

Vidarbha Region Crops: Cotton, Soyabean and Maize Disease Detection using Modified Autoencoder

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Abstract— Every nation's economy depends heavily on agriculture and India is recognized as an agro-based country. To produce healthy crops with free of disease is one of the primary goals of agriculture. The soil and water resources of our vidarbha are fertile and the climate is moderate. But numerous diseases affect crop production and cause enormous crop losses, endangering the lives of helpless farmers. Manual monitoring of these plant diseases is not possible as this plants are cultivated in huge acres of land. Early detection of diseases prevents the rapid spread of disease to the whole field. This study aims to use a Deep learning (DL) model to accurately classify three leaf datasets of cotton soyabean and Maize crop leaves as either infected or healthy. This paper presents exhaustive experimental evaluations on ensemble model to tune hyper-parameters named learning rate, optimizer and no of epochs. The suggested hyper-parameter settings can be directly utilized while employing the ensemble model for disease detection and prediction. Extensive evaluations on this dataset and another public dataset demonstrate the advantage of the proposed method. Our method outperformed the state-of-the-art techniques and displayed comparatively better results. Remarkably, our approach demonstrated even higher performance than widely used ensemble techniques, generally considered benchmarks in the field.

Index Terms— Auto encoder, Deep Learning, CNN, VAE.

I. INTRODUCTION

The agricultural sector is essential for producing revenue and satisfying the growing demand for food in the world [11]. With the growing population, the need for food continues to rise. One of the primary goals of agriculture is to produce disease-free crops. Crop diseases pose a significant challenge to agriculture, leading to substantial losses in yield and compromising food quality and quantity [12]. In agricultural farming, leaf diseases are the predominant challenges faced by the plants in producing a large number of agricultural products. Crop diseases constrain the sustainable development of agriculture and form one of the challenges that plague agricultural production [13]. Plant leaf disease detection has a considerable influence on the safety of crop quality. However, distinguishing different symptoms in leaves is a challenging task. Early detection of leaf diseases plays a crucial role in the crop production management process. Most agricultural specialists still rely on naked-eye observations as a fundamental method for detecting leaf diseases in plants. The traditional leaf disease detection of plants relies primarily on the on-site manual diagnosis, which has drawbacks of high workload and strong subjectivity, and cannot meet the real-time monitoring of large-scale diseases. With the development of modern computer technology, disease recognition technology is also upgraded.

Crop disease image recognition based on hand-designed features has also emerged. The method applies image processing algorithms to segment the leaves, extract the important disease spot information and finally selects the corresponding classifier to classify. Some of the most commonly applied techniques in plant disease detection/identification are those based on Machine Learning (ML)[14]. Methodologies like knearest neighbor (KNN), artificial neural networks (ANN), and support vector machine (SVM). Although the traditional machine learning method based on hand-designed features has gained good achievements in the field of disease recognition, this method is time-consuming and labor-intensive, and there is a great deal of objectivity in the selection of features, so it is difficult for this method to meet the practical needs. Therefore, several automated techniques have been integrated into the process of accelerating the human observation process in identifying leaf diseases. The techniques are very practical and important because they intend to identify diseases by analyzing leaf images.

Deep learning relies on neural networks made up of hundreds of layers rather than input, output and hidden layers. Convolutional neural networks, which are a subclass of deep learning networks, are concerned with the detection of features and relationships of images using a sequence of layers comprising convolution, pooling, and rectified linear unit (ReLU) feed into a fully connected layer. CNN architectures have the "moving window" feature, which extracts only the local information of the image, not the global features. In addition, CNN architectures take the whole image as an input that is unable to identify small lesions, thus affecting the classification.

Unlike traditional approaches, the deep learning model is able to automatically extract features.[16] On the basis of a large number of data, the deep network can extract deeper feature representations to the disease image and thus makes the recognition effect and generalization ability of the model better. However, deep learning models become increasingly and more multi-layered, which often requires much more training samples with a large number of parameters and high computational overhead.

