG19 have obtained an accuracy of 98.6% [4].

Diabetic retinopathy is a disease that is diagnosed in diabetic patients. The Diabetic retinopathy classification achieved a best result through the combination of a Gaussian mixture model, visual geometry group network (VGGNet), singular value decomposition and principle component analysis (PCA), and SoftMax, for high dimensional feature extraction, image classification. The experiment performed using a standard KAGGLE dataset. The proposed model VGG-19 DNN based DR model achieved better than AlexNet and spatial invariant feature transform model.[5]. Rupal Agarwal et al., The classification of an image of a cooking object into one of its states using deep convolutional neural network. To train the model, transfer learning approach was used with VGG19 used as a pretrained model. The architecture of VGG19 was slightly modified to get the effect of different optimizers, regularizes and layers. The dataset consisted of 17 cooking objects with 11 different states. There was a total of 9309 images which were randomly divided into three sub datasetstraining, validation and testing. The model was able to classify the images with 70.58% accuracy on test dataset [6]. Xiang Wan et al., The surface defects region of strip steel and various defect types and has complex gray structures. There would be a large number of false defects, which lead to the traditional machine vision algorithms to be unable to detect defects for different types of strip steel. Image classification techniques based on deep learning require a large number of images to train a network. Through verification of the mixed dataset, composed of the NEU surface dataset and dataset, the recognition accuracy of the improved VGG19 network reached 97.8%. The improved VGG19 network performs slightly better than the baseline VGG19 in six types of defects, but the improved VGG19 performs significantly better in the surface seams defects [7]. Tomatoes are the most commonly and widely grown crop across the world. The plant diseases easily and immediately affect the quantity of produce as well as the quality of tomato. An attempt at contributing towards the detection andidentification of diseases in tomato leaves using machine learning. Analyze the efficiency of algorithms such as XGBoost and Convolutional Neural Network (CNN) and its architectures such VGG19 withdata as augmentation transferlearning and over conventional machinelearning algorithms such as Support Vector Machines (SVM) and Random Forest and test their efficiency in the detection and classification of tomato plant leaf diseases in terms such as accuracy, precision, recall and training time. In convolution neural network's VGG19



architecture with transfer learning reached the best result with overall accuracy of 96 percent compared to other models. And it has faster training time [8]. In breast cancer images classification for early detection of the disease. The fully-trained network on the imaging modality by using 3 pre-trained networks such as VGG16, VGG19, and ResNet50. All the three networks performed well when the training data is 90% of the total dataset, but the situation is somewhat different for full training. VGG19 performed well for the 80%-20% training-testing data splitting. However, the performance of ResNet50, VGG16 network for the entire splitting fashion was almost same. The deviation of VGG19 from the usual trend is due to its more sensitivity towards benign and malignant during 90%- 10% and 70%-30% splitting, respectively [9]. The silkworm, Bombyx mori, is an significant economic insect in silk production. There are different types of silkworm diseases exist in sericulture industry. They cause large number of economic loss to the sericulture industry, among them the serious disease is B. mori nucleopolyhedrovirus (BmNPV), (Jiang and Xia, 2014; Xu et al., 2015).BmNPV disease is very dangerous, and infected approximately 96 h. The body wall of infected silkworms breaks effortlessly and, thus, the pathogen pollutes, which spreads the disease easily to whole batch of the silkworm production (Bao et al., 2009).

III. METHODOLOGY

A. Proposed Method

The proposed model here is VGG-19. VGG-19 is a Convolutional neural network, used to classify images. VGG-19 is 19 layers deep. The Reason to choose VGG-19 is that we can load the pretrained version of the network which is trained on millions of images from the ImageNet dataset. The Network that are pretrained will classify the images into object categories. Rich features representation for a wide range of images is learned by the network. This network has 47 layers. 19 layers with learnable weights, in those 19 layers there are 16 convolutional layers, 3 fully connected layers, 5 MaxPool layers, and 1 SoftMax layers. The model's default input size is 224x224.

> Total params: 20,074,562 Trainable params: 50,178 Non-trainable params: 20,024,384

1. Convolutional Model:

In silkworm classification, we use the convolutional layer for feature extraction. These layers are arranged at the top so that to increase the depth level. The first convolutional layer i.e., 64 kernels is used to extract features from input images.

2. Fully Connected Layer:

Feature vector is prepared using fully connected layer. The Feature vector is further subjected to dimensional reduction for better classification results.

3. MaxPool Layer:

It is used as a handler. MaxPool layer along with convolutional layer is used to minimize feature dimensionality.

4. SoftMax Layer:

Here we used SoftMax layer for feature classification that is extracted from the fully connected layer. Table 1 shows the architecture of VGG-19.

