

AN AI BASED AUTOMATED METHOD FOR THE DETECTION OF TUBERCULOSIS IN LUNGS USING GENERATIVE ADVERSARIAL NETWORKS

Roopa N K¹, G S Mamatha²

¹ Sri Siddhartha Institute of Technology, Karnataka, India

² R V College of Engineering, Karnataka, India.

1 roopank@ssit.edu.in

Abstract - Tuberculosis is considered one of the deadliest diseases. It is caused by a Mycobacterium Tuberculosis. The life of the person becomes very severe if it is not treated at an early stage. The introduction of new technological methods, software and hardware devices, is encouraging researchers to come out with more powerful computer-aided methods for diagnosing TB at an early stage. However, the use of deep learning methods requires an ample amount of datasets. Because of the non-availability of enough volume of the dataset, in this work, we are using a generative adversarial neural network which has a special feature of synthesizing the images such that one cannot differentiate whether the image is original or fake. This study uses chest x-ray images of the infected persons, performing data pre-processing including resizing and converting them to grayscale and the input images are labeled. The input data consists of 4200 total images both healthy and unhealthy images. This work uses a deep learning-based technique, GAN. It consists of two sub models, the generator model and the discriminator model. The results were plotted using standard library functions. Classification accuracy of 96% was obtained, the precision of 96%, recall 79%, and 98% f1 score. This is observed to be the outstanding performance obtained compared to the similar kind of works in the literature.

Keywords - Generative Adversarial Network, Tuberculosis, Convolution Neural Network, Mycobacterium, CT-Scan

Introduction

Nearly 25% of all over the world is suffering from the infectious disease tuberculosis (TB). This is a bacterial infection caused by Mycobacterium tuberculosis. Till today 1.45 million people have died because of TB [1]. As per the survey by World Health Organization (WHO), it is South-East Asians that are suffering from TB the most. From the studies it has been identified that around 24% of Africans, 18% of Western Pacific people, 3% of the people from both America and Europe, and 8% of the people from the Mediterranean region are suffering from TB [2]. 15% of people with TB are asymptomatic. This indicates that using bacterial approaches to diagnose these patients is challenging.

On the other hand, in recent years, only up to 70% of the 5.9 million individuals with pulmonary TB had their diseases bacteriologically proven. The remainder of the patients were therefore clinically identified based on symptoms, CXR abnormalities, and medical records. Given the situation, a prompt and precise diagnosis would be crucial to the treatment and management of the condition [3]. The method for isolating bacteria continues to be the gold standard for case determination testing. The approach has a somewhat low sensitivity despite having a very high specificity. Additionally, such a test is a lengthy procedure that might take at least three

weeks to provide the findings. Additionally, diagnostic methods for molecular and immunological disorders both have benefits and drawbacks [8][9].

The procedure for analyzing TB molecular markers in patient samples Polymerase Chain Reaction (PCR) basically overcomes the limitations of the two aforementioned methods. Unfortunately, not all medical institutions are capable of performing PCR techniques due to the high cost. Many times the patient with tuberculosis remains asymptomatic. In such cases, it is difficult to detect the presence of tuberculosis with bacterial methods. On the other hand, many patients with pulmonary TB can be diagnosed using bacterial methods. Another method of diagnosing called Polymerase Chain reaction (PCR) is more accurate and powerful compared to traditional bacterial methods. Because it is very expensive the institutions are not ready to take up PCR. The standard imaging techniques which can be used for lung disease detection are magnetic resonance imaging (MRI), chest X-ray, and computed tomography (CT-scan).

Since MRI and CT-scan are very expensive and involve lot of radiation exposure, in almost all medical institutes chest X- ray is commonly used for TB detection. Chest X-ray is cheap and affordable by all kinds of people. Chest X-rays read by different radiologists result in different opinions and variations. Also, chest x-ray is used in the detection of many other diseases and pandemics. This increases the load on radiologists and hence decreases the correctness and efficiency. Therefore it is very crucial to go for automated methods that can detect not only the tuberculosis bacteria but also other lung-related diseases so that the right treatment at the right time can be prescribed. Many artificial intelligence automated methods are made available by researchers for diagnosing TB. The World Health Organization approved the use of automated methods for the analysis of chest X-rays in 2020. This reduced human errors in reading the X-rays.