A. Leaf and Disease

It is very early disease detection, allowing farmers to respond appropriately before the spread of diseases, and they minimize losses. Healthy plants yield more. Detection of disease ensures optimal production through the maintenance of plant health. Identification of disease fosters sustainable agriculture since the reduction in the need for chemical interventions enhances integrated pest management strategies. Early disease detection would save much water, fertilizers, and pesticides, hence reducing costs and environmental impact. Vidarbha is one of the agricultural divisions of Maharashtra, India, having a variety of crops such as cotton, maize, and soybean. Following section explain crops taken for experimentation and list is mentioned in Table 1,2,3 respectively

Cotton crop

India is the world's largest producer of cotton but recently, the production of cotton has significantly declined due to various cotton plant diseases. Vidarbha is one of India's major cotton-growing regions, often called the "Cotton Bowl" due to its favorable climate and soil conditions. The bacterial and fungal diseases reduce the growth of the cotton and contribute to the decline in cotton yield. Cotton is one of the most cultivated crops. Its cultivation is often infected with pests and diseases. Real-time monitoring and data analytics could help farmers and researchers catch potential problems early, make corrective action, thereby reducing risks and promoting the health of crops.

B. Soybean Leaf Diseases

Soybean (*Glycine max* L. Merrill) is one of the highly important seed legumes in Vidarbha. It serves as the primary source for edible oil and contributes close to 25% to the total edible oil. Nutritional value of soybean helps prevent heart diseases and diabetes to a certain degree. Soybean has increased its popularity in Vidarbha because of its content of protein and demand for the oil. The annual loss of soybean due to these diseases is about 10%, and the serious ones can be more than 30% [14]. So the accurate identification of soybean leaf diseases is especially important for early prevention and control of the disease [16].

C. Maize Leaf Diseases

Maize or corn is a mass agricultural crop produced worldwide. It serves for food and as a forage crop. This has high importance in the Vidarbha cropping system. The same is consumed directly as edible food, while serving the basis for several products used in the kitchen for instance cooking oil, starch, flour, sugar, biofuels, alcohol, among many others, besides providing livestock feed. Corn grows under varied environmental conditions and is regarded as one of the most important crops with high genetic diversity and production potential besides rice and wheat.

These crops have significant potential in the local economy and food security in Vidarbha. Sustainable farming practices and technologies have increased over the years in which the farmers to improve productivity use these crops.

The organization of the remaining paper is as follows: The materials and methodologies are discussed in Section II, which consists of the theoretical background, and the outlines of proposed method. The experimental setup, performance matrices, results, and the related discussions are in Section III. At last, it is concluded with discussion in the Section IV

II. METHODOLOGY OF PLANT DISEASE DETECTION USING SPARSE ENCODER

Variational Autoencoders (VAEs) are a type of generative model that can be effectively applied to plant leaf disease detection.

VAEs are neural networks designed to learn latent representations of input data. They consist of an encoder that compresses the input into a latent space and a decoder that reconstructs the input from this compressed representation. [15]

- Encoder: This component compresses the input images into a lower-dimensional latent space, capturing essential features that characterize healthy and diseased leaves.
- Latent Space: The VAE learns to represent the input data in a probabilistic manner, allowing for variability in the encoded features.
- Decoder: This part reconstructs the input images from the latent space, enabling the model to learn important patterns associated with diseases.

Back-propagation is used to minimise the loss function whereas forward-propagation is used for calculating outputs. The loss function is a measure of how much predictions deviate from the desired value. To do this, we must reverse the weights and biases. The latent representations can be clustered to differentiate between healthy and diseased samples, allowing for classification.

The VAE is trained using a loss function that combines reconstruction loss (how well the model can recreate the input images) and a regularization term (Kullback-Leibler divergence) that ensures the latent space follows a Gaussian distribution.

The KL divergence is a measure of how one probability distribution diverges from a second, expected probability distribution. In the context of VAEs, it serves two main purposes:

Regularization: It regularizes the latent space by encouraging the learned distribution of the latent variables to be close to a prior distribution (usually a standard normal distribution, $\mathcal{N}(0,1)$). This ensures that the latent space is structured and can generalize better.

Encouraging Diversity: By promoting a distribution that resembles the prior, KL divergence helps the model to avoid overfitting to the training data, thus encouraging the generation of diverse outputs.