Layer (type)	Output Shape	Param a
input_1 (InputLayer)	[(Mone, 224, 224, 3)]	0
Black3_conv& (Conv20)	(None, 224, 224, 64)	3792
N3INCH3_CONV2 (Conv2D)	(Norue, 224, 224, 64)	36928
blucsi_pool (MasFooling2D)	(Nume, 112, 112, 64)	ø
himch2_convi (Conv26)	(fermer, 112, 112, 128)	73856
bluck2_conv2 (Conv2D)	(Norw, 112, 112, 128)	147584
bluck2_pool (MaxPooling2D)	(Nume, 56, 56, 128)	-01
bluck3_conv1 (Conv2D)	(Mone, 55, 56, 256)	29516#
block3_conv2 (Conv2D)	(Norme, 55, 56, 256)	5504440
bluck3_conv3 (Conv2D)	(Mone, 56, 56, 256)	\$90080
D]mck3_conv4 (Conv2D)	(Mone, 56, 56, 256)	55494880
block3_pool (MaxPooling20)	(Mone, 28, 28, 256)	49
bloch4_conv1 (Conv2D)	(Minue, 20, 28, 512)	\$100100
block#_colv2 (Corv20)	(Nume, 28, 28, 512)	2359808
tilictul_conv3 (Conv20)	(Norm, 28, 28, 542)	2319808
bluch4_convet (Conv20)	(Mane, 28, 28, 512)	2359808
blucké_pool (MasPooling20)	(Nume, 14, 14, 512)	0
bluck5_conv1 (Conv2D)	(None, 14, 14, 512)	2359808
hisech5_conv2 (Conv2D)	(None, 14, 14, 512)	2359808
Eliick5_conv3 (Conv2D)	(None, 14, 14, 512)	2355808
himch5_conv4 (Conv2D)	(None, 14, 14, 512)	23508408
DINCKS_pool (MaxPooling2D)	(None, 7, 7, 512)	-0
flatten (flatten)	(Norw, 25888)	- 47
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Table 1.Detailed architecture of VGG-19





Fig 1: Basic VGG19 Architecture.

Fig 1 shows basic architecture of vgg-19. In this VGG19 model first two layers are convolutional layers with 3*3 filters. The first two layers uses 64 filters, result in 224*224*64. The filters are continually 3*3 with a stride of 1. After this pooling layer with max-pool of 2*2 size with stride 2, which decreases image size from 224*224*64 to 112*112*64. This is headed by 2 more convolution layers with 128 filters, which outcomes in the new dimension of 112*112*128. Again, pooling layer is applied, which decreases the size to 56*56*128. Two more convolution layers are integrated with 256 filters, where each layer is followed by a down-sampling layer, which reduces the size to 28*28*256. There are still two more stacks, each with 3 convolution layer is separated by a max-pool layer with 7*7*512 volume, which is

flattened into a Fully Connected (FC) layer and followed by a SoftMax layer as output.

B. Dataset

To perform deep learning method for our proposal work, we use silkworm image dataset. Where the dataset consist consist of 1000 silkworm images in which 800 images for training and 200 silkworm images for testing. Our dataset contains two categories: Diseased and Undiseased as shown in Fig 2. There are at least 500 images in each category. For the assessment, we divide the images into 8:2 train/test sets for each category. Since the images were choosen at random for each collection, the accuracy varies depending on which image was chosen, and we report the average accuracy and loss.



(c) (d)

Fig 2: Example images from dataset (a) test- diseased (b) test-undiseased (c) train-diseased (d)train-undiseased

IV. PERFORMANCE

In this paper we have got the overall performance in VGG19 model. We have trained and tested the data by using our dataset images. The whole system is enforced in Python language on Windows 10. We have used Google Colab. Hardware details that we have used are Processor: Pentium 4 or above, RAM:8GB, Hard Disk: 80GB, Input Devices are Keyboard and Mouse, Output Device is High Resolution Monitor.



While doing VGG19 model compilation, this model trained for 15 epochs. Given below table shows the end result of training that is train accuracy, test accuracy, train loss, test loss and epochs.

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Table 2. Training Result Per Epoch

A. CONVERGENCE ANALYSIS

The convergence analysis of this model on our silkworm Dataset. The accuracy and loss from the model are monitored and it is shown in Figure 3(a) and 3(b). And achieves the result 98% of accuracy. The graph is obtained by using vgg19 model on our silkworm datasets.



In the above graph, X-axis is having epoch values. Y-axis in Model Loss (Figure 3(a)) is Loss values, in case of Model Accuracy (Figure 3(b)) is having values of accuracy. The accuracy is varying per epoch. We have enhanced the epoch value from 15 to 20 in our model. The training accuracy is sort of stable in 0.97 and 0.05 loss once more or less 15 epochs.



B. RESULT

By using vgg19 model, the image classification of silkworm as diseased and undiseased is successfully obtained. We have achieved 98% of accuracy using small set of data. It is observed that image classification using CNN-VGG19 is very efficient and easy to implement.

V. CONCLUSION

In this paper, we determined a CNN model using a VGG-19 architecture that is to classify the silkworm images based on diseased and undiseased. This project is to classify the silk worm images using Deep Neural Network that will helps in optimizing the seed production of silkworms, which increases silk production. We have used the subset of the images an achieved accuracy of 98%. The accuracy would increase if we use whole Currently peoples datasets. are manually classifying the diseased and undiseased silkworm. This technology will help in the field of sericulture, when the disease spread to the entire set and destroys. This helps to maintaining the quality and quantity of the silkworm production.

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