The rest of the sections in the paper are organized as follows: Section II gives a detailed description of some of the similar works identified in the literature, section III gives the architecture and the detailed working process of the Generative adversarial neural network, section IV gives the complete details about building the model, experimental setup, the metrics used to evaluate the model performance and the results obtained. The next section is the conclusion which is followed by the references.

Related Work

This section describes the various works done in the literature to understand the gap analysis. We briefly mentioned various related work details.

Muhammad Rahman et al [5], have worked to develop a method for detecting tuberculosis using XGBoost technique with pre-trained deep neural networks for feature extraction. Tuberculosis is one of the most severe deadly diseases. More than 1.8 million people are losing their lives because of this disease. The authors in this work have used chest x-ray images as input data for developing an automated method. A total of 7000 x-ray images were used to train the deep neural network, out of which 3500 were healthy images and the remaining 3500 images were unhealthy. Three different pre- trained networks were used in this work, ResNet, VGGNet and DenseNet for feature extraction. XGBoost was used for classifying normal images from unhealthy images. A very impressive result of 99% accuracy, 99% precision, and

99% F1 score and specificity was observed for DenseNet neural network architecture. This was the highest among all the 3 types of networks.

Mohammad Momeny et al [1] used generalized deep CNN to build an auto-augmented classification method for classifying tuberculosis lung images. In the images of the input dataset, the parts which are not so significant are identified and removed using a most sophisticated algorithm called square rough entropy. The authors used 10 best policies for data augmentation in the proposed method using a greedy autoaugment algorithm. This helped them to avoid overfitting. They used CNN to enhance the generalization property of the model. They also employed batch normalization, Dropout and PReLU to improve the classification performance. The classification was also compared with other machine learning classifiers like KNN, Naive Bayes, and SVM. The results proved that the CNN performance with outstanding results compared to the mentioned ML techniques. The CNN model gave promising results with 93% accuracy for diagnosing tuberculosis.

Abhinav Sharma et al [6], have done an exhaustive literature survey to understand the statistics and the state-of-the-art of applying machine learning techniques for the diagnosis of tuberculosis. The authors say that World Health Organization has made a strategy "End TB" defining its target to end the disease by 2035. They mentioned that during 2019, there were 0.5 million active cases of Drug-resistant tuberculosis, out of which 78% were drug-resistant to multiple TB drugs. The authors also mention that identifying all the mutations of the bacteria and documenting the same is a time-consuming process and therefore, it is very crucial for doctors and researchers to go with machine learning technology for predicting the presence of tuberculosis bacteria. This helps to get early treatment and early recovery compared to the traditional method of diagnosis.

Satyavrat Govindarajan et al [4], have worked on classifying pulmonary tuberculosis in chest X-ray images using an extreme learning machine with integrated local feature descriptors. The input images are segmented. This is done using Reaction-Diffusion Level set method. Local binary features and local ternary features are extracted using local feature descriptors. Extreme Learning Machine is used as a classifier and the performance of the model is evaluated using standard evaluation metrics.

Thomas E. Tavolara et al [7], have implemented an automatic discovery method for detecting the clinical interpretable biomarkers for images of susceptible mycobacterium tuberculosis using a deep learning approach. In this work, Gradient-boosted trees are used for extracting features. An attention-based multiple-instance model was used for regression purposes. This was used to identify the gene expression from a lot of input data expressions.

Zhi Zhen Qin et al [2], tried to develop computer-automated software products to help researchers working on tuberculosis. The authors say that TB programs should take into account not only the diagnosis accuracy but also the relevant features like operational characteristics, the output format, the method of deploying the product to the patient environment, privacy-related issues, etc. They used the landscaping method or collected information from CAD developers. This work helped the tuberculosis community by reaching them the updates about the latest CAD software products available.

The dataset for the work was taken from the US National library of medicine. It comprises of two datasets of postero-anterior (PA) chest X-ray images. The first set is the MC set and the

second one is the Shenzhen set. Both sets are associated with the readings of the radiologists. Also, MC set consists of manually segmented lung masks to evaluate or assess the automatic lung segmentation methods. MC was collected from Health and Human Services department, Maryland, USA. It comprises 138 chest x-ray images, out of which 80 are normal lung images and the remaining 58 are from people having tuberculosis infection.