Before making any changes to the weights, the total error (E) is calculated:

$$E = \sum (0.5 * (T_i - H_i)^2) \quad (1)$$

where T_i is target values. Next, the learning rate (L_i) multiplied with the derivative of the total error w.r.t weights are subtracted from the given weights:

$$\frac{dE}{dW_i} = \frac{dE}{dH_{i+1}} * \frac{dH_{i+1}}{dH_i} * \frac{dH_i}{dW_i} \quad (2)$$

$$W_i = W_i - (L_i * \frac{dE}{dW_i}) \quad (3)$$

Either choose a learning rate that results in a severe loss function, or decrease it gradually between training iterations.

The input image is resized to 512x512 and normalized before being fed into the network.[16]

$$X = [x_1, x_2, \dots, x_k] \quad (4)$$

K denotes the input image pixels. Then normalization carried out by adjusting and scaling the activations. It computes the mean and variance of the mini-batch and uses these to normalize the activations. This helps to reduce internal covariate shift and allows for higher learning rates. Normalization layers are essential for stabilizing and accelerating the training of VAE.

$$x = \left[\frac{x - \min}{\max - \min} \right] \quad (5)$$

Convolutional layers enable learning features at multiple abstraction levels. Each module of the Layer 3,5,&5 contains several convolutional filters of different sizes (1x1, 3x3, 5x5) which run in parallel. This multi-scale approach allows the network to learn various features effectively. 1x1 filters are especially important for reducing the dimensionality before applying larger convolutions, thus limiting the number of parameters and computation load. After convolution layer we got estimated the weight(w), bias (bj).

$$x_i^{l,j} = \sigma[b_j + \sum_{a=1}^m w_a^j x_{i+a-1}^{l-1,j}] \quad (6)$$

Activation function is symbolized by the variable σ . The architecture is proposed by which a healthy gradient may flow through the network to prevent vanishing gradients, which might occur while training issues. This happens partially because the convolutional layers are of specific structure, and with the use of auxiliary classifiers. Max pooling reduces spatial dimensions of the feature map that decreases the number of parameters and computation in that network. It captures the most dominant characteristic within a pooling window often of size 2x2 by taking the maximum. This retains important spatial details and discards the much less significant details to describe the feature maps in sum. Max pooling thus picks the maximum value in its region, which has its own form of invariance to small translations in the input image as well as distortions. This means that the difference in the input does not seriously affect the output. So, the model's stability is improved.

$$x_i^{l,j} = \max_{n=1}^r (x_{(i-1)*T+n}^{l-1,j}) \quad (7)$$

where n is pooling size and T is pooling stride.

Reducing the size of feature maps through max pooling leads to faster training times and lower memory usage, which is critical when dealing with large datasets and complex models.

Following equation models the Hidden layer to output .Proposed method have this capability

$$h_t = g(W_{xh}x_t + W_{hh}h_{t-1} + b_h) \quad (8)$$

$$z_t = g(W_{hz}h_t + b_z) \quad (9)$$

here, g indicates elementwise nonlinearity(it can be sigmoid or hyperbolic tangent), x_t is the input $h_t \in R^N$ is the hidden state having hidden units equals to N. Output is denoted by Z_t at instant t.pixel sequence $(x_1, x_2, \dots, x_T)$ having T number of coefficient, then h1 (letting $h_0 = 0$), $z_1, h_2, z_2, \dots, h_t, z_t$.

Algorithm: 1 Sparse autoencoder based disease detection

Inputs: ϵ : Choose $(x^0, s^0) > 0$ stop accuracy ϵ (e.g. $1e-6$),

Total Epochs is k_{max} .

for $k = 1, 2, \dots, k_{max}$ do

Perform Prediction Step : set $\sigma \leftarrow 0.001$

$$(x^k, s^k, \alpha_p, \alpha_d) = \text{UPDATE}(x^{k-1}, s^{k-1}, \sigma)$$

if $\mu_k \leq \epsilon h(x^k)$ and $\|r_d^k\|$ then

e Break

Outputs: x^k

Function: $\text{UPDATE}(x^{k-1}, s^{k-1}, \sigma)$

Compute $\Delta x, \Delta s$ with σ, x^{k-1}, s^{k-1}

Compute α_p, α_d with $x^{k-1}, s^{k-1}, \Delta x, \Delta s$

$$\text{Update}(x^k, s^k) \leftarrow (x^{k-1} + \alpha_p \Delta x s^{k-1} + \alpha_d \Delta s)$$

Return $(x^k, s^k, \alpha_p, \alpha_d)$

The proposed model can learn meaningful latent representations that capture essential characteristics of the healthy and diseased leaves. They can generate synthetic images of diseased leaves, which is useful to augment datasets and improve their training. With proper training data, they can easily adapt to various types of leaf diseases and plant species. This Study is carried out in Badnera city of western Vidarbha on the available internet data sets images of Cotton, Soyabean and Maize Images. We have calculated all the parameters of Images in the computer lab of our department in Prof Ram Meghe College of Engineering and Management Badnera-Amravati- Maharashtra-44470

TABLE I: FREQUENT DISEASES ON COTTON LEAF

S N	Disease Class	Symptom
1	Alternaria Leaf Spot	Dark spots on leaves
2	Bacterial Blight	Water-soaked lesions on leaves
3	Fusarium Wilt	Wilting and yellowing of leaves
4	Powdery Mildew	White powdery coating on leaves
5	Leaf Curl	Curled or distorted leaves

TABLE II: FREQUENT DISEASES ON SOYABEN LEAF

S N	Disease Class	Symptom
1	Soybean Rust	Orange-brown texture on leaves
2	Powdery Mildew	White, powdery on leaf surface.
3	Septoria Leaf Blight	Dark, water-soaked spots leaves
4	Bacterial Blight	Water-soaked lesions with dark leaves

TABLE III: FREQUENT DISEASES ON MAIZE LEAF

S N	Disease Class	Symptom
1	Anthrachnose Leaf Blight	Dark, sunken lesions on leaves
2	Downy Mildew	Yellow patches on leaf
3	Gray Leaf Spot	Narrow, elongated gray spots on leaves
4	Corn Smut	Grayish-white galls on leaves
5	Leaf Blight	yellowing and browning of leaf tips and edges

III. EXPERIMENTAL SETUP AND PROPOSED RESULTS

This section describes the experiments performed to assess the model's performance, figure 2, demonstrates the distribution of the crop wise dataset. For cotton 1155 images, for Soyabean 2590 and 1870 for Maize is considered. Main features of the implementation environment, experiments setup, initialization of parameters and performance metrics are presented in the subsequent subsections. Finally, details of the results are mentioned along with their discussion.

The ensemble model performed better when the learning rate parameter was set to 0.0001 at 20 epochs. However, Adam optimizer was used in the above studies. Therefore, further testing to tune the optimizer hyper-parameter is conducted using the SGD and RMSprop optimizers, while keeping the learning rate at 0.0001. The following figure provides the results of this experimental investigation. The SGD optimizer results greatly improved the training-testing accuracy of the ensemble model. It also reduced the losses observed during the training of the ensemble model. By comparing with the above classical detection frameworks, we can find that the proposed framework can achieve the best results.

Evaluations include accuracy, recall, precision and F1 score of sparse autoencoder images used to assess models for disease detection. It measures the performance of how well the model can make correct predictions regarding positive cases. Specificity measures its ability to detect negative cases correctly. Precision is calculated in terms of positive cases as a fraction of all positively classified cases in the result. The F1 score presents a balanced measure both in terms of precision and recall, hence providing the healthcare practitioners with a holistic tool that informs their decisions and improves patient care, ultimately. Below are the equations for accuracy, precision, recall, and F1 score.

Accuracy

This is the most important metric for evaluating a model and is defined as the proportion of correct predictions to the total number of predictions made by the model. It is evaluated using Eq.

$$Accuracy = \frac{(TP + TN)}{(TP + TN + FP + FN)}$$

The evaluation of the model's accuracy involves the examination of true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN)..

Precision

Higher-precision classifiers produce fewer false positives. High accuracy reduces the likelihood of misclassifying negative instances as positive in numerous applications where false positives have severe consequences. Precision is calculated by Eq

$$Precision = \frac{(TP)}{(TP + FP)}$$

Recall (sensitivity or true positive rate)

Classifiers with higher recall have fewer false negatives. The classifier captures positive cases and reduces false negatives. A classifier with lower recall has more false negatives. The recall is determined by Eq.

$$Recall = \frac{(TP)}{(TP + FN)}$$

F1 Score

The F1 Score is the harmonic mean of precision and recall, indicating patterns between them and calculated using Eq.