The images are of 12-bit grayscale in portable network graphics format collected using Eureka stationary x-ray machine. The size of the images is either $4,020 \times 4,892$ or $4,892 \times 4,020$ pixels. All the images are having the file name prefixed with MCUCXR. (MCUCXR xxxx N.png). The xxxx is a 4 digit number; N is either 0 or 1. 0 indicates a healthy image and 1 indicates an unhealthy image. The readings of the radiologists are kept in a text file with the extension .txt. The readings include the details like patient's age, sex, and the abnormality in the image if it is unhealthy.

On the other hand, Shenzhen set was collected from People's Hospital, Shenzhen China. The X-ray images in this set were collected from outpatient clinics on a daily basis for a period of one month. These images were captured using a Digital diagnostic system. The set comprises 662 chest X-ray images in total out of which 326 were healthy lung images and the remaining 336 were unhealthy images. Just like the MC set images, these images are also embedded with a text file with the extension .txt which includes the details like a person's age, sex, and the abnormality seen if it is an unhealthy image.

Deep Learning and Generative Adversarial Networks

Deep learning is continuously gaining popularity in the field of scientific computing and is used to solve many complex problems in real-time applications. There are different types of deep learning neural networks with different architectures like recurrent neural networks, convolutional neural networks, generative adversarial networks, long short-term memory, Radial basis function networks, self-organizing maps, etc. Each type of network has its own speciality. Deep learning networks work with complex network structures and can handle very large volumes of data. Deep learning works with a set of libraries irrespective of the type of network architecture. The libraries include Keras, Theano, TensorFlow, Torch, etc.

A generative adversarial network is a method for generative modeling based on a deep learning approach convolutional neural network. Using the generative model, the data is generated based on a probabilistic theory [10]. Then the model is trained in an adversarial fashion. The whole network is trained using deep learning artificial intelligence techniques. GAN is an unsupervised learning technique that has the ability to learn the deep insights of the input data. The speciality of GAN is that it can be used to generate data similar to the input data. It works with two sub-models. The generative model generates new fake samples similar to the input data and the discriminator model discriminates the real input data from the generated fake data. The learning speed of GAN is higher than that of CNN.

The two neural networks of GAN are more powerful in making predictions more accurate. Both neural networks are trained together [11] [22]. Each network competes against each other. The generator works for generating more and more accurate input data images while the discriminator works for detecting the generated fake images. The generator network of the

GAN is capable of generating realistic birds, animals, humans, trees, and plants images. The working of a GAN can be illustrated as shown in figure 1.

The generative model is trained such that, it increases the probability of the discriminator model to make mistakes. Whereas the discriminator computes the probability that the received input is from the training dataset not from the generator. Thus the GANs can be considered as a minimax game which means, the discriminator tries to minimize its reward, whereas the generator tries to maximize the loss. The working of the generator and discriminator can be formulated as given below:

$$\text{minimax} Vp(Di, Ge) \tag{1}$$

$$Vp(Di, Ge) = E_{x \sim p_{data}(xd)}[\log Dd(xd)] + E_{z \sim p_{dz}(zd)}[\log(1 - D(Gg(zg)))] \tag{2}$$

Where, Ge is a generator,

Di is a discriminator

data(xd) is the real data distribution

pdz(zd) is the generator data distribution

xd is the sample data from pddata(xd)

zd is the sample data from pdz(zd)

Dd(xd) is the network for the discriminator

Gg(zg) is the network for the generator

GANs can be used in various applications involving images. For example, generating images to boost the input dataset, generating human face images, realistic photos generation, cartoon characters, image-to-image translation, text-to-image translation, face front view, side view, different poses generation, clothes changing for the same human images, generating Emojis etc.