$$F1\ Score = \frac{2 * Precision * Recall}{(Precision + Recall)}$$

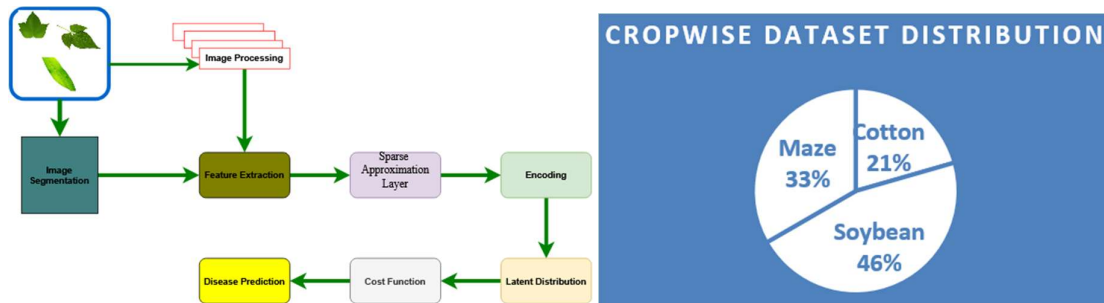


Figure 1. Process Flow

Figure 2: Cropwise Dataset Distribution

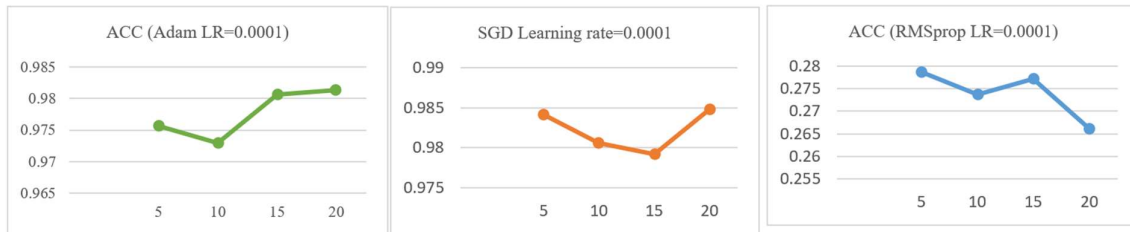


Figure 3: epoch vs Accuracy for a) Adam b) RMSprop c) SGD

TRAINING ACCURACY (%)

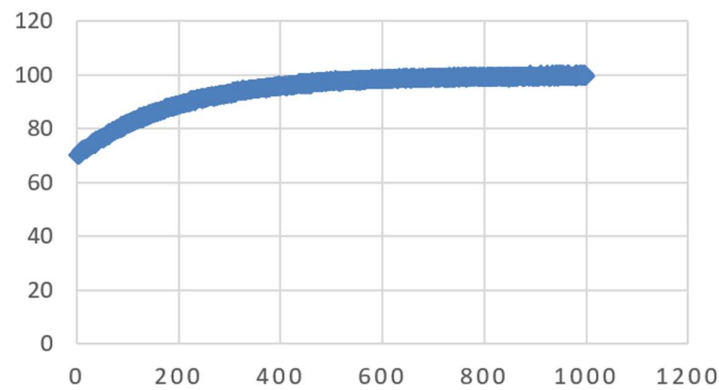


Figure 4: Training accuracy vs Epochs

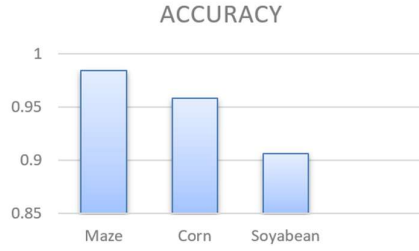


Figure 5: Comparison of Accuracy of Selected Crops

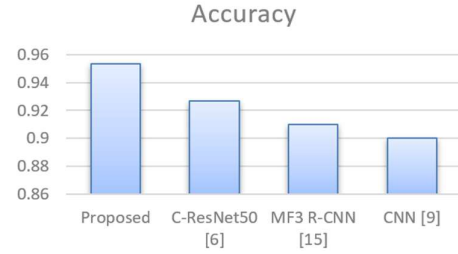


Figure 6: Comparison of Accuracy of State of the Art Methods

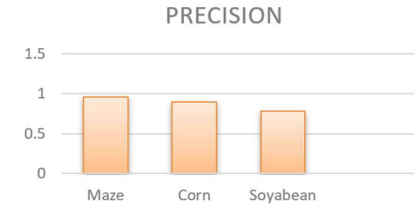


Figure 7: Comparison of Precision of Selected Crops

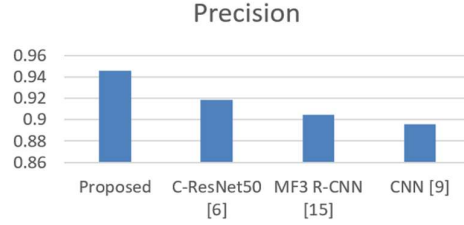


Figure 8: Comparison of Precision of Various Methods

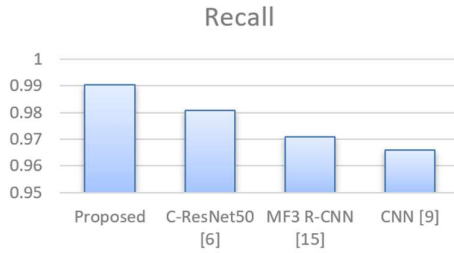


Figure 9: Comparison of Recall of Selected Crops

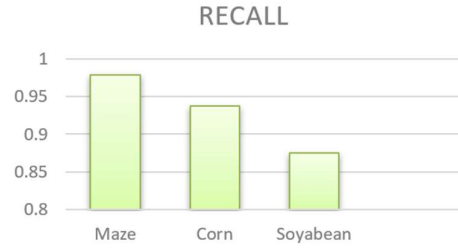


Figure 10: Comparison of Recall of various Methods

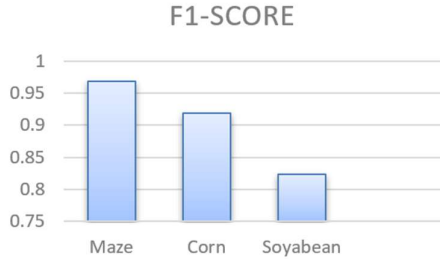


Figure 11: Comparison of F1-Score of Selected Crops

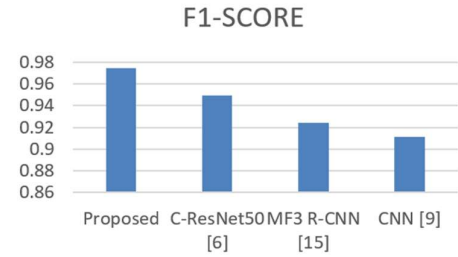


Figure 12: Comparison of F1-Score for Various Methods: Showing the sampling sites

TABLE IV: COMPARATIVE ANALYSIS WITH STATE-OF-THE-ART DEEP LEARNING MODELS [1][2][3][4][5][6][7][8][9][10]

Model	Type	Strengths	Limitations
CNN (VGG16, ResNet50)	Convolutional Network	Strong in spatial feature extraction; widely used	Needs large datasets; struggles with small lesions
YOLOv5 / YOLOX	Object Detection	Fast, real-time detection; bounding box-based	Less effective for uniform leaf symptoms
Vision Transformer (ViT)	Transformer	Captures global features; scalable	High compute demand; large dataset needed
MobileNet / EfficientNet	Lightweight CNN	Optimized for mobile and edge devices	Lower accuracy in complex classification
Proposed Sparse Autoencoder	Latent Encoding	Good for low-data regimes; captures abstract patterns	Needs careful tuning; less field adoption

IV. CONCLUSION

Experts usually rely on bare eyes to detect and identify such plant diseases and pests that may be brought about by lower accuracy in identification. Thus, an early detection of cotton disease using AI-based systems would help to increase the production of cotton by detecting the leaf disease significantly. Machine learning algorithms are playing a very important role, as they can learn an image dataset of crop effects and thus identify them properly. They have achieved recognition in the identification of a significant proportion of plant diseases ranging across many categories and are remarkable in terms of disease detection through patterns and early warnings of plant diseases in advance by deep learning algorithms. Compared to standard CNN architectures and object detection models such as YOLO and ViT, the proposed Sparse Autoencoder achieves higher accuracy and generalization with fewer samples. Its ability to learn compressed latent features enables robust classification even in the presence of noise, overlapping symptoms, and minimal data augmentation.

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