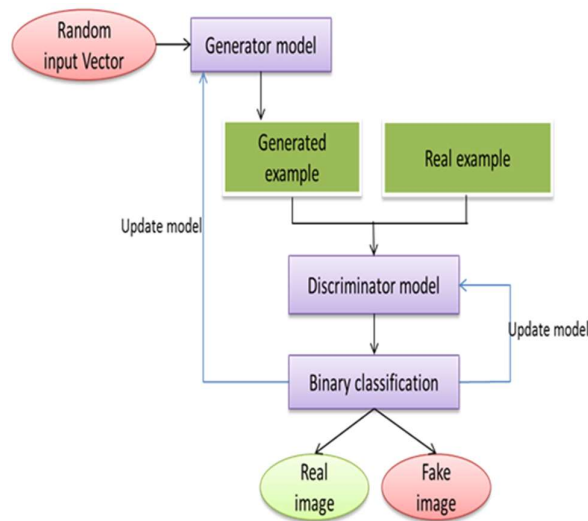


Fig. 1 Generative Adversarial Network for Image Classification

Results and Discussion

The experiment was carried out using the Keras, NumPy, and pandas in the Jupyter notebook. The work started by importing all the required library packages. The packages include Keras models, the layers such as input, reshape, flatten, leakyReLU, dropout, lambda, and activation.

Pyplot from matplotlib, backend from keras, image and imageOps from PTL, and some of the NumPy functions like expand dims, zeros, ones, as arrays for numerical array operations [12][13]. From TensorFlow Keras [15], some of the layers like sequential, Conv2D, MaxPooling2D, flatten, and dense were used. Evaluation metrics from Scikit learn were imported [14]. Some of the modules like glob, OS, PIL, and time were included for building the model.

Two types of datasets were used for the experiment, normal images, and tuberculosis images. Two different arrays image list and label list were used for storing the input x-ray images and the corresponding labels respectively. The preprocessing of the input dataset is performed before passing them to the model for training purposes. The preprocessing stage includes resizing the images to improve their resolution of the images. The images were also converted to grayscale. The label for each input image is created. If the image is a normal healthy image, the label is given as 0. If the image is a tuberculosis- affected image, the label is set to 1. The dataset consisted of a total of 3500 normal images and 700 tuberculosis images. In the next step, the dataset is converted to data frame format with the help of the pandas function. The input dataset is split into a train set and a test set. The train set included 80% of the images and the test set included the remaining 20% of the images.

The GAN model was built by building two submodels, the generator model and the discriminator model. The complete flow of building the models till classification is shown in figure 2. The generator model was built with a number of layers. It started with a sequential layer followed by a dense layer, batch normalization layer, and leakyReLU layer. The next layer was reshaped layer. After reshaping the model's output shape was defined. After this, the convolution 2D transpose layer was added with strides equal to 1X1, with padding set to "same". This was followed by defining the output shape. After that, batch normalization was added followed by one more leakyReLU layer. After this one more combination of convolution 2D layer transpose layer, batch normalization layer, and leakyReLU layer was added. After that, at the end one more convolution 2D layer transpose layer was added and then the final outcome of the generator model was defined.

Similarly, the discriminator sub-model was built. This model was also started with a sequential layer followed by a convolutional 2D layer with 2X2 strides, padding set to "same" and passing the input with shape 28X28X1. After this layer, the next layer was a leakyReLU layer, then the dropout layer. After these layers, one more combination of a convolutional 2D layer, a LeakyReLU layer, and a dropout layer was added [21] [23]. Finally, a flattened layer and a dense layer were added to the discriminator model.

Both the generator model and the discriminator models were optimized using the optimizer adam [24]. First, the generator model was run, and then the discriminator model was run. Both are optimized using adam. Proper checkpoints were used to keep track of the working of both models. The summary of the discriminator is given in the figure. The model was able to train 212,865 total parameters. The summary of the model is shown in figure 3.

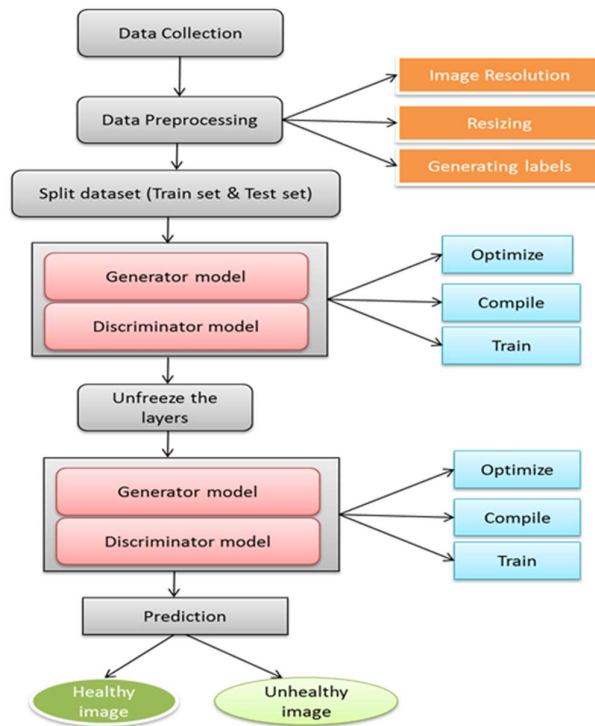


Fig. 2 Workflow of the Proposed Model

Model: "sequential_20"

Layer (type)	Output Shape	Param #
conv2d_75 (Conv2D)	(None, 14, 14, 64)	1664
leaky_re_lu_119 (LeakyReLU)	(None, 14, 14, 64)	0
dropout_17 (Dropout)	(None, 14, 14, 64)	0
conv2d_76 (Conv2D)	(None, 7, 7, 128)	204928
leaky_re_lu_120 (LeakyReLU)	(None, 7, 7, 128)	0
dropout_18 (Dropout)	(None, 7, 7, 128)	0
flatten_16 (Flatten)	(None, 6272)	0
dense_30 (Dense)	(None, 1)	6273

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 Total params: 212,865
 Trainable params: 212,865
 Non-trainable params: 0

Fig. 3 Summary of the Discriminator Model

It takes a lot of time to train deep neural networks (DNNs). While the majority of current systems attempt to plan or overlap computation and communication for effective training, this research takes things a step further by avoiding computation and communication altogether using DNN layer freezing [25]. To precisely assess the training flexibility of each layer, safely freeze the converged layers, and preserve the appropriate backward computation and communication. Although freezing layers might save training costs, freezing untrained layers too rapidly can affect ultimate accuracy. The summary of the freezing layer is given in the

figure. The model was able to train 12,546 total parameters. The summary of the model is shown in figure 4.

```

Model: "sequential_21"
Layer (type)                Output Shape                Param #
-----
conv2d_75 (Conv2D)          (None, 14, 14, 64)         1664
leaky_re_lu_119 (LeakyReLU) (None, 14, 14, 64)         0
dropout_17 (Dropout)        (None, 14, 14, 64)         0
conv2d_76 (Conv2D)          (None, 7, 7, 128)          204928
leaky_re_lu_120 (LeakyReLU) (None, 7, 7, 128)          0
dropout_18 (Dropout)        (None, 7, 7, 128)          0
flatten_16 (Flatten)        (None, 6272)                0
dense_31 (Dense)            (None, 2)                    12546
-----
Total params: 219,138
Trainable params: 12,546
Non-trainable params: 206,592

```

Fig. 4 Summary of the Freezing Layer Model

The model was trained with 3360 images. And it was tested with 840 images. The compilation of the model was done with an optimizer, “sgd” (Stochastic gradient descent), and loss calculation was done using the “binary crossentropy” method and evaluated using the performance metrics “accuracy” [16]. The “sgd” is an optimization algorithm that calculates the gradient for each variable. It calculates the step size for each feature and then finds the new parameters. Binary cross entropy is used especially for binary classification. The equations are shown below. Accuracy is the percentage of correct predictions over a total number of predictions [17][18].

The training of the model was done with 5 epochs, setting the batch size 10. All the layers were unfrozen; once again the training is done using the same parameters, “sgd”, “binary cross-entropy” and “accuracy”[19][20]. This time batch size was set to 10 and epochs to 8. 96% of accuracy was obtained for the validation set. The accuracy plot was plotted using matplotlib shown in figure 5. The plot was plotted with epochs on the x-axis and accuracy on the y-axis.

$$St_{sz} = gr * lr \quad (3)$$

$$nw_{fr} = old_{fr} - St_{sz} \quad (4)$$

Where, St_{sz} is the step size
 gr is the gradient
 lr is the learning rate
 nw_{fr} is the new feature
 old_{fr} is the old feature

$$Bi_{ce} = \frac{1}{n} + \sum_{i=1}^n (-y_i \cdot \log(p_i) + (1 - y_i) \cdot \log(1 - p_i)) \quad (5)$$

Where Bi_{ce} is the binary cross entropy loss
 n is the number of features
 y_i is the i^{th} features
 p_i is the probability of the i^{th} feature

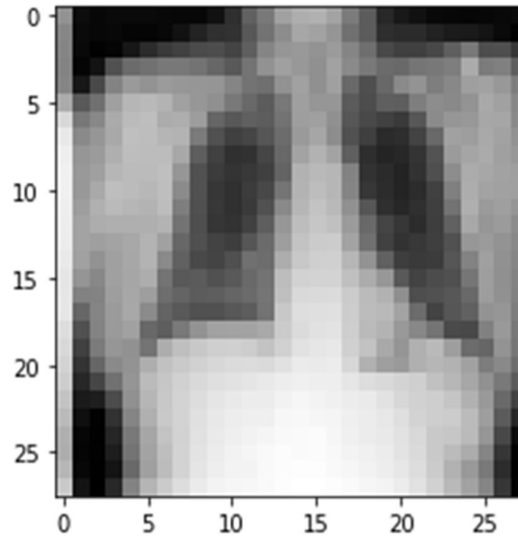


Fig. 5 Accuracy obtained for the Validation Set

The model was run once again, for demonstrating the prediction for the new test image. Once again the probability distribution and classification were done for the test image. The predicted accuracy for the test image was 99.7%. The predicted image is shown in figure 6. The entire test set was run again and the results were obtained. The classification report obtained is shown in figure 7.

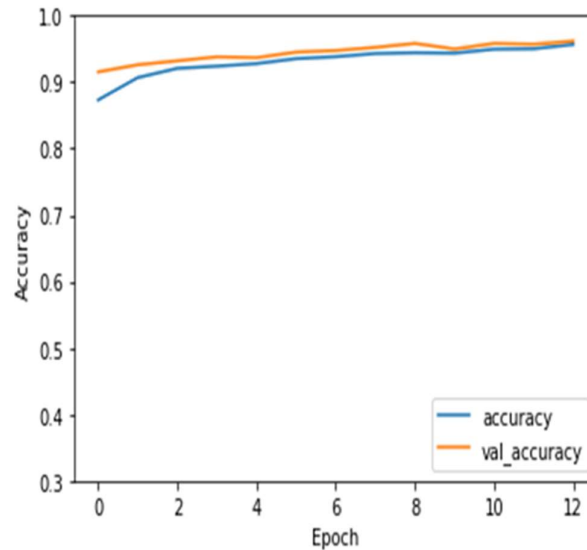


Fig. 6 Predicted Image by the Model

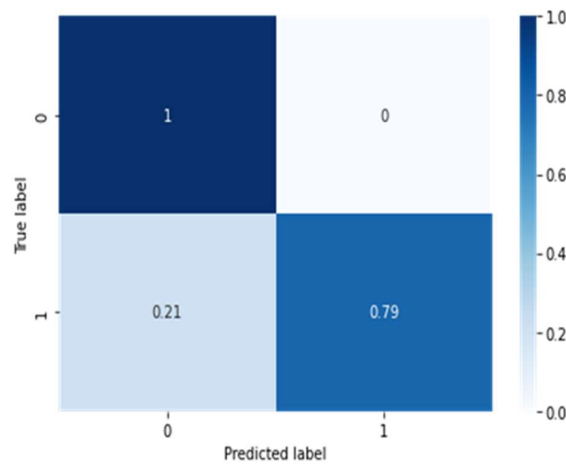


Fig. 7 Classification Report

The confusion matrix obtained is shown in figure 8.

	precision	recall	f1-score	support
0	0.96	1.00	0.98	701
1	0.97	0.79	0.87	139
accuracy			0.96	840
macroavg	0.97	0.89	0.93	840
weightedavg	0.96	0.96	0.96	840

Fig. 8 Confusion matrix

Conclusion

In this study, we made an effort to come out with an automated method for diagnosing tuberculosis mycobacterium using chest x-ray images. So far many researchers have tried experimenting with different approaches like statistics, machine learning, deep learning, etc. Many works were observed to be really good and worth enough to use in real-time clinical use. But the accuracy obtained was still not satisfactory in the works observed in the literature. In

this study, we used a generative adversarial network. This helps in generating more images similar to the one we have in the input dataset. This increases the volume of the data and improves the learning of the models. The deep learning approaches are data thirsty. The more data better is the learning. This study gave improved results compared to previous works of the same kind.

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